Submitted Abstracts for Botany 2023

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Ecophysiology

Topic: Colloquium — Ecological and Evolutionary Consequences of Genome Size Variation in Plants

Title: Quantifying genetic variation in physiology and functional traits in subspecies of big sagebrush (Artemisia tridentata) in a common garden setting.

Author: ***Spencer Roop @ Idaho State University***

Keywords: Artemisia tridentata,common garden,ecophysiology,Semiarid Grassland,big sagebrush

Abstract:

Big sagebrush (Artemisia tridentata) is a widespread and locally dominant shrub throughout many ecosystems in western North America. Based mainly on differences in microsite occurrence and morphology, there are three broadly recognized subspecies of big sagebrush. These subspecies are found at varying elevational and soil moisture gradients and have also been found to differ in palatability, digestibility, chemical composition, and genome size. Several studies have reported subspecies-level differences in survivorship and physiology in A. tridentata, however these studies have been often limited in population sample size. More recent genecological studies have found evidence that subspecies has little to no contribution to survivorship, fecundity, and freeze resistance in big sagebrush, and suggest that cytotype and climate-of-origin may play a larger role in phenotypic variation for big sagebrush than previously thought.

To explore possible differences in ecophysiology among purported subspecies of big sagebrush, I measured morphological and physiological traits in a big sagebrush common garden to understand how genetic and environmental variables (subspecies, cytotype and climate-of-origin) contribute to phenotypic expression in this widespread, drought-adapted shrub species. Despite previous evidence of purported-subspecies driven phenotypic variation in A. tridentata and variation in survival, size, fecundity, and freeze resistance based on cytotype and climate-of-origin, this study found no strong evidence of morphological and physiological variation driven by purported subspecies, cytotype, nor climate-of-origin in mature A. tridentata when grown in a common garden. These results are important as understanding what drive phenotypic expression in big sagebrush can give better insight into how climate change may affect migration and extirpation, as well as help increase the effectiveness of restoration efforts. As a keystone species in sagebrush steppe ecosystems, this is integral to the survival of these habitats.

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Pteridology

Topic: Colloquium — Neotropical Pteridology: A Dedication to Robbin Moran

Title: Discovering Parablechnum: a complex evolutionary history within the youngest fern family.

Author: ***Sonia Molino @ Universidad Complutense de Madrid***

Keywords: phylogenomics,phylogeny,pteridophyte,systematics

Abstract:

Parablechnum is a fern genus with 68 species, the most speciose of the Blechnaceae (the youngest fern family, together with the Onocleaceae). It is widely distributed in Central and South America and the Austropacific, with some representatives in southern Africa, Madagascar, and the Mascarenes. The interpretation of this distribution proved to be challenging, with conflicting evidence supporting Gondwanan vicariance and long-distance dispersal (LDD). To contribute to its resolution, we performed a molecular phylogeny based on 5 plastid markers of 127 accessions from over 60 taxa, the largest molecular sampling of the genus to date, and a molecular dating analysis. Our results support the monophyly of the genus and show a complex evolutionary history, probably due to events of hybridization, cryptic diversification, and rapid radiations. The origin of Parablechnum occurred around 38 million years BP, and probably reached its distribution by several LDD events. A high diversification is seen in America with active cladogenesis in the Late Miocene, coinciding with the Andes uplift, which could have triggered the American radiations. Very likely, a substantial cryptic diversity within the genus remains unaccounted. Further research including nuclear genes will be needed to fully resolve the phylogeny of this genus. To achieve this, we will perform a new reconstruction based on Hyb-Seq of the GoFlag 408 nuclear loci set. We will also carry out gametophyte cultures to describe their morphology, mostly unknown in this genus, and as a source of tissue with simplified genomes to investigate ancestry of allopolyploid hybrids.

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Pteridology

Topic: Colloquium Neotropical Pteridology: A Dedication to Robbin Moran

Title: Ecological correlates and evolution of adaptive traits in the fern genus Pleopeltis (Polypodiaceae)

Author: ***Sarah K. Morris @ University of Vermont, Pringle Herbarium***

Keywords: adaptive traits,ecological niche,Pleopeltis,American tropics

Abstract:

The relationship between niche breadth and adaptive traits is central to studies of diversification. Field observations indicate that species of the fern genus Pleopeltis (Polypodiaceae) tend to exist in two ends of the environmental spectrum ranging from hyper-humid to arid. Two innovative traits in this clade likely facilitated opposing niche selection: absorptive laminar scales appear to be an adaptation to dry habitats and green spores appear to be an adaptation to wet habitats. The species found at the ends of the ecological spectrum tend towards having a more extreme version of the two traits. Is the evolutionary history of Pleopeltis a result of traits responding to the exploration of new ecological niches or the exaptation of morphological traits that already existed? Based on extensive observations of these species in the field at various climatic and elevational zones in Mexico, Costa Rica, Colombia, and Ecuador, we hypothesize that absorptive laminar scales and achlorophyllous spores represent adaptations of Pleopeltis to habitats with significant water stress, and that chlorophyllous spores and fewer scales are adaptations to wetter habitats. We further hypothesize that these innovative adaptations allowed this lineage to diversify into new habitats with less competition. Using phylogenetic comparative methods, we evaluated the interplay between evolution of adaptive traits, movement into new ecological niches, and speciation.

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Bryology and Lichenology

Topic: Colloquium One World Many Kingdoms: Conservation of Bryophyte and Lichen Biodiversity

Title: Sounding the alarm: Rare lichens may be rapidly declining in the Pacific Northwest

Author: ***Jesse Miller @ Washington Natural Heritage Program***

Keywords: fire,lichens,wildfire,biotic homogenization,fire regimes

Abstract:

Lichens, critical members of terrestrial ecosystems globally, may be particularly sensitive to global change pressures because they respond to the environment at fine scales. Losses of lichen diversity and biomass will likely disrupt food webs and alter nutrient cycles.
Because lichens do not have known adaptations to wildfire, altered fire regimes pose a particular risk to lichens. Wildfires may catalyze range shifts by settling the "climate debt" of lichen communities that are currently at the edge of their thermal limits. Government rarity rankings for lichens in the United State and Canada are generally based on the assumption that lichen populations observed in a single historical survey remain extant, but if wildfires and other global change pressures have caused widespread extirpations of lichen populations, extinction risks of numerous lichens species may be much greater than previously estimated. In this study, we use spatial analyses to estimate the proportion of rare lichen populations that have likely been extirpated because of recent wildfires in Oregon and Washington, USA. We also perform an analysis of long-term population trends in the old-growth-forest-associated lichen based on field observations and assessments of changes in habitat quality.

We found that as many as approximately one-third of rare lichen populations in Oregon and Washington, USA, may have experienced wildfires in the last 20 years. While exact extirpation rates cannot be calculated without field visits, as many as one quarter of known rare lichen populations may have been extirpated in these wildfires given that lichens rarely survive high severity fire. In our case study with a rare old growth forest lichen, we estimate 35-45% population declines across all previously known populations, largely because of wildfire, logging, and other forms of habitat degradation. Our findings highlight that rare lichen rankings in the Pacific Northwest, and likely globally, should be reevaluated in light of effects of widespread, recent wildfires and other global change pressures. Extinction risks for lichens may be greater than previously estimated, and major range contractions may have already occurred for some species. Extensive field monitoring will be critical for providing more specific data on the status of rare lichen species. There may be little time remaining to save some of the most vulnerable lichens in the Pacific Northwest.

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Topic: Colloquium

One World Many Kingdoms: Conservation of Bryophyte and Lichen Biodiversity

Title: Imperiled wanderlust lichens in steppe habitats of western North America

Author: ***Steven Leavitt @ Brigham Young University***

Keywords: endemism,genome skimming,Intermountain West,Rhizoplaca,sage steppe,vagrant lichens

Abstract:

The northern North American Cordillera is a globally significant center of endemism. In western North America, arid steppe habitats support a number of unique species, including several endemic lichens. However, processes driving diversification and endemism in this region remain unclear. In this study, we investigate diversity and phylogeography of the threatened wanderlust lichens (mycobiont=Rhizoplaca species) which occur free on calcareous soils in steppe habitats in western North America. Wanderlust lichens comprise three species of lichen-forming fungi (LFF) – Rhizoplaca arbuscula, R. haydenii, and R. idahoensis (endangered, IUCN Red List) – which occur in fragmented populations in Idaho and Wyoming, with limited populations in southeastern Montana and northern Utah. These lichens reproduce almost exclusively via large, asexual vegetative propagules. Here, our aims were to (1) assess the evolutionary origin of this group, (2) investigate genetic diversity across populations throughout the distribution of these species, and (3) create species distribution models (SDMs) to better understand potential factors limiting distributions. Using a genome-skimming approach, we generated a 19.1Mb alignment, spanning ca. half of the complete LFF genome, from specimens collected throughout the entire range of wanderlust lichens. Based on this phylogeny we investigated phylogeographic patterns using RASP. Finally, we used MaxEnt to estimate SDMs for R. arbuscula and R. haydenii. We inferred a highly structured topology, with clades corresponding to distinct geographic regions and morphologies represented throughout the group’s distribution. We found that R. robusta, a sexually reproducing taxon, is clearly nested within this asexual lineage. Phylogeographic analyses suggest that both dispersal and vicariance played a significant role throughout the evolutionary history of the wanderlust Rhizoplaca clade, with most of the dispersal events originating from the Salmon Basin in eastern Idaho – the center of diversity for this group. Despite the fact that vagabond lichens are dispersal limited due to large, unspecialized vegetative propagules, we inferred multiple dispersal events crossing the Continental Divide. Comparing herbarium records with SDMs suggests that wanderlust lichens don’t fully occupy the areas of highest distribution probability. In fact, documented records often occur in areas predicted to be only marginally suitable. These data suggest a potential mismatch between contemporary habitats outside of the center of diversity in eastern Idaho with the most suitable habitat, adding to the vulnerability of this imperiled complex of endemic lichens.

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Topic: Colloquium

Title: Intraspecific variability in heat stress tolerance across and within habitats in the tropical plant Marchantia inflexa

Author: ***Hansika Herath @ University of Kentucky***

Keywords: bryophytes,Marchantia inflexa,field studies,intraspecific variation,Phenotypic variation,Thermotolerance

Abstract:

A plant's ability to withstand abiotic stress is important for their survival and reproductive success. Due to climate change and global warming, increasing temperature has become a major abiotic stress factor which can impact the stability of plant population dynamics, ecosystem functions, and agricultural productivity. The ability of plants to survive heat stress varies among and within species. Individuals within a species can vary because populations occur across a range of temperatures and are subjected to selection based on the temperature regimes they occur. While intraspecific variation in heat stress tolerance exists, it is rarely studied, and such studies can elucidate the underlying molecular mechanisms that can be used to improve crop thermotolerance and for in-situ and ex-situ species conservation. Here, we targeted a tropical liverwort, Marchantia inflexa growing in the island of Trinidad, the Republic of Trinidad and Tobago to examine the intraspecific variation of heat tolerance and sex differences in tolerance. Marchantia inflexa is an ideal candidate to study variation in heat tolerance across populations as they typically grow along cool, moist natural habitats along forested streams but are also found along novel habitats of exposed roadsides that are warm and dry. Multiple thallus tips were collected from four stream-sides and three roadside-sides, and their baseline physiologies were noted. Then the samples were subjected to a short high temperature stress (55 oC for 45 minutes). Percent recovery was calculated by measuring quantum efficiency of photosystem II over a period of ten days. Additionally, environmental data were recorded from the collection sites. By the fifth day in the recovery period, we detected a significantly higher recovery in the roadside collected plants than stream-side plants. Further, we noted a trend of higher recovery in male plants compared to female plants. We are under way with a common garden study to gain a more thorough understanding of the genetic and plastic effects of these varying heat stress responses. Identifying heat stress driven phenotypic variations within a species and their underlying molecular responses will contribute to the growing body of knowledge on thermotolerance.

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Bryology and Lichenology

Topic: Colloquium One World Many Kingdoms: Conservation of Bryophyte and Lichen Biodiversity

Title: A New Era of Collections-based Bryology at the University of British Columbia Herbarium (UBC)

Author: ***G Karen Golinski @ University of British Columbia***

Keywords: bryophytes,Biodiversity,conservation,Herbarium curation,herbarium specimen,partnerships

Abstract:

British Columbia is a hotspot for bryophyte biodiversity, and the University of British Columbia Herbarium (UBC) in the Beaty Biodiversity Museum houses one of North America's largest and most comprehensive collections of mosses, liverworts and hornworts.

As UBC strives to share materials and resources in aid of discovering and understanding biodiversity and addressing current conservation concerns, we face many challenges: large pockets of the province are unexplored and under-represented in the collection; a small fraction specimens of taxa represented in collection are 'fresh'; curation of the specimens has been opportunistic in recent decades; the backlog of undetermined specimens is large; and georeferencing is inadequate to meet the needs of 'big data' type studies. We have fallen behind.

To address these challenges and to increase the utility of the collection for biodiversity and conservation purposes, in 2022 we convened a meeting to identify opportunities for synergistic research and teaching in collaboration with partners at other universities, museums, government agencies, conservation groups, and communities. So far, members of the group have compiled up-to-date draft checklists of the mosses, liverworts and hornworts of BC; contributed samples of curated specimens to a DNA-barcoding initiative and begun to analyse data; conducted fieldwork and embarked on integrative taxonomic studies of select bryophytes at-risk; and modelled climate change in areas occupied by bryophytes-at-risk. In these initiatives we have focused on training and supporting the next generation of bryologists. The future is bright!

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Bryology and Lichenology

Topic: Colloquium

Title: Biocrust responses to wildfires without livestock grazing

Author: ***Heather Root @ Weber State University***

Keywords: bryophytes,biocrust,lichen,wildfire

Abstract:

Dryland ecosystems in the western US are affected by invasive species, climate change, wildfires, and livestock grazing in ways that can be difficult to distinguish. Biocrusts perform important ecological roles in these systems and are sensitive to all of these pressures. We revisited a site in eastern Washington that had been extensively sampled for biocrusts in 1999, allowing us to focus on effects of climate change, exotic annual grass invasion, and wildfires in the absence of livestock grazing. Within two decades, exotic annual grass cover increased in all and unburned plots by 16% and 18%, bunchgrass cover decreased by 21% and 25%, and biocrust cover decreased by 8.9% and 9.8%. We developed a causal model to examine changes between 1999 and 2020 that suggested decreases in bunchgrass increased exotic annual grass, which reduced biocrust cover. Surprisingly, wildfires did not appear to influence changes in bunchgrass, exotic annual grass, or biocrust cover. Biocrust lichen and bryophyte communities were composed of different species that were less abundant and diverse in areas dominated by exotic annual grass. We observed a reduction in cyanolichens that may be associated with warming nights and less moisture availability. Our study represents an unusual opportunity to examine the effects of wildfires in the absence of livestock grazing. In this context, the minimal influence of wildfire on exotic annual grass and biocrusts suggests that some apparent negative impacts of wildfire at other sites are due to exacerbation by livestock grazing or other surface disturbance, such as rodent burrowing and off-road vehicle use.

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Population Genetics/Genomics

Topic: Colloquium Shifting baselines and altered landscapes: Botany in the Anthropocene

Title: Rapid adaptation following the worldwide introduction of cosmopolitan weed

Author: ***Nic Kooyers @ University of Louisiana, Lafayette***

Keywords: adaptation,biological invasions,colonization,genomics,introgression,Trifolium,plant defense

Abstract:

Classic invasion biology theory posed that invasions stem from introductions of few individuals that create a limited pool of genetic and phenotypic diversity for future adaptation. However, a rising number of examples highlight high levels of genetic diversity, extensive admixture, and the potential for rapid adaptation following introduction. The worldwide introduction of white clover, Trifolium repens L., to multiple different regions during the 1700's and subsequent establishment and spread presents a unique opportunity to examine the role of rapid adaptation in invasions. Here I leverage a transcontinental provenance study conducted in the native and introduced ranges of white clover as well as a large worldwide population genomics dataset to determine the extent and costs of adaptation following introduction as well as regions of the genome underlying adaptation. Introduced populations show distinct signatures of local adaptation to novel conditions within the introduced range. However, there is a clear cost to adaptation as introduced population have lower fitness in native populations with similar abiotic climates. Native and introduced populations form nearly entirely non-overlapping clusters in PCA analysis stemming from distinct introduction histories, introgression with cultivars, as well as adaptation. Population genomic outlier analysis between native and introduced populations suggest that many genomics regions show signatures of selection. While many more of these regions are shared between different introductions than expected by chance, few regions are shared across all introductions. We focus on one key candidate region of the genome containing a putative inversion that segregates at relatively high frequency in North and South America, but that is at low frequency within the native range. This region co-locates to a large-effect fitness QTL within common garden sites in the introduced range suggesting that this locus may underlie adaptation to novel environments during invasion. Together, our results emphasize the complex and intertwined roles that colonization history, introgression and selection play in adaptation to novel environments during an ongoing invasion.

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Ecology

Topic: Colloquium

Shifting baselines and altered landscapes: Botany in the Anthropocene

Title: Variation in phenological responses to climate within and among wind-pollinated dioecious plants

Author: ***Yingying Xie @ Northern Kentucky University***

Keywords: Populus,flowering phenology,herbarium specimens,leaf out

Abstract:

Significant shifts in the timing of life history events (i.e., phenology) of plants corresponding to anthropogenic climate change were reported worldwide, affecting their reproduction, survival, and interactions with other species. Recent studies have uncovered significant intra- and inter-specific variation in plant flowering phenology and its response to changes in climate. However, most of this research has been limited to animal pollinated species with large and/or showy flowers, and variation in phenological responses to climate remain largely unexplored among and within wind-pollinated dioecious species, and across sexes. Based on herbarium specimens and ground observations from volunteers of cottonwood (Populus) species in North America, here we examined how phenological sensitivity to climate varies among species, across species ranges, between sexes, and between different phenophases to assess how climate change may affect their phenology and related synchrony and reproduction of wind-pollinated dioecious species. The timing of flowering varied significantly across and within species, as did their sensitivity to winter temperature. In particular, we found that male flowering generally happens earlier in the season than female flowers. Male flowering phenology was more sensitive to warming than female flowering. Further, the onset of flowering was more sensitive to changes in temperature than leaf out. Increased temporal gaps between male and female flowering time and between the first open flower date and first leaf out date were predicted for the future time periods (2041-2070 and 2071-2100) under two climate change scenarios (SSP2-4.5 and SSP5-8.5). Our study demonstrates significant intra-specific variation in phenology and its responses to environmental cues, across species' ranges, phenophases, and sex. These variations need to be considered in predicting and mitigating the effects of climate change, due to the critical associations with the ecological synchrony and their community and evolutionary processes.

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Biodiversity Informatics & Herbarium Digitization

Topic: Colloquium

Title: Phenological shifts across the invaded range of Blue Mustard (Chorispora tenella, Brassicaceae)

Author: ***Kathryn Turner @ Idaho State University***

Keywords: biological invasions,climate,climate change,Climate Gradients ,Climatic variability,Herbarium,Herbarium Digitization,herbarium specimens,invasion,Invasive,invasive species,phenological shifts,phenology,phenophase,Plant invasion,time since invasion,Tempera

Abstract:

Invasive species represent excellent evolutionary test cases for understanding how species may rapidly adapt to novel environments, for example, in the face of climate change. Often invasion biology relies on comparisons between contemporary populations or ranges (i.e. current populations from the invaders native and invasive ranges), inferring that any differences should be the result of evolution in the invaded range. However, natural history collections such as herbaria offer the opportunity to compare invasive individuals across the timeline of an invasion. Native to Eurasia, blue mustard was introduced to North America by 1894, and has since spread to 31 US states and 3 Canadian provinces. It is a weed of both rangelands and croplands, and to date most research has focused on management. Using phenological data scored from 528 digitized herbarium specimens collected in western North America between 1920 – 2020 and monthly climate data during this time (CRU v4.06), we ask 1) does phenology change over the course of invasion? and 2) how does regional climate influence the phenological timing of blue mustard across its invaded range? We find that mean annual temperature and interannual temperature variability were the most predictive of phenology day of year. The average timing of phenology, across all life stages, occurs earlier in warm regions than in cold regions. Plants in the coldest and most temperature variable regions of the range experience the most delayed phenological timing, likely serving as a strategy to avoid winter frost. Interestingly, interannual temperature variability was less deterministic of phenology in warm regions. Warm regions have long growing seasons, such that temperature unpredictability may not impose a large frost risk on plants and thus have a reduced effect on phenology. In this dataset, phenological variation along this mean annual temperature gradient is contingent on the predictability of the temperature regime itself, a pattern which has not been show before in this type of system to our knowledge. This may have implications for this plant under climate change, which should increase temperatures, but also unpredictability, across this range. This spatial pattern may be driven, to some degree, by adaptive genetic variation in the phenological strategies of blue mustard.

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Floristics & Taxonomy

Topic: Colloquium

Title: Scientific and Societal Ramifications of Floristic Studies in the Boise Front

Author: ***Barbara Ertter @***

Keywords: Floristics,invasive species,new species,rare plants,Idaho,Boise Front,shrub-steppe habitat

Abstract:

On-going floristic studies, even in such relatively accessible and presumably well-known areas as the Boise Front, can result in wide diversity of results with both scientific and societal ramifications. Significant range extensions of native species, possible taxonomic novelties in need of further investigation, and a variety of other worthwhile research questions have come to light as a result of the current floristic survey, which itself provides a slice-of-time status report that can be used to determine long-term trends when compared to earlier records, as well as serving as a baseline for comparison with future surveys. In the Boise Front, these trends include an under-acknowledged decline in native forb diversity, a continual rain of novel exotic species in various stages of naturalizing, and the on-going degradation and loss of quality shrub-steppe habitat. The floristic work has also triggered a closer look at the rarity status of several declining native species, which were subsequently added to the Idaho Rare Plant List, and one potential invasive was treated as an Early Detection, Rapid Response Idaho Noxious Weed. These results are regularly brought to the attention of biologists in local, state, and federal land management agencies, and also communicated to the general public with the goal of triggering an appreciation of our unique local flora.

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Ecology

Topic: Colloquium Shifting baselines and altered landscapes: Botany in the Anthropocene

Title: Comparing long-term patterns of spread of co-occurring native and invasive plants in a regenerating forest

Author: ***Matthew Yamamoto @ Connecticut College***

Keywords: deciduous forest,invasive species,New England,plant succession

Abstract:

A fundamental question in invasive plant ecology is whether invasive and native plants have different ecological roles. Differences in functional traits have been explored but we lack a comparison of the factors affecting the spread of co-occurring natives and invasives. Some have proposed that to succeed, invasive plants would colonize a wider variety of sites than native plants, that invasive plants would disperse farther, or that invasive plants would be better at colonizing sites with more available light and soil nutrients. Others have argued that native and invasive plants are more similar than we typically perceive and share similar environmental preferences. We examined patterns of spread of shrubs and lianas over 70 years in a regenerating forest in Connecticut where both native and invasive species acted as colonizers. We compared the characteristics of colonized plots, the variation in characteristics of colonized plots, and the importance of site variables for predicting colonization between seven invasive and 19 spreading native species. We found little support for the hypotheses that invasive plants succeed either by dispersing farther than native plants or by having a broader range of site tolerances. In addition, colonization by invasive plants was not more dependent on light than colonization by native plants and in fact, light availability had relatively low impact on colonization success for most species. Similar to native understory species, invasive plants were able to spread into closed canopy forest and species rich communities despite earlier predictions that these communities would resist invasion. The biggest differences between natives and invasives were that soil nitrate and the forest being younger increased the odds of colonization for most invasives but only for some natives. The narrower range of spread patterns for invasives with respect to these variables is consistent with a known bias in the selection of nonnative plants for introduction. In large part, the spread of native and invasive plants was affected by similar factors, adding to growing evidence that research in native community assembly and succession is also useful for understanding invasive plant spread.

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Ecology

Topic: Colloquium

Title: Alpine plant responses to human trampling disturbance in the Nch'kay Region (Garibaldi Provincial Park, British Columbia)

Author: ***Philippa Stone @ University of British Columbia***

Keywords: alpine ecology,disturbance ecology

Abstract:

Despite a large increase in hiking recreation in the Coastal Mountains of British Columbia, how human trampling affects alpine plant communities that are already impacted by warming is unknown. To quantify this, we established a trampling study in Summer 2022 in the Nch'kay region (Garibaldi Provincial Park, British Columbia) as part of the International Tundra Experiment (ITEX). We established 14 paired disturbed (trail-side) and undisturbed (off-trail) transects along three major hiking trails in the Nch'kay region. At each transect, we measured maximum plant height and diameter (growth proxies), and recorded the number of buds, flowers, and fruits (reproduction proxies) for mountain heather, blueberry, and sedges. We took standardized photographs of each transect to compute plant percent cover and buried tea bags at selected transects to measure litter decomposition rates. We found that trail-side ericaceous plants were smaller than those located off-trail, suggesting lower growth rates, lower survival rates, or both. However, we found the opposite was true for sedges, with trail-side sedges being larger than those located off trail. Both of these effects were exacerbated at increasing elevation, indicating that plant communities are more sensitive to the effects of disturbance at higher elevations. We found no significant difference in reproductive outputs of species growing in disturbed or undisturbed transects. Understanding which plant types are more susceptible to the effects of human trampling than others will help inform land managers on where to establish recreational sites and trails to minimize the effects of human trampling.

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Ecology

Topic: Colloquium

Title: Decline in Mycorrhizal Activity Decreases Foliar Micronutrients After Arctic Wildfire Recovery

Author: ***Natalie Kashi @ University of New Hampshire, Villanova University, Colorado College***

Keywords: Mycorrhizae,Nitrogen and Phosphorus,stable isotopes,succession,wildfire,arctic,Micronutrient

Abstract:

Wildfires in the Arctic are historically uncommon but in recent decades have increased in frequency and intensity. Phases of post-fire succession depend on wildfire severity and the initial effect is species loss such as Sphagnum and the combustion of plant and soil organic matter. After 5-10 years of recovery, vegetation growth increases, especially shrubs, likely as a response to higher nitrogen and phosphorus availability from the wildfire combustion of organic matter and associated permafrost thaw. However, the long-term post-fire succession dynamics in the tundra are not fully understood as this increased growth response can taper 9-12 years post-recovery. Additionally, wildfires reduce microbial biomass and abundance by over 90 %, with little recovery a decade post-wildfire. Here, we investigated how four dominant Arctic plants with different mycorrhizal relationships respond to nitrogen (N), phosphorus (P), and nitrogen and phosphorus (NP) fertilization in both unburned and burned tundra. We hypothesize that higher N and P availability post-wildfire may decrease mycorrhizal-mediated nutrients and subsequently reduce foliar micronutrient concentrations. Ectomycorrhizal and ericoid mycorrhizal species increased foliar d15N by 4.0 ± 1.9 ‰ in response to the wildfire, whereas the non-mycorrhizal species Eriophorum vaginatum and arbuscular mycorrhizal Rubus chamaemorus showed little change. These d15N patterns were even stronger after adding N or NP, indicating wildfires alleviate nutrient limitation and reliance on mycorrhizal symbiosis for ericoid and ectomycorrhizal plant species. Lower foliar d15N in N and NP treatments for non-mycorrhizal and arbuscular mycorrhizal plants likely reflect the N fertilizer signature. Wildfire increased foliar N and P concentrations across all species by 24% and 17%, respectively. In contrast, wildfire decreased concentrations of four of the five micronutrients (barium, sodium, sulfur, and zinc) but increased foliar potassium concentrations. The ectomycorrhizal species Betula nana had highest micronutrient concentrations including aluminum, barium, boron, calcium, manganese, and zinc. For non-mycorrhizal Eriophorum vaginatum, micronutrients were significantly lower than in the other plants, except for silicon. There was a strong negative correlation between d15N and micronutrients (barium, r = -0.67; boron, r = -0.54; calcium, r =-0.44; manganese, r =-0.58, and zinc, r = -0.34) and a positive correlation for potassium (r = 0.49), suggesting that micronutrient concentrations decline with higher d15N (less mycorrhizal mediated nutrients). We compared the change in nutrient concentrations between each of the three unburned fertilization treatments to the control burned treatment to compare how wildfire and nutrient enrichment affects various nutrient foliar concentrations. There was a strong correlation (adj r2 = 0.47) for the NP treatment, with a positive change for N and P and a negative change for barium, calcium, copper, iron, zinc, magnesium, manganese, and silicon. These data indicate N and P enrichment on Arctic vegetation negatively affects a variety of other nutrient foliar concentrations. Despite 12 years post-wildfire recovery, our results suggest decreased plant-mycorrhizal symbioses may lead to micronutrient limitation, a mechanism responsible for slower vegetation growth rates during the later post-fire succession.

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Topic: Colloquium

Strategic uses of herbaria, specimens, and digital specimen data

Title: Extending Specimens: Integrating iNaturalist Observations into Symbiota

Author: **James Mickley @ Oregon State University**

Keywords: extended specimens,herbarium specimens,iNaturalist,symbiota

Abstract:

The iNaturalist citizen science platform is rapidly becoming the largest source of plant biodiversity data for many regions. Therefore, it is an important and complementary resource to physical herbarium specimens. Symbiota, a widely-used software tool to manage biodiversity data and serve it to the public contains a number of tools for interacting and visualizing herbarium specimen data, that could benefit from including the data that iNaturalist provides. To integrate this data into Symbiota, I will demonstrate new Symbiota-based tools to facilitate the import and use of iNaturalist data on Symbiota portals. These tools will be introduced on the OregonFlora.org Symbiota portal. The importer can be used in several different ways. First, when collecting physical specimens, iNaturalist can be used as a digital collection notebook, automatically collecting data, and avoiding the need for field data transcription. These iNaturalist records can then be imported into Symbiota, with the iNaturalist record linked as an associated occurrence, providing additional extended specimen data. Second, an iNaturalist observation of an organism that was subsequently preserved as a vouchered specimen can be linked to that specimen record. Finally, un-vouchered iNaturalist observations can be selectively imported into Symbiota as observations instead of specimens, and can be searched for, displayed and mapped, or added to checklists to provide a complement to specimen data. Careful curation of observational records chosen for import is advised in order to maintain the quality criteria of the portal integrating the data. These new tools will augment OregonFlora's public engagement with its floristic and biodiversity resources. More broadly, these tools improve the ability of Symbiota portals to take advantage of iNaturalist biodiversity data to complement and extend existing specimen data.

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Topic: Colloquium

Title: Linking phenotype, genotype and environmental data from museum specimens in the Prunus serotina (black cherry) species complex

Author: **Richie Hodel @ Smithsonian Institution**

Keywords: morphology,environmental gradient,herbariomics,Hyb-Seq,Machine Learning,Phylogeography

Abstract:

The phenotypes of organisms have been used for centuries to quantify biodiversity in museum collections, and represent the primary tool early naturalists used to study evolution. Phenotypes are the targets upon which selection acts, and therefore affect the survival and success of organisms in variable environments. In order to understand patterns of biodiversity, an understanding of genomic as well as phenotypic variation is necessary as both contribute to species diversification. However, the relationship between genotype and the environment to shape phenotype is complex, and can be difficult to study. In the genomic and big data age, we can relatively inexpensively obtain genomic and environmental data from field-collected and/or herbarium specimens to investigate genetic patterns across environmental gradients. However, we lack methods to obtain phenotypic data in a high throughput fashion. Recent advances in computer vision-based machine learning approaches hold the promise to extract high-throughput phenotypic data from digitized biological image data, such as herbarium specimens.

The black cherry (Prunus serotina) tree species complex occupies a variety of environmental conditions across its wide native range in North and Central America. Within the species complex, there are five named subspecies that have distinct morphological features, such as leaf shape, size, margin, and texture. Previous genetic investigations indicate some differentiation among subspecies, but genome-scale data are needed to resolve genetic relationships within and among subspecies. Here, using herbarium specimens from the US collections, we aim to explicitly connect genotypic, phenotypic, and environmental big data sets to determine how the phenotypic characters observed on herbarium sheets may have arisen via ineteractions between the genome and environment.

We use 610 nuclear loci and plastid genomes generated via Hyb-Seq to quantify genomic variation among herbarium specimens from across the range of P. serotina in the U.S., Mexico, and Central America. For the same specimens, we quantify the environment using bioclimatic variables associated with each specimen's georfereferenced coordinates, and we investigate phenotypic traits present on each herbarium sheet by extracting leaf traits using the versatile machine learning tool LeafMachine. This study has the potential to revolutionize how we collect phenotypic data from herbarium sheets, as well as redefine the scale of data we can expect to include in future studies of phenotypic variation using museum specimens, or specimens mounted as herbarium specimens.

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Biodiversity Informatics & Herbarium Digitization

Topic: Colloquium

Strategic uses of herbaria, specimens, and digital specimen data

Title: New objectives of the Herbarium of Economic Botany of Ecuador (QUSF)

Author: ***Hugo Valdebenito @ Universidad San Francisco de Quito***

Keywords: Bioprospecting,Economic Botany,Ecuador

Abstract:

The Herbarium of Economic Botany of Ecuador (QUSF) of Universidad San Francisco de Quito (Ecuador), established in 1995, contains around 28,000 preserved vascular plants of the Ecuadorian flora. These specimens contain a wealth of information on uses and economic value that, along with field notes acts as a major regional as well as national reference center. Research is primarily focused on the taxonomy, distribution, use and conservation of Ecuadorian plants.

Recently associated with the new USFQ Bioprospecting Institute, our herbarium is involved in the search, extraction, isolation, purification and identification of molecules from natural sources. We also have a library of extracts obtained mainly from plants. Additionally, we have started an economic botany collection to show how local communities from Amazon to the Coast, obtain artifacts derived from plants such as food and medicine.

In this presentation, new goals and objectives for the QUSF are presented.

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Biodiversity Informatics & Herbarium Digitization

Topic: Colloquium

Title: Nondestructive estimation and evolution of arid-associated traits from herbarium specimens

Author: ***Aaron Lee @ University of Minnesota***

Keywords: herbarium specimens,Phylogenetic comparative methods,reflectance spectrum,Polygonaceae,Eriogonoideae,Fagopyrum

Abstract:

Herbarium specimens capture variation across spatial, temporal, and taxonomic scales. In the "extended herbarium specimen" concept, researchers have developed creative approaches to utilize specimens and their metadata. Recent work has used nondestructive, indirect approaches, such as reflectance spectroscopy, to obtain leaf reflectance spectra and estimate functional traits from pressed leaves. However, these models have focused on using recently collected specimens from temperate lineages. Here, we present our workflow for obtaining leaf level reflectance spectra from herbarium specimens, highlight some challenges of working with spectra obtained from herbarium specimens, and insights learned about trait evolution in Polygonaceae. Polygonaceae is a compelling system to test hypotheses about repeated evolutionary trajectories in spectral and spectra-derived traits associated with ecological function. This group includes at least two major transitions to xerophytic (arid-adapted) lineages from wet-tropical lineages, including the radiation of iconic North American eriogonoids. This group also includes a diversity of habits and life histories, all with flat leaves that are amenable to the measurement of leaf reflectance. We obtained reflectance spectra from herbarium specimens, and plan to predict functional traits associated with leaf construction and nutrient content using previously constructed universal prediction models. We will model both the evolution of predicted traits and reflectance spectra, and use phylogenetic comparative methods to ask whether independently evolving xerophytic lineages converge in similar functional and spectral trait spaces.

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Biodiversity Informatics & Herbarium Digitization

Topic: Colloquium

Title: From leaves to labels: building modular machine learning networks for rapid herbarium specimen analysis with LeafMachine2

Author: ***Will Weaver @ University of Michigan***

Keywords: Herbarium,herbarium specimens,large datasets,leaf traits,Machine Learning,Computer Vision,Optical Character Recognition

Abstract:

Quantitative plant traits play a crucial role in biological research. However, traditional methods for measuring plant morphology are time-consuming and have limited scalability. We present LeafMachine2, a suite of machine learning and computer vision tools that can automatically extract a base set of traits from over 100 angiosperm families and calculate pixel-to-metric conversion factors for more than 20 commonly used ruler types.

LeafMachine2 was trained on 494,766 manually prepared and expert-reviewed annotations from 5597 herbarium images obtained from 288 herbaria, representing 2663 species. LeafMachine2 employs object detection and segmentation algorithms to accurately identify and isolate individual leaves and petioles, even in cases of partial occlusion or overlap. Additionally, our landmarking network identifies and measures nine pseudo-landmarks that occur on most broadleaf taxa, including apex and base angles, lamina length and width, midvein length, petiole length, and lobe tips. Archival processing algorithms prepare labels for optical character recognition and interpretation, while reproductive organs are scored.

Our results demonstrate that LeafMachine2 is a highly efficient tool for generating large quantities of plant trait data, even from field images and non-archival datasets, making it a valuable asset for trait-based research. Our project, along with similar initiatives, has made significant progress in removing the bottleneck in plant trait data acquisition from herbarium specimens and shifted the focus towards the crucial task of data revision and quality control, which is essential for validating autonomously collected measurements.

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Biodiversity Informatics & Herbarium Digitization

Topic: Colloquium

Title: Humans in the Loop: Citizen science and machine learning synergies for overcoming herbarium digitization bottlenecks

Author: ***Robert Guralnick @ University of Florida***

Keywords: Community science,digitization,herbaria,Machine Learning,OCR

Abstract:

The slowest step in natural history collections digitization is converting imaged labels into digital text. This long-recognized efficiency bottleneck can be overcome and we present a working solution that leverages synergies between citizen science efforts and machine learning approaches. We present two new semi-automated services. The first detects and classifies typewritten, handwritten or mixed labels from herbarium sheets. The second uses a workflow tuned for specimen labels to OCR label text. The label finder and classifier was built via humans-in-the-loop processes that utilize the citizen science Notes from Nature (NFN) platform to develop training and validation datasets to feed into a machine learning pipeline. Our results showcase >93% success for finding and classifying main labels. The OCR pipeline optimizes pre-processing, multiple OCR engines and post-processing steps, including an alignment approach borrowed from molecular systematics. This pipeline yields >4-fold reductions in errors compared to off-the-shelf open source solutions. The OCR workflow also has a human validation using a custom NFN tool. Our work showcases a usable set of tools for herbarium digitization including a custom-built web application accessible to all. Further work to better integrate these services into existing toolkits can support broadest community use.

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Biodiversity Informatics & Herbarium Digitization

Topic: Contributed Papers Biodiversity Informatics & Herbarium Digitization

Title: FieldPrism: a system for creating snapshot vouchers from field images using photogrammetric markers and QR codes

Author: ***Will Weaver @ University of Michigan***

Keywords: Field Botany,Fieldwork,Herbarium curation,herbarium specimen,Imaging,Live imaging,Machine Learning,Photogrammetry,snapshot vouchers

Abstract:

Field images are important sources of information for research in the natural sciences. However, images that lack photogrammetric scale bars, including most iNaturalist observations, cannot yield accurate trait measurements. We introduce FieldPrism, a novel system of photogrammetric markers, QR codes, and software to automate the curation of snapshot vouchers.

Our photogrammetric background templates (FieldSheets) increase the utility of field images by providing machine-readable scale bars and photogrammetric reference points to automatically correct image distortion and calculate a pixel-to-metric conversion ratio. Users can generate a QR code flipbook derived from a specimen identifier naming hierarchy, enabling machine-readable specimen identification for automatic file renaming. We also developed FieldStation, a Raspberry Pi-based mobile imaging apparatus that records images, GPS location, and metadata redundantly on up to four USB storage devices and can be monitored and controlled from any Wi-Fi connected device.

FieldPrism is a flexible software tool designed to standardize and improve the utility of images captured in the field. When paired with the optional FieldStation, researchers can create a self-contained mobile imaging apparatus for quantitative trait data collection.

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Biodiversity Informatics & Herbarium Digitization

Topic: Contributed Papers

Title: Introducing www.plantsofhawaii.org: A species information and identification system for the Flora of Hawai‘i

Author: ***Timothy Gallaher @ Bishop Museum***

Keywords: bioinformatics,digital floras,Floristics

Abstract:

Our new webiste, Plants of Hawaii (www.plantsofhawaii.org), brings together information about all native, naturalized, and cultivated plants in our state. The site will include descriptions of every plant taxon, specimen and field images, cultivation and cultural information, and maps indicating the known distribution for each species. The site is constantly updated as new information about our flora becomes available. Ongoing projects will extend the site's scope to include information on bryophytes and algae so that all of our flora, from the mountains to the ocean, are represented. The site serves natural resource managers and biosecurity programs by providing critical information so that potentially harmful species can be prevented from entering the islands, established noxious weeds can be tracked, and native species can be restored into natural areas. The site is easy to use and searchable using binomial and vernacular names. We hope the site will be a valuable resource for the general public. We further hope that anyone interested in or currently working on the flora of Hawai‘i will help us improve the site by providing field images, editing descriptions, or contributing other data.

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Biodiversity Informatics & Herbarium Digitization

Topic: Contributed Papers

Title: Database upgrade, digitization, and increasing accessibility of the Atlanta Botanical Garden Plant Collections

Author: ***Lauren Eserman-Campbell @ Atlanta Botanical Garden***

Keywords: Botanic gardens,Collections,digitization,Botanical Gardens

Abstract:

The Plant Collections at the Atlanta Botanical Garden house 106,028 individual plants from 25,335 genetically unique accessions representing 12,096 taxa (species, subspecies, and varieties) from 276 plant families and over 1,800 genera. Most notably, ABG maintains the most diverse living collections of orchids (Orchidaceae) in the United States with 2,328 taxa. Other major foci of the Collections include rare, threatened, and endangered plants of the southeastern United States, plants of New Caledonia, tropical conifers, carnivorous plants, and neotropical blueberries. The ABG Plant Collections are divided into two separately managed collections. The Living Collection falls under the purview of the Horticulture & Collections Department, and the Conservation Collection is managed by the Conservation & Research Department. These two collections differ in their mission and intent. Whereas the Living Collection is intended for research, education, display, and public enjoyment, the Conservation Collections support research on rare and endangered species, safeguard globally and regionally imperiled species, and place an emphasis on long-term maintenance of population-level genetic diversity. The Conservation Collection also supports Metacollections that add safeguarding depth to collections of endangered plants. Use of the Collections by outside researchers is limited to those with existing knowledge of the collections. We have embarked on a multi-phase project to (1) upgrade collections data to the Brahms botanical garden data management system, (2) share collections data via external data aggregators (e.g. GBIF, GGBN, iDigBio), (3) photograph and GPS map priority collections, and (4) update protocols related to collections management and research requests. This will enable collection information to be shared with the greater research community via outreach to professional botanical societies and on the Garden’s social media pages. We expect utilization of the collection to significantly increase and to allow for creative and impactful research to be done with plants in the collections.

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Biodiversity Informatics & Herbarium Digitization

Topic: Contributed Papers

Title: Best Practices and Guidelines for Digitized Lichen Herbarium Specimens

Author: ***Eli Denzer @ New York Botanical Garden***

Keywords: Georeferencing,Herbarium Digitization,Imaging,lichen,Lichenology,Data Standards

Abstract:

Digitization is an increasingly important part of collection management and collections-based research. Imaging and digitizing specimens allows access to collections without in-person visitation, limits risk of loss or damage caused in shipping and transport, and increases efficiency by allowing the collections user community to better focus inquiries or loan requests. Having publicly accessible digital records, that are populated with high quality, standardized data and images, opens up a collection for new and innovative uses. In lichen collections, where specimens can be small, cryptic, and require different workflows than vascular plants, there is an urgent need for digitization best practices and standards to maximize the usability of specimens both now and in the future. These practices include standards for all aspects of the digitization process including georeferencing, accurate data capture and transcription, and high-quality images. Given the amount of resources (time, effort, support and expertise) required to digitize lichen specimens, establishing and implementing standardized best practices is particularly urgent to avoid the additional resources of reimaging or retranscribing the majority of collections in the future. This talk will present guidelines aimed at maximizing the usefulness of digitized specimens during lichen digitization based on experience gained from a large-scale project on Appalachian lichens.

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Biodiversity Informatics & Herbarium Digitization

Topic: Contributed Papers Biodiversity Informatics & Herbarium Digitization

Title: Spatial phylogenetic patterns of the vascular flora of Florida

Author: ***Lauren Gillett @ University of Florida***

Keywords: ecological niche modelling,rbcL,chloroplast,matk

Abstract:

Hosting over 4,200 species of vascular plants, Florida overlaps two globally recognized biodiversity hotspots, the North American Coastal Plain (NACP) and the Caribbean Islands. Unfortunately, habitat destruction and climate change pose serious threats to the maintenance of this floristic diversity. Quantifying biodiversity for conservation purposes has typically relied on methods that evaluate Species Richness (SR), which does not incorporate the evolutionary history of the community, and how this may influence the community assembly. The massive amount of digitized herbarium specimen records available through data aggregators like iDigBio, GBIF, and SERNEC, facilitate the aggregation of records representing species in the vascular flora of Florida. The goal of my research is to locate current concentrations of significant biodiversity, using a phylogeny representing 99% of the vascular flora of Florida. This phylogeny was generated by generating an alignment using MAFFT using open source DNA sequences from GenBank representing the rbcL and matK gene regions of the chloroplast. These two alignments were concatenated and used to generate a phylogeny using RAxML. With this phylogeny, I plan to use spatial phylogenetic metrics, such as Phylogenetic Diversity (PD), to assess the diversity of plant assemblages with an evolutionary context. Other metrics such as Phylogenetic Endemism (PE), Relative PD (RPD), Relative Phylogenetic Endemism (RPE), and Categorical Analyses of Neo- and Paleo- Endemism (CANAPE). The overlap between currently conserved land in Florida and areas of significantly high PD patterns will be assessed. These analyses will provide a more thorough understanding of the spatial phylogenetic diversity patterns in Florida Here we present results from a phylogeny representing 99% of the vascular plants of Florida. This phylogeny can be used to analyze various spatial phylogenetic patterns in Florida and make recommendations for conservation efforts and land managers for bettering the conservation of Florida's evolutionary biodiversity hotspots.

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Biodiversity Informatics & Herbarium Digitization

Topic: Contributed Papers

Title: Announcing the eDNA Explorer web tool for managers and researchers to process and share eDNA qPCR and metabarcoding projects

Author: ***Rachel Meyer @ University of California Santa Cruz***

Keywords: conservation,Environmental DNA,Interdisciplinary,management,Metabarcoding,web resource,qPCR

Abstract:

Environmental DNA is a rapidly growing tool for bioinventory and tracking environmental change. Single species qPCR assays and cross-kingdom multiplex metabarcoding are some of the now familiar approaches to census species non-invasively, from soil, water, leaf surfaces, honey, air, and other substrates. In conservation and management, rapid biodiversity monitoring needs are growing as environments experience climate change, land use intensification, keystone species dropout and increased pressure to fulfill ecosystem services. In an initial uX study on managers and researchers working on these challenges, we found that there's a lot of need for eDNA and interest in such data, but adoption of eDNA methods requires collaborations over years between managers who are constantly acclimating to new policies and the researchers who must acclimate to the rapidly evolving state of science around eDNA. We are acting on an opportunity to help ease collaboration activities from describing assays to data manaagement and comparing eDNA results to remote sensing (via Google Earth Engine) or visual on-the-ground observations such as from GBIF. We created the eDNA Explorer web tool for people to learn about projects, events, and trainings, to find resources and protocols, and to manage their own projects. Our tool includes a reference database maker and Tronko, the first phylogeny-based taxonomy assignment software that can handle rich NGS data as part of reference DNA databases. We present use cases of the website for biodiversity inventories of flora, fauna, and microbes from the Los Angeles River and other locations recovering from disturbances from alien invasive species to wildfires. Our hope is that the eDNA Explorer will catalyze accessibility and interoperability of eDNA results across projects, and will help create a culture of sharing information prior to publication, which will help ease collaborations, improve project success rates, and speed up appropriate adoption of eDNA as a tool in the biodiversity manager's toolkit.

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Biodiversity Informatics & Herbarium Digitization

Topic: Contributed Papers

Title: Spatial Phylogenetics of Vascular Plants in the South-Central U.S.

Author: ***Sierra Hubbard @ Oklahoma State University***

Keywords: Biodiversity Informatics,Oklahoma,phylogenetic diversity,Texas

Abstract:

While traditional measures of biodiversity are typically based on the species present in an area, phylogeny-based measures are able to capture information about the evolutionary history represented in an assemblage of taxa. Investigations of diversity using a phylogenetic framework can reveal the distributions of evolutionary lineages and the relative ages of plant assemblages. The South-Central United States (made up of Oklahoma and Texas) is a floristically diverse region that contains ~8,000 vascular plant species. This region is also climatically diverse, with strong abiotic gradients in temperature, precipitation, and elevation. The current understanding of spatial phylogenetics in this region comes from a few continental scale studies utilizing herbarium data. However, the South-Central US has not yet been included in any regional-scale studies, which could potentially reveal finer-scale patterns not apparent across broader study regions. Additionally, much fewer data have been available from Oklahoma and Texas compared to many other regions of North America; this may have led to incomplete conclusions about the spatial phylogenetics of plants in this region. Recent and ongoing digitization and georeferencing efforts have addressed this data gap by mobilizing a wealth of herbarium records from Oklahoma and Texas. In this study, we aim to use these newly available herbarium data to characterize the spatial patterns of phylogenetic diversity (PD) and relative phylogenetic diversity (RPD) seen in the vascular flora of the South-Central US. This approach highlighted regions that contain young plant assemblages in the High Plains and Southwestern Tablelands and identified concentrations of old lineages in the Eastern Temperate Forest and Edwards Plateau. In addition, we tested for associations between PD, RPD, and climatic gradients in precipitation, temperature, and elevation. We found that bioclimatic variables related to precipitation were the best predictors of PD and RPD.

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Topic: Contributed Papers Biogeography

Title: Biogeography, phylogeography, and disjunctions in the Florida Panhandle: A center of diversity and endemism within a biodiversity hotspot.

Author: ***Elizabeth White @ University of Florida***

Keywords: areas of endemism,Biodiversity hotspots,biogeographic patterns,Biogeographic regions,Southeast US

Abstract:

The Florida Panhandle is a unique region within the North American Coastal Plain (NACP), which is the 36th recognized biodiversity hotspot in the world. There are over 1,500 plant species endemic to the NACP, roughly 20% of which are present in the Florida Panhandle. The NACP more broadly, but particularly the Florida Panhandle, exemplifies the unique nature of the region as a biogeographic model– lacking stark elevational changes or clear barriers to gene flow aside from a few major rivers. I provide a review of what is known about this region's high plant diversity and endemism by presenting a comprehensive review of biogeographic affinities as well as the complexities of these patterns at the phylogeographic level. My results show numerous overlapping affinities corresponding to distinct habitats found in the region such as sandhills, wet flatwoods, seepage-fed fens, limestone outcrops, and steephead ravines. These findings showcase this region as being at a crucial location historically for various migration events, but also the importance of the region in more recent times as home to multiple different refugia, which have ultimately contributed to the region's high diversity of plants. An overview of the region's geology, history, and the overlapping disjunctions that seem to converge here will provide insight as to how these plant communities formed and changed through time. This in turn stresses the importance of the conservation of this region generally, while also pointing towards a better understanding of how ecosystem-level management can best take place in an area that is so richly mosaiced with multiple distinct plant communities which are separated by small changes in microclimate or topology.

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Biogeography

Topic: Contributed Papers

Title: Identifying the drivers of range limitation using transplant gardens within and beyond the range edge of sexual and apomictic Townsendia hookeri reveals signatures of dispersal and niche limitation.

Author: ***Jeannette Whitton @ University of British Columbia***

Keywords: apomixis,asexual reproduction,Asteraceae,Autopolyploid,Diploid and polyploid ,niche differentiation,transplant study

Abstract:

Differences in the distribution of close relatives represent the outcome of factors acting during or after their establishment. In apomictic complexes, sexual diploids and their derivative apomictic polyploids often occur in a distribution pattern known as geographical parthenogenesis. This pattern is characterized by sexuals having a more southern and smaller range than their related apomicts, with apomicts often occurring primarily or exclusively in previously glaciated areas. The varied forces that could produce this pattern potentially include more rapid or more successful post-glacial colonization by apomicts due to advantages associated with uniparental reproduction, niche divergence that excludes apomicts or sexuals from the other's range, and reproductive interference that prevents sexuals from invading sites occupied by apomicts. We have been working to disentangle these forces in Townsendia hookeri, a perennial plant system from the Rocky Mountains' east slope that displays a classic pattern of geographical parthenogenesis. Here we present the results of a 5-year multiple transplant garden experiment that included a total of eight experimental gardens spanning the sexual and apomictic ranges. We transplanted greenhouse-grown seedlings from 12 source populations and measured survival, growth and reproduction annually. We used Aster models to summarize fitness over the five years in the transplant gardens. We found that the fitness of apomicts transplanted into the sexual range was lower than in their own range, but sexuals did show consistent declines in fitness when planted in the apomictic range. We also conducted a separate seedling establishment trial at each garden site. Analysis of seedling establishment trials using generalized linear mixed models revealed that seedling establishment differed among garden regions, but not between sexuals and apomicts. In the context of range limit theory, our results suggest that dispersal limitation may limit the northward expansion of sexuals, while niche limits may prevent apomicts from extending into the sexual range to the south. Integrating the transplant garden results with additional data on the ecology, genetic structure, and reproductive dynamics of the system gathered to date suggests that apomicts likely originated near the northern range limits of sexuals, with favoured clones spreading northward into previously glaciated areas. Sexuals that disperse into the apomictic range may be precluded from establishing due to asymmetric reproductive interference via the pollen of apomicts, while the southern expansion of apomicts may be limited by biotic interactions.

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Biogeography

Topic: Contributed Papers

Title: Morphological variation and geographic distribution in Hillia subg. Hillia (Rubiaceae): Dissecting a species complex

Author: ***Laymon Ball @ Louisiana State University***

Keywords: biogeography,Neotropics,Rubiaceae,species complex

Abstract:

Hillieae (Rubiaceae) is a widespread Neotropical tribe of 29 epiphytic species, with spectacular variation in floral morphology: species display the hawkmoth, hummingbird, and bat pollination syndromes. In addition, species occur in a variety of habitats and fill different abiotic niches. Species in Hillia subg. Hillia (includes species Hillia parasitica, Hillia wurdackii, Hillia killipii, and Hillia macrophylla) have highly similar floral and leaf morphology. Corollas are white, long, and narrow tubular, exhibiting the hawkmoth pollination syndrome. These species also overlap in geographic range and are mainly distributed along the eastern side of the Andes Mountain range in South America. To better understand and define the boundaries between these species, we integrate a series of methods including RADseq, biogeographic reconstruction, ecological niche modeling, and principal components analyses of floral and leaf traits.

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Biogeography

Topic: Contributed Papers Biogeography

Title: Biogeographic history, floral morphology, and realized climatic niche of the Neotropical genus Palicourea

Author: ***Ana Maria Bedoya @ Louisiana State University***

Keywords: Andes,biogeograpy,Climatic niche,Neotropics

Abstract:

Palicourea is a species-rich genus of Neotropical plants in the family Rubiaceae. It consists of >800 species (several species of Psychotria are now transferred to the group) with center of diversity in South and Central America. Palicourea includes predominantly shrubs and subshrubs living in habitats that range from lowland to montane, and from seasonal to usually wet ecosystems. The genus is remarkable for its diverse inflorescence and flower morphology ranging from small white flowers that are pollinated by insects, to colored flowers, with well-developed corolla tubes, and abundant nectar that are hummingbird pollinated. In this project we inferred evolutionary relationships of Palicourea using a target enrichment approach with recently developed probes for Rubiaceae. Our species tree is the most comprehensive phylogenetic study of the group to date, both in terms of genomic and taxon coverage. We modeled biogeographic range evolution in Palicourea and estimated climatic niche overlap of species pairs to propose hypotheses for the interplay between floral, geographic, and niche evolution in this diverse group of Neotropical plants. Stay tuned for what we find and present!

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Biogeography

Topic: Contributed Papers

Title: The Phylogeny and Biogeography of Neotropical Bellflowers Centropogon subgenus Centropogon (Campanulaceae)

Author: ***Janet Mansaray @ Louisiana State University***

Keywords: molecular phylogenetics,mutualism,Neotropical biogeography

Abstract:

Centropogon subgenus Centropogon (Campanulaceae), a clade of 65 species that occur in low-to-mid elevation forests in the Neotropics, has some of the most curved flowers among all angiosperms. The curvature represents coevolution with the sicklebill hummingbird (Eutoxeres: Trochilidae), which is an obligate pollinator of most (but not all) species of Centropogon subgenus Centropogon. Despite the available molecular data, the relationships among species in this group remain poorly understood. This highlights the complexity of their evolutionary history and the need for further research to uncover the underlying processes that have led to their diversity. A previous phylogenetic hypothesis of the clade included limited taxon sampling (I.e. 20 out of 65 species) that demonstrated the monophyly of the subgenus and the non-monophyly of many widespread species (a notable exception is C. cornutus, the species with the broadest range that falls sister the rest of the subgenus). I improved on the previous phylogeny by more than doubling taxon sampling (i.e., 46 out of 65 species) using targeted sequence capture with probes designed to isolate low-copy nuclear loci Neotropical bellflowers. I applied phylogenetic methods that incorporate incomplete lineage sorting and introgression (e.g., ASTRAL) as these evolutionary processes are likely important in the clade, which represents a young, rapid radiation. In addition, using occurrence data from georeferenced herbarium specimens, I investigated the biogeographic history of the groupusing BioGeoBEARS. By integrating these results, I provide insight into the evolutionary relationships of the subgenus as well as biogeographic patterns, which has not been done before.

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Biogeography

Topic: Contributed Papers

Title: Modeling dispersal potential of American amphitropical distributed species [VIDEO]

Author: ***John Schenk @ Ohio University***

Keywords: ecological niche modelling,biogeography,Dispersal,long distance dispersal,Species Distribution Model,vicariance,American amphitropical distribution

Abstract:

Plant species that occur in temperate areas in North and South America, but are absent from interleaving tropical areas, is one of the most striking biogeographic patterns. This distribution pattern, referred to as the American amphitropical distribution, has evolved in 237 land plant species. Despite this relatively common distribution, we know little about the biogeographic processes that have led to such a remarkable pattern. Three hypotheses have been postulated to explain the American amphitropical distribution pattern. The first is long-distance dispersal. Some evidence has supported long-distance dispersals from North to South America being the predominant pathway. The second is vicariance in which species historically occupied temperate and tropical areas continuously, but interleaving populations have since gone extinct. The third is a stepping stone model in which smaller patches of suitable habitat intermittently connect temperate areas and allowed for multiple migration and establishment events that occurred repeatedly in relatively shorter distances. To test the above hypotheses, we applied a species distribution modeling approach to estimate the probability of species occurrences based on current distributions and the species' bioclimate conditions. Under the vicariance model, we predicted that a continuous distribution of suitable environmental conditions would connect the Northern and Southern Hemispheres, even if species do not currently occupy those areas. Under the stepping stone hypothesis, we predicted that discontinuous patches of suitable habitat would connect the Northern and Southern Hemispheres. Although our approach does not allow us to explicitly test for long distance dispersal, rejecting the stepping stone and vicariance hypotheses would inform the probability of long distance dispersal as the remaining hypothesis. We tested our hypotheses with 25 species based on current bioclimate data and distributions, and projected the models into current climates and the last glacial and interglacial maxima. The majority of species distribution models across time scales failed to show suitable tropical habitat based on the model's thresholds per species. We rejected the vicariance hypothesis in all but one case (Tiqullia nuttallii [Boraginaceae] in the last interglacial maximum). We failed to reject the stepping stone hypothesis in 11 out of 75 analyses. Although the vicariance and stepping stone models remain a possible explanation for the amphitropical pattern, our best explanation is that long distance dispersal was the predominant mode.

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Biogeography

Topic: Contributed Papers Biogeography

Title: Biogeography and diversification of the Southern Andean Loasa (Loasaceae)

Author: ***Dylan Cohen @ Chicago Botanic Garden***

Keywords: Andes,Diversification,Historical biogeography,Loasaceae,RADseq

Abstract:

The Andes of South America are most biologically diverse mountain chain on the planet. There are many speceis rich groups which experienced adaptive, rapid, and recent radiations in the northern and central Andes. Most of this research has argued high diversificaton rates are associated with increased mountain uplift rates. In addition, the insular nature of high peaks, low valleys, plateaus, and contrasting periods of uplift have contributed to high levels of endemism and habitat diversity. The Huancabamba deflection zone is a low-lying area separating the northern from the central Andes however the central and southern Andes do no have a geographical break. Instead, they are separated by an arid and elevational barrier located in northern Chile called the western Southern American Dry Diagonal (wSADD). Historical biogeography and diversification studies have focused on the enigmatic radiations from the northern and central Andes, while far less has been revealed about the biogeography and tempo of diversification from the central and southern Andes. Here we focused on the Southern Andean Loasa (SAL, Loasaceae), a diverse clade that includes five genera distributed across the central and southern Andes. We applied a single digest restriction site next generation sequencing method (RADSeq) to obtain thousands of nuclear markers from species across SAL to 1) reconstruct a phylogeny, 2) generate divergence time estimates, 3) investigate ancestral areas, and to 4) determine the tempo of diversification across SAL and species from the central and southern Andes. Phylogenetic results were largely congruent with past studies apart from Grausa not being monophyletic. BioGeoBears results suggested that the ancestors for SAL were in arid regions during the Oligocene throughout the early Miocene. The uplifting of the central Andes indirectly created more arid habitats (rain shadows), and thus facilitated diversification of arid adapted Loasa. Montane SAL first arose within the southern Andes during the Miocene, followed by only Caiohora into the central Andes during the late Miocene. Overall, diversification rates were slow, but highest during expansion of arid habitats, and into the Andes. Diversification largely correlates to the age of habitat; high Andean SAL were the most recent to diverge; temperate rainforest SAL were found to be on long branches with much older ages. A taxonomic revision is need for Grausa and increased sampling is needed to resolve species complexes in Loasa, Pinnasa, and Caiophora. The Andes are the most diverse mountain system on the planet and increased study in all parts is urgently needed to understand its diversity and how it evolved through time and space.

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Biogeography

Topic: Contributed Papers

Title: Exploring patterns of lichen diversity across scales

Author: ***Klara Scharnagl @ University of California Berkeley***

Keywords: Biodiversity,lichen,symbioses,functional biogeography

Abstract:

Lichens are terrestrially ubiquitous, yet not all lichens are everywhere. In fact, most lichen species are rare. How does this work, what environmental filters are in place to create unique lichen communities in different areas and at different scales? Here I present work from four different studies, investigating the patterns and potential drivers of lichen diversity and community composition at four different scales. I will present on patterns of lichen diversity on different sidewalk squares in an urban environment, across a moisture gradient on an alpine tundra, across individual trees from the base to the canopy, and across a latitudinal gradient in the Americas. I will introduce the lichen species and functional communities found at each of these scales, and explore the macro- and microclimatic, substrate, as well as biotic factors driving these patterns.

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Biogeography

Topic: Contributed Papers

Title: The END of Vaccinium as we know it? A comprehensive phylogenomic and biogeographic investigation of the blueberry tribe (Vaccinieae)

Author: ***Anna Becker @ University of Florida***

Keywords: Vaccinium,Ancestral state reconstruction,biogeography,Classification ,divergence time,Historical biogeography,Taxonomy,molecular systematics

Abstract:

Vaccinieae is a morphologically diverse and species-rich tribe in the Ericaceae. While the majority of its diversity is tropical, Vaccinieae is best known for temperate crops (i.e., blueberries, cranberries, huckleberries) of the genus Vaccinium. Vaccinium itself has been previously suggested as highly polyphyletic, and taxonomic boundaries of the remaining genera have been untenable. To better understand the extent of polyphyly of Vaccinium in the context of closely related genera, and gain insights into the evolutionary history of Vaccinieae as a whole, we assembled a nuclear dataset for over 200 taxa, representing 30 of the 34 genera in the tribe, and 25 of the 30 sections of Vaccinium. We additionally constructed a plastome dataset for a subset of these taxa. We present results from various phylogenetic and time-calibrated biogeographic analyses to address the following questions: 1–What are the phylogenetic patterns within Vaccinieae? 2–How do the recovered clades compare with current sectional and generic boundaries? 3–Where and when did major dispersal and diversification events take place? We additionally discuss the taxonomic implications of a polyphyletic Vaccinium (and other genera). We recovered seven major clades corresponding to previously delimited genera and sections of Vaccinium and approximately 30 more that do not correspond to previously delimited groups. Instead, groups generally align with geographic boundaries. Biogeographic reconstruction suggests that tropical diversity of Vaccinieae appears to be the result of multiple, independent movements into tropical habitats from temperate, mostly North American ancestors. Divergence time and diversification results reveal dispersal events aligning with major geographic changes such as the uplift of the Andes, and some of these events coincide with increased diversification rate. Traditionally significant morphology that was used to circumscribe many genera and sections did not follow natural groupings in Vaccinieae with the exception of the pseudo-ten-locular ovary, for which we were able to place the evolutionary origin from the five/four locular ovary state. Given the extensive polyphyly of Vaccinium detected here, we recognize several options for reclassification and favor a move to elevate all sections of Vaccinium to the rank of genus, rendering Vaccinium monospecific, including solely the type, Vaccinium uliginosum.

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Biogeography

Topic: Contributed Papers Biogeography

Title: Phylogenetic diversity and regionalization of the mimosoid clade: Drivers of diversity in dry tropical forest

Author: ***Ryan Folk @ Mississippi State University***

Keywords: beta diversity,legume-rhizobia symbiosis,Mimosoid clade,legumes,spatial phylogenetics,nodule

Abstract:

The seasonally dry tropics stand out among tropical biomes for their distinctive plant communities as assessed along environmental, functional, structural, and phylogenetic axes. The distinctiveness of dry tropical forest species is driven particularly by high niche conservatism and strong spatial turnover compared to other tropical biomes. The legumes, as the pre-eminent dry tropical forest family by a margin of nearly two-fold (many of them mimosoid legumes), can be safely claimed as an archetypal group for the study of tropical dry forest. While only marginally present in cold to warm temperate areas compared to subfamily Papilionoideae, the other major legume radiation outside of moist tropical regions, they are some of the most prominent legumes of the semi-arid tropics and subtropics globally, concentrated between 36°N and 36°S and dominant in savannah biomes, particularly in Africa and Australia. To better understand global patterns of diversity and endemism in the dry tropics, here we determine centers of species richness (SR), relative phylogenetic diversity (RPD) and paleo- and neo-endemism in the mimosoid clade. We also use distance methods to regionalize phylogenetic diversity and understand spatial breaks in phylogenetic diversity and the relationships of recognized diversity centers in terms of shared lineage diversity. Finally, because mimosoid legumes are one of the richest clear examples of nodule loss, important to interpreting the drivers of diazotrophic symbiotic strategies, we map the distribution of mimosoids lacking RNS (root nodule symbiosis).

Using data from the NitFix sequencing iniative, we built a phylogenetic tree covering 1313 species and high-quality species distribution models covering 1128 species. Centers of significant RPD and endemism were identified using a randomization approach, the latter using CANAPE. Phylogenetic regionalization used a distance-based phylogenetic beta-diversity approach. RNS species were identified using a recent authoritative RNS database, also assembled through the NitFix iniative.

We recovered nine distinct SR hotspots, which are partly incongruent with centers of RPD and phylogenetic endemism. Regionalization of phylogenetic diversity showed partial congruence with previous legume biome classifications but failed across continents to recover a clear split between tropical dry forest and scrub biomes. This suggests that scrub and dry forest mimosoid communities, while distinct, are assembled from closely related lineages. Lineages lacking RNS are distributed in hotspots in Africa and the Americas, and specifically associated with relatively moist tropical environments with low temperature seasonality and high nitrogen.

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Biogeography

Topic: Contributed Papers

Title: Montane speciation in the Greater Antilles – using Melastomataceae as a test case

Author: ***Lucas Majure @ University of Florida, Florida Museum of Natural History***

Keywords: sky islands,speciation,neotropical cloud forest,Caribbean biogeography,long-distance dispersal

Abstract:

The pantropical family Melastomataceae is most diverse in the Neotropics with ca. 3500 species occurring there. Although the continental distributions of the family demonstrate the highest species richness, the Greater Antilles are also a major diversity hotspot, especially for the genus Miconia. There are close to 385 species of Miconia in the Antilles, with around 345 of those endemic to the region. Curiously, putative sister taxa within Miconia in the Antilles tend to show allopatric distributions and therefore may likely follow a speciation pattern of isolation-by-distance through long-distance dispersal among adjacent or non-adjacent mountain ranges. We wanted to test this hypothesis using robust phylogenetic topologies based on phylogenomic data and through mapping sister species pair populations across the islands of the Greater Antilles, but with a focus on Hispaniola. We indeed find evidence for speciation through long-distance dispersal within islands, but we likewise see evidence for stepping-stone speciation among mountain chains involving several species within clades, as well as putative niche specialization for species pairs within the same mountain range. Thus, montane speciation in Melastomataceae of the Greater Antilles is a complex pattern of within and among mountain range processes, which has led to the current species richness in this insular system. We will compare patterns seen in Melastomataceae with other montane Antillean groups.

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Biogeography

Topic: Contributed Papers

Title: Areas of Endemism of Plants in the U.S.A.

Author: ***Anna Saghatelyan @ McMurry University***

Keywords: areas of endemism,Biogeographic regions,North America,floristic connections

Abstract:

The history and connections of the flora of North America have been studied and summarized in biogeographic regionalization. However, some studies show contrasting delineations of the North American provinces that could be better determined using quantitative methods. We aimed to find spatial patterns of a set of plants in the United States by conducting endemicity analysis (EA) on different scales. We first built a dataset with 215,772 specimen point records of 731 species from 235 genera and 76 families of angiosperms and two genera of gymnosperms using digitized specimen data from iDigBio. We then performed EA at four different scales to identify the areas of endemism (AoEs). We obtained 31 AoEs with different cell sizes by selecting each AoE under the grid size that yielded the highest number of high-scoring species. The study region split into three floristic centers, the Northwestern and Eastern, both supporting the Boreal subkingdom of Takhtajan, and the Madrean, supporting the namesake subkingdom of the Holarctic Kingdom. The Madrean Subkingdom showed two significant centers of accumulation of nested or partially overlapping AoEs: the SW and SC consensus areas. In these parts of the study area, many genera/clades, among those in the dataset, showed a geographic split into western and eastern clades. Most significant in endemism AoEs, the Sonora–Mojave arid center, Chihuahuan Desert, the California Floristic province, Gulf Coastal Plain, and southern Appalachians, harbor basally branching taxa of several genera, subfamilies, and even families, based on the observations o some species, which allowed identification of the AoEs. Northwestern AoEs showed connections to East Asia across the Bering Land Bridge, Madrean AoEs – had mostly southern, especially along the backbone of the Andies and amphitropical, connections, while eastern AoEs– showed tmperate connections mostly across the Atlantic and, in Gulf Coastal Plain, to the tropical New World, or broader tropical floras.

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Biogeography

Topic: Contributed Papers Biogeography

Title: The Spatial, Historical, and Evolutionary Correlates of Hybridization in Vascular Plants

Author: ***Lydia Morley @ Texas A***

Keywords: hybridization,Vascular Plants,Biogeogrpaphy

Abstract:

The central task of any evolutionary biologist is understanding what lead to the evolution and diversity of life on earth. Thus, the ecological, spatial, genetic, and historical, drivers of vascular plant speciation have been extensively investigated over the last century, leading to the accumulation of genomic data for an increasingly large number of vascular plant taxa. Emerging from this growing body of work is the recognition that hybridization has played (and continues to play) a fundamental role in vascular plant evolution. In this way, gene flow (both hybrid speciation and introgression) is an evolutionary process that is inextricably linked to speciation—it's not an aberrant phenomenon that occasionally plagues unlucky systematists. Thus, we should not only be asking "How frequently does hybridization occur, and what are its evolutionary consequences?", but also "Under what conditions are evolutionary trajectories of lineages driven towards hybridization?" The probability of hybridization and its success should depend on a combination of: (a) the historic and geographic context under which the parental species evolved, (c) the historic and geographic context under which the parental species hybridized, and (d) relevant life-history traits of the parental species.

We use a combination of available trait, phylogenetic, and distribution data to hypothesize that: 1) Hybridization will be more frequent in temperate versus tropical regions (even when accounting for phylogeny); 2) Hybridization will be more frequent in plants with certain life history characteristics; 3) Current rates of congener co-occurrence differentially predict hybridization frequency depending on region/life history traits.

In general, this study emphasizes the fact that, like divergence, gene flow is a regular evolutionary event predicted by historical, geographic, and phylogenetic factors.

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Biogeography

Topic: Contributed Papers

Title: Spectral phylogeography in live oaks across the tropical-temperate divide

Author: ***Mariana Hernandez_Leal @ Universidad Nacional Autonoma de México***

Keywords: Genetic variation,natural selection,Phylogeography,population genetics

Abstract:

Local adaptation and genetic differentiation between populations is improved by selective differences among populations and little or total absence of gene flow. However, determining whether population differentiation is caused by selection of certain traits is complicated by the fact that other forces such as genetic drift can also cause population differentiation in the absence of gene flow. The Quercus subsection Virentes includes seven species (Q.virginiana, Q. geminata, Q.minima, Q. brandegeei, Q. fusiformis, Q. oleoides and Q.sagrean.) distributed from southeastern US, through eastern Mexico, southern Baja California, Central America, and Cuba (Nixon & Muller 1997). Due to its wide distribution, this group presents a great variety of adaptations that could be the cause of the divergence between the populations of the species that share the same geographical site. For example, little differentiation has been found between Q. minima and Q. geminata when using SSR simple sequence repeat or chloroplast data in populations where both species co-occur. However, both species have different habitats, one being fire-dependent and the other fire-tolerant. (Kurz & Godfrey 1962; Cavender Bares et al. 2004b). All these habitats and environmental differences in a group of so closely related species are of great evolutionary interest in determining to what degree population differentiation is caused by local adaptation (selective traits) versus neutral (stochastic) processes. During this research, we focused on testing whether spectral information of dried samples can be used to detect divergence between genetic groups at different hierarchical levels using natural populations of seven closely related species in the Virentes subsection. Our main goals are 1) to identify spectral regions in dry leaf spectra that are important for discriminating closely related oak species; and 2) to elucidate if phenotypic variances in spectra between populations are the product of demographic history (genetic drift) or genetic variation and environmental factors (adaptation). Methodology We measured leaf spectral reflectance (400 – 2500 nm) on pressed specimens collected from 2006 through 2011 from individuals in which there were nuclear single sequence repeat (nSSR) amplification data (from Cavender-Bares et al. 2015). We ran two clustering algorithms within STRUCTURE v. 2.3.4 (Pritchard et al., 2000), first we include 428 individuals of the seven species. Then, we include only individuals of Q. oleoides given that these species have shown phenotypic variation across its distribution (Ramirez-Valiente et al. 2015). We used partial least square discriminant analysis (PLS-DA) (Chevallier et al., 2006) to assign spectral samples to different hierarchical groups (genetic groups, and species). Results Genetic data of the nSSR showed seven genetic groups for all species in accordance with Cavender-Bares et al. 2015 and five distinct groups for Q. oleoides (Fig 2). Classification using PLS-DA models for the seven species of Virentes using raw pressed-spectra showed good performance at classifying species and correctly predicted the taxonomic identity of 295 of 302 samples in the training dataset.

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Biogeography

Topic: Contributed Papers

Title: Lessons on gypsophile gene flow from the Chihuahuan Desert

Author: ***Mike Moore @ Oberlin College***

Keywords: biogeography,Chihuahuan Desert,Dispersal,Edaphic Endemism,gypsum,México,phylogeny,Phylogeography,soils,gypsophiles

Abstract:

Edaphic "islands" have long been thought to have reduced gene flow among them, but how much is gene flow restricted, and are there asymmetries between seed and pollen dispersal? Using DNA sequence data in exemplar taxa from the gypsophile flora of the Chihuahuan Desert, we demonstrate that seed movement is often very limited, even among relatively close exposures of gypsum. Likewise, there is some evidence for persistently low population sizes from plastid data. However, pollen flow seems to be more variable among taxa, with some evidence that pollination syndrome affects nuclear gene flow.

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Biogeography

Topic: Contributed Papers Biogeography

Title: Reconstructing the biogeographic history of three widespread manzanita (Arctostaphylos) species of western North America

Author: ***Glen Morrison @ UC Riverside***

Keywords: California Floristic Province,ddradseq,manzanita,Phylogeography,RADseq

Abstract:

The region of western North America with a Mediterranean-type climate, known as the California Floristic Province (CFP), is a hotspot of endemic plant diversity, largely due to a number of plant lineages that have high diversity within the CFP, but aren't especially diverse elsewhere. The assumption has long been that the bulk of endemic diversity of these particular lineages in the CFP is due to diversification within the CFP. However, at least some of this endemism may be due to the survival of some species in the CFP whose ranges may have shrunk as southwestern North America became the more arid, desert-dominated region that it is today. Manzanitas (genus Arctostaphylos) are the most diverse woody genus in the CFP, and are seen as emblematic of a within-CFP diversification hypothesis, but interestingly, several species have much larger ranges over extensive areas in western North America. The goal of this study is to evaluate two hypotheses regarding the present-day distribution of these species: (1) these species originated in the CFP and dispersed outward, or (2) they originated well outside of the CFP, and dispersed into the CFP. In this study we sampled multiple populations across the ranges of three such widespread species. Each of these species occur in multiple western US states, and one extends deep in mainland Mexico. We used reduced representation genome sequencing (ddRADseq) data to infer the relationships among populations across the range of each species, and recover the best supported hypotheses about their biogeographic history. Additionally, we examine these data for any hidden structure that may exist that is not recognized by the current taxonomy, and in the case of at least one o the focal species, preliminary findings lend some support for older taxonomy that had treated that species as several distinct species. Understanding the biogeographic history of these widespread species can add valuable context to how lineages like the manzanitas became so endemically diverse in the CFP, and shed light on historical biogeography of other plant lineages in western North America.

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Topic: Contributed Papers

Title: East Asian-North American disjunctions and phylogenetic relationships within subtribe Nepetinae (Lamiaceae)

Author: ***Bryan Drew @ University of Nebraska Kearney***

Keywords: Eastern Asia – Eastern North America floristic disjunction,Nepetinae,Lamaiceae,Agastache,Meehania,Dracocephalum

Abstract:

Biogeographic disjunctions are found across plant lineages and have been of major interest to biologists for centuries. Research on this subject has been reinvigorated by recent advances in molecular dating and associated comparative methods. One of the "classic" disjunction patterns is that between Eastern Asia and Eastern/Western North America. It has been speculated that this pattern is the result of vicariance following the sundering of a widespread Acrto-Teritary flora. The subtribe Nepetinae in the Lamiaceae (mint family) is noteworthy because it contains three genera with this intercontinental disjunction pattern: Agastache, Dracocephalum, and Meehania. These disjunctions are ostensibly the result of three separate events, allowing for concurrent testing of the tempo, origin, and type of each biogeographic event. We use phylogenies based on chloroplast and nuclear data to estimated divergence times and analyze the historical biogeography of Nepetinae. We show that the three disjunctions are "pseudo-congruent", with unidirectional movement from East Asia to North America occurring at slightly staggered times during the late Miocene and early Pliocene, about 3.5-10 million years ago. With the possible exception of Meehania, we find that vicariance is likely the underlying driver of the disjunctions.

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Biogeography

Topic: Contributed Papers

Title: Leaf Evolution in the Hawaiian Lobeliads

Author: ***Jeff Rose @ University of Wisconsin-Madison***

Keywords: adaptive radiation,Geometric Morphometrics,Hawaii,Campanulaceae

Abstract:

Lobeliads (Campanulaceae: Lobelioideae) arrived on Hawai'i from a single ancestor ~15 mya. Since then, they have diversified to become the archipelago's largest plant radiation, comprising ~12% of the native species diversity. With ~140 known species spread across 6 genera, the Hawaiian lobeliads have undergone an adaptive radiation which encompasses a panoply of growth forms, habitat types, floral forms, photosynthetic rates, and morphological leaf traits. The morphological diversification of leaves includes shape, size, margin, armature, and perhaps most notably, changes in leaf shape within the lifespan of an individual (heteroblasty). The latter is restricted to the genus Cyanea, which in itself makes up more than half of the species diversity in the clade. We quantify leaf size and shape in Hawaiian lobeliads, and examine the partitioning of morphological diversity across genera, islands, and habitat types. We also quantify disparity in juvenile and adult leaves in heteroblastic species. These results are discussed in light of new, time-calibrated phylogenetic hypotheses for the clade based on analyses of hundreds of nuclear loci and nearly complete plastomes.

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Biogeography

Topic: Contributed Papers

Title: Climatic niche differentiation of African acacias (Senegalia, Vachellia; Fabaceae)

Author: ***Joey Charboneau @ University of Michigan***

Keywords: drought tolerance,environmental niche modeling,Mimosoid clade,fire resistance,savanna

Abstract:

Following the retypification of non-monophyletic Acacia Mill. s.l., the ca. 140 acacia species found in Africa are now about evenly split between two genera: Senegalia Raf. and Vachellia Wight & Arn. The extant species of Senegalia and Vachellia both date from common ancestors that lived about 5-8 Mya, concurrent with the rise of C4 grasses and increasing diversity of large mammalian herbivores. As many of these species became established in African savannas and came to dominate them, their seedlings have needed to overcome stressors such as competition with grasses, herbivory, fire, and drought. Differences among species in geographic range, phenotypic traits, and ecological interactions suggest species likely vary in their tolerances to these stressors. We will use GBIF occurrence data (including iNaturalist observations as well as herbarium specimens) to examine species' differences in climatic niche using ordination methods and niche modeling. We also will compare species-specific tolerances to stressor treatments in a common garden experiment in Arusha, Tanzania to tolerances estimated from occurrence data.

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Botanical History

Topic: Contributed Papers Botanical History

Title: Herbaria and botanical gardens have a tightly entwined history that will be discusssed in this presentation.

Author: ***Maura Flannery @ University of South Carolina, Columbia***

Keywords: botanical garden,herbaria,biodiversity conservation,plant taxonomy

Abstract:

Herbaria and botanical gardens have a tightly entwined history. Luca Ghini, an early proponent of documenting plants by pressing and preserving them, was also director of the first botanic garden at the university in Pisa where he taught materia medica to future physicians. He took his students into the garden to learn about plants and also used specimens so they would be able to identify both living and dried plants. The latter were usefu when teaching during the winter months when fresh material wasn't available, hence an early name for an herbarium was hortus hyemalis or winter garden. This connection between herbaria and gardens continued and broadened as the study of plants moved beyond medicine. There are plant collections documenting what was growing in the Oxford University garden at the time of Jacob Bobart in the seventeenth century and of Herman Boerhaave in the eighteenth century at Leiden. After the taxonomic innovations of Carl Linnaeus, herbaria became even more essential to research, and they moved beyond educational institutions to become part of gardens that were in essence governmental institutions such as the Jardin des Plantes in Paris and the Royal Botanic Gardens, Kew. At its inception, the Smithsonian Institution included both living and preserved plants from the Wilkes Expedition. In all these instances, herbaria also developed as important hubs for plant science research.

While not all botanical gardens have herbaria, many of them do, and more are beginning to preserve material at least from their own living collections. In the 21st century, the role of these gardens is changing, becoming more focused on efforts to identify and preserve biodiversity, and to support sustainable horticulture and agriculture around the world. There are cases where the only living representatives of a species are in gardens. In some cases, these are being propagated to be grown in their home ranges. There are also efforts to build research infrastructures, including herbaria, particularly in the global South, to establish the same synergy between living and preserved specimens that has been so successful throughout the history of botany. Gardens and herbaria both are seeking to broaden involvement in their work with outreach efforts to the larger community. While many people visit gardens for the restorative pleasure they provide, few are aware of the research going on at many of them, and the important role herbaria play in that work. Just as Luca Ghini saw a close connection between living and preserved plants, the goal is to make the vital interplay between them become better known. Many of these herbaria now sponsor community science projects where volunteers input label data and mount specimens. Making the various aspects of botanical gardens more familiar makes them more vibrant, and the idea of dead plants being vital to the study of the green world becomes better known and appreciated.

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Botanical History

Topic: Contributed Papers

Title: The mycological discoveries of Swiss naturalist Jean-Frédéric Chaillet (1747-1839) in the works of Christian Hendrik Persoon (1761-1836) document the early understanding of European fungal diversity

Author: ***Jason Grant @ University of Neuchatel***

Keywords: collaboration,herbaria,mycology,new species,botanical history,Fungi

Abstract:

Christian Hendrik Persoon (1761-1836) was a prominent and independent mycologist living in Paris who prepared taxonomic treatments of fungi based on dried specimens. He reached out to a broad network of naturalists to send him specimens to describe. When he saw the name "Chaillet" referenced in Candolle's Flore Française (1815) he sought out a connection through a mutual acquaintance. Jean-Frédéric Chaillet (1747-1839) in retirement became a fervent local naturalist in Neuchâtel, Switzerland with a broad interest to catalogue the plants, algae, mosses, lichens, and fungi of the region. He documented this through an extensive and meticulously prepared personal herbarium by identifying them himself using his own library or through specialist identifications. Persoon and Chaillet quickly set up a system where over eight years (1816-1823), Chaillet would send specimens of fungi to Persoon with an accompanying list. Persoon would then identify the fungi, annotate the list with identifications and remarks, and send back to Chaillet who could then update his collection. Chaillet would contentedly acknowledge the identifications but sometimes even debate taxonomy and nomenclature, to the point of even discouraging some of Persoon's proposed new species. Their complete transcribed correspondence demonstrates both the authority and interest of Persoon to ask questions about ecology, morphology, color of the fungi, and to request additional material or color illustrations if needed. Their collaboration led Persoon to name 72 new taxa of fungi from the limestone substrate Jura mountains around Neuchâtel, Switzerland.

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Botanical History

Topic: Contributed Papers

Title: Reconstitution and valorization of a regional scientific and historical heritage: The herbarium of vascular plants collected Jean-Frédéric Chaillet (1747-1839) in Switzerland

Author: ***Jason Grant @ University of Neuchatel***

Keywords: herbaria,Switzerland,Vascular Plants,botanical history

Abstract:

The use of herbaria became important in the 18th century when linked to advancements of the field of botany as well as a general desire to know and describe the flora of different regions. Like his predecessors and contemporaries, the Neuchâtel (Switzerland) botanist Jean-Frédéric Chaillet (1747-1839) inventoried and collected the plants he encountered and preserved them as dried specimens. While he devoted most of his life to the study of cryptogams, for which he was most recognized, he naturally began with the study of flowering. Self-taught and persevering, Chaillet established the most complete collection of plants in Neuchâtel, a region he botanized in for more than 40 years. After his death in 1839, a first sorting of his collection was undertaken before its integration in the local institution. Subsequently, after various moves, the entire collection was reconditioned at the end of the 20th century. Today, his flowering plant specimens can be found intercalated in the herbarium of the University of Neuchâtel (NEU). His specimens that were collected between 1788-1830 comprise more than 2,000 specimens and over 1,800 taxa. Moreover, a handwritten catalog of his herbarium containing a list of more than 3000 taxa, allows to evaluate the number of specimens between 3000-4000. The richness of the information present on the labels is quite exceptional for the time. The virtual reconstitution of the Chaillet herbarium, which includes many challenges, makes it possible to consult, complete and develop this collection as a scientific and historical heritage.

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Topic: Contributed Papers Botanical History

Title: Microhistories of Botany 1: Where in the World Was Charles Wilkins Short?

Author: ***Jordan Teisher @ Missouri Botanical Garden***

Keywords: botanical history,Microhistory,Philadelphia,Kentucky botany

Abstract:

Dr. Heather Sharkey, a history professor at the University of Pennsylvania, was doing some volunteer work transcribing herbarium specimens for the Mid-Atlantic Megalopolis digitization project when she came upon a note on a specimen from Charles Wilkins Short. The note reads, “With this specimen, plucked in Bartram's Garden in the spring of 1816 (in company with the Abbé Correa, the venerable William Bartram, and my friend and fellow student Dr. Edward Barton, all of whom are long since dead) this collection commenced. C.W. Short, M.D., Kentucky, 1857.” This otherwise unremarkable specimen – just a twig and a few flowers of yellow root (Xanthorhiza simplicissima) – was the start of what would become one of the largest and finest private herbaria in the world, amounting to roughly 15,000 beautifully prepared and preserved specimens now housed at The Academy of Natural Sciences of Drexel University in Philadelphia. The conditions surrounding the start of such a prominent collection (Short distributed tens of thousands of high-quality specimens to dozens of botanists around the world) provide a unique lens through which to examine the development of American botany in the early to mid-19th century. However, subsequent investigation into Short’s biography and correspondence identified a small problem – he was not in Philadelphia in the spring of 1816. In this presentation, we present evidence that the year on the label was recalled by Short in error, and in the process explore his training and growth as a botanist as well as his role in the national and international botanical community in the 1800s.

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Topic: Contributed Papers

Title: The World of José Francisco Correia da Serra and the Herbarium of Charles Wilkins Short

Author: ***Heather Sharkey @ University of Pennsylvania***

Keywords: Herbarium labels,botanical history,Xanthorhiza,Charles Wilkins Short,José Francisco Correia da Serra

Abstract:

Among well over a million botanical specimens preserved at the Academy of Natural Sciences of Drexel University – a collection which volunteers since 2016 have been transcribing online for the Mid-Atlantic Megalopolis (MAM) Project – is a sprig of Xanthorhiza apiifolia, or yellowroot. Picked in Philadelphia around 1815 but only mounted in 1857, this specimen bears a label that speaks to the history of botany in the United States and the wider world. The brief cursive caption indicates that the sample came from the eminent American botanist, Charles Wilkins Short (1794-1863), and that it launched his collection de novo. It reveals, further, that Short collected the sample with three companions, two of whom were significant naturalists of the age: namely, William Bartram (1739-1823) and the Portuguese priest and polymath José Francisco Correia da Serra (1750-1823), known to his American friends as “the Abbé Correia.”

This paper treats Short’s yellowroot specimen as a point of departure for studying the life and career of José Correia relative to the trans-Atlantic scientific and political world of the late eighteenth and early nineteenth centuries. It approaches this subject through microhistory, a way of studying the past that examines little things and ostensibly minor occurrences to grasp larger events and social phenomena. Here, microhistory can help us to see how a shared love of botanical (as well as zoological and geological) research drew Correia into a scholarly network that included not only Pennsylvanians like Bartram and Henry Muhlenberg (1753-1815), but also an international set of Enlightenment thinkers ranging from Carl Linnaeus (1707-1778) and Joseph Banks (1743-1820) to Thomas Jefferson (1743-1826) and Antoine Laurent de Jussieu (1748-1836). Just as powerfully, the experiences of Correia show how scientific research in this period could become entangled in political upheavals and subject to political pressures. In Correia’s case, the Portuguese Inquisition and the French Revolution disrupted his life and propelled migrations that led him to Philadelphia, where for a few years he found refuge and intellectual companionship. The label on Short’s yellowroot specimen obviously remains silent on these larger issues. It nevertheless offers clues for investigation while suggesting the potential value of herbaria for historical research in and beyond the field of botany itself.

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Botanical History

Topic: Contributed Papers Botanical History

Title: Microhistories of Botany 3: Going Meta with Metadata--Herbarium labels as digitized paper trails of history

Author: ***Richard McCourt @ Academy of Natural Sciences of Drexel***

Keywords: Herbarium labels, metadata, Lewis and Clark, botanical history

Abstract:

Herbarium labels contain seemingly modest amounts of data on what, who, where, and when specimens were collected. But with the advent of massive digitization efforts in herbaria, scientists and others are discovering there's more there there. The recent wave of digitization has taken the modest amount of data on individual specimens and converted them from dark data into a more integral part of the published record. Online availability allowed us to mine individual bits of information as well as combine them into big-data analyses. We sport here on examples of how label data can be used to discover novel insights into history surrounding collecting and indigenous knowledge.

As an example, we will examine the paper trail of Lewis and Clark, who, after their 8,000-mile journey in 1804 to 1806 returned with more than 200 specimens, which have accumulated a variety of field labels, taxonomic annotations, and other metadata that enhances their value as “extended specimens." Included in this paper trail are 34 original hand-written labels by Meriwether Lewis including several mentions of indigenous uses of plant species and additional field notes. Hundreds of additional annotations made by later botanists, such as Frederick Pursh (1774-1820) and Thomas Meehan (1826-1901), add to the original legacy of specimens and collecting notes. Cross-referenced with hundreds of journal entries describing plants and people encountered, the physical specimens and their labels provide fertile primary sources of information on collection practices, curation, research, and ethnobotany of this iconic American journey. The specimens are the physical heirlooms of the coming together of multiple cultures over a common botanical currency. We will describe how current and future digitization efforts offer not only novel and intriguing insights, but also offer opportunities to advance the use of collections and their data by diverse communities.

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Botanical History

Topic: Contributed Papers

Title: Timothy E. Wilcox: Army Surgeon, Botanist, and Naturalist

Author: ***Barbara Ertter @***

Keywords: botanical history,Timothy E. Wilcox,Fort Boise,Fort Niobrara,Camp Supply,Fort Huachuca,Smithsonian Institution,Wilcoxia

Abstract:

Recent sleuthing has cast light on Timothy E. Wilcox, a previously little-known early botanical collector and general naturalist who was active not only in Idaho but in several other states as well. As an army surgeon, Wilcox had multiple postings in the western territories following the Civil War, including Fort Boise, Fort Niobrara, Camp Supply, and Fort Huachuca; he also traveled widely in Alaska inspecting hospital service and sanitary conditions at military posts. At all of these locations he avidly collected plants and other natural history items, the majority of which were deposited at the Smithsonian Institution. Wilcox had several plants named in his honor, including the cactus Wilcoxia, and he published several observations on natural history topics ranging from earthworms to condors. A close look at Wilcox is inseparable from the army’s role in subjugating the indigenous inhabitants of these lands, with some intriguing complexities provided by Wilcox’s personal history.

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Botanical History

Topic: Contributed Papers

Title: Uncovering Women Botanists in New England’s Botanical History

Author: ***Lisa Delissio @ Salem State University***

Keywords: Economic Botany,Herbarium,invasive species,Medicinal Plants,native plants,New England,shrubs,Trees,women in science,History of botany,Peabody Essex Museum,New England History Society,New England Botanical Club,Massachusetts Horticultural Society,Essex Ins

Abstract:

As the field of botany was professionalized during the nineteenth century, highly accomplished women botanists were commonly pushed to the margins. Much of their work was not well preserved, and what remains is often hidden. That is one reason why women are in the minority in lists of nineteenth-century botanists, and why we lack both appreciation for their enduring contributions and access to historical women role models – essential to the recruitment of women into the sciences and reducing gender bias.

The good news is that herbaria can provide us with clues leading to the discovery of these significant scientists. An exploration of the Peabody Essex Museum Herbarium (PEM) revealed hundreds of outstanding specimens by women botanists who received only passing mention in accounts of the history of botany in New England. Through the collections of a dozen herbaria, both at PEM and elsewhere, and multiple libraries and archives, the life and work of one of these, Charlotte Nichols Saunders Horner (July 5, 1823 - July 18, 1906) was uncovered.

While not well known within today’s botanical community, Horner was among the most highly accomplished New England botanists of her time. Her outstanding botanical aptitude and interest were supported by an adventurous family background, a dedicated botany teacher, and a child-free marriage to an enthusiastically engaged husband. Active during a fertile perioc for botany, she rose to become an expert on the plants of the Northeast United States and Colorado. Unusual for a woman of her time, she was compensated for her expertise through her highly successful academic botanical supply business.

Horner made significant contributions to the botanical literature, prominent modern herbaria, and public education. Her many accomplishments included being one of only a handful of women in the Northeast United States to publish in scientific journals in the late 1800s, the first woman to give a scientific talk for the 50-year-old Massachusetts Horticultural Society, and the first person to be awarded its silver medal for expert displays native plants. More than 1,300 of Horner’s herbarium specimens, collected over three decades, still exist and add value to more than a dozen scientific collections. Horner’s contributions continue to make a difference to scientific progress around the world. We are fortunate that she left a legacy of herbarium specimens and published articles that secure her place in New England’s botanical history.

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Botanical History

Topic: Contributed Papers Botanical History

Title: 155 years of Botany at Emporia State University: a Case Study of College Botany in the U.S.

Author: ***Marshall Sundberg @ Emporia State University***

Keywords: botany curriculum,History of botany,enrollment trends

Abstract:

Two years after statehood, the Kansas Legislature established three colleges including the Kansas State Normal School of Emporia. The first catalog, in 1868, lists botany as one of three available natural history courses. The school burned to the ground in 1879. A new building was completed in 1880 and Holmes Sadler was hired to teach natural history. Botany including laboratory, was a 20 week course vs. 10 weeks for zoology and geology. Microscopy was required. During the next 20 years Sadler was replaced by two successive naturalists, but the prominence of botany remained. The second, Lyman Wooster, primarily a geologist, would hire one of his graduates, Elizabeth Crary, to be an instructor in the botany laboratories and eventually take over the lecture courses. Frank Agrelius, a Ph.D.-trained botanist, was hired in 1911 and he and Crary, who did some graduate work at Chicago, expanded the botany offerings adding Anatomy, Physiology, Taxonomy, and others. This curriculum remained basically intact into the early 1950s. In 1953 Biology 1 was introduced as a general education course and pre-requisite to botany, zoology and microbiology which were still required for all majors. In 1946 Merle Brooks was hired as an instructor and kept on after Gilbert Leisman was hired to replace Agrelius in 1955. Botany was growing, as was the department, with the baby boom anticipated, but also with the national concern for promoting STEM education. Several biology faculty members, national leaders in biology education, tapped into growing external grant opportunities. Between 1953 and 1968, the department received 4 major external grants, one from the National Wildlife Federation (6-yr) and three NSF (3-yr, 8-yr, 11-yr) totaling about $3 million. The department grew from 13 to 23 members and from 3 to 6 (+1 mycologist) botanists, peaking in 1968. In 1977 the universities name was changed to Emporia State University and the Biology Department was divided into 5 areas of concentration, including botany, but enrollments were already slowing so that by 1988 the department was down to 14 faculty with 3 botanists - comparable to 1950. For the next 25 years, university enrollment continued to decline while the department numbers remained more or less constant. Since the 1950s there had been two unsuccessful attempts, by externally hired department chairs, to restructure and modify the core curriculum of the department. Covid 19 ultimately drove change. In 2021, under strong pressure from the administration, the core biology curriculum was changed to come in line with the other Regents universities. Botany, zoology and introductory biology were dropped for a two-semester introductory sequence. Additional university-wide restructuring terminated thirty-three, mostly tenured, faculty members as their programs were cut. The botany emphasis was one of two programs cut from the biology department, allowing two botany positions to be eliminated. A single botanist remains to teach in the core organismal course and, in alternate semesters, Plant Taxonomy and Forensic Botany to serve the wildlife biology emphasis and Masters of Forensic Science program.

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Botanical History

Topic: Contributed Papers

Title: Hidden Cargo: Death, Survival, and Dispersion of Ballast-Associated Plant Species in the Northeastern USA

Author: ***Ryan Schmidt @ Rutgers University***

Keywords: biogeography,biological invasions,ecology,Floristics,Herbarium,Herbarium Digitization

Abstract:

Understanding how non-native plants establish and spread in new locations is increasingly important in the face of the homogenization of the global flora. To investigate both successful and unsuccessful plant introductions, we take a historical perspective, using digitized herbarium specimens to document the plants inadvertently introduced into Northeastern North America from Europe, Asia, Africa, South and Central America as a result of historical shipping trade. Specifically, we investigate the plants introduced into New Jersey through the deposition of solid ships' ballast during the 19th century. Such ships' ballasts were used to balance weight on sailing ships depending on the transported cargo, and included materials such as rocks, sand, soil fill, and used building materials. When steamships started to replace sailing ships for oceanic trade, solid ballast was replaced with water ballast (the type of ballast that is used today). We used digitized herbarium specimens from 75 herbaria to study the establishment and spread of 264 vascular plants associated with ballast deposition in New Jersey (a total of 6433 herbarium specimens from 1800-2022). Using temporal and spatial analyses of species retention and geographic spread we defined the trajectories these plants followed and quantified disappearance rate (species lost through time), survival (recollection in New Jersey), and geographic dispersion through time from 1800s to today (geolocation of observations and specimens). Four distinct trajectory groups based on species survival and spread were identified: Waifs (species only present during active ballast import times; 32% of total ballast species), Short-Term Introductions (species disappeared quickly after active import ended; 20%), Established & Limited Spread (species still survives locally, 30%), and Established & Widespread (species now geographically widespread, 18%). Species disappearance rate was high during the period of active ballast deposition and decreased following the end of ballast deposition (around 1900). We also demonstrate that the disappearance rate and spatial analysis are surprisingly robust to collection bias in the herbarium record. This is one of very few studies investigating the successes and failures of a large set of inadvertently introduced species through time and highlights the utility of herbarium specimens in studying plant introductions on large time scales and on a global scale.

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Bryology and Lichenology

Topic: Contributed Papers Bryology and Lichenology

Title: Internal and external biotic factors drive patterns of lichen species richness in the imperiled Southern Appalachian Biodiversity Hotspot

Author: ***James Lendemer @ The New York Botanical Garden***

Keywords: biodiversity hotspot,Biotic interaction,conservation,ecological gradient,ecology,lichen

Abstract:

Understanding the factors that generate and maintain biodiversity are foundational in ecology and evolution and critical for conservation. Despite generations of research and hundreds of proposed theories a cohesive and mechanistic understanding is still lacking. Moreover, existing theory derives strongly from studies of plants and vertebrates. The strongest correlates with global- and regional-scale biodiversity underscore the importance of climatic drivers, although the roles of biotic interactions remain weakly tested at large scales and in complex systems. We use data from comprehensive lichen inventories of 208 one-hectare plots throughout the southern Appalachian Mountains of southeastern North America to examine that how abiotic and biotic factors relate to species richness in this diverse and highly threatened system. Lichen richness strongly declined with increasing anthropogenic disturbance, as has been found in prior studies. After controlling for disturbance, we detected a mid-elevational peak in species richness that was repeated across separate latitudinal bands, but we detected no trend in latitudinal species richness. The strongest impacts on lichen diversity were biotic interactions, both internal and external to lichen symbioses.

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Bryology and Lichenology

Topic: Contributed Papers Bryology and Lichenology

Title: Flying First Class: Lichen Dispersal By Icelandic Migratory Birds

Author: ***Carly Russell @ Ludwig Maximilian University Munich***

Keywords: lichen,Lichenology,Ornithology,Ectozoochory,Dispersal Ecology,Bird-Lichen Interactions

Abstract:

Lichens have wide, often disjunct ranges, but little is known about their dispersal. Birds may play a key role as dispersal vectors of lichens, but there is a large gap in knowledge concerning which lichens birds regularly carry via ectozoochory, where they collect lichens in their environment, and how fungal and lichen propagule loads differ between bird species, seasons, and geographic regions. Many migratory bird populations in Iceland come into close contact with lichen due to its prevalence in this tundra-dominated Arctic-boreal habitat. As part of my PhD thesis on the role of migratory birds as vectors for dispersal of Arctic fungi, I am investigating the hypotheses that Icelandic birds often encounter epiphytic, saxicolous, and terricolous lichens, and that these birds collect and carry propagules of lichens on their feet and feathers. Here, I will present this methodology and its application at Icelandic bird ringing stations and nest sites over the past 3 years, demonstrating the ability of birds to collect lichen propagules from their environment on their feet, legs, and feathers. With this important data, I aim to link the transport of lichen propagules with the intercontinental migration routes of the birds in order to provide insight into important hypotheses on the long-distance dispersal of lichens.

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Bryology and Lichenology

Topic: Contributed Papers

Title: Digitizing the bryophyte and lichen collections of the University of Florida herbarium (FLAS)

Author: ***Alan Franck @ University of Florida***

Keywords: Biodiversity,bryophytes,digitization,Florida,lichen

Abstract:

The University of Florida Herbarium (FLAS) houses approximately 100,000 specimens of bryophytes and 20,000 specimens of lichens. The most substantial contributions were made through the efforts of Severin Rapp (1900s-1940s) and Dana Griffin, III (1960s-2000s). The FLAS collections have an excellent representation of Florida's diversity, of which nearly all specimens are digitized but with images only of the labels. Recent efforts via our TCN from NSF (DBI #2001500) have focused on digitizing the international specimens to include images of the actual collected organism and the label. Images of the dried bryophyte and lichen organisms will be useful for identification as well as visualizing their phenotypic diversity. The FLAS bryophyte collection is especially rich in Neotropical specimens, but only a small portion of these are fully digitized. Current plans are to fully digitize (or nearly so) the entire collection over the ensuing years. What remains particularly daunting is the large assemblage of unaccessioned material and unprocessed duplicates which need to be worked through.

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Bryology and Lichenology

Topic: Contributed Papers

Title: A Preliminary Bryophyte Flora of Henry W. Coe State Park

Author: ***John McLaughlin @ San Jose State University***

Keywords: bryophytes,California,California Floristic Province,Floristics,Mediterranean ecosystems

Abstract:

Henry W. Coe State Park (HWCSP) is a botanically important preserve in the central interior Coast Ranges of California that until now has been overlooked bryologically. Comprising 177 species including 1 variety and 3 undescribed taxa, the bryophyte flora of HWCSP currently represents 22% of California's bryophyte diversity. Situated along the Diablo Range, this state park contains relictual taxa from the exterior coast ranges as well as rare and disjunct populations from within California. Thirty species from Santa Clara County and sixty-two species from Stanislaus County are reported for the first time further highlighting the state's need for bryological surveys.

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Bryology and Lichenology

Topic: Contributed Papers

Title: Asexual Offspring Germination is Dependent on Water Vapor and Source Habitat

Author: ***David Nicholas McLetchie @ University of Kentucky***

Keywords: bryophytes,Marchantia inflexa,liverworts,relative humidity,Gemmae,water vapor deficit

Abstract:

Water is essential for all life but while most studies focus on liquid water, few studies focus on water vapor. The amount of water vapor is informative of the habitat and can provide an organism information on the favorableness of a habitat. Plant species where individuals vary along moisture gradient are good candidates to test for variation in a trait's response to relative humidity. In the liverwort Marchantia inflexa, water stress responses differ by the sex of the plant and vary across habitats differing in moisture levels. Further, germination responses are critical for successful establishment of populations. To test for differences in M. inflexa germination responses due to water vapor, asexual propagules were floated on water and exposed to air with high (100%) or low (65%) relative humidity (RH). Twenty female and male laboratory-grown M. inflexa plants from two locations (East Turure (high moisture) and North Oropuche (low moisture)) in Trinidad and Tobago were used in this study. Germination was measured after one day. Four trials were completed. Germination was significantly higher in high RH compared to low RH, significantly higher in plants from the drier, more exposed habitat compared to plants from the moist, less exposed habitat and, the sexes did not differ. Despite floating on liquid, the lower RH reflects less optimum moisture conditions. Higher germination in plants from the less mesic relative to more mesic habitat suggests selection for quicker germination response when conditions are favorable. This finding is evidence that genetic variation occurs in M. inflexa response to water vapor. Response to water vapor is a critical response where the sensors remain unknown.

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Topic: Contributed Papers Bryology and Lichenology

Title: A Potential Symbiosis of Nitrogen-Fixing Bacterial Endophytes and Their Bryophyte Hosts

Author: **_Blair Young @ Rutgers_**

Keywords: bacteria,endophyte,liverworts,microscopy,mosses,nitrogen fixation,bryology,bryophytes,Symbiosis,Microbiome,STRUCTURE,Anatomy, Development,cell biology,microbiology

Abstract:

Plants host endophytes within their tissues, but much more is known about vascular plant symbioses, while bryophyte symbioses remain poorly understood, especially intracellular associations with bacteria. Vascular plants have complex relationships with the endophytes in their roots where the rhizophagy cycle provides the plant with nutrients sourced from bacteria, especially nitrogen. Bryophytes lack roots but possess many unique structures capable of hosting bacterial endophytes that may contribute nutrients. Pre-existing research on bryophyte bacteria associations have focused on macroscopic relationships such as epiphytic bacteria, hornwort mucilage cavities, or whole microbiome studies. Here, the presence of nitrogen transfer from bacteria to bryophyte was tested to understand the function of intracellular bacterial endophytes in bryophyte cells. The stem vasculature of mosses and the oil bodies of liverworts consistently host large numbers of bacteria in species across the phylogeny. At both sites sugars are concentrated around the bacterial endophytes, and in the mosses, nitrate is often present surrounding bacterial membranes. The extent of this association is hypothesized to be widespread, with benefits to bryophyte growth. The mechanism governing the regulation of the relationship is likely comparable to the rhizophagy cycle in vascular plants. This is a potential mutualism between bryophytes and their endophytic bacteria, where plant carbon is exchanged for bacterial nitrogen within the plant’s cells. The presence of this relationship in both mosses and liverworts across their respective phylogenies would suggest the mutualism is ancestral to at least the Setaphyta, and perhaps all bryophytes.

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Topic: Contributed Papers

Title: Microclimate and substrate shape lichen community composition and functional diversity in the foothills of the Southern Rocky Mountains

Author: **_Jacob Watts @ University of Colorado at Boulder_**

Keywords: Community composition,functional traits,lichens,microclimate,Symbiosis,elevational gradient,reflectance spectrum,functional diversity

Abstract:

Lichens are an impressively stress-tolerant photosynthetic symbiosis between at least two partners, the fungus and alga – mycobiont and photobiont respectively – and a host of accessory fungi, secondary photobionts, epicorticular bacteria, etc. They are often the only macroscopic organisms capable of living on bare rock in the dry, western US owing to a suite of adaptive traits unique to the lichen symbiosis. As such, they are essential for primary succession, soil formation, and a source of biodiversity in mountainous environments. Despite their importance for ecosystem functioning, few studies have attempted to link microclimate (relative humidity, temperature, vapor pressure deficit [VPD], and light), and substrate (soil, rock, bark) to variability in lichen community composition and functional diversity. As poikilohydric organisms, lichen thallus hydration status is always in equilibrium with the environment making VPD an important driver of lichen photosynthesis and metabolism. Yet, few studies have directly measured VPD at fine scale in relation to lichen communities. Further, the majority of past work on lichen functional traits has focused on either a small selection of quantitative traits such as specific thallus mass (STM) and water holding capacity (WHC) or many categorical traits such as growth form (leprose, crustose, squamulose, foliose, fruticose). Here, we assess many quantitative functional traits (thallus size, STM, WHC, growth form, layer thicknesses, hydrophobicity, symbiont proportions, photobiont trading, thallus reflectance spectrum, reproductive type, etc.) across a broad taxonomic and environmental range to better understand tradeoffs between traits and environmental drivers o functional strategies in lichens. To do this, we established 35 plots (0.25 hectares) distributed across an elevational gradient of native environments within the City of Boulder Open Space and Mountain Parks land in Colorado. At each plot, we measured microclimate, mycobiont community composition, and functional traits for each species. Preliminary results suggest wetter (low VPD) and lower light environments host a greater taxonomic and functional diversity of lichens, while more stressful environments host fewer, specialized lichen species with a characteristic set of stress tolerance adaptations. Despite these general trends, there seem to be many successful functional trait combinations exhibited by lichens. The results of this study provide an important step toward developing a unifying functional trait framework for the lichen symbiosis.

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Bryology and Lichenology

Topic: Contributed Papers Bryology and Lichenology

Title: Gymnomitrion as a treasure trove for bryophilous ascomycetes: new discoveries and a refined understanding of distributions across western North America

Author: ***W. Cuyler Bleecker @ University of Alaska Fairbanks***

Keywords: bryophytes,Alaska,epiphytes,Fungi,herbaria,lichens,liverworts,Pacific Northwest,parasites,bryophilous ascomycetes,Gymnomitrion,bryophilous fungi,Aleutian Islands

Abstract:

Bryophytes, far from being the infection-impervious organisms they are often misconceived to be, are colonized by a diversity of fungal parasites, saprobes and commensals, at least some of which likely recapitulate plant-fungal interactions in the first land plants. These fungi, the vast majority of described species of which belong to the phylum Ascomycota, and many of which are obligate parasites and host-species specific, have been deemed “bryophilous”. The leafy liverwort genus Gymnomitrion Corda (Jungermanniales, Gymnomitriaceae) is a predominately northern hemisphere genus that grows on exposed or somewhat sheltered rock surfaces, on well-drained tundra and among boulders in coastal and mountainous areas, and consists of six species in North America. The genus is known to be a common host for bryophilous ascomycetes, most of which have been documented on host plant collections from localities in Europe. Bryophyte specimens preserved in herbarium collections, at present still largely uninvestigated for the presence of bryophilous fungi, have high potential to reveal new species and new occurrences, at least for those ascomycete taxa which are desiccation and decay resistant (mainly Classes Eurotiomycetes and Dothideomycetes). The present study represents the first concerted effort to document bryophilous fungi from herbarium specimens of Gymnomitrion in North America. With the aim of increasing understanding of the variety and global distribution of different fungal taxa parasitic or epiphytic on Gymnomitrion, we screened over 100 specimens from multiple herbaria (mainly from ALA and OSC), mostly collected from western North America (the Pacific Northwest, Alaska and the Aleutian Islands) but also from Eurasia (Europe and the Russian Far-East). Our findings revealed a higher-than expected number of parasitic fruiting-body forming ascomycete taxa on Gymnomitrion. These included first records of previously known bryophilous taxa for North America; new occurrences of both lichenized and non-lichenized species as epiphytes and parasites, respectively, on the host genus and/or species; at least one new combination; and possibly one or more species new to science, including a true bryoparasitic fungus (Pleosphaeria sp). In addition to contributing to basic knowledge of these organisms, our findings reaffirm the value of herbarium collections as a tool for filling gaps in knowledge of bryophilous ascomycete biodiversity and biogeography. We hope the study will serve to both highlight the need for and encourage similar investigations seeking to further expand understanding of this fascinating but neglected field representing an intersection between bryology, lichenology and mycology, and conducted by only a handful of researchers worldwide up to the present.

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Bryology and Lichenology

Topic: Contributed Papers

Title: Bisexuality is not associated with increased diversification in mosses

Author: ***Katie Sanbonmatsu @ Texas A&M University***

Keywords: beta diversity,biogeography,bryophytes,chromosome counts,Diversification,monoecy,moss,Reproduction,Sex,sexual state,monoic

Abstract:

The frequency with which bryophytes transition between sexual states is unmatched by their vascular plant relatives. Yet, the ecological and evolutionary mechanisms that drive the evolution of separate and combined sexes in mosses remain somewhat obscure. Here, we re-evaluate the evolutionary ecology of sex in mosses. To do so, we use the largest sexual state database of mosses to date, the most comprehensive species-level phylogeny of mosses, and a massive geographic database to uncover the patterns and processes governing moss reproduction. We employed Hidden-State Speciation and Extinction analysis (HiSSE) to test the expectation that monoicous lineages have higher rates of diversification. We then used ancestral state reconstructions of moss chromosome numbers to test the hypothesis that increases in chromosome number coincide with transitions to monoicy. We used generalized dissimilarity modelling to determine the ecological drivers of turnover in moss communities partitioned by sexual state. Finally, we test the long-held hypothesis that monoicous lineages have larger ranges as a consequence of long-distance dispersal (LDD) by spores.

We found that changes in chromosome number are not associated with transitions in sexual state. We also show, using the most modern techniques, that sexual state is not associated with diversification, contrary to the results of previous studies. Most importantly, we demonstrate that monoicous lineages do not have larger range sizes, but instead have smaller ranges with low range overlap between closely related species. We interpret this as a phenomenon in which monoicous species may experience a ‘sweet-spot’ in the frequency of long-distance dispersal of spores. We postulate that LDD contributes to the formation of nascent selfing populations but is insufficient to maintain gene flow between daughter and parent populations, resulting in many incipient lineages that diverge allopatrically.

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Bryology and Lichenology

Topic: Contributed Papers

Title: Untangling Aquatic Transitions and Interspecific Relationships in the Moss Genus Fissidens

Author: ***Julia Butler @ University of Tennessee Knoxville***

Keywords: bryophytes,Aquatic plants,Evolution,GoFlag 408,herbarium genomics,molecular ecology,molecular phylogenetics,phylogenetics,bryology,moss

Abstract:

Bryophytes live in a diverse array of habitats from blazing deserts to arctic tundra. They can also occupy habitats ranging in moisture level from terrestrial to partially aquatic to completely submerged. Often when species move into aquatic habitats they lose morphological features, which can make it challenging to elucidate evolutionary relationships based on morphology. Species in the moss genus Fissidens reside in habitats across a range of moisture levels from terrestrial to aquatic. In this study our aim was to determine the evolutionary relationships between fully aquatic Fissidens species, including members of Subgenus Octodiceras, Section Sarawakia, and Fissidens brachypus, a species that grows exclusively on amazonian sponges. In order to address this aim, we conducted a molecular phylogenetic study using data generated from herbarium specimens. A total of 27 species were sequenced and analyzed, 12 of which are fully aquatic. Using a probe set for target enrichment (GoFlag408), we recovered hundreds of loci for each specimen, including a specimen collected in 1842. The resulting sequences were put through a multi-step pipeline in which we (i) trimmed the raw reads, (ii) assembled the targeted loci, (iii) probe trimmed, (iv) inferred orthology with reference genomes, (v) filtered contaminants, and (vi) aligned and merged isoforms. Post-processing scripts were run in order to prepare the resulting files for further analysis including file conversions, alignment pruning, and file concatenation. The resulting sequences were used to build two trees: a concatenated Bayesian Inference tree using MrBayes and a coalescent-based tree using RAxML and ASTRAL. Using the resulting trees, we determined how many times these species have transitioned to aquatic habitats across the genus Fissidens. Studies like this enable us to expand our understanding of habitat transitions and morphological evolution across plants.

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Bryology and Lichenology

Topic: Contributed Papers Bryology and Lichenology

Title: Molecular and phenotypic study put eastern North American Cetrelia in a global context of biogeography and phylogeny

Author: ***Jeremy Howland @ New York Botanical Garden***

Keywords: biogeography,lichen,Lichenology,molecular phylogenetics,morphological species delimitation

Abstract:

The family Parmeliaceae includes the largest diversity of foliose macrolichens, with over 71 genera and over 2,000 described species belonging to such iconic genera as Xanthoparmelia, Usnea, and Hypotrachyna. One genus, Cetrelia has been repeatedly shown to be monophyletic reinforcing its delimitation with phenotypic characters. Species of Cetrelia delimitated by chemical and morphological data have been largely supported by phylogenetic analysis of molecular data. While there is a robust, well-sampled global phylogeny for Cetrelia, it lacks sampling from Eastern North America (ENA) which is a region with important disjunct subpopulations of at least three species (C. chicitae, C. monachorum, and C. olivetorum). The focus of this study was to place the ENA subpopulations into the broader global Cetrelia phylogeny and confirm their taxonomic identities based on morphological and chemical characteristics. Targeted fieldwork was conducted by the first author in the Appalachian Mountains of North Carolina, Virginia, and West Virginia in 2022. Cetrelia specimens collected and sequenced for this study all were recovered in existing monophyletic or strongly supported groups when included with the global molecular dataset published by Mark et al (2019), and support three species (C. chicitae, C. monachorum, and C. olivetorum) being delimited by chemical and morphological characteristics in ENA. One species C. cetrarioides, also occurs in the region but was not successfully sequenced despite targeted attempts at new collections. Our study of C. cetrarioides suggests that morphological characters may not be enough to distinguish between it and C. monachorum in ENA and further molecular sequencing is needed to clarify this subpopulation as a chemotype of C. monachorum or phenotypic variation within C. cetrarioides.

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Bryology and Lichenology

Topic: Contributed Papers

Title: The Sphagnum cuspidatum complex: phylogeny, species delimitation, and morphology

Author: ***Sean Robinson @ SUNY Oneonta***

Keywords: Sphagnum,RADseq,species delimitation,Morphological variation

Abstract:

The use of species as a concept is an important metric when assessing biological diversity and ecosystem function. However, delimiting species based on morphological characters can be difficult, especially in aquatic plants that exhibit high levels of variation and overlap. The Sphagnum cuspidatum complex, which includes plants that dominate peatland hollows close to or at the water table, provides an example of challenges in species delimitation. Microscopic characters that have been used to define taxa and the possibility that these characters may simply be phenoplastic responses to variation in water availability make species delimitation in this group especially difficult. In particular, the use of leaf shape and serration, which have been used to separate species in the complex, have resulted in divergent taxonomic treatments. Using a combination of high-resolution population genomic data (RADseq) and a robust morphological assessment of plants representing the focal species, we provide evidence to evaluate putative species in this complex. Our results are broadly relevant to other aquatic groups where leaf shape and marginal teeth are used to distinguish species.

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Bryology and Lichenology

Topic: Contributed Papers

Title: Custom-made regional DNA barcode databases increase successful specimen identification of lichen-forming fungi

Author: ***Michael Kerr @ Brigham Young University***

Keywords: database,ITS,lichens,Metabarcoding,taxonomic identification

Abstract:

DNA barcoding and metabarcoding have proven to be indispensable tools for characterization of diversity, both genetic and taxonomic. The relatively low cost of metabarcoding, in terms of time and money, increases its attractiveness as a tool for ecological studies. However, metabarcoding approaches are hindered by poor representation of multiple organism groups in barcode databases, particularly in fungi and lichen-forming fungi. We propose that small, regionally focused, single organism group barcode databases can help address the current lack of species representation. We assessed this for lichen-forming fungi by creating a barcode database focusing on the ITS barcoding region, made up of over 4800 sequences representing over 600 formal and provisional species. We then compared our regional database and the UNITE fungal DNA database with respect to identification success of bulk sequences from samples across the Intermountain West. The regional database successfully identified more than twice the number of the 473 recovered species hypotheses that UNITE successfully identified. We show that regional databases can be a powerful tool in filling gaps in barcode databases with broader scope, as robust regional databases can focus on single regions and single groups before being linked to wider databases.

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Comparative Genomics/Transcriptomics

Topic: Contributed Papers Comparative Genomics/Transcriptomics

Title: Differentially expressed genes and signatures of selection highlight the genetic underpinnings of floral syndromes in multiple species of Calochortus (Liliaceae)

Author: ***Jacob Landis @ Cornell University***

Keywords: Calochortus,comparative transcriptomics,RNA-Seq,flower morphology

Abstract:

Floral traits such as flower size, shape, and pigmentation are major factors in pollination biology, providing cues for pollinator attraction or mechanisms for effective pollen transfer. To understand the evolutionary processes and the genetic mechanisms that drive adaptive morphologies, we investigate the genetic regulatory mechanisms that give rise to the wide diversity of floral traits across the genus Calochortus. The highly charismatic genus is an excellent model to investigate the genetic mechanisms underlying developmental evolution due to the high diversity of suites of traits or 'floral
syndromes'. The four floral syndromes are characterized by variation in trichome densities and placement on petals, diversity of flower size, a wide spectrum of floral pigments, and variation in floral posture (i.e., erect v nodding flowers). A three-pronged comparative transcriptomic approach using RNA-Sequencing data is employed to
identify candidate regulatory genes expressed in floral tissue: 1) comparing expression patterns across three species at three developmental times points using a high quality reference transcriptome, 2) comparing expression patterns within each of three species across three developmental stages using species-specific transcriptomes, and 3) identifying ortho groups across six species and looking for signatures of selection on the coding regions of candidate genes identified from expression analyses. With this approach we can examine key players regulating the development of floral traits that have been recruited across floral syndromes and determine if key genes are similarly expressed during the same developmental stage across syndromes. If expression of candidate genes does not change across floral syndromes we can determine if there are structural changes in the genes associated with different phenotypes.

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Comparative Genomics/Transcriptomics

Topic: Contributed Papers Comparative Genomics/Transcriptomics

Title: Hybridization, ploidy, and genome size variation in the toxic alga Prymnesium parvum

Author: ***Jen Wisecaver @ Purdue University***

Keywords:

Abstract:

Harmful algal blooms (HABs) of the toxic haptophyte Prymnesium parvum are a recurrent problem around the world. Strains of P. parvum vary in the toxins they produce and in other physiological traits associated with HABs, but the genetic basis for this variation is unknown. To investigate genome diversity in this morphospecies, we generated genome assemblies for fifteen phylogenetically and geographically diverse strains of P. parvum including Hi-C guided, near-chromosome level assemblies for two strains. Comparative analysis revealed considerable DNA content variation between strains, ranging from 115 Mbp to 845 Mbp. Strains included haploids, diploids, and polyploids, but not all differences in DNA content were due to variation in genome copy number. Haploid genome size between strains of different chemotypes differed by as much as 243 Mbp. Syntenic and phylogenetic analyses indicate that UTEX 2797, a common laboratory strain from Texas, is a hybrid that retains two phylogenetically distinct haplotypes. Investigation of gene families variably present across the strains identified several functional categories associated with metabolic and genome size variation in P. parvum including genes for the biosynthesis of toxic metabolites and proliferation of transposable elements. Together, our results indicate that P. parvum is comprised of multiple cryptic species. These genomes provide a robust phylogenetic and genomic framework for investigations into the eco-physiological consequences of the intra- and inter-specific genetic variation present in P. parvum and demonstrate the need for similar resources for other HAB-forming morphospecies.

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Comparative Genomics/Transcriptomics

Topic: Contributed Papers

Title: High diversity of Type I Polyketide genes in lichen-forming fungi as revealed by comparative analysis of 23 lichen genomes

Author: ***Julia Gerasimova @ Senckenberg Research Institute and Natural History Museum Frankfurt***

Keywords:

Abstract:

Fungi synthesize an extensive array of chemically and functionally diverse natural products, termed secondary metabolites, with roles in defence, self-protection and development. Based on their properties and the core enzymes and precursors involved in their biosynthesis, four major groups of fungal secondary metabolites are distinguished: polyketides, non-ribosomal peptides (NRPS), terpenoids, and tryptophan derivatives. The mos common lichen secondary metabolites polyketides—are synthesized by polyketide synthases, particularly by Type I PKS (TI-PKS). We conducted a comparative genomic analysis of the TI-PKS gene content of 23 lichen-forming fungal genomes from Ascomycota, including the de novo sequenced genome of the crustose lichen Bacidia rubella. Our comparative analysis included 1) an identification of a putative atranorin cluster in Bacidia rubella, 2) an overview of TI-PKS gene diversity in lichen-forming fungi, and 3) a reconstruction of the most comprehensive Type I PKS phylogeny of lichen-forming fungi to date, including 624 sequences. We revealed a high number of biosynthetic gene clusters and examined their domain composition in the context of previously characterized genes, confirming that PKS genes outnumber known secondary substances in lichens. Similar to previous studies, we observed a large diversity of PKS genes in lichen-forming fungi as well as B. rubella, much larger than expected based on their recorded secondary metabolite profiles. Particularly, our results reveal that a biosynthetic gene cluster, including PKS23, is likely involved in the biosynthesis of atranorin in Bacidia rubella. Although many PKSs remain without functional assignments, our findings highlight those genes from lichen-forming fungi represent an untapped source of novel polyketide compounds.

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Comparative Genomics/Transcriptomics

Topic: Contributed Papers

Title: Gene Co-expression Networks Across Phylogeny in the Study of C4 Photosynthesis

Author: ***R. Shawn Abrahams @ Yale University***

Keywords: Brassicaceae,Brassicales,C4 photosynthesis,Cleomaceae,Co-expression network,photosynthesis

Abstract:

C4 photosynthesis is a carbon concentration mechanism that has evolved multiple times across plants as an adaptation to low atmospheric CO2 and hot and dry environments. The molecular mechanisms underlying C4 photosynthesis are complex and involve the coordinated expression of many genes. Here, we investigated the co-expression patterns of genes involved in C4 photosynthesis in the C3 species Arabidopsis thaliana and Taranaya hassleriana and the C4 species Gynandropsis gynandra.

Using publicly available transcriptomic data, we constructed gene co-expression networks for C3 and C4 species. We found that the co-expression networks of the C3 species were more similar than that of the C4 species, suggesting that this method can be utilized in a phylogenetic framework. In addition, we identified several interesting patterns of co-expression within and across the networks. For example, leaf-based phosphoenolpyruvate carboxylase (PEPC), a key enzyme in the C4 pathway, appeared loosely correlated with the Calvin Cycle in Arabidopsis and increasingly in Tarenaya. This copy of PEPC is a part of the syntenic locus from which C4-acting PEPC in Gynandropsis is recruited. Additionally, we observed that ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit (RBCS) copies were not co-expressed within Gynandropsis as they were in the C3 networks. This could indicate a different regulatory mechanism for RBCS in C4 species. Finally, we found that the mean co-expression was lower in C4 species compared to C3. This may reflect the more specialized nature of the C4 pathway and the cell-specific regulation required for its function. In conclusion, our study provides insights into the gene co-expression networks underlying C4 photosynthesis. These findings have important implications for understanding the evolution and regulation of this key process in plants.

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Comparative Genomics/Transcriptomics

Topic: Contributed Papers

Title: Pleiotropy and adaptation in the silverleaf sunflower, Helianthus argophyllus

Author: ***UZEZI OKINEDO @ University of Massachusetts Boston***

Keywords: gene expression,Gene Regulatory Netvwork,genomics,population genomics,sunflower

Abstract:

Pleiotropy is the control of multiple phenotypes by a single locus. According to Fisher’s model, pleiotropy is expected to slow down local adaptation unless populations are far from being optimally adapted to their environment. A recent study found that candidate locally adapted loci were enriched for high gene network connectivity, a measure of pleiotropy, in populations of common ragweed. Here we conduct comparative analyses in another member of the Asteraceae, the Texas endemic silverleaf sunflower. We used transcriptome sequences from 22 individuals in two regions (coastal and north) that represent divergent locally adapted life history strategies. We assessed genotype-expression associations, constructed gene networks, and tested for associations between genetic signatures of local adaptation and gene network connectivity. As in common ragweed, we find that silverleaf sunflower candidate loci for local adaptation are centrally located in gene network maps, substantially pleiotropic, and have higher odds of controlling the expression of other

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Comparative Genomics/Transcriptomics

Topic: Contributed Papers Comparative Genomics/Transcriptomics

Title: Sex determination is complicated: Exploring the genomic architecture of sexual dimorphism in the meadow-rues (Thalictrum, Ranunculaceae)

Author: ***Melody Sain @ Bucknell University***

Keywords: Dioecy,eudicot,Evolution,genomics,k-mer,Ranunculaceae,sex determination,Sexual system,short read data,Thalictrum,WGS,XY

Abstract:

The evolution of dioecy, the condition of having populations with distinct male (with only staminate flowers) and female (with only carpellate flowers) plants, has been widely studied in angiosperms. A key to understanding the evolution of dioecy is to understand the genetic mechanisms responsible for the differentiation of male versus female plants. This research builds on the existing knowledge of sexual system evolution, by investigating the genomic architecture of sex determination in the genus Thalictrum (the meadow-rues, Ranunculaceae). The goal was to build a foundation for determining whether similar or different genetic mechanisms were utilized in the two independent origins of dioecy within the genus. Thalictrum is a particularly interesting genus for the study of sex determination because flower developmental studies have suggested that it may use a homeotic mechanism to achieve unisexuality: numerous similar primordia in the center of each flower develop as either stamens or free carpels depending on the sex-determining genetic regions. Using Illumina short read sequencing from pooled same sex individuals of T. dasycarpum and T. dioicum, representatives of each dioecious clade, I developed a k-mer based pipeline to make inferences about the architecture of sex determination and evaluate the likelihood that similar or distinct genomic regions determine sex in each clade. I found evidence of XY sex determination systems in both T. dasycarpum and T. dioicum, yet it seems the two species use different genetic mechanisms.

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Comparative Genomics/Transcriptomics

Topic: Contributed Papers

Title: Exploring the evolutionary history of MADS-box genes in Carex (Cyperaceae): genome-wide analyses of seven Carex species

Author: ***Seungyeon Lee @ Sungshin Women's University***

Keywords: Carex,Cyperaceae,genome,Nanopore,transcriptome,MADS-box gene

Abstract:

MADS-box genes are transcription factors that control eukaryote development and growth, particularly in regulating flower development in plants through the ABC(D)E model. Revealing the functions of MADS-box genes and their regulatory network, together with other related genes, will play a key role in understanding the evolution of angiosperms. However, studies on floral MADS-box genes in many major lineages of angiosperms have not yet been conducted. Carex, with approximately 2,000 species, is the fifth largest genus in angiosperms and has unique floral morphology, including the perigynium, a sac-like structure covering gynoecium. Detection of MADS-box genes and their functional studies in Poales have primarily focused on Poaceae, which includes several model plants, rather than Cyperaceae. In this study, we detected MADS-box genes in Carex as a representative of Cyperaceae. We first determined draft genomes from five Carex species (C. siderosticta, C. paxii, C. dickinsii, C. breviculmis, and C. capricornis) based on both long-read (Nanopore) and short-read (Illumina and MGI) sequences. The genomes were of high quality, with 48 to 168 contigs, and had BUSCO values over 94.5%. We analyzed three previously reported Carex genomes and representatives of other Poales lineages, in conjunction with five newly sequenced genomes from this study. The MADS-box genes from Amborella trichopoda, Oryza sativa, and Arabidopsis thaliana were used as references in the detection process. The maximum-likelihood tree using amino-acid aligned DNA matrix showed unique duplication and deletion events in the evolutionary history of MADS-box genes in Carex. We produced transcriptomes of each floral organ from two representative species and compared them with those in Arabidopsis and rice. We also compared various methods for detecting MADS-box genes and discussed the boundary of the MADS-box gene family. Our findings will shed light on the floral structure evolution and genome evolution of Carex, which serves as a representative for the Cyperaceae.

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Comparative Genomics/Transcriptomics

Topic: Contributed Papers

Title: Genetic cascades driving developmental desicions from single-cell transcriptomics

Author: ***Philip Shushkov @ Indiana University***

Keywords: comparative transcriptomics,developmental trajectory,vascular tissues

Abstract:

Changes in transcriptional profiles are at the heart of development. Understanding transcriptional dynamics at the single-cell level is a central challenge in deciphering developmental processes. Current sequencing technologies allow the estimation of transcription profiles at unprecedented single-cell resolution but the inference of developmental progressions of cells is hampered by sampling sparsity, technological noise, and loss of spatial and temporal information. I use noise-resilient diffusion mapping-based approaches to infer and recapitulate developmental trajectories from large single-cell datasets. Our new methods allow us to reconstruct multiple branching trajectories that occur on substantially different timescales in development and infer waves of gene expression changes along the developmental progressions. We analyze the development of vascular cell types, i.e., sieve elements, companion cells, and vessel elements, in different plant organs. We recover known regulators of vascular development that follow expected developmental dynamics based on previous studies and identify putative regulatory factors. We identify waves of gene expression changes of transcription factors and their downstream targets, which provide substantial resolution of transcriptional dynamics in vascular cell development.

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Comparative Genomics/Transcriptomics

Topic: Contributed Papers

Title: The Open Green Genomes Initiative (OGG): Filling Gaps in the Phylogenetic Distribution of Chromosomal Genome Assemblies for Land Plants.

Author: ***Jim Leebens-Mack @ University of Georgia***

Keywords: genome composition,genome evolution

Abstract:

Open Green Genomes (OGG) is a Department of Energy Joint Genome Institute community science program initiative working to improve the phylogenetic representation of reference genome sequence assemblies and annotations across land plants. With contributions from more than 100 scientists around the world, OGG aims to generate land plant genome sequences to enable comprehensive analyses of evolutionary changes in gene content, regulatory networks and metabolic pathways influencing plant growth, responses to environmental stress, and production of valuable plant products. The resulting comparative framework will drive translation of genome science into predictive understanding and inform engineering of efficient production of plant-based products for the growing bioeconomy. The talk will provide a progress report for the initiative, highlighting how new genomes for several land plant species are improving our understanding of the evolution of genome content and structure, as well as gene function.

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Comparative Genomics/Transcriptomics

Topic: Contributed Papers Comparative Genomics/Transcriptomics

Title: Subgenome-dominant expression and alternative splicing in response to Sclerotinia infection in polyploid Brassica napus and progenitors

Author: ***Keith Adams @ University of British Columbia***

Keywords: alternative splicing,Brassicaceae,differential gene expression,polyploidy,Transcriptomics

Abstract:

Polyploidy has played an extensive role in the evolution of flowering plants. Allopolyploids, with subgenomes containing duplicated gene pairs called homeologs, can show rapid transcriptome changes including novel alternative splicing (AS) patterns. The extent to which abiotic stress modulates AS of homeologs is a nascent topic in polyploidy research. We subjected both resynthesized and natural lines of polyploid Brassica napus, along with the progenitors B. rapa and B. oleracea, to infection with the fungal pathogen Sclerotinia sclerotiorum. RNA-seq analyses revealed widespread divergence between polyploid subgenomes in both gene expression and AS patterns. Resynthesized B. napus displayed significantly more A and C subgenome biased homeologs under pathogen infection than during uninfected growth. Differential AS (DAS) in response to infection was highest in natural B. napus (12,709 DAS events) and lower in resynthesized Brassica napus (8,863 DAS events). Natural B. napus had more up-regulated events and fewer down-regulated events. There was a global expression bias towards the B. oleracea-derived (C) subgenome in both resynthesized and natural B. napus, enhanced by widespread non-parental down-regulation of the B. rapa-derived (A) homeolog. In the resynthesized B. napus, this resulted a disproportionate C subgenome contribution to pathogen defense response, characterized by biases in both transcript expression levels and the proportion of induced genes. Our results elucidate the complex ways in which Sclerotinia infection affects expression and AS of homeologous genes in resynthesized and natural B. napus.

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Comparative Genomics/Transcriptomics

Topic: Contributed Papers

Title: Comparative analysis of grass defense responses to Poacea-adapted and generalist lepidopteran herbivores

Author: ***Kate Eastman @ Purdue University***

Keywords: comparative transcriptomics,defense pathway,herbivory,Maize,Poaceae,specialized metabolism,caterpillar

Abstract:

Herbivorous insects in the order Lepidoptera cause massive losses to agricultural yields. One such species, the fall armyworm (Spodoptera frugiperda) causes the greatest damage to maize and exhibits host plant preference for Poaceae species. The beet armyworm (Spodoptera exigua) also feeds on monocots but is more commonly a pest on dicot vegetable crops. In response to herbivory, plants produce toxic and deterrent metabolites. For example, maize synthesizes indole-derived benzoxazinoids that limit the growth of non-adapted insects. Green foxtail (Setaria viridis), the wild progenitor of domesticated foxtail millet (Setaria italica), synthesizes the neurotransmitter serotonin as a defensive compound. Although insect feeding induces the accumulation of hundreds of metabolites in both maize and green foxtail, the biosynthetic pathways and defensive functions of most of these metabolites remain unknown. This work aims to compare the transcriptional and metabolic impacts of herbivory from the monocot-adapted fall armyworm and the generalist beet armyworm on maize and green foxtail. The results of these experiments show transcript-level changes in plant defensive pathways, including jasmonic acid biosynthesis and signaling, and secondary metabolic pathways such as indole-derived metabolism and terpenoids. Global analyses of differentially expressed genes between herbivory and controls show enriched gene ontology functional categories, including terpene synthase activity, indole metabolism, and lipid metabolism. Differences in plant defense responses against the two caterpillars also identify genes that are specifically affected by the monocot-selective fall armyworm. Additionally, these results show both shared defensive pathways, as well as divergent strategies between the domesticated and undomesticated plant hosts. Defense responses unique to green foxtail may contribute to herbivore resistance that is lacking in domesticated crops such as maize. The experimental results may alsobe utilized to further define defense-related metabolic pathways in both maize and green foxtail.

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Comparative Genomics/Transcriptomics

Topic: Contributed Papers

Title: Genomic comparison of freezer stored DNA to herbarium sheet DNA in diverse Hawaiian taxa

Author: ***Edward McAssey @ University of Connecticut***

Keywords: chloroplast DNA,DNA extraction,genomics,Hawaiian Islands,herbaria

Abstract:

Many studies have highlighted the broad utility of herbaria in plant evolutionary biology by analyzing DNA obtained from specimens of variable ages. However, the breadth of species found in herbaria presents issues regarding methods used for molecular studies, including DNA isolation. Some species may preserve better than others, while others may produce significant secondary compounds that inhibit DNA isolations. The Hawaiian Plant DNA Library presents a unique opportunity to investigate the quality of DNA in herbarium specimens compared to long-term freezer storage. For decades, herbarium specimens of Hawaiian endemic species have been paired with a contemporary DNA extraction (i.e., herbarium sheet made in 1995 and DNA extraction performed in 1995), which has been stored in a freezer. We have used this unique collection to compare how herbarium sheet DNA and their frozen isolated DNA counterparts perform in high-throughoput sequencing for speices in 12 genera of Hawaiian plants. By assembling chloroplast genomes, as well as mapping reads to Angiosperm 353 genes, we sought to quantify the effects of herbarium storage of tissue vs. freezer storage of isolated DNA. Herbarium samples were statistically more fragmented and produced fewer complete circular chloroplast genomes compared to their freezer stored DNA counterparts. However, there were numerous species-specific instances of herbarium samples performing exceptionally well. Overall, this study highlights the importance of obtaining high quality DNA at the time of vouchering a plant for herbarium storage. This is especially important in areas of the world with high concentrations of endemic and/or threatened taxa, such as Hawai‘i.

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Comparative Genomics/Transcriptomics

Topic: Contributed Papers

Title: Whole-genome-based paleogenomics reveals angiosperm karyotype evolution during their early history

Author: ***Susanne Renner @ Washington University***

Keywords:

Abstract:

Chromosome-scale genomes provide a basis for inferring ancestral linkage groups and processes of karyotype evolution. We have reconstructed the karyotypes of the major groups of flowering plants, using an approach that starts from retained intact chromosomes and syntenic blocks. Using genome assemblies representing Amborella, Nymphaeales, and Austrobaileyales (newly generated) as well as the five lineages of mesangiosperms (Ceratophyllales, Chloranthales, eudicots, magnoliids, monocots), we reconstructed the 16 unique protochromosomes ancestral in the angiosperms, the 14 of the mesangiosperms, those of the monocots before and after the divergence of Acorus, and those of the eudicots. Nine of the protochromosomes are still retained in at least one extant species without any fusion or fission. Other protochromosomes underwent rare and probably irreversible fusion events, detectable through repeated polyploidizations. These findings reject the low ancestral numbers for ancient angiosperms inferred with non-genomic approaches over the past 90 years.

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Topic: Contributed Papers Comparative Genomics/Transcriptomics

Title: Morus rubra L (Moraceae) Chloroplast Genome Sequencing and Phylogenomic Analysis of the Genus Morus

Author: ***Madhav Nepal @ South Dakota State University***

Keywords: Chloroplast genome,endangered species,native species,phylogenomics,Morus rubra,Morus,Red Mulberry,Mous Phylogeny,Organeller DNA

Abstract:

Genus Morus (Family Moraceae) comprises 13 species of mulberries distributed throughout temperate and subtropical regions of the world. Morus rubra, also known as red mulberry, is an endangered species native to North America and is found in riparian areas of eastern North America. Species integrity of M. rubra is threatened by introgressive hybridization with its invasive exotic congener M. alba (white mulberry). The interspecific hybridization is believed to pose a challenge of species identification. In order to address this challenge, and threats posed by hybridization to the species integrity of M. rubra, we conducted an analysis of chloroplast genomes of M. rubra, M. alba and hybrid individuals. The M. rubra chloroplast genome is 159,421 bp with 128 genes that code for 83 proteins, 8 ribosomal RNAs (rRNAs), and 37 transfer RNAs (tRNAs). Analysis of the genome size, GC content, and pattern of simple sequence repeats (SSRs) revealed a high degree of similarities between the two species. The chloroplast genome of M. rubra is larger than that of M. alba by 120 bp. Phylogenomic analysis of the chloroplast genomes of 11 species supported previously published Morus phylogeny with well-resolved Asian and North American clades. Nine hypervariable sites were identified across the genomes, which are yet to be tested for their effectiveness as species-specific markers. The research outcomes of this study not only provide insights into the chloroplast genome structure and organization of M. rubra but also help address taxonomic challenges and serve as an important genomic resource for future studies on Morus species

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Topic: Contributed Papers

Title: A novel loss of photosynthesis in fully mycoheterotrophic Afrothismia (Dioscoreales), and its effect on plastid genome evolution

Author: ***Nathaniel Klimpert @ University of British Columbia***

Keywords: Gene loss,Mycoheterotrophy,Plastid,genome evolution,Dioscoreales,plastid gene code

Abstract:

Mycoheterotrophic plants obtain most or all of their carbon from fungal associates instead of photosynthesis. This transition in trophic mode is associated with at least 50 independent losses of photosynthesis in land plants. These losses provide multiple evolutionary experiments in the convergent, divergent and unique ways in which plastid genomes evolve in heterotrophic lineages. Afrothismia represents one such independent loss in the yam order, Dioscoreales. Comprising up to 23 species, the lineage is endemic to tropical Africa; more than half of the species are endangered or critically endangered. The taxon was recently inferred to be the sister group of Taccaceae and Thismiaceae in Dioscoreales, but has received only limited attention in molecular systematics studies, and to date only nuclear and mitochondrial genes have been recovered from Afrothismia species. Here we sequenced and assembled full plastid genomes of three Afrothismia species to characterize the consequences of photosynthesis loss in the clade. All three plastid genomes have experienced extreme reductions in size and gene content (lacking all photosynthesis-related genes), and represent among the most reduced plastid genomes known (~12–15 kb). These plastomes lack the large inverted repeats typical of most photosynthetic taxa, but are otherwise nearly colinear with photosynthetic relatives, ignoring the gene losses and their substantially reduced intergenic spacer regions. Group IIA cis-spliced introns are retained in two plastid genes despite loss of the matK maturase gene, and a trans-spliced intron is retained in two of three species. All three species retain only 12 of 79 protein-coding genes, with just one of these (accD) involved in a function (fatty-acid biosynthesis) unrelated to protein synthesis. The protein-coding genes display massive rate elevation in phylogenetic analysis; despite this, they are predicted to all be evolving under strong purifying selection. The plastomes retain only two (of four) ribosomal RNA genes (16S and 23S rDNA), and one (of 30) transfer RNA gene (trnfM), implying import of nuclear or mitochondrial homologs for some or all of the missing translation apparatus genes, if plastid translation is functional. The trnE gene, which serves a critical role in heme biosynthesis in most heterotrophic plants in addition to its role in plastid translation, has been lost from the plastid genome, which has not been observed in any other mycoheterotrophic lineage. The plastid protein-coding genes of two species (Afrothismia hydra and A. winkleri) have multiple premature and in-frame TGA stop codons, and consistently use only one type of stop codon (TAA) at the end of genes. This pattern is potentially consistent with a change in the plastid genome genetic code, rather than RNA editing.

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Topic: Contributed Papers Comparative Genomics/Transcriptomics

Title: A gall-inducing herbivore influences transcriptome-wide changes in tall goldenrod (Solidago altissima L.)

Author: ***Robert Witkowski @ The Pennsylvania State University***

Keywords: GC-MS,herbivory,plant-animal interaction,RNA-Seq,Solidago,Transcriptomics,Eurosta,priming,chemical ecology,goldenrod

Abstract:

Through the “arms race” of antagonistic co-evolution, plants have evolved to recognize herbivore-specific volatile chemicals in their environment. After perceiving such a cue, plants may induce preparatory chemical defenses, a phenomenon referred to as “priming”, which readies a rapid defense response to a later challenge such as herbivory or infection. Recent discoveries in the co-evolutionary relationship of tall goldenrod (Solidago altissima L., Asteraceae) and the goldenrod gall fly (Eurosta solidaginis Fitch, Tephritidae) have demonstrated that priming plays an important role in the mediation of their host-parasite interactions: adult male gall flies emit a volatile pheromone on goldenrod plants to attract mates, then mated E. solidaginis females lay their eggs in the growing apical bud of S. altissima, where the larva hatches and induces a gall. Nearby S. altissima plants are primed by the male pheromone signal and are more resistant to galling from the E. solidaginis larva as well as specialist beetle herbivory. Despite a rich body of research on the chemical ecology of goldenrod and its gall fly, the molecular underpinnings of priming, including what gene expression patterns are involved in the rapid mobilization of plant defenses post-pheromone perception, are still not well understood. Until now, the Solidago-Eurosta system has not been studied using transcriptomic tools; this ecological model system is fertile ground for understanding the genes underlying plant priming. Additionally, primed S. altissima plants are less palatable to specialist herbivores, but it is not confirmed whether generalist species are similarly deterred. We investigated the phytohormone and transcriptomic profile of S. altissima plants primed by E. solidaginis pheromone before and after herbivory from a generalist caterpillar. To measure chemical defense, we extracted leaf phytohormones from primed and naïve (unprimed) plants that were damaged by caterpillars and quantified defense-related hormones such as jasmonic acid and salicylic acid with gas chromatography-coupled mass spectrometry (GC-MS). Illumina RNAseq was obtained for damaged leaves and the Trinity pipeline was used for assembly and differential gene expression (DGE) analyses. Our phytohormone results coupled with DGE analysis illustrate the influence of a co-evolved specialist on generalist herbivory and offer insight into the molecular signatures of defensive priming in plants.

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Topic: Contributed Papers

Title: RNA-seq study revealed difference in drought-tolerant mechanisms in various Pelargonium geophytes.

Author: ***Noorpreet Kaur @ University of Connecticut***

Keywords:

Abstract:

The biodiversity of geophytes is higher in Greater Cape Floristic Region (GCFR) of South Africa than anywhere else in the world. The GCFR is a winter rainfall region where geophytes survive hot and dry summers as below-ground tubers. Winter rainfall is predicted to become less consistent due to climate change which will impact survival of some geophyte species. To study the effects of drought during the growing season, three geophytic species of Pelargonium (sect. Hoarea) were subjected to an acute dry-down experiment. Leaf tissue was collected from control and treatment plants. Differentially expressed genes (DEGs) were identified using a computational pipeline including Trimmomatic, Trinity, EnTAP, GO annotation with g:profiler, and Gfold and R package-DESeq2. In all species, most enriched drought-responsive genes were related to protein processing in the endoplasmic reticulum, plant hormone signal transduction, response to abiotic stimulus, and response to stress. Differentially expressed genes in P. oblongatum were primarily associated with aging, plant organ senescence, and leaf senescence. Interestingly, this species had the largest leaves and was the only species to show plastic reduction in leaf size under drought stress. On the other hand, P. auritum had the smallest leaves out of all three species and an earlier study showed that it was physiologically the most resilient to drought. Drought-responsive genes in P. auritum were implicated in signal transduction, ion homeostasis, and Abscisic acid (ABA) signaling. In contrast, in P. incrassatum, major enriched genes categories involve plastids, thylakoids, and chloroplast stroma, implying that drought in this species affects photosynthetic machinery. Despite their common growth form, each species responds uniquely to drought in terms of gene regulation and physiology.

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Comparative Genomics/Transcriptomics

Topic: Contributed Papers Comparative Genomics/Transcriptomics

Title: Transcriptomics and metabolomics in the field: analysis of flavonoid biosynthesis across a latitudinal gradient

Author: ***Chloe Drummond @ Mount Holyoke College***

Keywords: Vaccinium,Flavonoid Biosynthesis,Latitude,metabolomics,Transcriptomics,Bilberry

Abstract:

Vaccinium membranaceum Douglas ex Torr. (tall bilberry, Ericaceae) grows along a latitudinal gradient in the Pacific Northwest and the Rocky Mountain Region where grizzly bears, American black bears, ungulates and birds rely on its leaves, stems, and berries for food. Flavonoids in the leaves are important nutrients for animal wildlife, they contribute to the value of the leaf as a medicinal herb, and they are important metabolites involved in photoprotective response. Previous research shows that flavonoid content of Vaccinium leaves changes in response to light intensity and along latitudinal gradients. Latitudinal variation in Vaccinium membranaceum flavonoid content has not yet been studied using transcriptomic and metabolomic tools and may reveal latitudinal patterns in light stress response and expand our understanding of the interaction between geography and digestibility of leaves by animals. We hypothesize a greater induced flavonoid photoprotective response at higher latitudes due to longer growing season daylight length and lower temperatures that reduce photosynthetic capacity. We reason that excess light, exceeding photosynthetic capacity, can induce photoprotective responses to avoid cell damage. To test our hypothesis, we analyzed transcriptome and metabolome data from V. membranaceum leaves collected from seven populations along a latitudinal gradient, within a three-week period in August 2021. Environmental data such as soil pH and canopy cover were collected, alongside genotyping-by-sequencing data, to account for covarying effects of environment and genetic background. RNA-Seq transcriptomic data were de novo assembled and analyzed using differential gene expression analysis with gene ontology enrichment to identify flavonoid or defense-related enrichment. To identify gene expression networks correlated with latitude, the eigengene from weighted gene correlation network analysis was used in statistical regression correcting for environmental and genetic co-variables. Gene expression networks correlated with latitude were annotated with GO enrichment analysis to identify flavonoid or defense-related enrichment. LCMS untargeted metabolomic data were processed by alignment, normalization, and peak identification. Metabolites differentiating by latitude were identified using principal component analysis followed by partial least squares discriminant analysis correcting for environmental and genetic co-variables. Functions of these metabolites were annotated using the Kyoto Encyclopedia of Genes and Genomes database to identify metabolites related to flavonoid biosynthesis. Results from transcriptomic and metabolomic analysis were compared. Our study illuminates the challenges and benefits of field-based transcriptomic and metabolomic experiments. In addition, our results help to illuminate geographic patterns of abiotic stress and leaf nutrient quality. Finally, this study may serve as a foundation for understanding how this species may respond to greater UV exposure or movement to higher latitudes in the future due to climate change and inform attempts to commercially grow this species, an effort that may reduce stress of over harvesting on natural populations.

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Comparative Genomics/Transcriptomics

Topic: Contributed Papers

Title: Comparative expression of genes involved in regulating nectar composition across species of Aquilegia with different animal pollinators

Author: ***Maria Alcaraz @ California State University, Sacramento***

Keywords: Aquilegia,comparative transcriptomics,Development,Nectaries,Pollination

Abstract:

Plants have evolved different mechanisms to attract pollinators and promote outcrossing. One of these mechanisms is the production of floral nectar. Nectar is a sugary substance that plants produce to attract pollinators to visit their flowers. This sweet liquid is composed of mainly carbohydrates, water, amino acids, and secondary metabolites. When analyzed, the composition of nectar follows specific trends. The nectar of a plant that is primarily pollinated by a hummingbird is very different than that of a plant that is pollinated by a bee or hawkmoth. For example, the nectar of a plant that is pollinated by hawkmoths has a higher sucrose concentration than a plant pollinated by bees or hummingbirds. The genetic intricacies that control this phenomenon are not well defined. Currently, the literature on the genetic control of nectar composition in plants is very limited. Most of the work done has concentrated on isolating specific genes involved in nectar production. Very few studies have looked at entire genetic pathways involved in nectar production and secretion. Here, I will use comparative transcriptomics to identify the genes that influence nectar composition across related species of Aquilegia with different animal pollinators. To determine which genes are associated with variation in nectar composition between species with different animal pollinators, I will examine gene expression in nectary tissue from four species of Aquilegia, including a primarily bee-pollinated species, two primarily hummingbird pollinated species, and a hawkmoth-pollinated species at different developmental stages. I will then identify genes that are differentially expressed by using Illumina sequencing to compare the RNA present in the nectary at the point of collection. I intend to then use Gene ontology enrichment analysis to define the identity or functions of expressed orthologs in other species.

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Conservation Biology

Topic: Contributed Papers Conservation Biology

Title: Conservation Genetics and the Maintenance of Flower Color Polymorphisms in a Non-Model System of Erythranthe discolor (Phrymaceae)

Author: ***Selena Vengco @ California Botanic Garden***

Keywords: Erythranthe,_{conservation biology},flower color polymorphisms

Abstract:

Angiosperms have a broad diversity of biotic and abiotic factors that maintain floral color throughout many lineages. Similarly, intraspecific taxa with corolla variation can be maintained through parallel biotic and abiotic pressures that influence flower colors across angiosperms. Erythranthe discolor (Phrymaceae) is a rare California endemic annual that occurs in the Southern Sierra Nevada and is known to have discrete flower color polymorphisms (FCP) in yellow and pink. A previous study found that precipitation was only partially responsible for the maintenance of yellow and pink corollas in this system. This study aims to detect mechanisms that maintain FCP in this non-model system by assessing gene flow between color morphs and through pollinator observations. Additionally, E. discolor is not recognized by California or the Federal Endangered Species Act as a species of conservation concern despite its narrow distribution. This research will provide the necessary baseline data including population structure and genetic diversity metrics to consider E. discolor as an endangered species.

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Conservation Biology

Topic: Contributed Papers Conservation Biology

Title: The potential distributions of African Azolla species and their implications for African wetland ecosystems for the future

Author: ***Mwihaki John(MJ) @ University of Florida***

Keywords: Africa, Azolla, climate change, ecological niche modeling, MaxEnt, wetland ecosystems

Abstract:

Aquatic ecosystem species are expected to be impacted by climate change. In Africa, conditions that may affect how aquatic species adapt are poorly understood and challenging to predict. In this study, we investigated the possible distribution of three Azolla aquatic fern species in Africa under several scenarios of future climate change. The three species' ecological niche models were developed using MaxEnt using occurrence data and environmental factors. AUC and TSS values for all models were reasonable and above 0.801, suggesting high prediction precision. The results suggested that the major determinant factors restricting the species' future range expansion were elevation and precipitation. Furthermore, we detected notable differences in the three species' unique climatic niches and suitable places. The species' current probable distribution areas ranged from 2,328,726 km2 to 4,026,363 km2. The range of the Azolla species may have extended beyond the known and recorded places, but under future temperature conditions, the species was predicted to lose between 8.1% and 48% of their suitable habitats as a result of climate change. Our findings can be used to devise aquatic species conservation programs that are sustainable and to inform people about the consequences of climate change.

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Conservation Biology

Topic: Contributed Papers

Title: Using environmental niche modeling and next generation sequencing to understand the factors promoting endemism of the critically-imperiled, hybrid Florida Pondweed (Potamogeton floridanus)

Author: ***Kaitlyn Sampson @ University of South Alabama***

Keywords: ecological niche modelling,_{conservation biology},Aquatic plants,endemism,hybridization,phylogenomics,Potamogetonaceae,freshwate

Abstract:

The southeastern United States is a global biodiversity hotspot, meaning it is a center of endemism that is highly threatened by human activity. Much of this biodiversity is supported by a wide range of freshwater ecosystems. Freshwater aquatic ecosystems are also essential to a variety of economic services and ecological processes that humans rely on, but they are especially impacted by climate change and anthropogenic disturbance. Freshwater aquatic macrophytes form the foundation of food webs, remove excess nutrients and minerals from the water column, and serve as critical bioindicator species; they play a key role in maintaining community structure. However, aquatic plants, especially endemics, are understudied and under-collected, ultimately impeding conservation efforts. The pondweed family (Potamogetonaceae) is one of the most species-rich submersed aquatic plant families in the northern hemisphere. Pondweeds provide food, shelter, and habitat for organisms such as insects, fish, turtles, and waterfowl and can improve water quality. Potamogeton floridanus, the Florida pondweed, is a rare, endemic species currently known from few populations in the Blackwater River drainage in Florida. It has recently been suggested that P. floridanus is a hybrid between P. oakesianus and P. pulcher. Potamogeton species are known to readily hybridize, and it is estimated that there are more hybrids than distinct species in the genus. Hybrids may form a significant proportion of pondweed diversity in North America. However, hybrid species do not receive the same considerations for protection from policymakers and therefore, don't receive necessary attention for conservation efforts. This study aims to (1) identify the factors contributing to the endemism of P. floridanus so that it may be better assessed for conservation, (2) develop a custom hybseq probe set for Potamogetonaceae to test its hybrid origin, and (3) advocate for better recognition of hybrid taxa in policy.

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Conservation Biology

Topic: Contributed Papers

Title: Conservation genomics and species delimitation in the threatened Magnolia pyramidata

Author: ***Lauren Eserman-Campbell @ Atlanta Botanical Garden***

Keywords: Angiosperms353,Coastal Plain,target-capture,Magnolia,Magnolia pyramidata

Abstract:

One longstanding taxonomic question in the genus Magnolia is whether Magnolia pyramidata (=Magnolia fraseri ssp. pyramidata) is truly a subspecies of Magnolia fraseri or whether these represent two independently evolving lineages. This question presents real challenges for conservation collections and in situ conservation management (e.g. assisted migration, genetic rescue). Magnolia pyramidata individuals are currently threatened (IUCN Red List Endangered) by habitat loss and climate change. Whereas M. fraseri inhabits more mountainous regions in the United States, M. pyramidata is found within the coastal plain, with a concentrated distribution in southern Alabama and the Florida Panhandle. We are assessing population genetic diversity and structure and the species status of M. pyramidata using high throughput sequencing. We have sampled individuals from the wild as well as botanic gardens and herbaria. We are utilizing the Angiosperms353 bait set in addition to the Magnoliaceae specific bait set. We will present results of population genetic and phylogenomic analyses.

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Conservation Biology

Topic: Contributed Papers

Title: Conservation genomics of island mallow, Malva assurgentiflora (Malvaceae)

Author: ***Kristen Hasenstab-Lehman @ Santa Barbara Botanic Garden***

Keywords: _{conservation biology},Malvaceae,population biology,Taxonomy

Abstract:

Malva assurgentiflora (Kellogg) M.F. Ray [Lavatera assurgentiflora] (Malvaceae) is a shrub endemic to four of the eight California Channel Islands: San Miguel, Anacapa, San Clemente, and Santa Catalina. Earlier population genetics and morphological studies have supported the recent recognition of subsp. glabra on San Clemente and Santa Catalina Islands. Subspecies assurgentiflora of the northern Channel Islands is quite rare, originally documented on San Miguel and on two of the three islets of Anacapa Island. Both Middle and West Anacapa islets populations have been extirpated over the last two decades, although seed from Middle Anacapa Island has been used to generate plants that have been introduced on East Anacapa San Miguel Island has two naturally occurring populations with fewer than 300 plants total. Here we use population genomic techniques to 1) assess if genomic data continues to support taxonomic circumscription of northern island plants as differing from southern island plants; 2) investigate the within-island and between island genomic diversity of remaining plants on San Miguel and Anacapa; 3) determine the genetic provenance of plants in horticultural settings on the mainland and across the archipelago; and 4) identify the highest value conservation seed banking targets. Our sampling includes 150 individuals from across the range of both currently recognized subspecies as well as horticultural settings. Our results are consistent with earlier microsatellite studies and show a clearly that populations of subsp. glabra on San Clemente and Santa Catalina samples are as genetically distinct from each other as from the northern Channel Island populations, and merit taxonomic recognition. Samples from presumed horticultural settings share ancestry with plants from Anacapa Island. Unexpectedly, results also identify plants from a presumed historic horticultural setting on Santa Rosa Island as genetically most similar to those on San Miguel Island. These results forced a careful reanalysis of the provenance of the Santa Rosa Island plants and potential focused conservation efforts to preserve these unique genotypes.

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Conservation Biology

Topic: Contributed Papers Conservation Biology

Title: Conservation and Paleoclimate Applications of the Endangered Dawn Redwood:

New Directions Based Upon Enhanced Paleobotanical Techniques

Author: ***Josh Turner @ Bryant University***

Keywords: _{conservation biology},Cuticle morphology,paleobotany,Paleoclimate,Conifers

Abstract:

The endemic Metasequoia glyptostroboides Hu & Cheng 1948 (Cupressaceae), the Dawn Redwood, is the only extant representative of the Metasequoia genus which has an abundant fossil record in the Northern Hemisphere since the Cretaceous. With only a small native population restricted to south-central China, the Dawn Redwood is facing serious challenges today due to its low genetic diversity, urbanization, and climate change, although cultivated trees have thrived around the globe. Metasequoia has been used as a model taxon for studies in paleobotany, paleoecology, and paleoclimatology, drawing on data from its extensive fossil record, cuticular micro-morphology, biomolecules, stable isotope signals, etc.

Two types of cuticles, the even type and the uneven type, have been characterized in its native living population with the vast majority of trees having uneven type cuticles. The even type is rarely found: From only a single tree in Paomu Village, Luota Town, Longshan County, Hunan Province, China (the “Paomu Tree”) and occasionally from some high branches of mature trees or juvenile seedlings. However, fossils all over the world are represented by the even type cuticle except for two recent reports of the uneven type in Miocene fossils from Yunnan and Inner Mongolia in China. Competing hypotheses exist regarding the origin and relationshi of these two cuticular types—whether they were caused by genetic mutation(s), different ecological conditions or combined influences. Ultimately, the resolution of this question will have critical implications in the conservation plan for this living fossil species and the application of its cuticular features for paleoecology and paleoclimate research.

Metasequoia’s thin and uneven type cuticle is notorious for being difficult to prepare in order to recover large pieces for accurate measurements of cell dimensions. The development of a cleared leaf epidermis (CLE) technique, modified from the conventional cleared leaf method solved the problem by obtaining a complete and transparent epidermal layer, allowing accurate measurements of three-dimensional epidermal features in both types of both fossil and modern Metasequoia. By applying this method to fossil leaves from the mid-Miocene Clarkia deposit in Idaho and various modern leaves, we carried out a statistical comparison of guard cell size and geometry of Metasequoia. Our data indicates that fossil leaves have relatively smaller guard cells compared with their living relatives, but the range of the two groups are still overlapping, implying that guard cell size is related to taxonomy and likely influenced by atmospheric CO2 levels as the Miocene Metasequoia lived under much higher CO2 conditions.

Through pyrolysis analysis of various conifer fossil compressions with different levels of preservation, we demonstrated that the CLE technique is readily applicable to other plant taxa for both modern and fossil specimens. We believe its wide usage can solve a variety of botanical and paleobotanical issues which bear conservation and paleoclimate applications.

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Conservation Biology

Topic: Contributed Papers

Title: Fire management after farming can recover phylogenetic structure of former longleaf grassland

Author: ***Natali Ramirez-Bullon @ U.S. Fish and Wildlife Service***

Keywords: ecological restoration,fire,longleaf pine savannah,biodiversity conservation

Abstract:

Biodiversity loss due to human activities is likely to increase due to projected increase of human populations. Humans have transformed forest, grasslands and savannas to produce food, fiber and timber (DeFries et al. 2004, Ramankutty et al., 2008). Models of land conversion predict a reduction species richness by 40.3% globally (Newbold et al. 2015). The projected decrease in species richness might be underestimating the loss of unique or similar species because those measures assume all species are equal. Phylogenetic diversity not only accounts for the number of species present but also for their evolutionary relationships. Phylogenetic diversity is a biodiversity index that can reflect the diversity of features or characteristics represented in a community (Faith 1992), thus a community that lost phylogenetic diversity would lose functional diversity. Functional diversity refers to the value and range of species traits in an ecosystem, such as leaf size, nitrogen content, and canopy heights (Díaz and Cabido 2001). Even in areas where species richness remains the same, it has been suggested that agricultural history has altered community composition and reduced phylogenetic diversity (Turley and Brudvig 2016).

We examined the effects of human activities on phylogenetic diversity and structure in the longleaf pine savannas. We quantified measures of phylogenetic diversity for plant communities described by vegetation surveys conducted in the uplands of the Red Hills Region of Florida and Georgia during 2017 and 2018 (Dixon et al. 2021) as part of study investigating ecosystem services in the area and their relationship with species richness. The areas surveyed comprise 10 different land use types including annually tilled row-crop fields which were all tilled within the year, five different periods of time since abandonment (5-15 years, 15-30 years, 30-50 years, 50-75 years, and 75-100 years, which we will refer to as restored savanna), and reference sites (never-plowed, frequently burned pine savanna). There were 2 to 4 replicate 100 m2 plots per land use type at each property for a total of 101 plots. The plots contained more than 386 plant species. Phylogenetic diversity doubled within five years of fire management. Continuous fire restoration helps recover phylogenetic structure after 15 years (mean nearest neighbor taxon distance, mean pairwise taxon distance). Communities affected by human activities species tend to be less closely related than in never plowed communities. Species that did not return after anthropogenic disturbance were not a random subset of species. One explanation for this clustering is that abiotic filtering influences recovery after disturbance.

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Conservation Biology

Topic: Contributed Papers

Title: A population genomic assessment of federally threatened Astragalus magdalenae var. peirsonii in California

Author: ***Carrie Kiel @ California Botanic Garden***

Keywords: Astragalus,Californina,conservation,Fabaceae,population genomics

Abstract:

Astragalus magdalenae var. peirsonii (Fabaceae - Peirson’s milkvetch) is a perennial herb that is native to dune habitats in southern California USA, Baja California, MX. This species is presently listed as Threatened under the Federal Endangered Species Act (ESA) and Endangered under the California ESA. Throughout the species range, habitat fragmentation and degradation, impacts from OHV use, low reproduction rates, and climate change have been documented as threats. Here we present new results of a robust, range-wide population genomic study for this endangered species in California. Specifically, we will address genetic structure, genetic diversity, in-breeding, and current patterns of gene flow within and among populations. We will also discuss how these results will inform future management and restoration efforts to protect this imperiled species.

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Conservation Biology

Topic: Contributed Papers Conservation Biology

Title: Getting our feet wet to bypass collection bias in Neotropical rivers: research in riverweeds (Podostemaceae) and its implications on conservation of threatened ecosystems

Author: ***Ana Maria Bedoya @ Louisiana State University***

Keywords: Andes,Collections,conservation,Neotropics,Podostemaceae,rivers

Abstract:

Riverweeds (Podostemaceae) are the largest group of strictly aquatic angiosperms. The family is unlike any other group of flowering plants in the Neotropics in that they live attached to rocks in fast-flowing aquatic ecosystems like river rapids and waterfalls. It is generally known that the Podostemaceae have a center of diversity in the Neotropics. However, the extent of species distribution and evolutionary history of the family is hindered by the fact that Neotropical Podostemaceae remains underrepresented in herbaria. Past research has shown that the future of rivers and of riverweeds are linked. I will talk about how current efforts in increasing collections of Podostemaceae have implications to conservation of rivers, and to advancing our understanding of evolutionary processes in the dynamic landscape of the tropical Andes. This talk is a call for international collaborative projects supporting local collectors and institutions in Latin America to bolster research in the under-collected river plants. Lets get out feet wet and do research in the increasingly threatened Neotropical rivers.

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Conservation Biology

Topic: Contributed Papers

Title: Threats on the horizon: Conserving rare plant species in the American West using the Endangered Species Act and other advocacy tools for scientists

Author: ***Naomi Fraga @ California Botanic Garden***

Keywords: California,climate change,conservation,endangered species,Endangered Species Act,Mojave Desert,Nevada

Abstract:

Beyond research, scientists have a number of tools available to advance conservation of rare and threatened species. Advocacy, including Endangered Species Act listing petitions, media messaging, and organizing with environmental advocates provides some of the most accessible and high value tools towards addressing critical and immediate conservation needs. Threats such as mining, habitat conversion, off-highway vehicle use, cattle grazing, invasive species, climate change and catastrophic drought are degrading and eliminating habitat for numerous rare plant species that occur on public lands in the American west. In this presentation we will discuss three plant species as case studies: Chloropyron tecopense (Tecopa bird's beak, Orobanchaceae), Eriogonum tiehmii (Tiehm's buckwheat, Polygonaceae), and Nitrophila mohavensis (Amargosa niterwort, Amaranthaceae), where the advocacy tool kit has either advanced conservation or is in the process of being employed to address urgent conservation issues.

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Conservation Biology

Topic: Contributed Papers

Title: Conservation genetics of the imperiled Mountain Purple Pitcherplant, Sarracenia purpurea var. montana

Author: ***Amanda Carmichael @ Atlanta Botanical Garden***

Keywords: conservation,Genetic diversity,inbreeding,RADseq,pitcher plant,sarracenia

Abstract:

Sarracenia purpurea var. montana is a pitcher plant native to the Southern Appalachian mountain bogs. This variety is currently under review for listing under the Endangered Species Act and is considered S1 or critically imperiled by NatureServe due to threats of habitat destruction and degradation. There is only one existing population of this endemic variety left in the state of Georgia. In the early 1990s, horticulturists from the Atlanta Botanical Garden (ABG) propagated two of ten remaining plants from this population at the ABG Greenhouse. These two plants were crossed to generate F1 individuals, which were then outplanted at the natural site as well as six in situ safeguarding sites around north Georgia. Since then, garden-grown plants have become naturalized and have been interbreeding on their own. We are interested in testing 1) the level of genetic diversity at in situ safeguarding sites, and 2) whether inbreeding has occurred at the extant natural site where F1 offspring were outplanted. DNA was isolated from 190 individuals using a modified CTAB extraction method. Genomic DNA was converted into nextRAD genotyping-by-sequencing libraries and sequenced on a Novaseq 6000 with one lane of 122 bp reads (SNPSaurus, University of Oregon). Genetic analyses show that the full extent of genetic diversity is not represented in each of the six safeguarding sites. Clonal analyses show a high level of relatedness but the plants are likely not clonal, implying a high level of inbreeding. This study is important in informing the future management of these safeguarding sites, and future outplantings need to target genetically distinct individuals that are not represented at the particular safeguarding site to ensure that sites capture full genetic representation in this taxon.

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Conservation Biology

Topic: Contributed Papers

Title: Developments in the race to conserve critically endangered Florida ziziphus (Pseudoziziphus celata; Rhamnaceae)

Author: ***Sterling Herron @ Archbold Biological Station***

Keywords: _{conservation biology},Florida,Pseudoziziphus celata,Ziziphus celata,Florida scrub,Lake Wales Ridge,Florida jujube

Abstract:

Florida ziziphus (Pseudoziziphus celata (Judd & D.W.Hall) Hauenschild) is a federally listed endangered, clonal shrub endemic to the Lake Wales Ridge of central Florida, restricted to jus 12 extant wild populations, many of which are at critically low numbers. Since its rediscovery in 1987, myriad challenges to its recovery have been identified including low genetic diversity, self-incompatibility, low seedling recruitment, and diminishing habitat. Efforts to save Florida ziziphus from extinction have focused on 1) finding and monitoring new wild populations, 2) propagating seeds and stem tissue, 3) characterizing genotypic diversity in these populations and propagules, and 4) using propagules to establish genetically guided augmentations and introductions with the goal to preserve and produce self-sustaining, stable populations of Florida ziziphus on protected lands. Florida ziziphus has been propagated successfully using tissue culture and seed germination, a critical resource for new translocations. To date, 41 extant, wild genotypes of Florida ziziphus have been discovered, in addition to numerous offspring that are crosses between the wild genotypes, most of which were produced through natural crossing in an ex situ population. From 28 years of demographic data, overall trends show slight to substantial declines in survival, with only three wild populations producing fruit. There have been 11 experimental introductions to seven protected properties and six genetic augmentations to two protected, uni-clonal populations of Florida ziziphus since 1998. Translocated populations have had relatively high survival rates, but relative growth rate has been quite slow and reproductive events rare, with an extended period before reproductive maturation. The most recent full census captured data on a total of 1,871 distinct ramets (1,454 living), including 672 wild ramets (537 living), 933 introduced / augmented ramets (691 living), and 266 ramets in the ex situ collection at Bok Tower Gardens (226 living). The new Plant Conservation National Collection site at a natural sandhill restoration at Bok Tower Gardens offers an additional ex situ repository for Florida ziziphus genetic diversity. Overall, the effort to conserve Florida ziziphus is a long-term endeavor, but we are optimistic for its ultimate recovery.

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Conservation Biology

Topic: Contributed Papers Conservation Biology

Title:

Quantifying grassland habitat suitability in North America for long-term restoration success under climate change

Author: ***Santosh Rana Magar @ Pennsylvania State University***

Keywords: climate change,range shift,ensemble species distribution modeling,prairies conservation,resilience & connectivity

Abstract:

Restoration theory suggests that using genetically- and species-rich seed mixes are necessary to ensure the long-term evolutionary potential of restored communities under global change. However, identifying suitable species and populations to source seeds for restoration is increasingly challenging given the rapid pace of climate change. Thus, new decision-making tools are required that integrate our understanding of species' contemporary and future niches into species and seed-sourcing decisions. In this study, we use ensemble species distribution modeling (eSDM) for single species and functional groups within a diverse plant community to forecast community response to global change. In addition, we model connectedness across fragmented landscapes to identify species-rich regions suitability needed to preserve communities in response to change. We tested these approaches using plant communities in North American grasslands, which are experiencing continued loss of native habitat and require extensive restoration efforts.

Using an eSDM approach, we modeled the distribution of 26 different grassland species that span four functional groups and are commonly for restoration in the North American Great Plains. We modeled species and functional groups in Biomod2 using contemporary environmental conditions and future (2050) climate projections. Across the community of grassland species, the environmental variables that contributed the most to grassland species' contemporary niche were 'growing degree days as heat units', 'soil characteristics', and 'cultivated and managed vegetation'. Interestingly, across all species, the factor that had the greatest predictive probability of species' presence was 'maximum temperature of the warmest month' suggesting the grassland species' community-associated ecosystem functions are associated with warmer, drier environments. While many regions exhibited stability in the predicted suitable distribution given contemporary and future conditions, the eSDM model predicted a northward expansion for many species into Canada. The greatest increase in predicted suitability was for the grass species, Boutleloua curtipendula (ca. 8%) while forbs such as Geum trifolium, were predicted to lose approximately 7% of suitable habitat across the western United States under the future (2050) climatic scenarios. This suggests the nuanced predictions associated with individual species may reshape the grassland community as a whole with expansion and loss of suitable habitat across North America.

Our research has identified key environmental factors that underlie the suitability of grassland communities under current and future conditions. Based on the current climate projections, the suitable climate for grassland communities may shift northward. This emphasizes the need to maintain connectivity across regions that exhibit hotspots of species suitability. The eSDM provides an invaluable tool needed to guide decision-making regarding grassland restoration and conservation efforts. Specifically, it suggests that restoration efforts should prioritize the selection of climate-resilient seed source populations and maintain connectivity to facilitate niche-tracking in response to climate change.

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Conservation Biology

Topic: Contributed Papers

Title:

High prevalence of clonal reproduction and low genetic diversity in Scutellaria floridana, a federally threatened Florida-endemic mint

Author: ***Richard Moore @ Miami Universtiy***

Keywords: Endemic Species,Florida,conservation genetics,clonal

Abstract:

The threatened mint Florida skullcap (Scutellaria floridana) is endemic to four counties in the Florida panhandle. Because development and habitat modification extirpated several historical occurrences, only 19 remain to date. To inform conservation management and delisting decisions, a comprehensive investigation of the genetic diversity and relatedness, population structure, and clonal diversity was conducted using SNP data generated by ddRAD. Compared with other Lamiaceae, we detected low genetic diversity (HE = 0.125-0.145), moderate evidence of inbreeding (FIS = -0.02-0.555), and moderate divergence (FST = 0.05-0.15). We identified eight populations with most of the genetic diversity, which should be protected in situ, and four populations with low genetic diversity and high clonality. Clonal reproduction in our circular plots and in 92% of the sites examined was substantial, with average clonal richness of 0.07 and 0.59, respectively. Scutellaria floridana appears to have experienced a continued decline in the number of extant populations since its listing under the Endangered Species Act; still, the combination of sexual and asexual reproduction may be advantageous for maintaining the viability of extant populations. However, the species will likely require ongoing monitoring, management, and increased public awareness to ensure its survival and effectively conserve its genetic diversity.

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Conservation Biology

Topic: Contributed Papers

Title:

Developing a common garden array to test adaptive genetic variation in priority restoration forb species in the Great Basin of the United States

Author: ***Francis Kilkenny @ USDA Forest Service***

Keywords: common garden,Local adaptation,seed transfer zones,dryland restoration

Abstract:

Seed transfer zones, developed from common garden data, can guide the selection and use o locally adapted plant materials in restoration. However, common garden studies are costly and time consuming. For logistical reasons, study approaches have emphasized either general models of adaptive variation across a species range (genecological studies) or the specific responses of a few seed sources across a range of environments (reciprocal transplant studies). Both axes of information are needed in the era of climate change, which requires flexible and dynamic seed transfer tools. A promising hybrid approach is to use common garden arrays where a large number of seed sources are planted in a set of sites that sufficiently cover the "environmental space" experienced by the study species; generating datasets on both general adaptive patterns and individual source variation in environmental response. Common garden array approaches can also generate economies of scale if technical resources are distributed efficiently and multiple species are tested simultaneously. This talk will describe the development of a common garden array in the Great Basin of the United States, run by a partnership of research groups and land management agencies, to develop high quality data on adaptive variation in multiple forb species. Currently, this array is made up of nine common garden sites covering a wide range of environments. Five priority restoration forb species have been planted and are being monitored, with four additional species in the pipeline. Some preliminary data will be shown.

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Conservation Biology

Topic: Contributed Papers Conservation Biology

Title: Towards the Conservaton of Endangered Trees in Nigeria: IUCN Redlisting and DNA Barcoding Approaches

Author: ***Temitope Onuminya @ University of Lagos***

Keywords: Bioconservation,DNA barcoding,endangered species,IUCN conservation status,Nigerian Trees,TETFUND

Abstract:

Biodiversity loss as a major cause of climate change is one of the greatest threats to sustainability of the environment. This is a growing issue in Nigeria as indigenes depend on resources obtained from the diverse fauna and flora in their environment. The reliance on biodiversity resources have led to its over-exploitation, endangerment and often extinction. Hence, the growing calls for strategies on how to conserve Nigerian trees. Our project aimed to use the ex-situ conservation strategies of DNA banking and barcoding to conserve endangered tree species in Nigeria. Twelve locations comprising 2 locations each from North East, North Central, South-South and 6 locations in South Western Nigeria respectively were visited for sample collection. The plant samples were randomly harvested from statutory forests, non-statutory forests, parks, roadsides, sacred grooves and farmlands. Samples of the plants were collected and processed for further treatment in the herbarium. Non-formal periodic interviews and Focus Group Discussion (FGD) were conducted on the inhabitants and the Park rangers for information about the plant uses and the problems of conservation that are prevalent in the areas. Samples were assessed using the IUCN criteria for category designation and those with high threat status were subjected to DNA Banking and Barcoding using standard procedures. A total of 274 tree samples were collected based on already established IUCN status and recommendations from local forest officials and rangers on the conservation status of species within the regions. Of these, 90 trees were designated as either endangered or vulnerable based on the IUCN criteria for category designation after assessment and these were selected for conservation. The species have a wide range of uses upon which the life of man is closely dependent. The species checklist, specific uses and use categories are presented. It was observed that the categories of the uses of the various plants (food, commercial and medicine) are closely related to their IUCN categorization. Genomic DNA extraction yielded high quality DNA materials which were deposited at the University of Lagos, DNA Bank. Also, amplification and sequencing of the genomic materials yielded DNA Barcodes from 3 gene regions (maturase K, ribulose 1,5-bisphosphate carboxylase large subunit and Internal Transcribed Spacer) which have been deposited in the gene bank for further studies. This project was funded by Tertiary Education Trust Fund, NRF grant (Ref: TETFund/DR&D/CE/NRF/STI/11/VOL 1) Nigeria.

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Conservation Biology

Topic: Contributed Papers

Title: Using Ecological Niche Modeling to better understand Pediomelum aromaticum, a Threatened Utah Plant

Author: ***Ian Eggleston @ Utah Valley University***

Keywords: ecological niche modelling,ENM,pediomelum,aromaticum,Pediomelum aromaticum

Abstract:

Ecological Niche Modeling (ENM) is a very useful technique that gives us insight into species' present and future ranges, habitats, and niches. ENM have applications within conservational biology as models can be used to understand the extent to which climate change may impact a species. Additionally, ENM can be useful for prospecting for and propagation of rare plant species. This project will use ENM to create predictive range models for a rare plant species, Pediomelum aromaticum, with the goal of defining an ecological niche, determining impact of climate change, and conservation of P. aromaticum. To better understand the niche and impacts of climate change of P. aromaticum multiple models will be created and compared using current climate data and predicted future climate data based on different shared socioeconomic pathways.

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Conservation Biology

Topic: Contributed Papers

Title: Patterns of genetic diversity within the endangered worm-vine orchid Vanilla barbellata (Orchidaceae) in south Florida and the West Indies have implications for conservation

Author: ***Ken Cameron @ University of Wisconsin-Madison***

Keywords: _{conservation biology},Florida,GBS,Orchidaceae,population genetics,Orchid

Abstract:

Genomics-based diversity analysis of natural populations is an indispensable tool for enabling informed, advanced, lineage-specific conservation strategies for threatened and endangered species, such as Vanilla barbellata (Orchidaceae). This leafless orchid native to south Florida faces severe environmental threats including rising sea-levels as a result of climate change. A total of 115 individuals from two Floridian populations and three Caribbean populations were sampled. The V. planifolia draft genome was used to identify a filtered set of 12,825 single nucleotide polymorphism (SNP) markers generated via Genotyping-By-Sequencing (GBS). Principal Component Analysis (PCoA) and fastStructure provided resolution of GBS markers confirming distinct populations. Discriminant Principal Components (DAPC), a Neighbor-Joining tree, Diversity statistics and the Fixation Index (Fst) were used to evaluate relationships among and within populations. Floridian populations within the Everglades National Park and the Florida Keys are significantly different and exhibit concerningly low levels of heterozygosity. In contrast, populations of the Guánica State and Susúa State Forests of Puerto Rico have relatively high heterozygosity, but exhibit no discernible gene flow. Finally, the U.S. Virgin Islands population is characterized by an even higher level of heterozygosity, but no gene flow is evident. These results suggest that ex situ conservation of this species is needed because of increased isolation and environmental change and will be best served by targeted collection that captures the greatest level of existing diversity possible.

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Topic: Contributed Papers Conservation Biology

Title: Where are they now? What Happened to the Plants First Proposed for Listing Under the Endangered Species Act?

Author: **Linda Howard @ Arizona State University**

Keywords: endangered species,Endangered Species Act,extinction,IUCN,NatureServe,plant conservation,policy,threatened species

Abstract:

When the Endangered Species Act (ESA) was passed in 1973, the Smithsonian Institute was asked to compile a list of plant species to recommend for protection under the new law. By 1975 they had amassed a list of just under 3,200 plant species from around the country which became the first bulk listing proposal under the ESA. During the subsequent fifty years that the law has been in place, fewer than 1,000 plant species have been listed and only 20 plant species have been de-listed due to recovery, which left me asking what happened to the rest of the species and why weren't they listed?

After tracking the species-level changes in taxonomy, I compiled threat assessments from NatureServe and the IUCN Red List to create a snapshot of endangerment for each species. Once I assembled the threat assessments, I excluded those species that have been listed, de-listed, or are currently under review for listing. Using the remaining species, I combed through the U.S. Fish & Wildlife service notices that are published in the Federal Register to track the justification for not listing each species. I searched in the Federal Register documents from 1980, 1985, 1990, 1993, and 1996 which were the years during which the listing proposal for these species were reviewed.

The taxonomic revisions made since 1975 have reduced the overall number of distinct species from the original list to a little more than 2,700 species and infraspecific taxa. I discovered that just over 20% of those species had been ESA listed during the last fifty years. These 550 species account for nearly 60% of all of the plant species ever listed. Approximately 2,100 species were never listed and threat assessments for those species indicate the highest levels of threat in an additional 54% of the species. The rationale provided by the U.S. Fish & Wildlife Service indicates that insufficient evidence was the primary reason for not listing more than 58% of the unlisted species.

Since 2000 the number of plant species being listed has declined at a time when threats against plants are increasing. The failure to list so many of the species that were first proposed for listing under the Endangered Species Act has resulted in further declines and presumed extinctions. The listing shortfall reveals flaws in the law itself and the listing process and undermines the value of the law for protecting plants. The lack of baseline knowledge of so many species is equally important and should be seen as evidence of the need for enhanced botanical capacity to prevent future extinctions.

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Topic: Contributed Papers

Title: Conservation and systematics of the critically endangered Nipomo Mesa lupine, Lupinus nipomensis

Author: **Gregory Wahlert @**

Keywords: California,Fabaceae,Taxonomy ,conservation,Lupinus

Abstract:

The Nipomo Mesa lupine (Fabaceae; Lupinus nipomensis Eastw.) is a critically endangered annual species endemic to San Luis Obispo County, California. The species has an area of occurrence of less than 6 km2, and yearly estimates of individuals have ranged from ca. 150 to 1,600—an exceedingly small number for an annual species. Nipomo Mesa lupine faces several threats to its survival, including invasive species, herbivory by small mammals and invertebrates, habitat loss and fragmentation, and increasingly variable rainfall and temperature. Because the threats to survival are coupled with a highly restricted distribution and low numbers of individuals, the Nipomo Mesa lupine is at risk of extinction. Ongoing conservation strategies have sought to establish ex-situ populations on adjacent protected lands, to bulk seed for long-term storage, to better characterize the habitat requirements and threats, and to develop a comprehensive conservation and management plan which will inform recovery efforts. Taxonomically, there has been some doubt about the species status of L. nipomensis. In the 1959 California Flora, Munz placed the species in synonymy under Lupinus concinnus, and a note in the current treatment in the Jepson Manual suggests that the species circumscription is somewhat unclear due to introgression with L. concinnus. These lingering taxonomic uncertainties have hindered conservation efforts. Here, we provide morphological and molecular phylogenetic evidence to demonstrate that L. nipomensis is a well circumscribed species evolving as a separate lineage from other closely related annual species, especially L. concinnus.

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Topic: Contributed Papers Conservation Biology

Title: Orchids for Peace

Reconciliation and Sustainable Development of Communities of the Andean-Amazonian Foothills

Author: ***Tatiana Arias @ Marie Selby Botanical Gardens***

Keywords: Colombia,horticulture,Orchidaceae,Orchids,conservation,Caqueta,Green economies,Biotechnology,invitro,circa situm

Abstract:

The 2016 Colombia Peace Agreement ushered in a new era for Colombia with the end of the longest-running conflict in the Americas. This period has faced significant challenges leading to further civil unrest in recent years. Caquetá is one of the most unexplored, diverse, and to this day, one of the most violent regions of Colombia and occupies an important geographical position in terms of diversity. Our research goal is to investigate and conserve orchids and their ecosystems by involving local communities in the creation of in situand ex situ conservation strategies, ultimately offering the communities an alternative mode of subsistence through tourism, cultivation, and legal orchid trade. During the development of this project, we recorded 96 genera and 414 species of orchids, exceeding a previous inventory by 272 species. The documented species diversity in the region could dramatically increase in the next few years with additional collecting efforts in the eastern slope of the Andes nested in Caquetá. About 9% (414/4600) of all Orchidaceae species recorded in Colombia are reported in this area, showing the important role of the Andean-Amazonian foothills and other ecosystems of this region. We have trained 10 local students and over 100 members of different local communities in vegetative and in-vitro reproduction of orchids. Native orchid nurseries have been built for research, propagation, and plant tourism in three municipalities of Caquetá. This research follows the reproductive aspects of orchids with ornamental value and conservation priorities, including seed germination. Orchids brought to our nurseries in Florencia-Caquetá were monitored weekly during 2021 - 2022. Twenty-four orchid genera were recorded, of which 49 species and 157 individuals have been followed. Orchids flowered mostly during the dry season (Nov.-Feb.). Twelve lowland growing species were prioritized for in-vitro reproduction. For this species manual auto-pollination was carried out with a success rate of 66.6% in the formation of fruits. The percentage of seed viability was tested with tetrazolium chloride before in vitro culture indicating 65% of the seeds for all tested species were viable. Although the germination and growing success is high, it has been limited to few species to date and is still being customized for our regional lab. We have developed two tourist interpretive trails near Florencia, Caquetá, field guides for hummingbirds and butterflies, for orchid inventories, and other resources. At least four different civil society reserves have adopted our traditional circa situm orchid breeding and conservation strategies. Next, we will work with former FARC combatants in the Departments of Caquetá and Meta implementing this project in the highlands of the eastern Andean Colombia mountain range.

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Topic: Contributed Papers

Title: Resilient Restoration: Drought Resilience Amongst Southern California Quercus agrifolia Populations on Tribal Lands

Author: ***Alexandra Hoff @ San Diego State University***

Keywords: climate smart restoration,drought tolerance,ecological restoration,native plants,Oaks,population genomics,climate resilient

Abstract:

The Coast Live Oak (Quercus agrifolia) is a keystone species, providing invaluable ecosystem services and cultural significance. With a large distribution throughout coastal California and northern Baja California, this species provides shelter and food sources for many animals, restores and improves watersheds and mycorrhizal activity through its root system. It is also culturally important to many Tribal communities, providing abundant harvests of acorns to their families. Unfortunately, this species is facing decline due to increased vulnerability to pests, disease, intense drought and high temperatures, exacerbated by climate change and increased urban development. As such, Q. agrifolia's resilience in the face of rapidly changing climate is integral to successful conservation and adaptation efforts. We are investigating whether drought tolerance varies amongst and within southern California Q. agrifolia populations, and which are more resilient. To achieve our goals, we collaborated with local tribes, the Climate Science Alliance and UC Riverside as part of the larger conservation project on 'Resilient Restoration'. We sampled Q. agrifolia acorns from eight populations across southern California, including local tribal lands. Within the Q. agrifolia, exist two varieties: Quercus agrifolia var. agrifolia which has more glabrous leaves and tends to be distributed closer to the coast, and Q. agrifolia var. oxyadenia which has more tomentose leaves and a more southern, inland distribution, potentially serving as an adaptation to prevent water loss. We predicted that trees from within the distribution of Q. agrifolia var. oxyadenia, where there is a hotter, drier climate, will be more resilient to climate change induced stressors such as drought and heat.

To assess the drought tolerance of the eight populations we have conducted a greenhouse experiment and are conducting genomic analysis. In the greenhouse experiment, half of each population were subjected to severe drought conditions, while the rest received a normal watering schedule. Throughout the greenhouse drought experiment, we measured several drought tolerance indicators such as germination, mortality, height, and stomatal conductance. The measurements of these indicators were compared among populations using an ANOVA test. Our results showed statistically significant differences in mortality and height among populations. With some populations having high levels of mortality. The four most southern populations (within the Q. agrifolia var. oxyadenia distribution) did have the lowest mortality rates of the eight sampled. After the drought experiment, resilient trees identified are being rematriated to the Tribal reservations for planting.

In our genomic analysis, we are currently investigating genetic diversity, based on SNP markers, within and between populations, as a potential additional measure of resilience. We expect populations and families with higher heterozygosity to be more resilient to drought. These findings, along with traditional ecological knowledge and cultural practices, will be used to inform conservation efforts on the tribal lands these oaks came from.

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Topic: Contributed Papers Conservation Biology

Title: DNA metabarcoding for accurately censusing natural populations of the endangered Gentner's Fritillary

Author: ***Aaron Liston @ Oregon State University***

Keywords: Chloroplast genome,endangered species,Fritillaria,genome skimming,plastomes,DNA Metabarcoding,Liliaceae,Illumina sequencing

Abstract:

Fritillaria gentneri (Liliaceae) is a U.S. Endangered species endemic to a portion of the Rogue and Klamath River watersheds of southwestern Oregon and adjacent California. Individuals of F. gentneri are predominantly triploid with low fertility, and it has been hypothesized to be a hybrid species originating from diploid individuals of F. affinis and F. recurva. These three Fritillaria species grow in mixed populations and are indistinguishable when not flowering. Furthermore, only 1-3% of individuals flower each year. Since the identity of most plants in a population is uncertain, efforts to accurately model demographic trends and predict the future viability of F. gentneri populations have been hindered. To address this obstacle, we set out to develop a high-throughput DNA metabarcoding assay for the species identification of vegetative samples. Using genome skimming, we assembled complete plastid genomes from ca. 10 billion base pairs of sequence (0.2-0.3X haploid genome coverage) from each of 24 individuals from 11 populations. The plastomes of F. gentneri and F. recurva are very similar, differing at 0-3 SNPs and 0-21 indels per population. Despite the low sequence divergence, candidate diagnostic polymorphisms were identified in 10 of the 11 populations. Among population plastome diversity was high, with most diagnostic SNPs unique to each population. Phylogenetic analysis resolved at least 5 independent origins of F. gentneri.
In a pilot study for species identification, leaf tissue was sampled from 38-40 non-flowering plants in each of five transects from one population and from 52 non-flowering individuals in a 1-meter radius surrounding a flowering individual of F. gentneri. Equimolar pools were created for each transect and a 250 bp plastid locus containing SNPs for each species was PCR-amplified and sequenced on an Illumina MiSeq. Results showed heterogeneity in the proportion of the 3 species from each transect; the radius plants were all F. gentneri.
With this diagnostic assay, accurate estimates of F. gentneri population size can now be made, facilitating the conservation, management, and recovery of this endangered species.

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Topic: Contributed Papers

Title: A comprehensive methodological guide for seed conservation of orchids

Author: ***Namrata Pradhan @ Xian Jiaotong Liverpool University***

Keywords: orchid seeds,seed banking,seed viability test,seed conservation,seed storage,dust seeds,orchid conservation,asymbiotic germination test,symbiotic germination test,orchid seed conservation guide

Abstract:

Seed conservation or seed banking of orchids is challenging because orchids have (1) minute seeds (dust seeds) that require specialized equipment and expertise to investigate, (2) complex reproductive biology that depend on specific pollinators, a non-typical seed germination process and association with mycorrhizal fungi for survival and growth, (3) species-specific seed storage behaviour, and (4) slow germination requiring long time and efficient tests for measuring the effectiveness of seed banking. Since seed banking has been established as an important tool for protecting orchids, a comprehensive, well-developed, and accessible orchid seed conservation guide that practitioners can follow prior to-, during- and post-seed conservation is much needed. Currently, standards followed by many seed banks for processing seeds are mostly based on theories and practical experience derived from studies and efforts on crops, which may not be applicable to other highly specialized, native and wild plant species such as orchids that urgently need efficient conservation planning. Here, with the aim of supporting orchid conservation, a comprehensive methodological guide with step-by-step protocols, identifying the challenges and potential solutions in each step, was developed by searching literature on established protocols used in different stages of orchid seed conservation, communication with experts in the field, and hands-on research experience in orchid seed conservation. Six successive stages were identified as important for effective, efficient, and comprehensive approach to orchid seed conservation: stage 1 - protocols to follow and procedures to adhere to during seed and data collection of orchids in the field; stage 2 - preliminary experimental assessment of the seeds in the laboratory after seed collection such as seed sterilization, extraction, moisture content assessment and dehydration; stage 3, 4 and 5 - seed viability assessment, symbiotic and asymbiotic germination assessments, respectively; and stage 6 - seed banking of orchids. This comprehensive methodological guide with the seed conservation protocols, the importance of each stage, the challenges involved and some potential solutions to those challenges provides a clearly defined stepwise roadmap to follow and prepare for prior to embarking on orchid seed conservation. This guide on orchid seed conservation can fulfill a vital need for comprehensive knowledge supporting orchid seed conservation planning, seed collection and processing, preparation for storage, storage, and pre- and post-storage testing. If used cautiously, by considering the high species-specificity in orchids, site specific conditions, local people's needs and customs, local, regional and country specific policy and legal frameworks, this seed conservation guide can contribute to stemming biodiversity loss, reversing ecosystem degradation and supporting the current Global Biodiversity Framework, which was agreed upon in Montreal at the Conference of the Parties (COP15) in December 2022.

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Conservation Biology

Topic: Contributed Papers Conservation Biology

Title:
Quantifying Research Effort for California's Flora: Evidence of bias against rare plants in literature and sequence data

Author: ***Kieran Althaus @ University of Chicago***

Keywords: rare plants,taxonomic bias,research effort,California flora

Abstract:

Without adequate data, the conservation and management of rare species can become unwieldly and increasingly expensive. Taxonomic bias, or taxonomically driven disparities in knowledge, can further make the job of conservation difficult. Here, we ask: Is there a bias in the amount of research effort given to rare species in California compared to non-rare natives and non-native species? To answer this question, we quantified the amount of literature available on Google Scholar and the number of sequences deposited in GenBank for California's rare plants, weeds, and non-rare natives. To account for the differences in species extent, we aggregated occurrence data for each species from GBIF to determine approximate ranges. We compared the amount of research published and sequences available amongst various rare plant ranks, non-native and non-rare native plants in California. Rare species were severely under-represented compared to non-rare natives and non-natives in literature and sequences, even after accounting for the differences in species extent. Furthermore, the more threatened the species is, the fewer pieces of both literature and sequence data were found. This research is important in understanding the research effort that has been distributed to plants of different kinds in California. Our results suggest that there is a lack of research on rare plants, making important conservation decisions and predictions related to climate change difficult.

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Crops and Wild Relatives

Topic: Contributed Papers Crops and Wild Relatives

Title:
The genomic origin of cultivated vanilla

Author: ***Paige Ellestad @ Boise State University***

Keywords: comparative genomics,domestication,hybrid,Orchidaceae,whole genome sequencing,plant genetic resources

Abstract:

Although the vanilla spice is so well-known, there is an unexpected lack of knowledge on the domestication processes that have shaped its genetic resources. Within the main vanilla producing plant species, Vanilla planifolia, which has a long history of cultivation primarily through vegetative cuttings, unexpected high levels of genome-wide heterozygosity have been found in the global "Daphna" cultivar and in accessions cultivated in Mexico, its center of origin. These findings have pointed to a hybrid origin within the crop; however, the source and quantity of hybridization events remained unclear. This study aimed to disentangle these events by identifying parental candidate species and investigating the domestication processes underlying its hybrid origin. The less commonly cultivated species, V. pompona, was identified as a likely parental candidate and hypothesized to have hybridized with V. planifolia causing the high levels of genome-wide heterozygosity observed within cultivated individuals. Chromosomal structure and SNP distributions were compared between a V. planifolia "Daphna" cultivar, 15 V. planifolia accessions from Mexico, and one V. pompona accession to answer the questions: 1) do both haplotypes of the "Daphna" genome show signatures of hybridization with V. pompona?, 2) do the highly heterozygous Mexican V. planifolia accessions exhibit the same hybridization signatures as the "Daphna" genome?, and 3) do the latter accessions show signatures of one or multiple domestication events? Results provided evidence for multiple genomic origins within cultivated V. planifolia and revealed more variation than previously recognized. At least two distinct hybridization events were shown to have occurred: one showing signatures of introgressive hybridization between V. planifolia and V. pompona in the "Daphna" cultivar, and at least one more in Mexican cultivars. This parental origin, however, has yet to be identified. Additional research incorporating genomic data from other crop-wild relatives is necessary to further disentangle these events observed in Mexico. Findings from this study offer a clearer illustration of vanilla's evolutionary history and genetic resources, highlight their importance for crop sustainability, and provide foundations for future research into the origin of this important spice.

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Crops and Wild Relatives

Topic: Contributed Papers

Title:
Early leaf shape variation in Brassica oleracea morphotypes and their wild relatives

Author: ***Makenzie Mabry @ University of Florida***

Keywords: Brassica,Machine Learning,morphometric analyses

Abstract:

Brassica oleracea is renowned for its diverse cultivars, such as broccoli, Brussels sprouts, cabbage, cauliflower, kale, and kohlrabi. However, distinguishing between these cultivars and their wild relatives during early growth stages is challenging. To address this issue, we aimed to investigate whether the variation present in B. oleracea can be detected from young leaves using traditional leaf descriptors and morphometric methods, including Elliptic Fourier Descriptors (EFDs). Our study revealed that there is indeed variation among the cultivars of B. oleracea and its wild relatives. However, clustering analysis using linear discriminant analyses (LDA) and machine learning confirmed the difficulty in classifying these species during early growth stages due to their similar morphological features. These findings have significant implications for the classification and breeding of B. oleracea and its wild relatives and could facilitate the development of new cultivars with improved traits.

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Crops and Wild Relatives

Topic: Contributed Papers

Title:
Chromosome-level and phased diploid genome assembly of the Andean tuber crop Ullucus tuberosus (Basellaceae: Caryophyllales)

Author: ***Romulo Segovia @ University of British Columbia***

Keywords: Crop Wild Relative,Ullucus tuberosus,Olluco,Basellaceae,Andean tuber crop,Phased genome assembly

Abstract:

The Andes are the domestication center of many important and minor crops. The list of Andean crops with available high-quality genome assemblies is biased towards crops with worldwide distribution, neglecting those cultivated locally that have significant agricultural and cultural value. After potato, olluco (Ullucus tuberosus, Basellaceae; 2n = 2x = 24) is the second most cultivated tuber crop in the Central Andes. Here we report phased diploid genome assemblies at a chromosomal scale. We assembled the haplomes (utub_hap1 and utub_hap2) from PacBio HiFi and chromosome conformation capture (Hi-C) reads into 24 chromosomes; the haplomes are 442 Mbp in size with 35.5 Mbp N50 (for utub_hap1), and 439 Mbp in size with 36.5 Mbp N50 (for utub_hap2). BUSCO results indicate 98.7% and 98% completeness for utub_hap1 and utub_hap2, respectively. We identified Arabidopsis-type telomeric repeats (TTTAGGG) at 40 chromosomal ends out of the 48. Repetitive element annotation reveals that 56.50% and 57.05% of utub_hap1 and utub_hap2 are repetitive, featuring Copia retrotransposons as the most abundant type (12.84% and 12.49%), and also supporting the presence of Helitron transposons (2.78% and 2.97%). Annotation of protein-coding genes based on protein similarity and RNA evidence predicts 28,913 genes and 30,584 transcripts in utub_hap1, and 28,852 genes and 30,696 transcripts in utub_hap2, a difference of only 61 genes between the haplomes. The assemblies will be used to facilitate ongoing research on mutational load, and to study the comparative and evolutionary trajectory of the species and a crop wild relative.

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Development and Structure

Topic: Contributed Papers Development and Structure

Title: COMPARATIVE MORPHOANATOMY OF THE FLOWER-TO-FRUIT TRANSITION IN ANDEAN LORANTHACEAE JUSS.

Author: ***Valentina Botero Castaño @ Universidad de Antioquia***

Keywords: endosperm,polycotyledonar embryo,viscin,inferus ovary

Abstract:

Loranthaceae Juss. (Santalales) is a widespread family of root and stem hemiparasitic plants with a staggering diversity in floral morphology, especially in the Neotropics. The family has species that range in floral size from small (a few millimeters long, pollinated by insects), to medium (3-5 cm long, pollinated by insects) to large (over 10 cm, pollinated by birds). The family exhibit atypical features, including a modified calyx, an extreme ovule reduction lacking integuments and a properly formed nucellus, an unusual development of the embryo sac into a placental-ovular complex called the mamelon, the embryo sac migration to the style and stigma, ectopic fertilization, and the repositioning of the proembryo(s) to the ovarian region. Fruits, traditionally described as berries, develop from inferior ovaries that are fused to the hypanthium, hereafter called dispersal units. Each unit contains viscin, a substance that facilitates dispersal and adhesion to the host plant prior to the formation of haustoria. Perhaps one of the most peculiar features described in the genus Psittacanthus is the occurrence of embryo dimorphism, with embryos forming two leafy laminar cotyledons, or 5-12 massive and prismatic cotyledons. Finally the absence of endosperm has also been described for both Aetanthus and Psittacanthus.

This work revisits the interpretations and assesses the homology of these unusual features, by undertaking a comparative developmental approach. Samples of Aetanthus colombianus A.C. Sm., Gaiadendron punctatum (Ruiz & Pav.) G. Don., Passovia pedunculata (Jacq.) Kuijt., Psittacanthus longerectus Roldan-Palacios & Alzate-Guarín, and Tristerix secundus (Benth.) Kuijt. were collected and fixed in 70% EtOH. Flowers to preanthesis to late anthesis and developing fruits were dehydrated in a series of absolute ethanol, followed by Ethanol-Histochoice (50-50%), ending in Paraplast Plus. Specimens were serially sectioned at 10 µm with a Leica rotary microtome, stained with safranin-astra-blue, and mounted in Entellan. Slides were observed in a Leica DM500 bright field microscope and photographed with a Leica ICC50W camera.

Our results indicate that: 1) The limits of the carpellary tissue remain detectable during ontogeny while the ovules are extremely reduced, 2) The epicarp (extracarpellary tissue) in all species undergoes profound tissue modifications forming the fleshy portion of the dispersal unit and the viscin; 3) There is a fully formed endosperm accompanying embryo development in Aetanthus and Psittacanthus. This project lays the morphoanatomical foundations necessary to carry out evo-devo studies to identify the genes responsible for such modifications and for the occurrence of successful fertilization in the absence of normal ovules.

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Development and Structure

Topic: Contributed Papers

Title: Genetics and development of nectaries in Cleomaceae

Author: ***Jocelyn Hall @ University of Alberta***

Keywords: Brassicales,Evo-Devo,Nectaries

Abstract:

Nectaries are fascinating as they display a wide range of morphologies and placement across angiosperms only unified by function of exuding nectar. Cleomaceae represents an ideal group to investigate the developmental and genetic bases of floral nectaries. The family houses considerable nectary diversity, including size, placement, and morphology. Developmental and anatomical studies reveal that the nectaries range from structured protrusions or concavities to inconspicuous and challenging to discern from the receptacle. Regardless of the diversity in form, nectaries share nectarostomata as the mechanism of nectar secretion in all species examined. Transcriptomic analyses and functional studies of Cleome violacea, a species with a conspicuous nectary, demonstrate some conservation in the genetic pathway in nectary formation with Arabidopsis thaliana and other core Eudicots. Specifically, CRABS CLAW, redundantly with AGAMOUS and SHATTERPROOF, is required for nectary initiation. Combined these data shed light on the extent and intricacies of nectary development flowering plants.

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Development and Structure

Topic: Contributed Papers

Title: How teff (Eragrostis tef) lets go of its fruits

Author: ***Elizabeth Kellogg @ Donald Danforth Plant Science Center***

Keywords: cell walls,programmed cell death,RNA-Seq,teff,abscission,shattering,Transmission electron microscopy

Abstract:

Eragrostis tef (teff) is a crop native to Ethiopia that is becoming increasingly planted worldwide because of its nutritious grain and drought tolerance. Most cultivated cereals retain their grains on the plant until harvest, i.e., the floral parts do not abscise, or shatter. In contrast, the grains in teff do abscise and are only retained on the plant because the surrounding floral bracts (lemmas and paleas) hold them in place. This mechanism is distinct from the shattering process in nearly all other grasses. In this study, we investigated the morphology, anatomy, cell structure, and gene regulation of the abscission zone in teff. The abscission zone (AZ) of tef is a slender, non-lignified stipe below the caryopsis whose morphology is shared among many other species of Eragrostis including E. pilosa. Cell walls in the AZ are thin and fracture at maturity, unlike the walls in the AZ of most other grasses, which separate at maturity, as shown by X-ray microscopy, scanning electron microscopy, transmission electron microscopy, and immunolocalization of cell wall components. The cells themselves die. Genes involved in cell wall modification and programmed cell death are upregulated in the AZ near seed maturity, as shown by RNA-seq, consistent with our cell-level observations. The lemma in the domesticated E. tef is thicker than that in E. pilosa, possibly explaining why the grains are clasped more tightly. Because shattering in many cereals is regulated in part by the YABBY transcription factor SHATTERING1 (SH1), we used CRISPR-Cas9 technology to disrupt it in E. tef. Shattering was normal in the mutant, indicating that SH1 is not involved in AZ regulation. Together these results point to a previously undescribed mechanism of abscission in E. tef, identify genes that may be involved in its regulation, and note genes that may be targeted for crop improvement.

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Development and Structure

Topic: Contributed Papers Development and Structure

Title: Assessment of the flowering genetic regulatory network in tropical orchids with different lifeforms

Author: ***Yesenia Madrigal @ Universidad de Antioquia***

Keywords: EvoDevo,Meristem development,Orchidaceae,RNAseq,Flowering transition

Abstract:

The reproductive transition in angiosperms includes morphological changes when a vegetative shoot apical meristem (VM) forming leaves, becomes an inflorescence meristem (IM) that forms bracts and flowers. This process is controlled in monocots, like Oryza sativa, by a Genetic Regulatory Network (GRN) that includes promoters like Heading date 3a (Hd3a) (FLOWERING LOCUS T-FT), Heading date 1 (Hd1) (CONSTANS-CO), FLOWERING LOCUS D (OsFD1) and 14–3–3 proteins that activate floral meristem identity genes. Repressors involved in the maintenance of the vegetative phases include TERMINAL FLOWER LOCUS 1 (TFL1) and OsMADS55 (AGAMOUS Like24/SHORT VEGETATIVE PHASE). Additionally, FLOWERING LOCUS C (FLC) and VERNALIZATION 2 (VRN2) are important in Poales species that respond to cold. Although flowering mechanisms have been studied in detail in monocot model species, little is known about how the same process occurs in orchids with different habits colonizing different niches. Terrestrial and epiphytic orchids vary in meristem hierarchies and the development of storage organs. We performed a comprehensive analysis of the morpho-anatomical changes from VM to IM in the terrestrial orchid Epidendrum fimbriatum with nearly continuous flowering all year long in cloud Andean forests. Using the landmarks for reproductive transition we performed comparative transcriptomic analyses in VM versus IM. We used a differential expression gene approach between those stages, and we found 40 DEGs between VM and IM involved in reproductive transition. Furthermore, we used a targeted search to isolate more than 30 orthologs from the canonical flowering GRN in parallel to the DEGs. In addition, we corroborated the results from our RNAseq data with spatio-temporal expression analyses using in situ hybridization and by protein-protein interaction studies using yeast two hybrid experiments. We are currently comparing these results with experiments performed in orchids with seasonal flowering, including Cattleya trianae, an orchid with storage organs and epiphytic habit, and Elleanthus aurantiacus with terrestrial habit and lacking storage organs. Our results allow us to re-evaluate the flowering GRN in orchids when compared to the model species O. sativa and other Poaceae. In general we have found evidence for: 1) high duplication rates for flowering integrators in orchids but a low percentage of homologs transcriptionally active; 2) the retention of canonical flowering integrators, at the expense of low expression, the loss of key protein interactions and possibly pseudogenization of some homologs; and 3) changes in the transcriptomic profiles in different orchids according to their habits.

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Development and Structure

Topic: Contributed Papers

Title: Virus induced over expression (VOX) in a ranunculid supports a novel role for a MIXTA-like ortholog in stigmatic papillae

Author: ***Veronica Di Stilio @ University of Washington, Seattle (WA)***

Keywords: polyploidy,Ranunculaceae,Thalictrum,trichomes,VIGS,WGD,wind pollination,VOX,Ranunculid,stigmatic papillae

Abstract:

The MYB family of transcription factors one of largest in plants of genes playing key roles in regulatory processes during plant development. One of these genes is MIXTA/MIXTA-like, known to modulate the differentiation of distinct cell identities in the epidermis of land plants. We had previously investigated the evolutionary history and function of the MIXTA-like gene family in the ranunculid Thalictrum, a representative of early-diverging eudicots, and found a lineage-specific duplication coinciding with a Whole Genome Duplication (WGD) in one large clade within the genus. We then functionally characterized a MIXTA-like ortholog from the diploid species T. thalictroides (TthMYBML2) via targeted virus induced gene silencing (VIGS) in leaves, finding a role a trichomes. Here, we add experiments in floral tissue and report for the first time the successful use of virus induced overexpression (VOX) to support a novel role for Thalictrum MIXTA-like in stigmatic papillae. Overexpression assays in a heterologous system (tobacco) provided further evidence for the leaf trichome function, while supporting the novel role in the promotion of stigmatic papillae elongation. The latter finding, combined with the high differential expression of specific paralogs in carpels of wind-pollinated polyploid Thalictrum suggests that MIXTA-like duplications likely contributed to the development of long stigmatic papillae in feathery stigmas during the evolutionary transition from insect to wind pollination.

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Development and Structure

Topic: Contributed Papers

Title: To Fuse or not to Fuse: Investigating the Evolution and Development of Floral Fusion in the Zingiberales

Author: ***Heather Phillips @ Cornell University***

Keywords: CUC1/2 genes,Development,Evolution,Floral Development,NAM/CUC3,Ontogeny,organ fusion,NAM

Abstract:

Throughout the evolution of the angiosperm flower, developmental innovations have enabled the modification or elaboration of novel floral organs enabling subsequent diversification and expansion into new niches, for example the formation of novel pollinator relationships. One such developmental innovation is the fusion of various floral organs to form complex structures. Multiple types of floral fusion exist; each type may be the result of different developmental processes and has likely evolved multiple times independently across the angiosperm tree of life. The development of fused organs is thought to be mediated by the NAM/CUC3 subfamily of NAC transcription factors, which mediate boundary formation during meristematic development. During this talk, I will show how I am utilizing the Zingiberales as a model lineage for investigating floral fusion, including my progress in (1) outlining the evolution of candidate fusion genes in this order and (2) characterizing fusion gene expression in Musa acuminata.

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Development and Structure

Topic: Contributed Papers Development and Structure

Title: Candidate genes underlying nectary development in banana and asparagus

Author: ***Irene Liao @ University of California, Los Angeles***

Keywords: candidate genes,comparative transcriptomics,Floral Development,monocot,nectary,single cell sequencing

Abstract:

Nectary function is central to many important ecological interactions. Across flowering plants, nectaries are diverse in positional location and morphology, yet few have used genomic approaches to better understand how diverse nectaries develop. Monocot flowers usually form septal nectaries, which are found on the margins between the three fused carpels that comprise the gynoecium. While key transcription factors underlying nectary development in eudictos have been characterized, the genetic basis of nectary development in monocots is virtually unknown. As a first step to identify candidate genes involved in monocot nectary development, we are using single nuclei RNA sequencing. We isolated and sequenced banana (Musa “Ice Cream”) nuclei from two sets of tissues—one region that is enriched in nectary cells found at the top of gynoecium (the “nectary”) and the other that primarily lacks nectary cells found at the base of the gynoecium (the “base”). We compare results from banana with nuclei sequences from asparagus (Asparagus officinalis) to determine whether putative nectary cell clusters from both species share a common core set of genes for nectary development. Results from this study will form the foundation for understanding nectary origins and losses in monocots and more broadly across flowering plants.

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Development and Structure

Topic: Contributed Papers

Title: The alteration to vegetative growth and gene expression supports the use of a novel aerial bulbil in Mimulus gemmiparus for reproduction

Author: ***Deannah Neupert @ Miami University***

Keywords: Mimulus,differential gene expression,Evo-Devo,Function-valued traits,Scanning electron microscopy (SEM),Structural novelty

Abstract:

The development of structural novelty is difficult to study, as novelty is ancient and lacks transitional forms. Mimulus gemmiparus, or Erythranthe gemmipara, reproduces almost entirely with a novel and asexual aerial bulbil. Within Mimulus, supernumerary axillary meristems are deposited in the leaf axils, where the leaf intersects the stem. For M. guttatus (E. guttata), M. floribundus (E. floribunda), and M. gemmiparus (E. gemmipara), the primary axillary meristem usually varies between becoming a branch or a flower. In M. guttatus and M. floribundus, the secondary axillary meristem may branch or flower (or remain quiescent) while in M. gemmiparus, the secondary axillary meristem typically expands into a vegetative propagule, which then arrests and is ensheathed by the subtending leaf petiole, resulting in a novel aerial bulbil that shares homology with both branches and leaves. To visualize the evolutionary divergence of whole plant and axillary meristem development in M. gemmiparus, I compared the growth of M. gemmiparus to two sympatric sister taxa, M. guttatus and M. floribundus. Throughout ontogeny, I measured height and node development to model the growth of the plants using a Function-Valued Trait (FVT) approach to determine how plant development has been modified to accommodate the novel reproductive structure in M. gemmiparus. Additionally, I imaged the development of axillary meristems over time within each species using scanning electron microscopy to create a cross-species comparative developmental series capturing axillary meristem fate and outgrowth. Pairing the results from the FVT modeling and developmental timeseries, we find that M. gemmiparus has a faster nodal development when compared to M. guttatus and M. floribundus. Therefore, showing that in M. gemmiparus, growth rates of axillary meristems have been increased to support growth of a novel reproductive structure, formed from modified leaves and meristems that, in related species, would be used to form branches. Additionally, I sampled homologous nodes between all three species to perform a comparative evolutionary analysis to determine the genes that are differentially expressed and responsible for the modifications to existing structures to evolve the novel structure in M. gemmiparus.

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Development and Structure

Topic: Contributed Papers

Title: A Morphological and Phylogenetic Comparative approach to investigating Branching Architecture Evolution in Monocots

Author: ***Jesus Martinez-Gomez @ University of California Berkeley***

Keywords: morphology,Architecture,Development,Inflorescence,Phylogenetic comparative methods,phylogenetics,evolution of development

Abstract:

The inflorescence is a specialized reproductive branch that dictates flower positions, necessary for effective pollination. Over evolutionary time, changes in branching patterns have led to the evolution of highly diverse inflorescence architecture. This work investigates the developmental and evolutionary origin of inflorescence branching architecture in monocots focusing on umbels, a type of branching architecture where all flowers appear to arise from a single point. Using comparative developmental morphology and anatomy we find that umbel homoplasy is underlained by at least three case convergent architectures that produce an umbellate phenotype. Of those, there are three cases of parallel evolution. This highlights the liability of achieving this unique inflorescence form. Given that umbellate structures have evolved via distinct mechanisms, wetest if umbellate inflorescences conferred an adaptive advantage in those lineages. To do so, data was collected on inflorescence structure in all major lineages of monocots, including fossils, totaling more than 2500 species. A statistical phylogenetic framework was utilized to infer ancestral states in the monocots and test if umbels are correlated with shifts in diversification, with respect to all other inflorescence morphologies. However the models in the aforementioned approach are based largely on models of nucleotide substitution for discrete states. To achieve a more realistic understanding of branching architecture evolution by incorporating morphospaces into comparative analyses. This was done by “rescoring” inflorescence states using a published inflorescence morphospace in conjunction with the threshold model, a more biologically realistic model. A series of simulations were performed using a new multivariate implementation of the threshold model and found that it is sufficiently accurate in ancestral state inference. Then, this model was used to test a 200-year-old conjecture on the origin of the monocot umbel found in the Amaryllis family (Amaryllidaceae). Overall, this research produced a framework that can broadly be applied to the study of other organisms in order to explore more mechanistic-based explanations for how macroevolution took place.

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Development and Structure

Topic: Contributed Papers

Title: Development and evolution of self-organizing pigmentation patterns in monkeyflowers

Author: ***Yaowu Yuan @***

Keywords: monkeyflower,Anthocyanin,pigmentation,reaction-diffusion,self-organizing,prepattern

Abstract:

Many organisms exhibit visually striking spotted or striped pigmentation patterns. The classical reaction-diffusion model predicts that such spatial patterns can form when a local autocatalytic feedback loop and a long-range inhibitory feedback loop interact. At its simplest, this self-organizing network only requires one self-activating activator that also activates a repressor, which inhibits the activator and diffuses to neighboring cells. However, we still know very little about the actual genes encoding the hypothetical activators and repressors underlying pigmentation systems, even less about the biophysical properties of these molecules, and virtually nothing about how modulation of the properties of these activators and inhibitors affects pattern evolution in nature. Through genetic analysis, transgenic experiments, and mathematical modeling, we have previously identified a pair of MYB proteins that constitute an activator-inhibitor, reaction-diffusion system underlying the formation of dispersed anthocyanin spots in monkeyflower petals. Here I present our most recent work on the genetic and developmental bases of pigment pattern evolution from dispersed spots to longitudinal stripes among species, through modulation of the prepattern of the R2R3-MYB activator and the biophysical properties of the R3-MYB inhibitor as well as two additional co-activators.

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Development and Structure

Topic: Contributed Papers Development and Structure

Title: Beyond lobed: molecular phylogeny and evolution of development of stem anatomies in the small genus Urvillea (Paullinieae, Sapindaceae)

Author: ***Israel Cunha Neto @ Cornell University***

Keywords: Anatomy,Ancestral state reconstruction,climbing plants,Evolution,phylogeny,vascular tissues

Abstract:

In seed plants, the procambium and cambium generates a cylinder of wood surrounded by a sheath of secondary phloem. However, independently, in numerous lineages, this conserved developmental pathway was altered to generate “vascular variants” i.e., a dramatic alternation to the location and distribution of xylem and phloem in stems. Paullinieae (Sapindaceae), a tribe of 6 genera of woody vines (lianas), contains the most diversity of vascular variants across plants. Although the evolution of vascular variants has been investigated in the large genus Paullinia, little is known about diversity housed in the small genus Urvillea (~18 species). This group stands out by having a diversity of growth forms including woody climbers (lianas) and even hemicryptophyte/rhizomatous species. In this talk, we focus on the evolution of development of stem ontogenies in Urvillea, investigated by using the first molecular phylogeny of the group, coupled with classical developmental anatomy, and Laser Ablation Tomography (LAT). We found that Urvillea have five stem developmental pathways: (1) regular ontogeny and (2) four variant ontogenies, which include (a) phloem wedges, (b) fissured stems, (c) lobed stems, and (d) successive cambia. We mapped these five ontogenies (regular and variants) in our molecular phylogeny and found that regular stem is ancestrally reconstructed in the genus. Lobed stems evolved in deep nodes, prior to the diversification of the three main clades of the genus. Phloem wedges and fissured stems evolved from lobed stems each once within the same clade. There is one reversal to regular stem in a second clade, which led to the evolution of successive cambia. A third clade comprises only lobed stems. Our findings illustrate that (1) there is an enormous developmental plasticity in vascular development in Urvillea and (2) vascular variants in the genus are developmentally similar to those found in closely related lineages, therefore, suggesting evidence towards repeated evolution of complex anatomies within Paullinieae lianas.

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Development and Structure

Topic: Contributed Papers

Title: A New Anatomical Examination of the Fern Onoclea sensibilis

Author: ***Jim Seago @ SUNY at Oswego***

Keywords:

Abstract:

A New Anatomical Examination of Onoclea sensibilis.

Most surprisingly, the anatomy of organs of the fern Onoclea sensibilis has been sparsely described over the centuries. Studied since 2016 from an often wet setting along a driveway, roots typically have a diarch or monarch stele with an endodermis of Casparian bands which are not revealed by all staining and microscopic methods; cortex cells are thin-walled, and the epidermis usually has root hairs in old roots. Rhizomes are typically dictyostelic and each of the six meristeles is surrounded by a distinct endodermis with Casparian bands; pith and most cortex cells are thin-walled, but hypodermis usually has sclerenchymatous cells and epidermis has a thick cuticle. Meristeles have bundles of xylem with phloem primarily located in two zones internal and external to the xylem. Near their connection to rhizomes, the upright megaphylls have at their bases two meristeles with primary xylem and phloem, and each meristele is surrounded by a distinct endodermis. The meristeles unite in the petiole to form a truncated V-shaped stele with phloem patches spaced around the xylem, surrounded by one endodermis, that then dichotomize just prior to entering blades with each meristele then vein surrounded by endodermis. Petioles usually have a prominent, multi-layered sclerenchymatous hypodermis.

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Development and Structure

Topic: Contributed Papers

Title: Micrometers of variation: Pollen morphology of a Castilleja species complex

Author: ***Magdalene Lo @ California Academy of Sciences***

Keywords: Lamiales,Scanning electron microscopy (SEM),Castilleja,pollen morphology,pollen preparation

Abstract:

Castilleja (the “paintbrushes”) is a genus of over 200 species of American wildflower whose systematics has been an ongoing challenge. Because of their hybridization potential and taxonomic difficulties, including species descriptions with overlapping qualitative and quantitative traits, many species are challenging to identify in the field and from preserved specimens. Morphology has largely driven species delimitation in Castilleja, including seed coat characteristics; however, pollen morphology, an important trait associated with pollination biology in angiosperms, has not been examined in the group. Pollen morphology has been used in the characterization of higher- and lower-order taxa, and pollen surface structure is potentially related to pollination syndromes, dispersal methods, and pollen-stigma interactions, which may affect reproductive potential. In this study, light and scanning electron microscopy of pollen from a species complex native to the California coast were used to describe their morphology, assess whether pollen morphology varies according to current taxonomy, and determine whether pollen morphology can be used to inform species boundaries in Castilleja.

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Development and Structure

Topic: Contributed Papers

Title: Evolution of the phloem genetic toolkit in plants

Author: ***Rafael Cruz @ University of Edinburgh***

Keywords: NAC gene family,Evo-Devo,Gene evolution,MYB transcription factors,Phloem,Vascular Plants,vascular tissues,Tracheophytes

Abstract:

Vascular tissues, xylem and phloem, are defining features of vascular plants and are predicted to have been key innovations during land plant evolution. However, it is unclear when the genetic toolkits of these tissues evolved especially the phloem. More data about the structural development and gene expression in seed-free plants will help us characterise the origin of the phloem genetic toolkit and test the homology between different food-conduction cells, including phloem sieve elements in different tracheophytes.

Some key proteins are described to regulate different stages of development of the phloem in Arabidopsis. The membrane protein OCTOPUS (OPS) is present in procambial cells that give rise to sieve elements, although the mechanism by which it acts is unknown. The transcription factor ALTERED PHLOEM DEVELOPMENT (APL) is expressed in protophloem poles and upregulates NAC45 and NAC86, which trigger the dissolution of nuclei and cytoplasmic organelles in sieve elements. These three groups of genes are major upstream regulators of the sieve cell development in angiosperms. The activity of orthologues of these proteins in other groups of plants is largely unknown, especially in seed-free plants. If they are present and expressed similarly in angiosperms and lycophytes, this would indicate that this is the genetic tool kit used by the common ancestor of tracheophytes during the development of their phloem. Moreover, the presence of these genes in bryophytes would shed light on the question of the homology of food-conducting tissues present in all land plants.

We investigated the evolution of homologs of OPS, APL, and NAC45/86 in land plants. To do this, we searched for homologs in genomes and transcriptomes, with a good representation of the phylogenetic diversity of tracheophytes and bryophytes. Phylogenetic trees were obtained from aligned nucleotide sequences partitioned by codon position, through the maximum likelihood method. The orthologues of these proteins are present in all major lineages of tracheophytes, revealing that they were likely to be present in their common ancestor.

Currently, we are working on RNA in-situ hybridization experiments in the model lycophytes Selaginella moellendorffii to detect if it is expressed in comparable cell types and stages considering what is known for Arabidopsis.

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Development and Structure

Topic: Contributed Papers Development and Structure

Title: Interspecific variation in the resting bud morphologies of Juglandoideae—a winter's tale?

Author: ***Kristel Schoonderwoerd @ University of Connecticut***

Keywords: bud burst,bud preformation,seasonality,temperate forest,heteroblastic,leaf morphology

Abstract:

In temperate environments, resting buds are frequently regarded as static units that require cataphylls, or bud scales, to protect preformed embryonic foliage leaves during winter dormancy. However, this winter-protective view is challenged by the existence of naked buds: buds that overwinter future foliage leaves without the protection of cataphylls. Could there be a connection between resting bud structure in winter and the dynamic patterns of shoot extension over the growing season?

We investigated this in Juglandoideae (the temperate subfamily of Juglandaceae), a group that contains remarkable variation in terminal bud structures. Some of its species bear scaly buds with cataphylls. Others bear naked buds and never initiate cataphylls. Still others develop cataphylls during the first phase of bud initiation that are subsequently lost before winter dormancy. Yet, many of these species have large ranges that experience very similar (winter) climate conditions.

To understand shoot ontogeny from bud initiation to mature shoot, we characterized the complete seasonal heteroblastic sequences of leaf forms in six species of Juglandoideae. The origin and developmental timing of metamers (foliage leaves, cataphylls, and intermediates) within the resting bud were investigated using micro-CT scanning. In addition, the dimensions of 2249 individual metamers were tracked from first exposure to abscission along the shoots of saplings and mature trees in a common garden setting over a seven-month growing season. For the metamers with prominent photosynthetic areas (n=1581), chlorophyll fluorescence data was collected monthly.

The occurrence of cataphylls is associated with a single cohort of foliage leaves that flush and abscise synchronously. This growing pattern is highly determinate, with next year's terminal buds initiated even before leaf out in spring. In contrast, in sequences without cataphylls, slightly shorter-lived foliage leaves appear and abscise in a staggered fashion. Neoformation featured more prominently in species without cataphylls.

Chlorophyll fluorescence data reveal that the effective light-capture area of species with determinate growth (and cataphylls) in most cases reaches a peak early in the growing season and slowly declines thereafter. An indeterminate growth pattern (without cataphylls), on the other hand, ultimately leads to a steady increase in effective light-capture area several months into the growing season with a peak in late summer. Therefore, the observed determinate and indeterminate modes of sequential leaf development in Juglandoideae, and their associated terminal resting bud types, may be reflective of distinct ecological strategies during the growing season.

While the protective role of cataphylls during the dormant season has been the subject of much speculation, the developmental consequences of inserting cataphylls into a dynamic seasonal sequence of leaf forms potentially reach far beyond winter in Juglandaceae. In a wider context, bringing a leaf economic spectrum mindset to seasonal heteroblasty could increase our understanding of the ecological functioning of shoot development in temperate, deciduous, woody species and their seasonal patterns of carbon sequestration.

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Development and Structure

Topic: Contributed Papers

Title: Preformation: Could development be the missing piece to flowering phenology?

Author: ***Lindsey Kollmer @ University of Connectucut***

Keywords: morphology,bud preformation,Development,Dormancy,flowering phenology,histology

Abstract:

One of the most well-documented effects of climate change is altered phenology (Forrest and Miller-Rushing 2010). Of particular interest is the phenology of flowering because of its importance to reproduction, ecology, and the interaction of plants with other species (Forrest and Miller-Rushing 2010). Many previous studies reveal that there is a general trend of earlier flowering with warmer spring temperatures (Fitter et al., 1995; Miller-Rushing and Primack, 2008; Fitter and Fitter, 2002; Parmesan and Yohe, 2003). Contrary to this general pattern, however, a significant number of species delay flowering or are seemingly unaffected by warmer spring temperatures (e.g., Bradley et al. 1999; Fitter et al., 1995). In many of these studies, preformation, the initiation of structures one or more years prior to maturation, may influence phenology, but the process is not well studied.

We examined dormant floral buds from a selection of Magnolia species to pursue two questions: First, what stage of development are the floral buds in winter dormancy? Answering this question will provide baseline data necessary to answer the larger question of how woody species that exhibit preformation might be affected by temperature increases imposed by climate change (Diggle and Mulder, 2019). Second, by investigating development, dormancy, and flowering time in the spring, we asked whether there is a relationship between floral developmental stage during dormancy and flowering time the following spring. In other words, do species with dormant buds in more advanced stages of development ultimately flower earlier than those with dormant buds at earlier stages? At dormancy, flower buds of each species bore all floral organs, but the later blooming species were significantly smaller and had less morphological development especially in the carpels. Additionally, in earlier flowering species, microspores were evident in anthers and ovule primordia were initiated while in late flowering species sporogenous tissue had yet to differentiate and carpels were not fully formed

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Development and Structure

Topic: Contributed Papers

Title: The Ontogeny of Disparity in Cupressaceae Seed Cones

Author: ***Stepfan Huntsman @ Stanford***

Keywords: Conifers,Cupressaceae,morphospace,Pollination,seed cone morphology,cone development

Abstract:

Ontogenetic shape change has long been recognized to be important in generating patterns o morphological diversity. Here we explore how patterns of seed cone disparity change over ontogeny across the Cupressaceae conifer clade by comparing two end-member developmental stages: pollination and seed maturity. We sampled cones at pollen release and just prior to seed release, measuring basic morphometric shape variables of their bract-scale complexes (length, width, thickness). We then used several multivariate statistical methods to characterize patterns of morphospace occupation; in particular, we used a hypervolume method to quantify percentage overlap in morphospace among taxa at pollination and maturity We found that bract-scale complexes at both pollination and mature stages exhibit substantial variability, but morphospace occupation is more discretized at maturity, such that taxa occupy less of the aggregate hypervolume and show less overlap with other taxa. This pattern results from two cone growth strategies that generate two distinct shapes of bract-scale complexes; relatively thin laminar scales that imbricate to enclose seeds and relatively thick, peltate scales that interlock to enclose them. By contrast, pollination-stage bract-scale complexes all exhibit laminar shapes and different taxa occupy slightly different positions within a broad cloud of variability. The two growth patterns occur across lineages, suggesting multiple shifts in growth strategies among clades. The morphological diversity observed among mature cones therefore largely happens post-pollination in Cupressaceae due to different strategies of cone growth that seal off seeds in divergent ways. These results highlight how morphological diversity in seed cones reflects the evolution of disparate trajectories of ontogenetic shape change, even i the ultimate functional role of the cones remains similar.

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Development and Structure

Topic: Contributed Papers Development and Structure

Title: How ectopic cambia form: Insights from the convergent evolution of successive cambia

Author: ***Israel Cunha Neto @ Cornell University***

Keywords: climbing plants,comparative transcriptomics,gene expression,vascular tissues,cambium

Abstract:

Among plants, body forms vary from tiny herbs to tall trees. A tree trunk enlarges mostly due to the production of wood and bark. This ability to expand in girth, or radial growth, is an extraordinary feature of plants because wood and inner bark comprises the bulk of vascular tissues. However, in many climbing plants radial growth is different from the typical pattern observed in a sequoia or a pine tree. Instead of forming the typical ring of wood and bark, many stems of climbing species display unusual organizations of vascular tissues which vary from cylindrical stems with heterogeneous distribution of wood and bark to the formation of asymmetrical stems. These anatomies have been hypothesized as adaptations to increased stem flexibility, mechanical support, and water/sugar translocation, contributing to the vine's ability to climb up on a support. But, how do these complex patterns develop? We aim to answer this question investigating aspects at the gene, tissue, and organismal levels. Towards this aim, we selected a type of radial growth that is very familiar to most people. When you cut open a sugar beet, you will observe concentric rings; this is multiple successively nested vascular cambia within a single root. Technically it is called "successive cambia". This aberration has evolved independently multiple times across the evolution of vascular plants, therefore presenting a natural experiment to investigate the emergence of de novo meristems from existing plant tissues. Among flowering plants (angiosperms), successive cambia have evolved in several groups, including the Fabaceae or Sapindaceae. In this talk, we focus on the developmental anatomy and molecular genetics underlying de novo meristems which has been investigated in a pair of species of the family Fabaceae; one species has successive cambia (i.e., Wisteria floribunda) and another species has regular anatomy (i.e., common bean, Phaseolus vulgaris). This research will generate the first comparative study of gene expression characterizing successive cambia development. In addition, we investigate processes in molecular evolution across the convergent evolution of successive cambia by testing for signatures of selection, gene duplication, and pseudogenization of conserved vascular genes in a phylogenetic context of species with and without ectopic cambia to reveal the molecular processes shaping their evolution across plants. Together these data will reveal which gene expression patterns are shared across lineages, and which gene expression patterns are specific to generating successive cambia within a lineage. Therefore, this research will shed light on how successive cambia form across vascular plants, which at the same time can illuminate how radial growth occur in ecological and economic important commercial trees.

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Ecology

Topic: Contributed Papers Ecology

Title: Soil Generalist, Erysimum capitatum, Shows Differential Adaptation to Serpentine Soil of Origin Across a California Latitudinal Gradient

Author: ***Charlotte Miranda @ San Jose State University***

Keywords: geoecology,Local adaptation,plant-soil interactions,Serpentine,Soil

Abstract:

The soil-plant interactions between serpentine and vascular plants have been well documented and serpentine is often used as a model system to understand evolution and adaptation. However, previous botanical studies often treat all serpentine as homogeneous environments ignoring the interspecific differences between serpentine formations of varying composition. As a result, little is known about how differences among serpentine soils may impact local adaptation in plants. Erysimum capitatum is a widespread soil generalist endemic to Western North America. In California, it can be found inhabiting non-serpentine soil as well as numerous serpentine soil formations across the state. Thus, E. capitatum provides the ideal system to explore the extent to which populations growing on soils derived from different serpentine formations are locally adapting to their serpentine soil of origin. The goals of this study were to: 1) Test if E. capitatum populations growing on serpentine soil are locally adapted to serpentine soil as compared to nearby non-serpentine populations and 2) Assess the extent to which E. capitatum populations experience differential success when grown in their soil of origin vs other serpentine soils. Seeds and soils were collected from four pairs of E. capitatum populations found growing on serpentine and non-serpentine soil sites along a latitudinal gradient across California and correlated with a gradient of annual precipitation. We conducted germination trials to establish if soil type impacted success and a reciprocal transplant greenhouse experiment to evaluate plant fitness across the serpentine soils. Preliminary results suggest that at least one serpentine population is better adapted to its serpentine soil of origin. These results suggest that plant adaptation to serpentine soils may be impacted by regional differences in soil characteristics and supports the need for targeted conservation efforts to protect the diversity of native plants growing on serpentine soils of varied origin.

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Ecology

Topic: Contributed Papers

Title: Evaluating the Effect of Anthropogenic Nitrogen Fertilization on Litter Decomposition, Microbial Community abundance, activity and Nutrient Cycling in Forest Ecosystems

Author: ***Ihsan Muhammad @ Guangxi University***

Keywords: Nitrogen Deposition,Litter Decay,Nutrient Cycling,Litter Quality,Amplicon Sequencing,Microbial Decomposer

Abstract:

Leaf litter decomposition responds differently to elevated nitrogen (N) deposition across various litter species. However, the potential of the microbial decomposer community to explain this apparent stochasticity remains largely untested. We conducted a litter decomposition experiment using litter bags under an N gradient to address how litter quality and litter-dwelling microbial decomposers jointly mediate the effects of exogenous N on the process of litter decomposition. The litter quality was differentiated by C/N ratio and lignin content, and the microbial community was assessed using a fungal internal transcribed spacer (ITS) and bacterial 16S rRNA gene (16S) amplicon sequencing throughout the decomposition process. We found that medium (70 kg ha-1 yr-1) and high (105 kg ha-1 yr-1) levels of N addition decreased the decomposition rate (k) of lower quality litter (Castanopsis chinensis, CC), whereas none of the N treatments reduced the decomposition rate of higher quality litter (Schima superba, SS). Unexpectedly, N addition generally increased the microbial alpha-diversity in the CC litter but decreased the microbial alpha-diversity in the SS litter. The reduced decomposition rates of the CC litter in medium and high N treatments correlated with a decrease in the relative abundance of ligninolytic fungi (Mycenaceae of Agaricales, Hydnodontaceae of Trechisporales, Corticiales). In the SS litter, these fungal groups did not decline with N treatments, and the relative abundance of the ligninolytic fungi, Agaricales (Marasmiaceae), increased with high N addition. The reduced relative abundance of the ligninolytic fungi contributed to a decreased litter decomposition rate of lower-quality litter via high N addition

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Ecology

Topic: Contributed Papers Ecology

Title: Seed Mucilage as a Defense Against Granivory is Influenced by Substrate Characters

Author: ***Madison Stessman @ University of South Carolina***

Keywords: seeds,seed mucilage,granivory,seed defense,seed ecology,context-dependency

Abstract:

Many seeds are consumed by granivores despite numerous adaptations to avoid detection or exploitation. The efficacy of defensive traits can be influenced by the environment. Therefore, understanding the mechanisms by which environmental factors modify defensive efficacy can be important for understanding this important context-dependency that may lead to patterns of plant distribution and recruitment. Seed mucilage is a sticky coating that binds wetted seeds to the substrate; this attachment has been previously demonstrated to lessens exploitation by granivores. Seed mucilage as a defense has been recognized for decades, though rarely investigated. Here, we investigated whether the environment alters this seed defense by addressing two questions: 1) Does substrate particle size affect attachment strength? And 2) Does a change in particle size lead to changes in mortality due to granivores? In the field experiment, ants removed more seeds from finer substrates. Across that same range of grit, seeds took less force to dislodge when mucilage-bound to fine sandpaper than when bound to coarser sandpaper; however, an investigation across a wider range of grits demonstrated nonlinearities occurred for many species. Small differences in substrate grit lead to differential mortality in mucilaginous seeds due to alterations in attachment strength, suggesting that the defensive efficacy of this trait differs across microsites. We propose several mechanistic hypotheses behind these somewhat idiosyncratic relationships. This work paves the way for a more integrative look at mucilaginous seeds. Seed mucilage is a widespread trait that is easily-studied and has important demographic implications. It represents an ideal system to examine dispersal, germination, and granivory to gain a more holistic view of seed ecology.

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Ecology

Topic: Contributed Papers

Title: The ecological implications of spatiotemporal patterns of leaf morphological traits

Author: ***Yaoqi Li @ Xi'an Jiaotong-Liverpool University***

Keywords: Geographic distribution,herbarium specimens,leaf morphological traits,environmental factors,ecosystem productivity

Abstract:

Leaves are morphologically and functionally diverse organs fundamental to the survival of photosynthesizing plants. Botanists have long attempted to explore the biological significance of leaf traits and their environmental drivers. Yet, studies of large-scale variation in leaf traits across wide geographical ranges are limited due to the quality of available data. Here, leaf morphological trait data of 11,405 Chinese woody species from online databases, herbarium specimens (>6000 specimens of 7 species spanning ~100 years since collection), published floras, and unpublished data from experts were combined with species distribution maps to generate spatial patterns of leaf traits, with the aim of exploring their environmental drivers, and evaluating their potential to predict ecosystem productivity. Results show that spatiotemporal variation of leaf size and shape responds to both temperature and precipitation two major environmental axes influenced by climate change. Further, leaf size was strongly linked with ecosystem primary productivity showing consistent patterns among species with different life-forms and evolutionary histories. The leaf size linkage with primary productivity may reflect mechanistically how natural selection optimizes leaf size to maximize photosynthesis through the physics of leaf energy balance and how climate limits the total leaf area of canopies in different environments. As both current and fossil leaf size is easy to measure, our findings identify key plant indicators scaling from individual adaptation to productivity of terrestrial ecosystems and provide an important methodological approach for studying plant structure to elucidate ecological patterns and future predictions using herbarium specimens housed in botanical institutions in situ plant collections.

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Ecology

Topic: Contributed Papers

Title: Community analyses of remnant forests in Shelby Co., TN reveal potential eastern old-growth forest

Author: ***Robert Laport @ The College of Idaho***

Keywords: community ecology,eastern North America,old-growth forest,Tennessee

Abstract:

European colonization of eastern North America resulted in widespread destruction of old growth eastern deciduous forest, negatively impacting native plant and animal biodiversity over the last several centuries. However, remnant old growth forest may be more common than previously thought, and urban forested natural areas may also contain old growth forest elements. While harboring important native eastern forest biodiversity and providing important ecosystem services, these forests may also be threatened by continued anthropogenic disturbance, especially if such forests remain “hidden” or uncharacterized. The objectives of this study were to investigate the presence of potential eastern old growth elements in several urban forested natural areas around Shelby Co., TN and to compare these forests to the Overton Park Old Forest State Natural Area in Memphis, TN to better understand how potential differences in land use history may have shaped the studied forests. We used stratified random plot sampling to obtain species composition, stem density, basal area, and coarse woody debris measurements. We also obtained cores from a subset of the largest trees to estimate minimum ages for each surveyed forest. We show that the studied urban forested natural areas meet some, but not all, commonly employed criteria for old growth forest elements consistent with ongoing recovery trajectories from anthropogenic disturbance. The studied forests are also distinct in species composition, likely due to unique land use and disturbance histories. Nevertheless, the urban forested natural areas of Shelby Co. harbor important native biodiversity in a region that has experienced intensive historical anthropogenic disturbance.

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Ecology

Topic: Contributed Papers

Title: Investigating the eco-evolutionary causes and consequences of plant species rarity with meta-analyses

Author: ***Jennifer Boyd @ University of Tennessee at Chattanooga***

Keywords: fitness,functional trait,Genetic diversity,meta-analysis,rare plants,rare specie

Abstract:

The enduring question of why some species are rare while others are common has important implications for ecological theory, rare species conservation, and overall biodiversity. We used a phylogenetically controlled meta-analysis to investigate eco-evolutionary factors that could influence existing patterns of rarity and elucide the vulnerability of rare species to rapid rates of contemporary environmental change. Specifically, we compared the population genetic diversity, fitness, functional traits, and/or mating systems of 252 rare and 267 common congeneric plant species reported in 154 peer-reviewed articles published from 1978 to 2022. Our findings revealed that rare plant pecies have reduced population genetic diversity, depressed fitness, and smaller reproductive structures than common congeners and that rare species also could suffer from inbreeding depression and reduced fertilization efficiency. These characteristics may constrain the current abundances, distributions, and/or habitat associations of rare species and suggest that rare species may have reduced capacity for adaptation and migration in the face of environmental change. Our meta-analysis was complicated by the various ways in which rarity can be defined, and we recommend that future studies include more nuanced descriptions of species rarity that could facilitate comparisons and syntheses. We also recommend future studies that include ecologically relevant treatments, such as reciprocal transplant experiments, and quantitative genetic and poopulation genomic analyses. Collectively, such research could improve our understanding of the factors that contribute to rarity and allow for predictions of how rare species are likely to respond to environmental change.

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Ecology

Topic: Contributed Papers Ecology

Title: Bison wallows bolster plant diversity and semi-aquatic habitat in tallgrass prairie

Author: ***Bess Bookout @ Kansas State University***

Keywords: Bison bison,community ecology,plant diversity,plant-animal interaction,tallgrass prairie,Herbivore

Abstract:

Plains bison (Bison bison) were a keystone species that once roamed the Great Plains in the millions but have now largely been replaced by domestic cattle. While cattle and bison share similar ecological roles within grasslands, bison, unlike cattle, create bare-earth depressions (wallows) through dust-bathing. Historically, as bison followed fire across the Plains, wallows would have been abandoned from months to years, likely creating a mosaic of unique plant communities and ephemeral wetlands. This study takes advantage of a long-term bison reintroduction (30 years), which is factorially crossed with fire frequency (1, 2, 4, and 20-year fire intervals) at Konza Prairie Biological Station (KPBS), a native, unplowed tallgrass prairie. One disadvantage of this landscape-scale experiment is that bison cannot migrate long distances and are less likely to abandon some wallows. To circumvent this limitation, we established exclosures within the bison area to mimic migratory patterns of wallow and pasture abandonment. We conducted plant surveys in 120 plots (fenced and unfenced wallows and non-wallows; n=24) to determine if wallows contribute to plant diversity in tallgrass prairie and, thus, if bison provide distinct services that cattle do not. Our results show that wallows support unique plant communities, increase overall plant diversity, and increase phylogenetic diversity, which may contribute to increased functional diversity and resilience. Wallows also house unique soil microsites with greater clay content, and in some wallows (about 20%), long periods of standing water and/or high salt concentrations similar to brackish wetlands. Our results suggest that the removal of bison from Great Plains tallgrass prairie may have reduced the plant biodiversity and the extent of semi-aquatic ecosystems.

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Ecology

Topic: Contributed Papers

Title: Pollination syndromes and patterns of disparity in Melastomataceae

Kopper Constantin, Agnes Dellinger, Jürg Schönenberger
University of Vienna

Author: ***Constantin Kopper @ University of Vienna***

Keywords: disparity,Melastomataceae,Pollination syndromes,Syndrome Evolution,functional floral traits

Abstract:

Pollination syndromes are defined as suites of floral traits, which have evolved repeatedly across angiosperms in adaptation to distinct functional pollinator groups. These syndromes were developed to classify flowers under a functional ecological perspective by their most efficient pollinator, irrespective of their phylogenetic relationship. Several studies show strong support for the concept of pollination syndromes while others raised concerns about their reliability.

Melastomataceae offer an ideal system to test the concept of pollination syndromes, since many different pollinators and specialized floral morphologies have been reported for the family. The large, pantropically distributed family is dominated by buzz-bee pollination (95.5% of species), where pollen grains are released from tubular, poricidal anthers through vibrations In eight (of 23) tribes, shifts to different vertebrate pollinators (i.e. bats, rodents, hummingbirds, passerine birds, flowerpiercers) have occurred. Although only studied at a small scale up to now, these shifts seem to associate with marked changes in floral functional traits such as reward type, mechanism of pollen release, and corolla shape. Shifts among major functional pollinator groups (e.g., bees and hummingbirds), are generally regarded as a major source of increased floral disparity (morphological diversty).

We recorded 44 pollination-relevant functional floral traits across 411 species (260 with pollinator observations, 151 without pollinator observations), spanning the whole family (at least 1 species per genus). We focused on system-specific functional floral traits (e.g., appendage shape, structure of thecal wall) but also include traits traditionally used in pollination syndromes (e.g., corolla shape, corolla color). We used machine learning algorithms to identify pollination syndromes for species with empirically documented pollinators and employed these trained models to predict pollinators for species with unobserved pollinators. We ran ancestral character state estimation to determine directionality in pollinator shifts in Melastomataceae, and tested whether pollinator shifts mirror shifts in selection regimes using Ornstein-Uhlenbeck models (OU-models). Furthermore, we contrasted floral disparity among the different syndromes, biogeography, and tribes to evaluate the relative role of pollinator shifts in generating floral diversity. Our results indicate strong support for four well differentiated pollination syndromes within Melastomataceae: (i) widespread buzz-bee pollination; (ii) pollination by mixed assemblages of nectar-foraging vertebrates such as birds, bats, and rodents; (iii) pollination by food-body-foraging passerines; and (iv) generalized systems. Pollination syndromes in Melastomataceae can be discriminated by six system specific floral traits of which reward type and pollen release mechanism are the two most important traits to distinguish the different syndromes. In addition, we found that the “buzz-bee” and “nectar-foraging vertebrate” syndromes are highly diverse and pollinator shifts contribute to floral disparity, which is not directly correlated with clade size. One explanation for the high morphological diversity within the “buzz-bee” syndrome might be the high diversity of bees that buzz-pollinate Melastomataceae. We reconstructed the “buzz-bee” syndrome as ancestral from which all other syndromes evolved repeatedly. Finally, we expect to find several subsyndromes within the “buzz-bee”, the “nectar-foraging vertebrate”, and the “generalist” syndromes as indicated by the PCoA and the output from the OU-models.

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Ecology

Topic: Contributed Papers Ecology

Title: What limits rare endemics? Testing the Center-Periphery hypothesis for occurrence and fitness.

Author: ***Anna Wyngaarden @ University of Georgia***

Keywords: endemic flora,Species Distribution Modeling,species distributions,rare plant,population fitness

Abstract:

Plant performance is predicted to decline toward range edges, due to the effects of geographic or climatic marginality. Alternatively, global change can create directional effects of range position, with declining performance toward equatorial or warm range edges. Although prior work has found support for these patterns in widespread species, few studies have tested whether they apply to rare or narrowly distributed species. Narrow-ranged species inherently experience less variation in range position or climate compared to widespread species, but conversely may be more sensitive to what variation does exist. In this study, I quantify range-wide variation in occurrence, abundance, and fitness for three federally endangered plant species endemic to granite outcrops in the Southeastern United States. I first test for effects of range position, building on traditional methods of defining a species’ range center. I then test for effects of multiple climate variables as well as overall climatic marginality by comparing local performance to the predicted habitat suitability obtained from Species Distribution Models. The results of this study will inform how broad-scale geographic and climatic drivers influence the fitness and persistence of three rare endemics of conservation concern.

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Ecology

Topic: Contributed Papers

Title: Patterns of Dispersal Syndromes on Gypsum Outcrops

Author: ***Kate Madsen @ Ohio University***

Keywords: community ecology,Dispersal,ecology,Edaphic,endemism,gypsum,southwestern US,evolutionary ecology

Abstract:

The discontinuous distribution of gypsum outcrops plays an important role in isolating and forming their edaphic floral communities. We know from insular island-biogeographic-studies that distance among islands plays an important role in selection for specific dispersal syndromes, but are different dispersal syndromes more common among the discontinuous gypsum outcrops? We hypothesize that selection can either favor dispersal syndromes associated with long distance dispersal or, alternatively, syndromes associated with limited dispersal. To determine whether selection has favored dispersal syndromes associated with long distance dispersal or limited dispersal, we compared the composition of dispersal syndromes among gypsum outcrops to paired sites of nearby non-gypsum communities. Presence and absence data were collected for 374 sites (187 paired sites in total) in southern New Mexico and eastern Arizona. Dispersal syndromes were assigned for all species using the following categories: anemochory (wind), epizoochory (attachment to animal), endozoochory (ingested by animal), achory (no discernable dispersal), hydrochory (water), ballochory (ballistic), barochory (gravity), myrmecochory (ant), and synzochory (scatter-hoarding). Each syndrome was analyzed separately using a paired t-test between gypsum and non-gypsum sites. To infer the relationship between dispersal syndrome frequency and gypsum site association, a chi-square test was conducted for all gypsum and non-gypsum sites. Dispersal syndrome frequency was significantly different between the site types. Anemochory and synzoochory was significantly more common on gypsum sites than non-gypsum sites. Conversely, epizoochory and myrmecochory was more common on non-gypsum sites than gypsum sites. Finally, the dispersal syndrome endozoochory, achory, hydrochory, ballochory, and barochory were not significantly different between gypsum or non-gypsum sites. Our results suggest that an ecological filter likely selects for particular syndromes either at the dispersal or evolutionary stage.

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Ecology

Topic: Contributed Papers

Title: Microsite influences on establishment of saguaro cacti (Carnegiea gigantea) on Tumamoc Hill, Tucson, Arizona

Author: ***Peter Breslin @ University of Arizona***

Keywords: establishment,Sonoran Desert,spatial mapping,microsites,desert ecology,saguaros

Abstract:

Plant seedling establishment often relies on facilitation from nearby plants, rocks, and other microsite characteristics, e.g. at a 1-meter scale. Favorable microsites may moderate temperature, increase available water, provide shade, and reduce herbivory, facilitating the risky transition from germination to establishment. Microsite characteristics vary considerably across the mesoscale. Establishment patterns of plants therefore often have strong spatial patterning related to microsite conditions. In arid environments, risks are especially pronounced. The giant saguaro cactus (Carnegiea gigantea) is an example of a long-lived arid land species occurring in remarkable heterogeneity of habitat conditions that facilitate establishment. The goal of this study is to investigate microsite patterns of saguaro establishment, important for saguaro conservation and restoration. On Tumamoc Hill (O’odham: Cemamagĭ Do’ag, “regal horned lizard”), long-term saguaro survey data of 5000 individuals has been collected since 1964. Previous research on Tumamoc Hill has shown that demographic patterns reflect slope aspect at the mesoscale. We are further investigating a smaller spatial scale, comparing random microsite features with establishment sites of saguaros, to better understand the variables that relate to the spatial pattern of saguaro establishment. We collected records of the species of associated vegetation, estimates of percent total vegetation cover, percent rock cover, percent non-native grass cover (buffelgrass), slope, aspect, elevation, and terrain ruggedness data for 30 randomly placed 1 meter diameter microsites within each of three subplots in each plot. We collected identical microsite variables where saguaros occur. Principal component analysis, generalized linear mixed models and other approaches are being used to detect contrasts between random microsite characteristics and those where saguaros have established, if any. We expect that patterns of saguaro establishment will be related to microsite characteristics and that establishment microsites will vary significantly from random sites. We further expect that these establishment patterns will help illuminate saguaro ecology, conservation, and restoration, and perhaps clarify why this important species occurs in such a wide variety of habitats across its range.

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Ecology

Topic: Contributed Papers

Title: Seasonal Dynamics of Endomycorrhizal Fungi in Two Congeneric Orchid Species from Southwest China

Author: ***Xiaoyin Wang @ Guangxi University***

Keywords: Metagenomics,Orchid mycorrhizal fungi,seasonality,Symbiosis,Diversity,biodiversity conservation

Abstract:

Mycorrhizal fungi are important factors driving niche partitioning in terrestrial orchids and may contribute to orchid coexistence. However, little is known about the mycorrhizal communities associated with sister taxa that occupy similar habitats, and even less is known about the changes in their fungal community composition over seasonal and annual cycles. Over a three year period, this study assessed the root mycorrhizal fungi of two coexisting congeneric species: Paphiopedilum dianthum and Paphiopedilum hirsutissimum using high-throughput sequencing to determine whether their fungal community and functional composition is determined by annual and seasonal variation, or the host species specificity. The results show that: 1) the fungal communities of the two orchid species were generally similar and belonged mainly to the phylum Ascomycota (77%), of which 30% were from the class Sordariomycetes, followed by 18% belonging to Dothideomycetes; 2). P. dianthum roots had a higher mycorrhiza alpha diversity compared to P. hirsutissimum, but not in all seasons; and that 3). The fungal communities of P. hirsutissimum were more sensitive to seasonal changes compared to P. dianthum. These results could provide a theoretical basis for the use of mycorrhizal technology as a foundation to restore the wild Paphiopedilum, and underpin further exploration of the relationship between the community structure of orchid endophytic mycorrhizal fungi and their temporal ecological function.

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Ecology

Topic: Contributed Papers Ecology

Title: Latitude and Urbanization, Do They Matter? Investigating Morphological Plant Trait Change in Cities of Eastern North America

Author: ***Megan King @ Rutgers University / Chrysler Herbarium***

Keywords: plant traits,Urbanization,weeds,leaf morphological traits,latitudinal gradient,urbanization gradient,cities

Abstract:

The impacts of environmental change on floras has been well documented, however far less is known about how urbanization drives morphological trait adaptation. While studies have used common garden experiments, they most often focus on examining a single species, not entire clades, or functional groups of species. As urbanization continues to rapidly increase, floras are changing around the world, with non-native species filling niches no longer favorable to the native flora. Additionally, recent studies have shown that some non-native species along an urban gradient become taller, demonstrate an increase in specific leaf area (SLA), and leaf production in the most urban environments. In this study, we collected individuals from six different species in nine cities on the eastern seaboard of the United States from Florida to Maine. In each city, we collected specimens within areas of high, medium, and low impervious surface cover for a total of 1,192 specimens. We investigated whether the selected species exhibit morphological change (i.e., plant height, internode length, seed mass) across the urban gradient within each city and across the continental latitudinal gradient. We hypothesize that morphological traits will shift in response to higher impervious surface cover across all cities. We also expect that variation in trait change will be greater in cities at higher latitudes, due to increased average temperature from high to low impervious surface cover.

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Ecology

Topic: Contributed Papers

Title: Characterizing the climatic and edaphic niches of the Temperate North American Clade of Asclepias

Author: ***David Kunkel @ Oklahoma State University***

Keywords: Asclepias,ecological niche,ecological niche modeling,lineage diversification

Abstract:

Niche divergence has been considered an important driver of speciation and diversification that has consequences for species coexistence. By characterizing the niches of species across a whole group it becomes possible to assess niche differences among closely related species and gain insight into the role that niches play in lineage diversification, as well as how that leads to coexistence across a landscape. To evaluate the role of niche differentiation in lineage diversification, I studied the Temperate North American Clade of Asclepias (milkweeds), which contains approximately 57 species. These species exhibit a broad range of ecological variation, from open deserts to forest understories, and can be found across much of North and Central America. I hypothesized that 1) species diverged along both climatic and edaphic niche axes, primarily precipitation and soil texture, and 2) niche differentiation among species in the southwestern United States and Mexico is greater than in the Eastern Temperate Forest. Here, I characterized niches by utilizing 19 bioclimatic variables, elevation, % clay content, % silt content, % sand content, coarse fragment content, nitrogen content, pH, and electrical conductivity. I used multivariate analyses, including principal component analysis (PCA), linear discriminant function analysis (LDA), and ecological niche modeling, to characterize niches and evaluate species differences. The degree of niche overlap between species was measured using Warren’s I.

Preliminary results from PCA and LDA show that species of the Temperate North American Clade are differentiated primarily along a climatic niche axis with mean annual temperature and precipitation being the most important. Soil characters, while still important for differentiation among some species pairs, did not contribute to differentiation as much as climate. In addition, species found in the southwestern United States and Mexico have high niche differentiation from each other, likely on account of the high ecological heterogeneity of the region. Counter to my original hypothesis, however, the niche differentiation of the species found in these regions is not significantly higher than among species in the Eastern Temperate Forest. These results indicate that the majority of the ecological variation of this group is not contained in one part of this group’s distribution, but rather is found across its range. This could suggest that the rapid diversification of this group, potentially associated with niche, may be consistent across their evolutionary history as well.

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Ecology

Topic: Contributed Papers

Title: Population impacts of rarity under native grazers and changing climate

Author: ***Sarah Herzog @ Kansas State University***

Keywords: Konza Prairie,population biology,Prairies,tallgrass prairie

Abstract:

Understanding if and how species can persist in a changing climate and landscape is critical to our ability to conserve and manage ecosystems over the long-term. Rare species are at higher risk of extinction overall; however, species that are rare in different ways (e.g., small range vs. low-density populations) might respond quite differently to environmental drivers such as climate change, herbivores, or land use. For example, species with small ranges might be more responsive to climate (if climate is constraining their range), or herbivores might strongly impact habitat specialists (if herbivores utilize specialists’ habitat). Here I use long-term vegetation cover and climate monitoring data from a research site (Konza Prairie) in the tallgrass prairies of the Great Plains to create density structured population models for 17 species differing in rarity type. I test how the response of species to different grazing regimes (bison presence vs. absence) and weather conditions (annual variability in weather) varies across rarity types. I find rare species can differ dramatically in weather and bison responses, suggesting that they may also differ in their response to changing climate and native grazer reintroductions. Understanding how species differing in rarity type respond to environmental drivers is critical for management considerations for long-term species persistence.

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Ecology

Topic: Contributed Papers

Title: Forest Type and Burn Severity Affect Understory Response to Historic Wildfires

Author: ***Kate Weimer @ Colorado State University***

Keywords:

Abstract:

The fire season of 2020 was unprecedented in the Western US. In one summer, three differen fires individually broke the record of Colorado's largest wildfire. Understading the recovery following these historic events can lend insight into the compounding effects of wildfire and climate change. Reorganization of the understory community after disturbance can indicate changes in conditions not yet reflected in tree communities. Understory dynamics also affect watershed characteristic, wildlife, and tree regerneration, so knowledge about the influence of wildfire on understory plant communities is crucial. The purpose of this study is to determine if a trend toward thermophilization is being shown in understory vegetation following 4 different wildfires in 2020 and to compare the relative importance of burn severity, forest type, and other environmental factors on community composition. Thermophilization is an process in which the relative abundance of warm-adapted taxa in an area increases due to a warming climate, especially in combination with disturbances. We found a trajectory of thermophilization in high elevation forests that burned at high severity. We also found that drivers of community composition varied by forest type. These findings help assess how wildfire is affecting plant communities in the 21st Century and highlight what future management concerns may be.

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Topic: Contributed Papers Ecology

Title: Investigating the function of the awn and its role in invasion success of Microstegium vimineum (stiltgrass)

Author: ***Lauren Kosslow @ West Virginia University***

Keywords: invasion,invasive species,Japanese stiltgrass,plant ecology,Plant invasion

Abstract:

Invasive species pose a threat to biodiversity, yet factors that determine why some species become invasive and others do not remains poorly understood. This research focuses on a specific trait, the awn, and its role in invasion success of Microstegium vimineum (stiltgrass), an invasive grass species in the US. The invasive range of M. vimineum is expanding northward and westward in the US, resulting in further habitat degradation and complicating conservation efforts. Along with climate change, a possible explanation for northern expansion is the geographic distribution of awn types across the invasive range. Awns are bristle-like extensions from the floret that respond to changes in moisture and are a hallmark of many grass species. Awns coil when dry then straighten when wet and have been shown to increase burial and germination under certain conditions in some grass species. Microstegium vimineum has multiple awn forms (awned, awnless, and intermediate-awned) with a distinct awned-awnless distribution from north-south in the native and invasive ranges, the only grass for which this geographic pattern of awn type has been documented. This north-south distribution of awn types suggests awns may be favored by natural selection in some environments, but the extent of awn function in M. vimineum remains largely unknown. We hypothesize awns allow florets to bury in the soil, which protects the seeds from freezing temperatures at high latitudes, leading to a selective advantage of awns in the north and increasing northern range expansion. Our goal is to determine the function of the awn and identify its role in invasion success through reciprocal transplant experiments of all awn types across various latitudes, elevations, and soil freezing conditions over three years. These experiments will provide evidence of awn function by examining the effects of awn type on germination and survival at each location. These experiments are being conducted at four locations including Erie, PA (northern), Clemson, SC (southern), Morgantown, WV (low elevation, mid-latitude), and Davis, WV (high elevation, mid-latitude). Five replicates of three awn types were used at each site, including the awned-type, awnless-type, and an awn-removed treatment to account for differences due to awned-type traits other than the awn itself. Results from year one show the awned-type had the greatest germination/survival at high latitude, suggesting greater survival of the awned-type at high soil freezing conditions. The awnless-type had the greatest mortality at high latitude and elevation, further supporting a survival advantage of the awned-type at high soil freezing. The awn-removed type had the greatest germination/survival at high elevation, which may suggest another associated trait of the awned-type, rather than the awn itself, confers a survival advantage in northern climates. Year two of the experiment will further investigate the function of the awn in survival by studying how awn type affects survival over multiple winters in the seedbank. The outcomes of this research will allow for elucidation of M. vimineum awn function, essential to explaining the geographic awn type distribution observed in the US, determining the likelihood of invasion success, and predicting future range expansion.

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Topic: Contributed Papers

Title: Disjunct populations of a hemi-epiphytic orchid (Vanilla trigonocarpa) show segregation of mycorrhizal niches

Author: ***SHAN WONG @ Texas Tech University***

Keywords: Orchid mycorrhizal fungi,Orchidaceae,disjunct distribution,spatial segregation,Vanilla

Abstract:

Orchids require orchid mycorrhizal fungi (OMF) for seed germination and seedling establishment. Because of this obligate relationship, host species' occurrence, distribution, fitness and environmental features can be linked to the identity, specificity, and availability of their fungal partners. The ecology of OMF associated with the genus Vanilla, however, remains largely unknown, despite its pan-tropical distribution with approximately 120 species. We investigated the patterns of mycorrhizal association in four populations of V. trigonocarpa in Costa Rica, comprising three populations in the Pacific region and one in the Atlantic region separated by three mountain ranges. The closest and farthest populations were separated by 2 and 220 km respectively. Within each population, we sampled the epiphytic and terrestrial roots separately to identify the associated fungal communities, including OMF communities. We hypothesized: 1) Pacific populations will show greater similarity in their OMF communities when compared to the Atlantic population; 2) similarity in the OMF communities will decrease with increasing geographic distance between the populations; and 3) OMF communities associated with the epiphytic roots will be distinct when compared to the terrestrial roots, both within each population and for the orchid host as a whole. Sequencing the nuclear ribosomal internal transcribed spacer (nrITS) region yielded 65 OMF Operational Taxonomic Units (OTUs) from 107 root samples. Thirty of the 65 OTUs across all data were assignable to the family Tulasnellaceae representing 52% of all fungal sequences, followed by the family Ceratobasidiaceae (17 OTUs) and order Atractiellales (2 OTUs), represented by 19% RA each. When comparing the OMF communities of the two regions, PERMANOVA ($p < 0.05$), hierarchical clustering, and Principal Coordinate Analyses (PCoA) showed a clear separation of the two regions. Although Tulasnellaceae OTUs dominated the roots in each population, the composition of the OTUs was differentiated. The Atlantic population hosted 6 unique OTUs (3 Tulasnellaceae; 3 Ceratobasidiaceae) that together represented 72% of all sequences. The Pacific populations altogether hosted 5 OTUs (4 Tulasnellaceae; 1 Ceratobasidiaceae) that were not shared with the Atlantic population but were shared by the three Pacific populations. Regardless of their native provenance, a Mantel test showed that the four populations followed a distance-decay pattern between similarity in OMF communities and geographical distance ($p < 0.05$). Further, we also detected different OMF community compositions in the two root types within each population and when data from all populations were combined, supported by PERMANOVA ($p < 0.05$) and PCoA. While the Atractiellales (1 OTU) and Serendipitaceae (9 OTUs) collectively made up 91% of the OMF community in the epiphytic roots, 13 OTUs of the Tulasnellaceae and 5 OTUs of the Ceratobasidiaceae dominated the terrestrial roots with a combined relative abundance of 83%. Taken together, our first evidence of geographic-scale OMF community niches of Vanilla indicates the capacity of a hemi-epiphytic orchid with large photosynthetic biomass to have specialized mycorrhizal niches, which are further stratified vertically between the epiphytic and terrestrial roots. The distinct OMF communities of disjunct populations reveal specialization at local levels while associating with a wider pool of OMF across space.

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Ecology

Topic: Contributed Papers Ecology

Title: Fire response and flammability across 20 C4 grasses

Author: ***Dylan Schwilk @ Texas Tech University***

Keywords: C4 photosynthesis,fire,functional traits,postfire

Abstract:

Grasslands in warmer regions are dominated by species with the C4 photosynthetic pathway and C4 grasslands are often maintained by frequent fire. Perennial C4 grasses with buds protected at or below the soil surface are resilient to fire, especially when such fire occurs outside of the growing season. Fire can, in fact, indirectly aid such grasses because grasses can fuel rapid fire spread and such fires can wound or kill woody plants that might otherwise overtop and shade grasses in the absence of fire. Grass species, however, are not uniform in their tolerance of fire. Furthermore, although much fire modeling has treated grass fuels as homogeneous, recent work suggests that grasses might also differ in their flammability. Understanding variation in flammability and how it correlates with fire response strategy can reveal eco-evolutionary patterns and help aid fire management in these grasslands. We grew 20 C4 grass species in a greenhouse experiment, measured leaf and canopy traits, and conducted flammability trials of entire individuals. We found that flammability differed across species and was driven by dead biomass retention and canopy volume. However, post fire responses were not related to observed fire behavior. These results indicate that species fire survival was independent of flammability traits and was instead idiosyncratic and species-specific. This does suggest, however, that any potential selection on increased flammability might not be constrained by negative effects on a plants own survival.

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Ecology

Topic: Contributed Papers

Title: Investigating the Turnover in Plant Species Biodiversity on Gypsum Soil Outcrops

Author: ***Lilly Osterday @ Ohio University***

Keywords: beta diversity,biogeography,Chihuahuan Desert,community ecology,ecology,Edaphic,Edaphic Endemism,gypsum,southwestern US

Abstract:

Gypsum soils have unique chemical properties that restrict edaphic communities of plants to them. Soils containing high levels of gypsum occur in patchy outcrops that form island chains throughout the southwestern deserts in North America. Island biogeography theory suggests that island communities should have higher species turnover than mainland communities due to isolation limiting dispersal events that would otherwise homogenize them. We tested the hypothesis that because of their discontinuous, island distributions, gypsum outcrops would have greater differences in species composition (beta diversity) than comparable populations from the surrounding non-gypsum floral communities. This result would show that the community assemblage of gypsum is governed by the same processes that lead to high species turnover in insular systems. We analyzed species presence/absence data collected from 148 gypsum sites and 148 paired nearby non-gypsum sites and compared the calculated beta diversity values between them using a paired t-test. We then ran a linear regression to determine whether beta diversity is influenced by the distance between sites. Beta diversity was not significantly different between gypsum outcrops and the surrounding non-gypsum communities. Both soil types had high beta diversity indicating low levels of similarity between sites whether the community was on or off gypsum. As expected, distance between the sites significantly influenced the beta diversity among non-gypsum sites. As distance increased, the differences in species composition increased. This pattern was not observed in the gypsum results. Distance had no effect on the beta diversity among gypsum sites. This result suggests that all gypsum sites were so isolated from each other that no matter the distance between sites, beta diversity is high. The equally high beta diversity among the non-gypsum sites, was not expected, but may be explained by the high environmental heterogeneity found in the landscape of southwestern North American deserts.

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Ecology

Topic: Contributed Papers

Title: Four range limit hypotheses tested in climate-manipulated common garden

Author: ***Laura Leventhal @ Carnegie Institution for Science***

Keywords: adaptation,common garden,Dispersal,drought,genetic swamping,mutation load,range limit

Abstract:

A species' range is a physical representation of the limits of evolution as it epitomizes a species' evolutionary niche in a specific period of time. Range limits are dynamic barriers affected by the abiotic and biotic environment, population dynamics, and, least well understood, genetic mechanisms. There are currently four hypotheses that best account for the genetic mechanisms behind the formation of range limits. 1) An increase in deleterious mutation accumulation as a result of low density at the edges of ranges relative to the center, making edge populations more susceptible to genetic drift and the fixation of deleterious mutations. 2) Higher levels of genetic swamping where because edge populations are also frequently locally adapted, gene flow from the center to the edge of a population can create maladaptive hybrids at the edge. 3) A high variance in fitness in extreme environments which present the opportunity for natural selection to act but also may allow fitness to aggressively decline to zero. And 4) the idea that the alleles for adapting beyond an edge exist in standing genetic diversity but are not in the right location and are therefore dispersal limited. We are testing each of these hypotheses using an outdoor common garden experiment with Arabidopsis thaliana on Stanford University's campus in Central California. To disentangle the genetic and ecological components of range limit formation, we used a sophisticated irrigation system that simulated 14 regimes of drought stress, varying in frequency and abundance, simultaneously. We selected ecotypes from the 1001 Genomes Project (1001genomes.org/) that fit the criteria of the four range limits by screening for Ka/Ks ratio, polygenic score for survival in drought conditions, distance to edge of A. thaliana's range, and fitness in previous drought experiments. In total, we planted 25,920 plants on the same day in November 2021 and monitored them throughout their entire life cycle. We measured fitness via survival and seeds produced, along with phenological variables including first day of flowering, day of death, and lifetime duration, as well as ecologically-relevant phenotypes such as stomata, trichome indices, growth rate, and ∂C13. This experiment will allow us to elucidate which hypothesis or combination of hypotheses contributes the most to the formation of range limits. It is essential that we understand the mechanism behind range limit formation as climate change is altering ecosystems at an alarming rate, and the capabilities of a population to respond may be the only way to avoid extinction.

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Ecology

Topic: Contributed Papers Ecology

Title: Using Genetically Defined Traits to Predict Competitive Interactions between Microstegium vimineum Genotypes

Author: ***Cynthia Huebner @ USDA Forest Service***

Keywords: competiton,invasive species,plant traits,genotype,microstegium vimineum

Abstract:

Microstegium vimineum (Japanese stiltgrass, JPS) is an annual shade-tolerant grass that has invaded much of the eastern US; its range continues to expand into new environments further west, north, and at higher elevations. This species is composed of several different genotypes that may help explain its ability to colonize novel sites rapidly. Some of these genotypes are defined by unique morphological traits, one of which is whether an awn is present on the florets. Some of our previous research has shown that awned JPS is found at northern latitudes whereas awnless JPS is found at southern latitudes in its native and US invasive range. We argue that the awn of the awned-type may facilitate burial into soil, buffering the seed against freezing temperatures or that awn presence is linked to cold-tolerance. However even if these predictions are supported by future data, they do not explain why the awned type does not appear to be expanding further south. Consequently, we hypothesize that the awnless, southern plants possess traits that give them a competitive advantage over the awned plants. To test this, we grew 72 second-generation populations (F2) that originated from plants collected from paired dry and mesic habitats, then grown in common greenhouse conditions to produce the F1 generation; F1 seed were then grown to produce the F2 plants and seeds. We evaluated 21 morphological traits that appeared to be conserved across generations. We also selected one awned and one awnless type to compete within the same pot, using six replicates. Our results show that the awnless type has significantly longer tillers, single tillers with greater biomass, larger total shoot biomass, more branches per tiller, more nodes per tiller, longer axillary roots that occur at higher nodes on each tiller, and wider leaves than the awned type. The awned type has more tillers per pot, suggesting a bunched growth habit compared with the awnless type's sprawling form. The two types do not differ in terms of total chasmogamous (open flowers) inflorescence biomass, but the awnless type produces more seeds while the awned type has heavier seeds. The awnless type takes 1.5x longer to flower, but the seeds of the awned type take 2x longer to mature. These same trait differences are found in the plants grown in direct competition, of which differences in tissue color made the plants easy to distinguish within the same pot. Although the awned plants may be producing heavier seed, the larger plants and higher seed production of the awnless type indicate the awnless plants could dominate when growing in the same area. The awned plants' investment in a longer reproductive period may ensure germination and survival in colder climates, whereas the more abundant, smaller seeds as well as a greater capacity to spread vegetatively may ensure rapid colonization in warmer climates by the awnless type. Future research will focus on these different growth habits as well address potential anatomical and physiological differences between plants of the two awn types.

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Conservation Biology

Topic: Contributed Papers

Title: Urban forest gaps across scales from 0.6 – 5.18 hectares are dominated by invasive species in a New Jersey national park.

Author: ***Steven Handel @ Rutgers University***

Keywords: invasive species,forest gaps,urban forest structure,national park conservatio

Abstract:

Disturbance gaps in forests can stimulate tree regeneration, maintain biodiversity, and promote forest heterogeneity. In urbanized regions, long term forest sustainability is threatened by many ecological stressors, such as high deer pressure and invasive plant spread, which are more intense than in non-urban landscapes. These pressures can affect regeneration capabilities in disturbance gaps. This study tested whether forest gaps promoted tree regeneration in comparison to the adjacent intact forests and if gap size was an influential factor in regeneration. This study was conducted across 54 natural disturbance gaps of different sizes (0.06 – 3.15 ha) in a 590-ha forest tract within an urbanized region in Morris County, northern New Jersey, within the Morristown National Historical Park. In each gap area, advanced regeneration data and species cover were collected in the understory stratum across three gap locations (gap center, gap edge, and adjacent forest). Results from 294 plots showed that advanced regeneration was greater in adjacent forest plots than in gap centers. Small Fraxinus spp. seedling numbers accounted for the difference among locations; when Fraxinus spp. were excluded there was no significant difference among locations. Gap size had no effect on advance regeneration. Overall, the mean stocking index was severely deficient and mainly due to excessive deer pressure; numbers of large seedlings and saplings were extremely low, but numbers of all smaller seedlings were sufficiently stocked. In addition, invasive plants dominated the understory. Stepwise multiple regressions showed that introduced shrubs and the introduced grass, Microstegium vimineum, displaced native tree regeneration. The only tree species that showed successful regeneration in gap centers was the introduced Robinia pseudoacacia which also had the greatest sapling numbers of all tree species. Without significant management intervention, natural disturbance gaps in this stressed forest tract will fail to promote native tree regeneration, allow R. pseudoacacia to dominate, and change the future composition and structure of the forest. This study serves as an example for the many forest tracts that have similar ecological stresses. Intensive deer control and invasive plant management are required to restore natural regeneration processes and the valuable role of disturbance gaps to promote forest sustainability and heterogeneity. These data offer an additional parameter to discriminate urban forest dynamics from processes in less human-dominated habitats which have dominated discussions of forest ecology. The fate of urban forest gaps in this study will not reiterate the surrounding mature forest structure.

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Ecology

Topic: Contributed Papers Ecology

Title: Vegetative and reproductive phenology in two populatios of Zamia encephalartoides D. W. Stev. (Cycadales), a threatened species endemic to Santander, Colombia.

Author: ***Jhon Alexander Carreño @ Universidad Industrial de Santander***

Keywords: Colombia,Endemic Species,phenology,Zamia,Dry forest

Abstract:

In this research we studied the reproductive and vegetative phenology in natural populations o Zamia encephalartoides Dw Stev, a Cycad species endemic to the department of Santander, Colombia. We observed and documented for approximately 27 months a group of 100 adult and reproductive plants in two populations of Z. encephalartoides with variable microhabitats, in relation to the availability of forest cover and humidity. We determined and described the phenological stages of Z. encephalartoides, the reproductive period, as well as the level of reproductive synchrony between males and females. We also observed the formation and development of new leaves to determine the production rate and leaf maturation time. The results obtained indicate that the reproductive periods of females and males are partially synchronous. Most of the observed female plants emerged strobili from May to August and showed a similar development time, reaching maturity and receptivity in synchrony. Likewise, male plants showed similar emergence periods extending over the same months but with different growth rates. We estimate that the period of correspondence in receptivity between male and female plants during the sampling time, occurred from October to November in most of the plants studied, however, with observations at the population level we recorded that some male plants continue with the development of strobili that achieve maturity in December and January. Regarding leaf phenology, we found that Z. encephalartoides can generate new leaves once in the year before or after the formation of reproductive organs and occurs synchronously in most of the plants studied. Finally, we discuss the ecological implications according to the characteristics observed in the phenology of Z. encephalartoides.

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Ecology

Topic: Contributed Papers

Title: Spatial, seasonal, and environmental phytochemical variation in a Great Lakes invasive aquaticplant

Author: ***Linden Taylor @ University of Wisconsin-Madison***

Keywords: Aquatic plants,chemical ecology,Myriophyllum

Abstract:

Myriophyllum spicatum (Eurasian watermilfoil; Haloragaceae)–a submerged aquatic plant that is highly invasive in the Great Lakes region and other areas in North America–produces phytochemicals that have been found to inhibit or reduce the growth of cyanobacteria and some aquatic insect herbivores. The native Myriophyllum sibiricum (northern watermilfoil) produces lower quantities of these inhibitory chemicals than the invasive Eurasian watermilfoil. Thus, increased chemical defenses and allelopathy, in addition to other competitive mechanisms, might have a role in native species displacement by invasive Eurasian watermilfoil. Although the chemical profiles of M. spicatum and M. sibiricum have been described, it remains unknown how watermilfoil phytochemistry varies within and between lakes over the growing season and along environmental gradients. This study aimed to determine the dynamics of watermilfoil phytochemistry in the field over the growing season and whether there are relationships between lake water column light availability, resource availability, and M. spicatum production of the phytochemical tellimagrandin II. We found minimal within-lake variation of tellimagrandin II production and significant between-lake and seasonal variation that may be driven by light availability. This research contributes to our understanding of Eurasian watermilfoil phytochemistry and ecology, which can inform aquatic invasive species management practices.

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Ecology

Topic: Contributed Papers

Title: The Little Mustard That Could: Is Phenotypic Plasticity Associated with Colonization Success in Arabidopsis thaliana?

Author: ***Maya Shamsid-Deen @ University of New Mexico***

Keywords: Arabidopsis thaliana,colonization,Phenotypic plasticity

Abstract:

As humans redistribute species across the globe and our climate changes at an unprecedented rate, it is urgent that we cultivate a robust understanding of the underlying mechanisms for colonization success, such as phenotypic plasticity. Phenotypic plasticity is the ability for a single genotype to differentially express alternative phenotypes based on the environment. By capitalizing on the abundant genomic and germplasm resources of the globally distributed species, Arabidopsis thaliana, we implemented a full-factorial design to test whether populations demonstrating recent successful colonization are more plastic. We selected twenty-two populations from A. thaliana's global range that represent the following groups based on their genomic cluster identities: "European colonizers", "North American colonizers", and "relicts". Using these group classifications, we are testing if plants that have a recent history of colonization (the North American colonizers) are more plastic than those in the native range but have expanded into available habitats (European Colonizers) and those that have remained in their glacial refugia (Relicts). Trait plasticity was quantified using the F-ratios generated from the following model: trait ~ treatment. We used a linear mixed effects model to empirically test for significant F-ratio differences between our groups of interest. The results of our study improve our understanding of phenotypic plasticity's role in plant colonization. This knowledge will enable us to forecast the changes we may see in our flora and ultimately, Earth's ecosystems.

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Topic: Contributed Papers Ecology

Pollen quality as a potential driver for bumble bee abundance and diversity in restored prairies

Author: ***Stephanie McFarlane @ Unversity of Wisconsin-Madison***

Keywords: floral rewards,pollen,tallgrass prairie,macronutrients,bumble bee

Abstract:

Many bee populations are declining globally, in large part due to habitat loss and the resulting nutritional shortages. Tallgrass prairie restoration efforts are often aimed at establishing vegetation that resembles undegraded historic conditions and to promote pollinator habitat. Restored prairies in southern Wisconsin have been shown to have increased floral resource abundance and to support a greater abundance and diversity of bumble bees than non-restored old agricultural fields. However, floral resource abundance does not appear to be the only driver of bumble bee abundance. Many factors have been shown to affect bumble bee foraging patterns: flower color, floral resource abundance, nectar availability, and the quality of pollen. Recent research has shown that, in experimental settings, bumble bees prefer pollen with a macronutrient composition that has a high protein:lipid ratio (P:L), suggesting that bumble bee larvae development and survival depends on specific pollen requirements. For this reason, we expect nutritional quality may be a potential mechanism for variation in local bumble bee abundance and diversity in restored prairies. However, the nutritional quality of pollen is typically unknown for most flowering species found in tallgrass prairies. Acquiring the pollen macronutrient composition of flowering species found in prairies would allow us to estimate the community-level nutritional quality of restored prairies. Here we ask, do restored prairies with high community-level P:L pollen have more abundant and diverse bumble bee populations than sites with a low community P:L pollen? To answer this question, we collected floral resource and bumble bee data during the summers of 2019-2022. Pollen from common herbaceous prairie species was collected and macronutrient assays were completed in 2021 and 2022. We conducted protein and lipid assays of pollen from 80 common flowering species in tallgrass prairies. We then calculated the community-level pollen P:L by multiplying the P:L of pollen for each flowering species found at a site by the flowering species abundance at that site and totaling all species at that site. Using preliminary data, we compared sites where we had over 80% of P:L ratios for the species observed (n=20; p-value: 0.056; r-squared: 0.25). A linear model with pollen nutritional quality and floral resource abundance explained 53% of variation in bumble bee abundance (p-value: 0.01). Our data support our hypothesis that pollen macronutrient composition drives bumble bee abundance, however it does not appear to affect bumble bee diversity.

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Topic: Contributed Papers

Come Hell or High Water, the Fate of Guzmania monostachia in Florida Rests with Humans

Author: ***Shelby Krupar @ University of Florida, Florida Museum of Natural History***

Keywords: _{conservation biology},Bromeliaceae,climate change,Species Distribution Model,Florida,guzmania monostachia,sea level rise

Abstract:

Anthropogenic land use changes in Florida have eliminated more than half of the state’s wetlands over the last 2 centuries, and additional losses are anticipated as a consequence of climate change, sea level rise, and continuing development activities that will accommodate a rapidly growing human population. These issues spell danger for Florida’s biodiversity and ecosystem services, and data are needed to inform future conservation priorities and. Guzmania monostachia (Bromeliaceae) is an endangered epiphyte native to freshwater forested wetlands within South Florida. We modeled the projected distribution of this species in response to changing climate and sea level conditions. We constructed ecological niche models (ENMs) under the current-day conditions using georeferenced occurrence points and projected them into the past and future under different climate and sea-level rise scenarios. Our future climate-based ENMs predicted small losses in suitable habitat for G. monostachia in South Florida, coupled with range expansions into more northern areas due to the warmer climate. In contrast, when sea-level rise conditions were included, our models predicted a considerable, although non-detrimental, loss of suitable habitat. These predictions suggest tha G. monostchia will not be driven to extinction in Florida by climate change and sea-level rise alone. Rather, these results when combined with land use data suggest that human activity is and will continue to be the largest threat to G. monostachia in Florida. Conservation efforts should focus on preserving existing habitats that will remain above sea level in the coming decades, and also should explore possibilities for assisted migration northward.

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Ecology

Topic: Contributed Papers Ecology

Title: Leafing, flowering, and fruiting phenology of tropical montane forests in Central Highland of Vietnam

Author: ***Ai Nagahama @ National Museum of Nature and Science***

Keywords: flowering phenology,Southeast Asia,fruiting phenology,leafing phenology,tropical montane forests

Abstract:

In East and Southeast Asia, various phenological patterns are known in each forest, such as temperate forests, subtropical forests, seasonal tropical forests, tropical rain forests, and tropical montane forests. However, the phenology of tropical montane forests has been less extensive than that of tropical lowland forests. To systematically understand the diversity of phenological patterns in East and Southeast Asia, we conducted (1) the field observation of tree phenology in tropical montane forests in Bidoup-Nui Ba National Park, Central Highland of Vietnam, where phenology had not been previously studied, and (2) the statistical comparison of phenological patterns among the nine well-studied areas in Southeast Asia. For (1) the field observation, five plots were installed at the elevation range from 1460 m to 1920 m in the national park, and monitored leafing, flowering, and fruiting events of 17–19 dominant tree species in each plot (five individuals per species; in total 91 species consisted of four deciduous and 87 evergreen trees) for seven times; in June, September, and December 2018, April, July, and October 2019, and January 2020. As a result, leafing, flowering, and fruiting events were observed for 91 spp. (100.0 %), 65 spp. (71.4%), and 54 spp. (59.3 %), respectively. The number of leafing species ranged from 20 spp. (22.0%) in June to 91 spp. (100%) in April, which was significantly influenced by all of day length, precipitation, and temperature. On the other hand, the number of flowering species ranged from 15 spp. (16.5%) in September to 33 spp. (36.3%) in December, which was influenced by day length and precipitation. The number of fruiting species ranged from 12 spp. (13.2%) in January to 27 spp (29.7%) in July, which was not significantly influenced by any of the meteorological factors. For (2) the statistical comparison of phenological patterns, we assembled the phenological data from previous studies in nine locations in East and Southeast Asia (2 temperate forests, 2 subtropical forests, 1 seasonal tropical forest, 2 tropical rain forests, and 2 tropical montane forests) and performed a cluster analysis for phenological patterns. As a result, the phenological pattern of Bidoup-Nui Ba National Park was similar to that of Mt. Kinabaru, though the two has different climatic patterns. This suggests the existence of other climatic factors that influence forest phenology. Based on the results of (1) and (2), we constructed a new hypothesis that showed the process of diversification of community phenology in correlation with local meteorological factors, though further observations are needed to assess the diversity of phenology in East and Southeast Asia.

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Ecology

Topic: Contributed Papers

Title: Can detection dogs improve biosecurity by finding invasive plant hitchhikers vectored by global trade?

Author: ***Rima Lucardi @ USDA Forest Service***

Keywords: biological invasions,Federal Noxious Weed,Plant invasion,seed dispersal,Working Dogs,Biosecurity,Global Trade,Propagule Pressure

Abstract:

Accidental nonnative invasive plant (NNIP) introductions occur cryptically, often with little or no observed data to determine a species' propagule pressure. Without such data, estimates of propagule pressure for subsequent successful establishment, spread, and systemwide negative impacts are difficult to determine. Our research team has been collecting directly observed data of plant seeds hitchhiking on shipping containers to assess propagule pressure of NNIPs at an international seaport, which is important because global maritime trade constitutes at least 90% of all trade. Our overarching research objective is to intervene at the onset of invasion by identifying and intercepting the diversity of high-risk plant species' propagules arriving on refrigerated shipping containers at an international maritime point-of-entry, thereby reducing propagule pressure and potential invasion success. Previous research discovered NNIP species with seasonal peaks in propagule pressure arriving into the Port of Savannah, GA, USA. Here, we specifically ask if specially trained detection dogs can discriminate among different plant seeds arrivals hitchhiking on containerized imports. We conduct novel research on the canines' capacity to: (1) detect seeds in varied abundances and environments, and with distractions and seed contaminants (e.g., hydraulic fluids, grease, grime, insects); (2) discriminate between NNIP target seeds from non-target seeds. This collaborative research among USDA Forest Service, Arkansas State University, and Working Dogs for Conservation (WD4C.org) aims to develop a novel tool to reduce plant invasions and biotic homogenization resulting from maritime global trade. This is the first research evaluation of the efficacy and potential role of detection dogs interrupting industrial-scale invasion processes at the introduction stage and in a direct effort to reduce propagule pressure of risky invasive plant species. Here, we present initial findings from this proof-of-concept trial with canine capacity on internationally vectored plant seeds via global maritime trade. The data we are collecting will allow us to determine if detection dogs can be employed for this purpose at scale, and if they can, we will work with them to improve biosecurity and reduce probabilities of plant escape that can start or exacerbate plant invasions.

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Ecology

Topic: Contributed Papers

Title: Using climatic niches to plan climate-resilient urban forestsPlanning resilient urban forests will ensure that benefits of urban trees are maintained as the climate in California continues to change.

Author: ***Natalie Love @ University of Illinois, Chicago***

Keywords: ecological niche modelling,climate change,urban forest,climate resilient

Abstract:

Planning resilient urban forests will ensure that benefits of urban trees are maintained as the climate in California continues to change. Selecting species that are well-suited for future climatic conditions will be a key component of this strategy. Tree species that are adapted to warm and dry climates will likely perform well in California's future climate. To understand the climatic requirements of urban tree species, we utilized data from the California Urban Forest Inventory and GBIF occurrence data from each species' native range. We used various ordination approaches to (1) characterize each species' climatic niche, (2) compare climatic niche of urban and native tree populations, and (3) develop region- and species-specific climate suitability scores for current and future climatic conditions in California. The results from this study can help guide species selection and planning for resilient urban forests, and suitability will be available to the public via the most widely-used tree website in the United States: SelecTree. The methods used here are also widely applicable to seed-sourcing efforts for ecological restoration or conservation.

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Ecology

Topic: Contributed Papers Ecology

Title: Pollination and herbivory differ across Abronia fragrans (Nyctaginaceae) populations but not between floral morphs: a reciprocal transplant experiment

Author: ***Sierra Jaeger @ University of South Carolina***

Keywords: Local adaptation,plant-pollinator interactions,Pollination syndromes,sand verbenas,floral trait evolution

Abstract:

Pollinator-mediated selection is considered a principal driver in floral diversification and shifts in functional pollinators frequently propel transitions in floral phenotypes. Abronia (sand verbenas), an ancestrally night-blooming and nocturnally-pollinated genus, contains striking trait shifts away from the nocturnal moth pollination syndrome, both within and between taxa. Throughout most its expansive range, Abronia fragrans has white, day-closing flowers, while a narrow portion of its range is populated by a pink-flowered morph that remains open into late morning. Previous work has demonstrated that only nocturnal pollinators contribute to A. fragrans reproduction in a white-flowered population, while a pink-flowered population also receives pollination by diurnal floral visitors (i.e., butterflies and day-active moths). To explore whether this shift in floral characters is driven by local pollinator or herbivore communities, we reciprocally transplanted white and pink floral morphs into a pink-flowered and a white-flowered population. We simultaneously applied day, night, and always-open pollinator-exclusion treatments to inflorescences, and estimated inflorescence and leaf herbivory. Pollination success (proportion seed set per inflorescence) and herbivory rates (percent tissue damaged) did not differ between floral morphs at either site for any treatment; thus, this experiment rejects local adaptation to pollinator or herbivore communities. However, diurnal pollination was significantly higher for both morphs in the pink-flowered population than in the white-flowered population, and the most-destructive herbivore guild changed between sites: leaf herbivory was greater in the pink-population, while florivory was greater in the white-flowered population. Therefore, it remains possible that population-specific biotic or abiotic agents of selection play roles in this floral trait transition.

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REVIEW TOPIC OPTION

Topic: Contributed Papers

Title: Nature's Velcro: Untangling Drivers of Complex Trichome Diversification in Mentzelia (Loasaceae)

Author: ***Rosemary Glos @ University of Michigan***

Keywords: Cornales,macroevolution,trichomes,plant defense

Abstract:

Trichomes are morphologically diverse and ecologically important structures that play a variety of roles across plant species. Although significant effort has been dedicated to elucidating trichome development and function in several (mostly model) taxa, we know relatively little about the evolutionary forces shaping trichome diversification across entire lineages. Here, we merge phylogenetic and ecological perspectives to reveal potential drivers of trichome evolution in the genus Mentzelia (Loasaceae, ca. 95 spp.), which belongs to the family that bears perhaps the most complex trichomes of any plant group. We measured microscopic trichome traits from vegetative and reproductive tissue across 40+ Mentzelia species representing wide variation in trichome morphology, geography, and habitat. We paired our dataset with the latest comprehensive phylogeny of the genus and applied phylogenetic comparative methods to test for correlations between trichome characteristics, life history traits, and bioclimatic variables. We evaluate existing adaptive and trade-off/synergism hypotheses and present initial evidence of correlations between traits. This is the first study to address longstanding questions about the adaptive value of elaborate trichomes produced by Mentzelia species and illustrate the evolutionary patterns of a complex phenotype that likely mediates interactions between plants, herbivores, mutualists, and the abiotic environment.

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Ecology

Topic: Contributed Papers

Title: Can flower colors in a rare cholla be indicative of their sex?

Author: ***Niveditha Ramadoss @ San Diego State University***

Keywords: Cactaceae,sexual dimorphism ,sexual dichromatism

Abstract:

Organisms with separate sexes usually exhibit sexual dimorphism, meaning morphological differences between the male and female individuals. Even though not as common as in animals, plants can also express sexual dimorphism. The study of sexually dimorphic traits is important because they influence the growth, physiology, pollinator visitation, and adaptation o different plant populations. A type of sexual dimorphism called sexual dichromatism is expressed by differences in color between the sexes. It is common in birds and reptiles and has not been documented in plants. Our research is based on a rare dioecious cactus called Wolf's cholla (Cylindropuntia wolfii, Cactaceae), that is distributed at the border of California and Baja California. This species serves as a good model to study sexual dimorphism and dichromatism as it has a functionally dioecious sexual system with six different flower color morphs within the same region. The main goal of our study is to identify sexually dimorphic traits including dichromatism in the male and female flowers of C. wolfii. To identify sexual dimorphism, we measured several categorical and quantitative factors that potentially influence pollinator visitation, such as flower color, UV emission, autofluorescence, filament color, tepal shape, flower display diameter, tepal length, tepal width, and number of flowers pe plant. The differences between the sexes were measured and assessed for significance using statistical analysis e.g., ANOVA. Our results suggested that C. wolfii has sexual dichromatism as male flowers are usually associated with brighter flower color morphs such as green and yellow. These features can make the male flowers more attractive to pollinators than females and it is predicted to be a consequence of intrasexual competition in dioecious species. Furthermore, we observed fluorescence dichromatism where female flower anthers fluoresce more than male flower anthers as a result of early degeneration of anther walls in females when they abort the male sex. Our study is the first to report floral sexual dichromatism and fluorescence dichromatism in a dioecious plant and will be a pioneer for future dichromatism studies in plants.

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Ecology

Topic: Contributed Papers Ecology

Title: Canopy coverage delays flowering phenology but does not reduce seed set for an herbaceous perennial in a subalpine meadow

Author: ***Scott Nordstrom @ University of Colorado, Boulder***

Keywords: flowering phenology,Reproductive Success,seed set,spatial autocorrelation,canopy,montane meadows,subalpine meadows

Abstract:

Timing (“phenology”) of flowering within a season can influence reproductive success and produce population-scale mating patterns. Flowering phenology is often partially dependent on environmental cues. Spatial variation in these cues within a population, e.g., due to microclimatic variation, can produce spatial structure in flowering time. Strong spatial structure in flowering time can produce temporal isolation for individuals in different environments, limiting sexual reproductive success or outcrossing, or creating genetic structure. Temporal structure in flowering phenology due to spatial variation in cues has been studied in alpine systems, where microtopography creates variation in the timing of snowmelt. However, environmental heterogeneity and spatial structure in flowering time has not been studied in subalpine meadow systems, despite being a model system for studying flowering phenology and being similarly threatened by climate change. Meadow systems are defined by contrast between open meadow interiors and forest canopy, producing variation in sunlight and soil characteristics. We answered the following questions: (1) does canopy coverage influence the flowering phenology of Thermopsis divaricarpa, a leguminous perennial common to the North American Rocky Mountains, and (2) what are the relative influences of canopy coverage and phenology on seed set in T. divaricarpa. We monitored flowering phenology over three summers in a large population (>10,000 individuals) within a six-hectare portion of an aspen-conifer meadow complex in Colorado, USA. We performed phenological censuses bi-weekly in 206 square meter plots over three years, recording the number of inflorescences and open flowers for each individual ramet in plots. Canopy coverage for each plot was estimated with a UAV-derived point cloud. In one year, we collected fruit from monitored plants, counting and weighing fruit and seeds. We evaluated relationships among canopy coverage, initiation of flowering, and seed set using spatial autoregressive regression models. In total we observed 490 T. divaricarpa ramets in 103 plots. Across years, canopy coverage delayed flowering, with plants in forest habitat flowering up to two weeks later than plants in open meadow interiors. However, plants in meadow interiors still had high variance in initiation of flowering date, such that there was still temporal overlap in flowering between plants in meadow interior and forest habitats. There was no relationship between initiation of flowering and seed set and only a weak negative relationship between canopy coverage and seed set. These results suggest that subalpine meadows show spatial structure in flowering similar to alpine systems, but it is not strong enough to reduce reproductive success or create strong genetic structure within the population.

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Ecology

Topic: Contributed Papers

Title: Creating ecosystem extent accounts to understand land use change in Irish forests

Author: ***Francesco Martini @ Trinity College Dublin***

Keywords: ecosystem services,forests,land use change,SEEA-EA,ecosystem accounting

Abstract:

In Ireland forests cover 11% of the land, making it one of the least forested countries in Europe. The government aims to reach 18% of forest cover by 2050. In doing so, it is key to develop resistant and resilient forests that can provide a wide range of ecosystem services (ES). Coillte, an Irish semi-State company, owns 49% of the forests in Ireland. Originally managed primarily for timber production, they now manage their forests for a range of ecosystem services including timber, carbon sequestration, biodiversity enhancement and recreation. One way to better understand changes in land use and associated ES is through natural capital accounting, and specifically the newly adopted System of Environmental Economic Accounting - Ecosystem Accounting (SEEA EA). The first step in the SEEA EA framework is developing the extent accounts, i.e., the total area of each ecosystem within an ecosystem accounting area.

We created the extent accounts for 25 diverse Coillte forest sites throughout Ireland, covering almost 9,000 hectares. We used CORINE land cover data for 2000 (opening extent) and 2018 (closing extent). In the 25 sites combined, there was a decline in coniferous forests (mostly Sitka spruce plantations) of 1,024 hectares (-20.1%), while broad-leaved forests cover increased by 230 ha (+73.2%) and mixed forest cover by 425 ha (+2,500%). Two sites with different management objectives (timber production and nature conservation) will be illustrated as examples. Following, we will produce the condition accounts and we will measure the flows of ecosystem services. This is one of the very first studies where the SEEA EA framework is being applied at a local scale.

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Ecology

Topic: Contributed Papers

Title: Forestry bias in provenance literature limits guidance for restoration seed sourcing under climate change

Author: ***Jessamine Finch @ Native Plant Trust***

Keywords: climate change,ecological restoration,Literature Review,provenance trial,seed sourcing

Abstract:

The question of from where plant material was collected, or provenance, is core to forestry and the younger practice of ecological restoration as it has profound implications for plant performance. Throughout a species’ range, intraspecific trait variation can be related to environmental differences and convey performance advantages in home environments, also known as local adaptation. This phenomenon has led to the dominance of the “local is best” provenancing strategy for seed-based restoration, also known as local seed sourcing. However, the continued impacts of climate change challenge this model, as adaptation to past climates may now prove maladaptive. In response, multiple climate-informed seed sourcing strategies have emerged, including sourcing from areas that resemble the predicted future climate of the restoration site (i.e., predictive provenancing) and mixing multiple sources from across a region to maximize evolutionary potential and climatic fit (i.e., regional admixture). Even so, there is a lack of empirical evidence to guide climate resilient seed sourcing, which is critical for the longevity and ecological function of restored natural communities. With the goal of characterizing, synthesizing, and applying experimental research to guide restoration practice, we conducted a systematic review of the global literature on plant provenance testing. A total of 176 papers met our criteria for inclusion, the majority of which focused on forest habitats (68%) and trees (esp. Pinaceae, 25%) in the global north (52% N. America, 31% Europe). This bias aligns with the finding that commercial forestry was the most common study motivation (42%), with ecological restoration a distant second (27%). Provenance trials considered a wide variety of response variables, limiting the potential for a meta-analysis, with the vast majority focused on traits highly related to industry, like height, survival, and biomass. We describe additional patterns and gaps our review identified, highlight topics which require further research, and provide practical suggestions of tools and actions that support restoration practice and the creation of resilient natural communities under future climate scenarios.

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Topic: Contributed Papers Ecology

Title: Individual and interactive effects of white-tailed deer and woody invasive plants on native tree seedlings in an early successional forest

Author: **David Gorchov @ Miami University**

Keywords: herbivory,non-native species,regeneration failure,Quercus rubra

Abstract:

Regeneration failure is a pressing issue exhibited in forests throughout eastern North America, potentially endangering the future health of forests. Densities of white-tailed deer (Odocoileus virginianus) have drastically increased in many of these forests and impact tree establishment and growth via browsing. Densities of non-native invasive plant species have also increased, with direct and indirect negative impacts on native tree seedlings. While the individual negative impacts of over-abundant deer and invasive plants are well known, the interactive effects are not as well understood. The goal of this study was to understand the individual and interactive effects of deer and woody invasive plants on tree seedlings in an early successional forest. The study was conducted in a stand of Juniperus virginiana forest near Oxford, OH (39°31'N, 84°42' W) with a basal area of 31.4 m^2/ha. The understory had very few native seedlings other than Fraxinus spp. and is heavily invaded by non-native shrubs Lonicera maackii and Ligustrum obtusifolium. A factorial experimental design was used with each combination of deer access/exclosure and invasive woody plants removed/not removed. In June 2022, we placed deer exclosures - 2.13m tall fences made of galvanized poultry wire using four trees as corner posts. The same month, plots designated for invasive removal had all woody invasive shrubs and vines removed via cutting and stump application of 41% glyphosate herbicide. Seedlings of four native tree species were selected for use in this study due to their relatively fast-growth and ability to grow in the future climate projected for these coordinates: Quercus rubra, Liriodendron tulipifera, Juglans nigra, and Carya cordiformis. Tree seedlings were planted in each plot in June 2022 and natural regeneration within the plots was also monitored. For planted Q. rubra, Northern Red Oak, the greatest height increase and greatest leaf count occurred in plots where deer were excluded and invasives were present. Modified canopy cover index at 0.3 m height was lowest in invasive removal plots. These preliminary results suggest that deer have greater impacts on tree seedlings than invasives, reducing seedling and leaf growth, despite invasives shading these tree seedlings. If these patterns persist, the results suggest that where tree regeneration is the primary goal, land managers should prioritize deer management over invasive plant removal, at least in early-successional forests.

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Topic: Contributed Papers

Title: Intra - and inter - specific effects of epiphyte - epiphyte associations in cloud forest in central Mexico

Author: **Elizabeth Victoriano-Romero @ Benemérita Universidad Autónoma de Puebla**

Keywords: Competition,epiphyte closest neighbor,facilitation,plan-plant associations

Abstract:

Mountain cloud forests hold a high diversity and abundance of epiphyte plants. This high abundance promotes the establishment of multiple associations among epiphytes, which have been scarcely studied. Using experimental epiphyte mats, positive and negative effects, as well as both effects occurring simultaneously were found. However, more studies are necessary to determine the effect of both intra- and inter-specific associations occurring among all the species within the epiphyte community. The goal of this study was to determine both intra- and inter-specific associations established among epiphytes and their effects (positive, negative or neutral) within the community. Epiphyte identification, abundance and distance between closest neighbors were determined in 0.25 ha of a cloud forest in Central Mexico. Chi-squared tests and Haberman residuals were used to test the existence of significant associations and their effects (positive, negative or neutral). A two-way ANOVA was applied to test the effect of the epiphyte species, the association type (intra- vs. inter-specific) and the interaction between them on the distance between pairs of closest neighbor epiphytes Significant epiphyte-epiphyte associations within the community were found ($\chi 2 = 6317$, d.f.= 196, $P < 0 .0001$). A total of 225 associations were found; out of these, 155 were neutral, 36 were negative, and 34 positive. Out of the total number of associations detected, 210 were interspecific and 15 were intraspecific. The fern Pleopeltis accicularis had the highest number of positive interspecific associations (4 with other ferns, 1 with the orchid Prostechea linkiana, and 1 with Peperomia tetraphylla). Contrastingly, P. tetraphylla (Piperaceae) and Tillandsia crypthanta (Bromeliaceae) had the highest number of negative interspecific associations (with 8 other epiphyte species). Among the intraspecific associations, 13 were positive; Prosthechea linkiana was the only species with neutral intraspecific associations, whereas Pleopletis acicularis was the only one with negative associations. Epiphyte-epiphyte distance was significantly affected by the species interacting ($F12, 3060 = 25.27$, $P << 0.0001$), the type of association ($F1, 3060 = 203.0$, $P << 0.0001$), and the interaction between those factors ($F12, 3060 = 12.16$, $P<< 0.0001$). Within interspecific associations Prosthechea linkiana (1.3 ± 0.55 cm) and Pleopeltis polylepis (25.9 ± 5.24 cm) had the shortest and greatest distance, respectively, with their closest neighbors. Likewise, Hintonella mexicana (8.5 ± 1.28 cm) and Tillandsia macoyana (16.16 ± 1.39 cm) had the shortest and greatest distance with their congeneric closest neighbors. Interspecific associations had a shortest mean distance (6.95 ± 0.29 cm) than the intraspecific ones (13.67 ± 0.4 cm). Six out of a total of 13 species included in the analysis had a significantly greater distance with their intraspecific closes neighbors (14.68 ± 0.76 cm) than with the interspecific ones (4.93 ± 0.32 cm). For seven epiphyte species, intra- and inter-specific mean distance (12.28 ± 0.36 cm) was similar. Intraspecific associations were predominantly positive (except in two species); whereas the interspecific associations were mainly neutral. Therefore, closest neighbor identity and distance between neighbors seem to have an important influence on the type of association established between pairs of epiphytes and, consequently, on the structure of the epiphyte community.

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Topic: Contributed Papers Ecology

Title: Sniffing out the link between nitrogen and floral scent

Author: ***Janelle Bohey @ University of California, Irvine***

Keywords: climate change,Floral morphology,Nitrogen,Volatile Organic Compounds,Floral Scent,Ipomopsis

Abstract:

Climate change poses a threat to many plant species and plant-pollinator mutualisms because environmental change can alter floral traits essential for attracting pollinators, like floral scent. Temperature, drought, and nutrient availability have the potential to alter the chemistry and composition of floral scents, which may disrupt pollination and defense against seed predators Temperature increases and changes in precipitation due to climate change are predicted to alter the availability of soil nitrogen via increased rates of nitrogen mineralization by soil microorganisms and increasing rates of atmospheric nitrogen deposition from human activity. Only a few studies to date have empirically tested how nitrogen availability influences floral scent emissions, and responses appear species-specific. More research is needed to understand the effect of nitrogen on floral volatile emissions, and the impact this may have on plant-pollinator mutualisms.

We tested how soil nitrogen availability affects floral scent in two subalpine species of Ipomopsis (I. aggregata and I. tenuituba) that serve as a model for studies of floral traits. We were especially interested in the effect of nitrogen addition on the nitrogenous compound indole in I. tenuituba, which is the primary attractant for hawkmoth pollinators. In this greenhouse experiment at the Rocky Mountain Biological Laboratory in Colorado, USA, we collected 20 plants of each species from natural populations, potted the plants in native soil and randomly assigned individuals to high or low nitrogen treatments. High nitrogen treatments received 0.5 g of ammonium nitrate applied weekly for 5 weeks during the growing season. Low nitrogen treatments received no additional nitrogen. We then measured floral scent, corolla length and width, maximum and minimum anther length, style length, flower number, nectar volume and sugar concentration, and inflorescence height. We used dynamic headspace sampling to collect floral scent from 1-5 flowers per plant during the day (09:00-13:00) and night (20:00-00:00) in addition to ambient air controls, and analyzed the samples using thermal desorption gas chromatography-mass spectrometry. Average volatile emissions per plant were compared using constrained ordination methods. Nitrogen availability affected daytime floral scent emissions of I. aggregata ($P = 0.009$), including a 56% increase in a dominant compound, the monoterpene α-pinene, in the high nitrogen treatment. In I. aggregata, higher nitrogen also increased inflorescence height by 22% and flower number by 71%. In I. tenuituba, higher nitrogen increased style length by 9% although there were no detected effects of nitrogen on floral scent or any of the other floral traits measured. Nitrogen had no detected effect on indole emissions, nighttime volatiles, corolla width and length, maximum and minimum anther length, and nectar volume and sugar concentration in either species. These results show that floral volatiles can respond to changes in soil nitrogen, but responses can differ even between closely related species. Future studies will examine the influence of soil microbes on this response to soil nitrogen.

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Topic: Contributed Papers

Title: Effect of plant growth regulators on multiple shoot formation in Afzelia africana Sm. Ex. Pers.

Author: ***Ejeoghene Ogbimi @ Obafemi Awolowo University, Ile - Ife, Nigeria.***

Keywords: Fabaceae,tissue culture

Abstract:

A. africana is a medicinal and multipurpose tree that is under permanent pressure from its continuous exploitation for medicine, food and timber products. In addition to this, the seeds are dormant and recalcitrant with a low rate of seed germination thus constraining propagation by conventional planting. There has been no literature documentation of any previous micro-propagation study on A. africana. Thus, this study is the first on callus induction and multiple shoot formation in Afzelia africana. Cotyledonary node, hypocotyl and nodal explants excised from in vitro seedlings and cultured on Murashige and Skoog (MS) medium 1962 with different concentrations and combinations of plant growth regulators and phloroglucinol. The experiment was carried out in two stages. The first evaluated the responsiveness of the different explants of A. africana in vitro while the second stage was done in 3 sets. The first set investigated the effect of plant growth regulators (benzyladenine BA, phloroglucinol Pg and Indole Acetic Acid IAA) interacting with age of cotyledonary node explants on shoot and callus initiation; the second investigated the effect of thiaduzuron TDZ, BA and Pg on shoot multiplication while the last experiment investigated the effect of BA and Pg on shoot elongation. The results obtained showed that cotyledonary node among other explants responded best., MS media incorporated with 15mg/L BA, 15mg/L PG and 5mg/L TDZ favored shoot multiplication producing 10 shoots per explant. Also, MS media incorporated with 15mg/L BA, 15mg/L PG and 15mg/L IAA was best for callus initiation and MS media incorporated with 15mg/L BA and 15mg/L PG produced the longest shoot (8.65 cm). This study has paved a path for the rapid regeneration of A. africana through in vitro propagation.

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Ecophysiology

Topic: Contributed Papers Ecophysiology

Title: Warming plus elevated CO2-induced leaf hyponasty in tomato may share chemical signaling pathways with shade avoidance and thermomorphogenesis

Author: ***Michael Thomas @ University of Toledo***

Keywords: Abiotic stress,climate change,tomato,survey,thermomorphogenesis,hyponasty,auxin,phytochrome

Abstract:

Atmospheric carbon dioxide (CO2) concentrations are increasing and may exceed 800 ppm by 2100. This is increasing global mean temperatures and the frequency and severity of heatwaves. Recently, we showed for the first time that the combination of chronic warming and elevated carbon dioxide (eCO2) caused extreme upward bending during growth (i.e., hyponasty) of leaflets and leaf stems (petioles) in tomato (Solanum lycopersicum), which reduced growth. Other compound-leaved species (marigold [T. erecta] and soybean [G. max]) displayed increased leaf angle and cupping as well, while simple leaved (sunflower [H. annuus] and okra [A. esculentus]) did not. That study, however, examined only two levels of CO2 (400, 700 ppm) and temperature (30, 37°C) at the young-vegetative-plant stage. Further, we did not investigate underlying mechanisms for this warming+eCO2-induced hyponasty, which is likely to involve the plant hormones auxin and ethylene, based on their role in thermal hyponasty. In this study, warming+eCO2 hyponasty was evaluated in tomato across a range of temperatures and CO2 concentrations, and at multiple life stages. Ethylene and auxin tomato mutants were examined to explore the potential role of these hormones in warming+eCO2 hyponasty, and a light-filtering experiment was used to evaluate how light quality may affect plant hyponastic responses to warming+eCO2 treatments. Lastly, other species, especially Solanaceous species, were examined to determine if warming+eCO2 hyponasty is restricted to compound-leaved species.

At eCO2 (800 ppm), petiole angle increased ca. linearly as temperature increased from 30-38°C. Under heat stress (HS, 38°C), petiole angle increased at all eCO2 concentrations compared to ambient (600/800/1000 vs. 400 ppm). All life stages examined (juvenile, pre-reproductive, and flowering) had increased petiole angle in leaves developed during warming+eCO2, such that most leaves exhibited hyponasty in juveniles but only young leaves did so in adults (previously fully-developed leaves were unaffected). Ethylene-insensitive and -constitutively-producing, and auxin-constitutively-producing, mutants displayed similar changes in petiole angle with warming+eCO2 compared to the non-mutant reference. Auxin-insensitive mutants grown with warming+eCO2 displayed similar leaf angle to those grown at optimal temperatures and ambient CO2, indicating that auxin and not ethylene is involved in this hyponastic response. Blue light filters increased the proportion of blue light and decreased the proportion of red and far-red light, resulting in reduced leaf angle in plants grown at warming+eCO2 compared to standard chamber lights, indicating a role for light in this hyponasty. Only compound-leaved Solanaceous species exhibited increased warming+eCO2 hyponasty compared to control conditions, warming, and eCO2 treatments, while plants from other families had varying responses. Warming+eCO2 hyponasty may have negative consequences for the productivity of certain wild and domesticated plants in the coming decades, and understanding the underlying mechanisms of this response may prove useful for developing climate-change-resistant crops.

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Ecophysiology

Topic: Contributed Papers

Title: Acclimation of functional traits drives biomass increases in leafy green species grown in aquaponics

Author: ***Courtney Campany @ Shepherd University***

Keywords: Stomata,Acclimation,Crops,Nitrogen,photosynthesis,aquaponics

Abstract:

As human population size continues to increase while climate change effects worsen, future food security has become a primary concern for agricultural industries worldwide. Yields of traditional agricultural farming are commonly limited by water and nutrient availability and many crop yields are predicted to decline. Alternative farming practices like aquaponics, which can alleviate these negative yield pressures, may become critical to reaching food production targets. Aquaponics is the cyclic joint production of fish and hydroponic plants where the fish efflux provides nutrients to plants that then purify the water to be recycled to the fish tanks. Here, we investigated acclimation of physiology and functional traits of plants grown in aquaponics versus soil for three leafy green crop species. We compared gas exchange, stomatal anatomy, water use efficiency, and foliar chemistry on newly formed leaves across weekly measurement campaigns. Increased photosynthetic rate, driven by higher stomatal conductance and increases in tissue nitrogen, led to higher harvested biomass in aquaponics for all species. Aquaponics plants adjusted stomatal behavior and to a lesser degree stomatal anatomy to become less water use efficient than plants grown in soil. Collectively, our findings demonstrate the ability of crops to acclimate quickly to aquaponics growing systems that largely remove water and nutrient limitations to plant growth. The increased biomass yield of aquaponics plants compared to soil-grown plants highlights the potential of small-scale aquaponics systems as an efficient and sustainable alternative farming practice.

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Ecophysiology

Topic: Contributed Papers

Title: Resilience to heat stress in natural accessions from contrasting climates, as well as in CRISPR-gene edited, high oleic acid lines, of the emerging oilseed plant pennycress (Thlaspi arvense: Brassicaceae).

Author: ***Nikhil Jaikumar @ Illinois State University***

Keywords: Thermotolerance

Abstract:

Field pennycress (Thlaspi arvense: Brassicaceae) is a winter annual currently undergoing domestication as a combined cash/cover crop. While pennycress has impressive cold tolerance, it is sensitive to heat stress, particularly during flowering. Previous efforts to improve oil quality, via CRISPR gene editing, have created lines with reduced polyunsaturated fatty acid content, through loss of function of the fatty acid desaturase (fad2) and reduced oleate desaturase (rod1) genes. This has the potential to alter heat and cold tolerance, as colder climates are often associated with greater lipid unsaturation. In several growth chamber experiments, we explored tolerance to heat stress during flowering in pennycress lineswith loss of function of either rod1 and fad2. Seed yield, lipid peroxidation (as an index of stress), and pollen viability at a series of temperatures were measured. We also conducted a study of heat stress tolerance, including pollen viability and photosynthetic assimilation under heat stress, in natural accessions selected from the northern and southern limits of their North American range. Both fad2 and rod1 lines had increased pollen viability (70% and 50% respectively) under moderate heat stress (28 °C) compared to their wild type parent (30%). They also showed smaller increases in lipid peroxidation, and smaller decreases in seed yield, following a 9 day treatment at 34 °C. . Southern accessions showed greater pollen viability at high temperatures than northern lines (e.g. 35% viability at 34 °C compared to 6%). Southern accessions also retained more of their photosynthetic capacity at 34 °C compared to northern lines. Our ongoing efforts serve as a starting point for improving heat stress in pennycress, both through gene editing and identification of natural variation, and rendering this emerging crop more resilient to global warming.

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Ecophysiology

Topic: Contributed Papers Ecophysiology

Title: A shift in the dominance of the xylem in hydrating Forsythia flowers could explain changes in freezing tolerance during floral development

Author: ***Jessica Savage @ University of Minnesota - Duluth***

Keywords:

Abstract:

The amount of carbon and water needed to support floral development changes dramatically between the early stages of bud development and anthesis. In a previous study, we suggest that these changes correspond with a shift in how flowers are hydrated. Early in floral development, when sugars are being imported into a bud and water loss is low, flowers could be hydrated mostly by the phloem, but once flowers open and demand for water is greater, there is a shift to xylem-dominated hydration. This hypothesis is consistent with evidence that some species like Forsythia do not exhibit xylem maturation in the pedicel of their flowers until immediately prior to anthesis. Therefore, it is possible that some flowers not only require minimum input from the xylem but are hydraulically isolated from the stem during the winter. This would explain why ice does not propagate into buds before budburst. To better understand whether there is a shift in the dominance of the xylem and phloem in hydrating flowers and how this shift might relate to floral freezing tolerance, we conducted an in-depth analysis of changes in the anatomy and physiology of Forsythia flowers during the spring. We measured anatomical changes in the vascular tissue, estimated xylem and phloem input based a carbon balance model and used thermal imaging to examine the propagation ice into flowers at different developmental ages. We found evidence that the phloem likely plays a larger role in floral hydration during bud expansion than after anthesis, as hypothesized. The timing of this change appears to correspond with a shift in floral freezing tolerance and the ability of ice to propagate into developing buds. Taken together, these results suggest that for plants that flower early in the spring, there could be a benefit to relying more heavily on the phloem before anthesis because it would reduce the risk of bud damage to young flowers.

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Ecophysiology

Topic: Contributed Papers

Title: Quantifying the physiological costs of flowers and their effects on whole-plant and ecosystem processes

Author: ***Adam Roddy @ Florida International University***

Keywords: Floral traits,flower,hydraulics,Reproductive Investment,functional floral traits,costs

Abstract:

For most angiosperms, producing and maintaining flowers for pollination is requisite for reproduction and population persistence. Historically, pollinators have been considered the primary agents of selection acting on flowers. Yet, the physiological costs of producing and maintaining flowers often oppose pollinator selection, and abiotic conditions (e.g. temperature, humidity, water availability) interact with floral traits to influence the total costs of flowering. Recent evidence has shown that abiotic conditions can have as strong an effect on floral traits as pollinators can. With increasingly anomalous and extreme weather events and declining pollinator abundance, the physiological traits of flowers may become increasingly important in determining floral production and success. Here, I present an approach to quantifying the physiological costs of flowers and how these costs may mediate physiological and evolutionary responses under global change, using data from temperate and subtropical plants. Despite originating from the same apical meristem as leaves, flowers often exhibit combinations of traits unique from leaves, which influence their physiological costs and responses to abiotic conditions. These early results suggest that floral physiological traits may be linked to climate, and may therefore be important in determining species distributions and community assembly processes. Yet floral traits are rarely included in most studies or in existing trait databases. I will further discuss how quantifying floral ecophysiological traits can be useful in understanding and predicting ecosystem and landscape processes.

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Ecophysiology

Topic: Contributed Papers

Title: Examining the effects of elevated [CO2] and temperature on plant performance and physiology in a perennial forb

Author: ***Derek Denney @ University of Georgia***

Keywords: Boechera,climate change,fitness,fitness landscape,life history

Abstract:

Anthropogenic climate change is altering the landscapes of populations worldwide. In the Rocky Mountains, elevated temperatures are causing decreased snowpack and greater drought stress.
Additionally, rising atmospheric CO2 concentrations ([CO2]) are affecting plant populations by increasing photosynthetic rates and enhancing plant growth. The negative effects of increased aridity may be offset by the fitness gains of elevated [CO2]. However, the interactive effects of [CO2] and temperature are rarely studied together. Here, we present the results of a multifactorial growth chamber experiment on Boechera stricta (Brassicaceae), a perennial forb native to the Rocky Mountains. We see increased photosynthesis in future [CO2] conditions but a decline in stress responses. Additionally, genotypes from lower elevations show elevated fitness and fecundity. These results are not evident under single factor manipulations and highlight the importance of examining climate change factors in multifactorial experiments.

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Topic: Contributed Papers Ecophysiology

Title: Does expression of the auxin biosynthetic protein family YUCCA change during drought?

Author: ***Samantha Pelletier @ Connecticut College***

Keywords: Populus,drought,Yucca,auxin

Abstract:

As drought becomes more pronounced due to climate change, it is important to characterize the responses of plants to water stress. One area of interest includes how auxin, the hormone most associated with growth and development, is affected by drought. In particular, mature lea size is often reduced in response to drought and auxin is known to play a key role in leaf expansion. The YUCCA proteins catalyze the conversion of indole-3-pyruvic acid to indole-3-acetic acid (IAA), the dominant form of auxin in most plants, and most of this IAA is produced in rapidly expanding leaves. However, in addition to synthesizing IAA, the YUC proteins are also associated with thiol reductase activity. This enzymatic function reduces reactive oxygen species (ROS), which can accumulate in plant tissue under stress such as drought. The YUCCA (YUC) gene family in Populus includes 12 YUCs, but they are not well described. This experiment was aimed to assess whether YUC genes in Populus leaves at different stages of development are differentially expressed in response to drought. Multi-shoot, one-year-old hybrid poplar plants (Populus tremula x alba; INRA 717-1B4) were either watered to field capacity daily (control; n = 5) or deprived of water (drought; n = 5) for nine days. Over that period, stomatal conductance and stem water potential both decreased significantly in the droughted trees relative to the control trees. The shoot apex, leaf 8, and leaf 16 (L8 and L16, counted down from the apex) were harvested for gene expression analysis, with the apex representing rapid growth, L8 representing a leaf approximately one half the size of the average fully mature leaf, and L16 representing a fully expanded leaf. Leaf relative water content (RWC) measured on leaf disks at the time of harvest and showed that the RWC of L8 (i.e., the eighth leaf beneath the shoot apex) was significantly reduced under drought compared to controls, but the RWC of L16 was similar between treatments. qRT-PCR was used to determine expression levels of five different YUC genes that had previously been shown to be expressed in Populus leaves: YUC1, YUC2, YUC4, YUC6, and YUC12. One gene, YUC2, was significantly upregulated in drought across all leaf developmental stages, where other YUCs either remained unchanged or were reduced. In shoot apices, YUC1 was downregulated. In L8, only YUC2 was significantly affected. In L16, YUC1, YUC4, and YUC12 were all downregulated in drought. The fact that YUC2 was upregulated in L8 but not in L16, where only L8 was shown a reduction in RWC, may suggest that YUC2 was increased in response to ROS production (RWC was not measured on apices). In contrast, the fact that no YUCs were significantly reduced in expression in apices or L8 suggests that IAA biosynthesis may not be directly affected by drought. Future work should measure IAA concentrations in leaf tissue under drought to better understand these hormonal cues.

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Topic: Contributed Papers

Title: Evaluating the early events in the evolution of C4 photosynthesis in Tribulus (Zygophyllaceae)

Author: ***Arthur Leung @ University of Toronto***

Keywords: C4 photosynthesis,gas exchange,trait evolution,Zygophyllaceae,C2 photosynthesis,C3-C4 intermediate,proto-Kranz,mitochondria

Abstract:

C4 photosynthesis is a complex evolutionary trait which evolved independently over 60 times. To study the mechanisms of how the C4 pathway evolved with such repeatability, it is useful to employ a comparative approach where its evolutionary acquisition by distinct lineages is evaluated. Genera known to have both C3 and C4 species and species with intermediate character states are prime candidates for comparative studies of C4 evolution. In this study, we characterize the physiology of C3-C4 intermediate species in Tribulus which are prostrate herbs of hot, semi-arid habitats. We grew ten Tribulus species under common conditions in growth chambers and examined leaf gas exchange, anatomy, and ultrastructure. C3-C4 intermediacy in this genus occurs in at least two species: T. cristatus and T. astrocarpus. Tribulus cristatus is a typical C3-C4 intermediate using C2 photosynthesis, a physiology where photorespiratory glycine is shuttled into the bundle sheath. Tribulus astrocarpus exhibited traits characteristic of an early phase of C4 evolution termed proto-Kranz, as demonstrated by concentration of mitochondria to the interior of the bundle sheath cells in the leaves. Other C3 species exhibited varying degrees of organelle concentration in the bundle sheath cells. We show that leaf structural modifications were associated with decreased photosynthetic CO2 compensation point, decreased ratio of intercellular to ambient CO2 concentrations, and increased intrinsic water-use efficiency. The proto-Kranz character state has only been identified in a few lineages of C4 photosynthesis (notably Steinchisma, Euploca, and Flaveria). With the addition of T. astrocarpus, we provide key evidence that the proto-Kranz character state is a common initial step in C4 photosynthetic evolution.

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Ecophysiology

Topic: Contributed Papers Ecophysiology

Title: Role of stem photosynthesis and elevated CO2 on the drought response of a late-successional Neotropical tree species

Author: ***Eleinis Ávila-Lovera @ University of Utah***

Keywords: tropical forest,water potential,stem photosynthesis,leaf photosynthesis,panama,non-structural carbohydrates,elevated CO2

Abstract:

It is widely known that stem photosynthesis plays important roles in the growth and survival of plant species from deserts and Mediterranean-type ecosystems. However, it is less clear how these advantages extend to species from wetter ecosystems, such as the wet tropical forests of Panama. We asked whether preventing stem photosynthesis had a negative effect on saplings of Calophyllum longifolium (Calophyllaceae), and whether this effect could be reverted by previously exposing plants to elevated [CO2]. We first exposed half of the saplings to 2000 ppm of [CO2], while the other half remained at ambient [CO2], for one month. We then placed the plants under a rain shelter and covered the stems of half of the plants in each of the [CO2] treatments to block stem photosynthesis and allowed the plants to dehydrate by withholding watering. We monitored pre-dawn leaf water potential (Ψpd), specific leaf area, leaf and stem temperature, leaf and stem gas exchange in light and dark every three days for two months, and also collected leaf and stem samples five times to analyze non-structural carbohydrates (NSC) as the drought progressed. There was no significant difference in Ψpd between elevated and ambient [CO2] treatments before or after the onset of drought, and there was no effect of light exclusion. However, Ψpd decreased from -0.20 MPa to almost -4 MPa as the drought treatment progressed. Before the drought treatment, leaf photosynthetic rate (A) was greater in the ambient [CO2] than in the elevated [CO2], despite lower stomatal conductance in the former. Stem photosynthetic re-assimilation rate (Ares) was also greater in the ambient [CO2] than in the elevated [CO2], although plants in both treatments had similar percent re-assimilation indicating differences in dark respiration in the stems with [CO2]. After the onset of drought, values of A in the ambient [CO2] treatment decreased more than those in plants subjected to elevated [CO2]. As expected, stem Ares was lower in the light-excluded stems, but light exclusion did not influence leaf mortality. Surprisingly, plants in the elevated [CO2] suffered greater leaf mortality. Overall, neither previous exposure to elevated [CO2], which did lead to greater NSC in plant tissues, nor allowing stem photosynthesis to occur had an important role in explaining plant responses during drought in Calophyllum longifolium saplings.

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Ecophysiology

Topic: Contributed Papers

Title: High-throughput phenotyping with laboratory cold tolerance assays

Author: ***John Butnor @ USDA Forest Service, Northern Research Station***

Keywords: freezing tolerance,Local adaptation,Phenotyping,relative electrolyte leakage,cold tolerance,Ulmus americana,Cicer arietinum,Pisum sativum

Abstract:

Plant tolerance of freezing temperatures results from plastic and genetically-based responses to environmental cues that trigger biochemical processes related to seasonal dormancy. It is not advantageous from a fitness standpoint to maintain high cold tolerance throughout the year, so populations have adapted to their local environment by fine-tuning phenological traits, including cold tolerance. Quantifying variation for cold tolerance may be especially important for conservation or restoration efforts (e.g., assisted migration), as well as breeding programs for disease resistance (e.g., American chestnut, American elm) or crop improvement, in which progenitors may be adapted to different climates than the offspring. These and other research efforts in plant biology would benefit from high-throughput phenotyping of cold tolerance to parameterize climate suitability.

Relative electrolyte leakage (REL) has been used for decades to provide a laboratory assessment of the degree of injury caused by exposure to cold temperatures. In the REL assay, replicates of tissue are exposed to increasingly cold temperatures in a test chamber and sequentially removed at specific minimum temperatures. When cells freeze and rupture, electrolytes are released and are detectable in solution with a conductivity meter. The data are commonly summarized on a relative basis as the temperature where 50% of the electrolytes have been released and cellular repair is unlikely. The laborious nature of handling thousands of samples necessary for the sequential temperature intervals, and the lack of commercially available multi-sensor equipment for measuring electrical conductivity has constrained widespread adoption of the REL approach. Recently, a new high throughput REL system for assessing plant cold tolerance was developed by the USDA Forest Service in Burlington Vermont . This has helped our group explore the potential of using REL for phenotyping variation in adaptation to seasonal environments, in addition to traditional growth and phenology measures.

Using examples from forest trees (Ulmus americana) and overwintering crop species (Cicer arietinum and Pisum sativum), we describe the diagnostic features of the REL temperature response curve and estimation of its parameters for use in phenotyping. The temperature response curve is very similar to a dose response curve fitted with a logistic or sigmoid model. The curve is bounded by Ymin and Ymax and the temperature where any percentage of electrolyte leakage i.e., 10%, 20%, 50%, may be determined. Using cold tolerance assays, we demonstrate the system’s high-throughput application to phenotyping two staple leguminous crops, Cicer arietinum (chickpea) and Pisum sativum (common pea) for sensitivity to freezing and to predict critical injurious temperatures. We also report an example for the forest tree Ulmus americana, in which differences in cold tolerance were observed in selections sourced from across a latitudinal gradient when grown in a common garden.

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Topic: Contributed Papers Ecophysiology

Title: The effects of competition × drought interactions on above- and below-ground traits in sorghum

Author: ***Shiran Ben-Zeev @ Pennsylvania State University***

Keywords: Competition,Sorghum

Abstract:

As soil resources worldwide are depleting, while the demand for food promises to continue to grow, there is a pressing need to produce more from less input. One important factor influencing stand- and community-level plant performance are plant-plant interactions under resource limitation. Plants compete for sunlight above ground by increasing leaf area and stem height. Belowground, competition mechanisms include increasing root biomass and reducing the size or changing the direction of competitors' root systems. While competition can benefit individuals, it may lead to negative outcomes at the stand level. Hence, understanding the developmental and physiological response to competition and its underlying genetic basis might enable the rational design of plantings and breeding for higher performance in agriculture. Sorghum plants from 10 traditional local varieties were grown with and without plants of a common competitor genotype, under well-watered and drought conditions in pots. Competitor stems were forced to grow sideways to prevent shading. Our results show that competition acts as biotic stress, limiting relative and absolute growth rates starting from 10 days after sowing and leaf area at 35 days after sowing. The presence of competitors under well-watered conditions had a comparable effect to drought without competitors. The genetic variance was observed between landraces, with some responding more severely to competition than drought. In addition, we demonstrate the relationship between the root system architecture of different landraces and their competition response. Our study reveals how early below-ground competition affects subsequent above-ground development. In this research's next step, we plan to use the lines reported here to identify the genetic basis of competition response.

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Topic: Contributed Papers

Title: Variation in mycorrhizal response traits across plant species and fungal isolates

Author: ***Katie Stahlhut @ Miami University***

Keywords: arbuscular mycorrhizal fungi,functional traits,plant-fungal interactions,response traits,function value trait modeling

Abstract:

While a majority of plant species allocate carbon to mycorrhizal fungi symbionts as a part of their nutrient acquisition and growth strategies, the effects of mycorrhizal symbiosis on plant growth are highly variable across plant and fungal partners. Even though plants can receive many benefits from mycorrhizal symbiosis, such as growth promotion, increased nutrient uptake, increased drought tolerance, and disease and herbivore resistance, aboveground biomass response is the primary trait studied to assess the effects of mycorrhizal symbiosis. The growth benefits provided by different mycorrhizal fungi isolates also vary, but how other benefits from mycorrhizal symbiosis vary across fungi is currently unknown. Here we present data from two different experiments assessing variation in mycorrhizal response traits across plant species and across fungal isolates.

In the first study, we assessed plant functional trait responses to mycorrhizal symbiosis. We identified two tradeoff axes for plant trait responses to mycorrhizal fungi. The first axis describes roughly half of the variation in plant response and is defined primarily by allocation to aboveground plant biomass. The second axis describes allocation to roots, and this axis was not associated at all with aboveground biomass response. We also used function value trait (FVT) modeling to assess the growth of plants over time, which shows that species have different growth rate and total biomass responses to mycorrhizal symbiosis. These results indicate that while aboveground biomass production is an important plant response to mycorrhizal fungi, only using mycorrhizal growth response as a proxy for mycorrhizal responsiveness may dramatically misrepresent the functional importance of mycorrhizal symbiosis in some plant species.

In the second study, we grew Andropogon gerardii with different mycorrhizal isolates and measured plant, fungal, and soil response traits. We measured how different mycorrhizal isolates affected above-ground plant growth over time. We also identified isolate differences in plant allocation to belowground tissues, and we measured the effects of different fungal isolates on soil properties including soil carbon and the formation of water stable aggregates. These results provide evidence that these mycorrhizal isolates are functionally distinct in their effects on plants and contribute to different mycorrhizal symbiosis traits. Combined with the first experiment, we show that plant and fungal identity both greatly impact mycorrhizal response, including those that are not often measured like root and soil traits. This data suggests that in order to adequately measure plant traits associated with mycorrhizal symbiosis, we must fully consider the impacts of plant and fungal identity on the whole plant physiology.

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Physiology

Topic: Contributed Papers Ecophysiology

Title: Photosynthetic performance and recovery potential of wild Juglans regia accessions under California natural heat waves

Author: ***Mina Momayyezi @ University of California Davis***

Keywords: germplasm,Photosynthetic capacity,Heat wave,Heat recovery,,Irrigation,Juglans regia

Abstract:

Heat stress reduces photosynthetic capacity, quality, and yields causing significant economic loss. In most cropping systems, the lack of cultivars with more resilience to heat wave cycles put perennial crops such as walnut commercial production under severe threat. The available walnut cultivars are highly sensitive to higher temperatures causing significant annual loss and inducing long-term susceptibility to other stressors. Germplasm collections provide a diverse cultivar option and hold the potential for improving crop productivity under heat tolerance. Over a two-year study, we screened 11 Juglans regia accessions for physiological responses to heat stress and recovery potential in the USDA-ARS National Clonal Germplasm. Net assimilation rate (An) under heat and recovery in response to irrigation differed significantly among accessions; accessions 3 and 5 with inherently higher An exhibited greater An under 35° and 40°C before irrigation and were the only accessions to have the highest An under those temperatures after irrigation. Stomatal conductance (gs) declined under higher temperatures for most accessions, while leaflet water potential decreased in a few accessions under high temperatures. When a subset of accessions including two high-performer (A3 and A5) and two low-performer (A1 and A8) were monitored over two full heat waves, we found the high-performer ones to keep their An higher than A1 and A8 under both 35°C and 45°C even before irrigation. A5 exhibited the highest performance under 35°C after irrigation, similar to its performance at the baseline which was prior to heat wave cycles. Greater An in A3 and A5 was supported by higher maximum carboxylation rate, electron transport rate, maximum photosynthesis, and photosystem II efficiency, in line with their higher carbonic anhydrase activity. In conclusion, J. regia accessions with inherently higher An and gs showed greater tolerance and recovery in response to irrigation under natural heat stress, supported by their greater biochemical and enzymatic activities.

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Ecophysiology

Topic: Contributed Papers

Title: Life at the extreme: understanding how hydraulics constrain some of the longest living pines to unique elevational positions

Author: ***Steven Augustine @ University of Wisconsin Madison***

Keywords: alpine,hydraulics,Pinaceae

Abstract:

Water moves through plant xylem conduits to replace the enormous volume of water transpired from leaves. This transport is driven by a negative pressure gradient and is inherently vulnerable because air entry into the system can render it dysfunctional. The air bubbles in the xylem that block water flow are most frequently caused by drought and freeze-thaw cycles. In response to freeze-thaw cycles, selection has favored narrower conduits. In tracheid-bearing conifers, drought tolerance is related to how much the torus overlaps the pit aperture, with drought tolerance increasing as torus overlap increases. Despite the importance of these traits to hydraulic functioning, there is a lack of information on how they vary within species. This study looked at how hydraulic traits, including both tracheid diameter and torus overlap, varied within three Pinus species (P. balfouriana, P. contorta, P. monticola) along an elevational gradient (2600 – 3300m). Within the three species, one spanned the entire gradien (P. contorta), while the others were excluded from either lower (P. balfouriana) or upper (P. monitcola) elevations. We found distinct species-specific trends, with each species having unique hydraulic syndromes. Species found at higher elevations had more conservative hydraulic traits (e.g., narrower conduits, lower hydraulic conductivity), while species at lower elevations were more hydraulically efficient, likely due to the underlying anatomy. While intraspecific variability was low, the large interspecific trends suggest that the underlying hydraulics of each species constrains it to distinct elevational positions.

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Ecophysiology

Topic: Contributed Papers

Title: Intraspecific Variation in Leaf Functional Traits in a Widespread Manzanita Species

Author: ***Angela Buehlman @ UC Riverside***

Keywords: functional traits

Abstract:

It has been suggested that populations of a species that occur at the edges of its range are more prone to collapse and generally do not perform as well as populations near the center of the species range, but this has yet to be established as consistent across species. Functional traits in plants are those that illustrate a particular aspect of how an individual or species has adapted to or is affected by its environment. These traits can be morphological, physiological, or phenological in nature. Leaf functional traits play an important role in various processes, including plant growth and response to abiotic stressors, and have been shown to vary between species, communities, and habitat types. There are, however, few studies which have looked at intraspecies variation in leaf functional traits. In order to better understand how these traits might vary between edge of range and center of range populations, as well as how a species might react to a changing climate, we will measure various leaf functional traits associated with drought tolerance in a widespread manzanita species, Arctostaphylos glauca.

Arctostaphylos glauca, the big berry manzanita, is one of the relatively few widespread species of the genus and has populations which occupy a range of habitat types throughout much of the California Floristic Province. The majority of A. glauca populations occur in chaparral habitats, but there are a few populations on the edges of its range which are in atypical environmental conditions, including maritime coastal locations, montane areas, and a known desert population. We examine a suite of leaf functional traits associated with drought tolerance to determine if there are significant differences in the means and variance of those traits between populations of A. glauca found at the edges of its range and those which occur in its more typical chaparral habitat. We also investigate if these drought-associated leaf functional traits vary with seasonal changes throughout a year.

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Ecophysiology

Topic: Contributed Papers

Title: Ecophysiological significance of photosynthetic nitrogen use efficiency and nitrogen allocation in an orchid community in karst limestone region

Author: ***Mei Yang @ College of Forestry, Guangxi University, China***

Keywords: Photosynthetic nitrogen use efficiency; Nitrogen allocation; Karst limestone region,Orchid

Abstract:

Orchid species are densely distributed in some karst limestone hilltop areas in southwest China, in which they become the dominant species in the herbaceous layer with epiphytic orchids having greater advantages over terrestrial orchids in both species number and population size. However, the ecophysiological adaptation of these sympatric orchids belonging to different growth forms are not fully understood. In this study, photosynthetic characteristics, leaf mass per area, leaf chlorophyll content traits, leaf nitrogen content and nitrogen allocation strategies in leaves of 22 epiphytic orchids and six terrestrial orchids in a karst limestone hilltop area in Yachang Orchid National Nature Reserve in southwest China were compared. The results showed that compared with terrestrial orchids, epiphytic orchids had lower light-saturated photosynthetic rate, photosynthetic nitrogen use efficiency, chlorophyll content, chlorophyll a/b ratio, leaf nitrogen content and leaf nitrogen content in photosynthetic apparatus, indicating that epiphytic orchids allocated more resources (nitrogen) into the construction of leaves with stronger resistance at the expense of photosynthetic capacity. The combination of these functional traits fits well with surviving and thriving in the karst limestone environment, under low-light intensity, low precipitation, low soil mass and low soil water retention. These results are essential for understanding the ecological adaptation of orchid species in subtropical karst limestone region.

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Topic: Contributed Papers Education and Outreach

Title: The Leo A. Galloway Herbarium at Missouri Western State University- showcasing floral specimens from North West Missouri and adjacent areas to build an educational and research tool

Author: ***Tilottama Roy @ Missouri Western State University***

Keywords: Biodiversity,Education,herbaria,Undergraduate Research

Abstract:

An herbarium is a critical resource for biodiversity, and ecological and evolutionary research studies. The Leo A. Galloway herbarium housed in the biology department at Missouri Western is comprised of dried, preserved and annotated specimens of over 3000 valuable plant species, particularly native to the mid-western United States. The herbarium collection is maintained and stored in Agenstein Hall in the biological sciences department. Dr. Leo A. Galloway, a former biology faculty, was a plant taxonomist and he worked on the genus Abronia, which belong to the Nyctaginaceae family. Dr. Galloway established the herbarium in 1972 and most of the specimens in the herbarium were collected by him. Most of the Leo A. Galloway Herbarium collections are from the midwestern United States, specifically northwest Missouri. So far, we have catalogued more than 10 gymnosperm families, 13 monocot families and more than 65 eudicot families in our herbarium (~ 1500 herbarium specimens), to complete work on the entire collection comprising of approximately 3000 plant specimens, housed within it. Our goal is to continue working on cataloging, databasing and circumscribing the taxonomical definitions of the remaining ~1500 specimens in our herbarium, to be indexed into the Index Herbarium, maintained by the New York Botanical Garden's William and Lynda Steere Herbarium. Future plans involve collaborative initiatives towards digitizing the specimens, and building a website showcasing the entire collection, with a link to access it virtually through Missouri Western's biology department's website. In a world of virtual research and learning, this will prove to be immensely valuable.

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Topic: Contributed Papers

Title: Using General Interest Science Books to Arouse Student Interest and to Substitute for an Introductory Textbook.

Author: ***Marshall Sundberg @ Emporia State University***

Keywords: General interest reading,textbook

Abstract:

For years teachers have provided students with lists of general interest books "for further reading" or even for supplemental assigned reading (see Knoblock, 1968, Plant Science Bulletin 14:4-6 for such a list). In the early 1990's, at LSU, I first began assigning students to read and critique up to three general interest biology books per semester, chosen from an annotated reading list. My objectives were first, to stimulate interest and introduce critical reading skills to students, but also to provide students an opportunity to earn a significant number of relatively easy points towards their class grade. I have continued to do this in all of my courses, both majors and nonmajors, undergraduate and graduate. Depending on the course, I limit students' choices to specific topic areas on the reading list. This annotated list will be shared. Beginning in 2000, I began teaching a mixed majors/non-majors honors Biology course. It serves as a general education lecture and lab for non-science majors and substitutes for the majors' introductory biology lecture and laboratory, the pre-requisite for all upper-level biology courses. The "lectures" are discussion-based; rather than a textbook I use four selections from the reading list, chosen to illustrate at least three of the following topics: organismal biology (structure/function); ecology; evolution/genetics; molecular biology; and critical thinking skills. Some of the books used will be highlighted. For reference, students have access to a number of standard majors' textbooks in the lab as well as the OpenStax Biology online textbook. On a standardized assessment, given to both majors' biology and honor students, the honors course typically outperforms the majors and some of the highest scores are from English and Economics majors. Choosing the "best" textbook for a majors course is less important than actively engaging students.

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Topic: Contributed Papers

Title: Seeing and questioning plants - a botanical perspective on nature journaling at the college level

Author: ***Lena Struwe @ Rutgers University***

Keywords: teaching,Education,Outreach,nature journaling,hands-on learning,art,informal education,plant awareness disparity,engagement,college teaching,sci-art,mental health

Abstract:

Nature Journaling, in the sense of the fantastic educator John Muir Laws' journaling and education methods (see https://johnmuirlaws.com/) is a superb tool to develop important scientific, art, and life skills among undergraduates (and others too, of course). Such skills include learning how to see, notice, and observe, how to ask open-ended and novel questions about what you see, to create a stronger sense of place, and how to synthesize that information into connected relationships between experiences, facts, observations, and memories. The integration of words, visuals, and numbers (quantitative data) is also important. In our recently developed nature journaling classes at Rutgers University where we have developed a college-level curriculum that is open to majors in any field, including students that have none to a lot of experience in art and/or science, and addresses many aspects of exploring and discovering everyday nature and biodiversity. Assignments can be tweaked to be plant-focused, and includes such as The Sit Spot, Zoom-in & Zoom-out, Modularity in Nature, String Safari, Fear of Nature, Mapping and Slicing Landscapes, Human Detritus, Natural History Collections, and Change over Time (many of these where invented by other educators; we provide descriptions in our outreach materials). Our assignments and topics are easily adapted as one-time assignments in plant science or other biological courses, which we also have implemented in botanical diversity and a study abroad course in tropical biology. Nature journaling is not about doing fine art, quite the opposite, and it is about developing skills in observation, thinking, and creating conclusions that go a step further. It has also turned out to be an excellent method to slow down high-paced lives, create meditative moments, and flow as part of creativity. We will discuss how to implement nature journaling in your class, present our curriculum for whole classes, and provide examples of one-time course assignments. Free teaching materials associated with nature journaling will be available for download on BotanyDepot.com at the time of the conference, we also strongly encourage you to visit John Muir Laws excellent website with additional resources (see link above).

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Topic: Contributed Papers

Title: Helping college students disentangle pollination, fertilization, and seed dispersal

Author: ***Dianne Anderson @ Point Loma Nazarene University***

Keywords: Education,flowers,seeds,Pollination

Abstract:

Teaching the reproduction of flowering plants is a central topic in general botany courses, yet students are often confused about the role of flowers and fruits in the process. In addition, pollination, double fertilization and seed dispersal are often entangled in students' minds. Having students develop a functional model of flowering plant reproduction requires them to identify the challenges of reproduction, and then list potential solutions accomplished by both flowers and fruits. Students then test their model by considering various unusual flower and/or fruit examples. When the new examples cannot be explained by their model, students must modify it to account for the new examples. Biology concept cartoons can also be used to enhance instruction on this topic by encouraging small group discussion, followed by deciding which character in the cartoon is correct. These cartoons provide the practice that students need in thinking about the topic to go beyond memorization to meaningful learning.

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Education and Outreach

Topic: Contributed Papers Education and Outreach

Title:

Teaching botany students how to identify wildflowers and grass-like plants in the winter condition: A simple three-step process that uses a multiple access visual key

Author: ***Bob Noyd @ U.S. Air Force Academy***

Keywords: identification,Undergraduate teaching

Abstract:

In the mountainous western part of the U.S., plants are in the winter condition for most of the spring semester. Therefore, students will need to encounter, collect, and identify plants in the dried winter condition to meet course learning goals. However, this is particularly challenging for beginning students because they encounter specimens in nature with parts that are shriveled and dried, bleached by the sun, shredded by the wind, broken, or shed by the plant altogether. Leaves, flowers, fruits, or seeds may or may not be displayed, which makes a traditional dichotomous key difficult to construct and frustrating for students to use. To overcome this challenge, I developed a simple three-step process that includes an observation checklist, which leads to a multiple access visual key, which in turn, leads to a plant profile page where students can confirm their identification. Each of the 185 plants featured in the key can be accessed through at least two different characters. For example, common cattail can be identified by following the key through plant height (tall), fruits-seed dispersal (fluffy plumose), or inflorescence type (spike-like) features. The instructional approach started with modeling the entire identification process for students. Next, students individually worked through the observation step to identify distinct features of several unknown plants. Finally, they were challenged with six unknown plants to identify. Once familiar with the 3-step process, my 40 students identified an unknown winter plant in an average time of 5-7 minutes. Students reported that the identification process using these tools was effective, efficient, and enjoyable.

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Education and Outreach

Topic: Contributed Papers

Title:

Teaching botany students the light reactions of photosynthesis: Applying the principles of cognitive load theory for more effective learning.

Author: ***Bob Noyd @ U.S. Air Force Academy***

Keywords: photosynthesis,Undergraduate teaching

Abstract:

Students frequently are overwhelmed by the complexity and difficulty of learning the light reactions of photosynthesis because there are many elements of the process for them to think about and master. This essential process involves several macromolecules, electrons, and protons moving in different compartments and locations, causing different chemical reactions to produce different products. The number of learning elements and their interactions, plus a lack of prior knowledge places a high demand on the minds of introductory botany students. This demand, or cognitive load, can be better managed by applying the principles of the cognitive load theory, which is a series of instructional recommendations based on how humans learn. I will present several strategies to optimize intrinsic load (nature of the material) such as pre-teaching vocabulary, segmentation, sequencing, and chaining, as well as reducing extraneous load (things we do as teachers) through creating more effective PowerPoint slides and reducing problems associated with animations. Many of these same principles can be applied to the Calvin cycle and other topics to create a more effective instructional design and increase student learning.

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Education and Outreach

Topic: Contributed Papers

Title:

An experiential learning approach to engage diverse student groups with climate change issues: Clarkia Miocene fossil flora as an example

Author: ***Taylor Vahey @ Bryant University***

Keywords: climate change,experiential learning,Plant fossil,Education,Clarkia,underrepresented students,middle Miocene

Abstract:

Climate change has emerged as the defining issue of the century for humanity with far-reaching impacts beyond the scientific community. Plant fossils help geoscientists understand ancient vegetation and their response to climate change, thus quantify surrounding environmental changes of millions of years, especially humidity and carbon dioxide concentration, through stomatal index, length and width of guard cells, shape, and quality of preservation.

New approaches to attract diverse student populations, especially women-identified, racial and ethnic minorities, and international students who are disproportionally underrepresented in geoscience fields but more affected by the climate changes are urgently needed. We advocate for an experiential learning approach to enhance learning of climate change and to effectively and creatively communicate the evidence of climate change to wider student populations.

We illustrate the advantage of such an experiential learning approach designed for the “Clarkia Miocene Climate Change Workshop: Facts, Forces, and Future,” an NSF-funded interdisciplinary and collaborative research and education program. The world-renowned Miocene Clarkia Lake in northern Idaho is closely associated with the Columbia River Basalt volcanic activities and facilitated the exceptional preservation of a diverse fossil flora and their biomolecules. The diversity, abundance, and exquisite preservation of the Clarkia fossil flora made it an idea outdoor laboratory for experiential learning. Our recent radiometric dating from interbedded volcanic ashes places the annually-resolved deposit at 15.78 ± 0.039 Ma, directly associated with the Miocene Climate Optimum. The atmospheric CO2 concentrations during that period was at the level that the human society is projected to reach in the coming decades, making it an attractive analogue to visualize the impact of near-future warming.

Designed to attract underrepresented students, several components were deliberately built into the real-world experience in questioning, reflection, and application process on top of the geoscience program to motivate and empower diverse student groups. Due to its global nature with differential local impacts, multi-disciplinary academic characteristics, and cross-cultural components, climate change topics are ideally suited in experiential learning programs with international perspectives, thus having the potential to generate life-long active engagements beyond traditional university settings for students to make a difference in the rapidly changing world

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Topic: Contributed Papers Education and Outreach

Title: Inspiring Collective Environmental Stewardship in an Urban Landscape by Increasing Science Accessibility and Building Community

Author: ***Tohmi Barrett @ The New York Botanical Garden***

Keywords: Citizen Science,community,community engagement,iNaturalist,Phenological tracking,Urban ecology

Abstract:

New York City is home to immense biodiversity. The NYC EcoFlora Project combines traditional outreach activities with the iNaturalist platform to increase awareness of and appreciation for urban biodiversity by engaging the public, fostering a sense of communal stewardship, and generating open source biodiversity data. The EcoFlora Project is a community science project led by the New York Botanical Garden to document and conserve the plants of NYC. It aims to amplify the role of community members in the scientific process of documentation and identification, who use iNaturalist to produce species checklists, track emerging invasives, document phenology, and make detailed observations of rare or potentially undescribed species. To date, nearly 20,000 observers have made about 900,000 observations of more than 6,000 species of plants and fungi in NYC. The NYC EcoFlora is a real-time, ongoing checklists of organisms—the first ever attempt to comprehensively document the diverse and ever-changing ecology that remains embedded within the city. The result is a dynamic resource for conservation planning as well as for New Yorkers who seek to increase their awareness about the more-than-human world.

In this talk we will share experiences and insights working with New Yorkers and iNaturalist to document biodiversity in a bustling urban landscape. Whether you have the resources of an institution like a botanic garden or university, or are a community-based, volunteer-run organization, we hope to continue to provide inspiration and support to similar initiatives to involve the community in the conservation of local and global biodiversity.

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Topic: Contributed Papers

Title: Budburst: Using community science in schools and with community organizations

Author: ***Emma Oschrin @ Chicago Botanic Garden***

Keywords: Citizen Science,climate change,Community science,monarch butterfly,plant-pollinator interactions

Abstract:

Budburst, a community science program hosted at the Chicago Botanic Garden, pursues two primary goals: Research and education. Budburst brings together researchers, educators, gardeners, and community scientists on a shared journey to uncover the stories of plants affected by human impacts on the environment. Budburst tells these stories through data collection, data sharing, education, and personal connections. We run three concurrent research projects broadly focused on plants and climate change and plant-animal interactions. We connect with community scientists by working with community organizations, libraries, and schools.

Budburst is building partnerships with local Chicagoland high schools and colleges to work on our Pollinators and Climate project. This project is ideal for high school and college students because they can observe plants and pollinators over the course of a semester, explore their own independent research questions in the context of the broader project, and learn valuable data management and analysis skills by examining both their own data as well as the larger project database. This project has been successful at giving students hands-on research experience, teaching content focused on place-based climate science, ecology, plant life cycles, plant-animal interactions, and more. We invite educators and researchers who engage with the public to learn about this research program and bring it to schools near them.

For our Milkweeds and Monarchs project, we investigate whether monarch butterflies preferentially lay eggs on flowering or non-flowering milkweed stems. We partner with local Chicago community organizations, libraries, and Forest Preserve sites to train participating community scientists, gather data, and disseminate educational information in English and Spanish. We've managed virtual and in-person trainings, run bilingual trainings, and found success by providing educational materials, take-home kits that included plants and magnifying glasses, and funding to both organizations and participants. Budburst would like to share successful practices, lessons learned, and ways we plan to iterate and improve. We invite community scientists and organizations to join the project; data can be collected across the entire monarch migration route.

Budburst is a project that can be adapted for students ages K-12, higher education, and adults and is an easy and interactive way to engage the public in authentic scientific research. We invite educators, researchers, community scientists, and conservation organizations to join the project and see what Budburst has to offer!

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Education and Outreach

Topic: Contributed Papers Education and Outreach

Title: Communicating the Effects of Toxic Plant Genera to Cat Owners

Author: ***Amelia Schmidt @ Virginia Tech***

Keywords: Outreach,Toxicology,Feline,Companion Animal

Abstract:

In the United States, feline poisonings account for approximately 7% of calls to the Animal Poisoning Control Center (APCC). Many house and garden plants are toxic to domesticated cats, and these cats are at risk of interacting with toxic plants due to behavior and innate curiosity. Owners must be aware of potentially toxic plants in their homes to properly ensure their animals' health and welfare. We compiled a guide to poisonous plants for cat owners in Virginia to increase owner efficacy in the identification of potentially toxic plant genera, as well as educate owners on the signs and symptoms of plant-generated toxicosis in felines. The guide addresses the 16 most reported plant genera recorded through the ASPCA poisoning hotline and provides information regarding plant identification and toxicological effects when ingested. Though a total of 200 plant genera were reported as toxic to felines via the hotline, those with under 20 occurrences were excluded from the guide. The genera Lilium, Spathiphyllum, Alstroemeria, Allium, and Hemerocallis constituted the most reports and thus were highlighted in the guide along with 11 other plant genera submitted to the call center. Most plant genera cited in the guide were non-native ornamental plants. These ornamentals are common house and flowering plants and are likely used in decorative settings such as flower bouquets or for aesthetic purposes. We performed a literature review in order to collect information on identifying features of toxic plant genera, symptoms, time of onset, and toxic portions of the plants. Literature findings were sorted by genera and then combined into paragraph form for the guide. Not all the genera reported are regarded as true toxins as certair genera, such as Alstroemeria, are classified as irritants and do not cause death. The most common affected areas of the animal after ingestion or contact with a genus regarded as toxic to cats include gastrointestinal tract and renal upset, nervous system disruption, throat and facial irritation, and cardiac dysregulation. Within the gastrointestinal and renal systems, symptoms of vomiting, anorexia, and irregular urination are common. Disorientation and ataxia are common symptoms regarding nervous system disruption while swelling and excessive salivation are associated with throat and facial irritation. Symptoms of cardiac dysregulation include irregular heart rate or breathing. Overall, the guide aims to provide owners with knowledge about toxins their cats may be exposed to prevent feline poisonings and ensure that their feline companion remains safe in their home environment.

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Education and Outreach

Topic: Contributed Papers

Title: Outreach and Publicity: The Ancillary (and Often Overlooked) Benefits of Canine Detection for Plant Detection, Biosecurity, and Early Detection and Rapid Response (EDRR).

Author: ***Pete Coppolillo @ Working Dogs for Conservation***

Keywords: Education,Invasive,Outreach,Biosecurity,Detection,Rapid Response,Prevention,Canine,Dogs,Publicity

Abstract:

The utility of specially trained dogs for plant detection is well demonstrated for rare, cryptic, and invasive species, and this utility can be instrumental in Early Detection and Rapid Response (EDRR) efforts. However, an often-overlooked benefit of canine teams is their value for outreach and education, which can significantly expand EDRR efforts by engaging a broader constituency. Here, we present two case studies from the Rocky Mountain regions of the U.S. and Canada demonstrating how canine teams can add value and impact to plant detection and management through increased public awareness, sympathy, and engagement. Strategic communications raised awareness of, and compliance with, invasive species control measures through earned media and direct contact with stakeholders at little additional cost. In one case, the estimated value of the publicity generated by the dog teams was over $CA1M. Practitioners using conservation canine teams should seize these opportunities when their programs depend on public support and/or compliance, and these benefits may make canine methods more cost effective compared to other approaches that do not provide concomitant outreach benefits.

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Education and Outreach

Topic: Contributed Papers

Title: The Hand Lens: Connecting Citizens with Cryptogamic Communities

Author: ***Amanda Chandler @ New York Botanical Garden***

Keywords: Decolonization,Outreach,Science communication,lichens,bryophytes,digitization,Cryptogams,GLOBAL TCN

Abstract:

The Hand Lens (THL) is an online public storytelling platform created with the goal of increasing access to botanical natural history collections (NHCs). By linking NHC data procured from digitization projects to relatable stories, information held within and surrounding herbaria can be made more accessible to groups other than what is traditionally considered as the scientific research community. One such digitization project is the large-scale GLOBAL Bryophyte & Lichen Thematic Collections Network (TCN), which links 25 herbaria across the United States with the baseline goal of digitizing all extra-North American lichen and bryophyte collections within them. A significant emphasis of the GLOBAL TCN lies in public education and outreach. Discussion surrounding the use of digital NHC data tends to center more on hov this information can further scientific research and less on how it can be used to enrich the general public and raise awareness of under-recognized groups of biodiversity. Since its launch in April 2019, THL has published 387 stories covering a variety of topics. Articles range from brief features of charismatic specimens to highlighting collectors from marginalized groups and the interwoven colonial history surrounding botanical expeditions and collections. I told with a sense of accountability and honesty, collections-based stories can publicly support a more inclusive dialogue concerning the social and cultural issues that are inevitably coupled with botanical history. THL also provides an opportunity for digitization interns to participate in writing science communication articles and to delve further into the cultural and social conversations surrounding the history of the collections they are working with. Here we explore how this public platform has been used to connect the general public with the relatively underrepresented realm of cryptogamic botany and the stories of the people who have contributed to the field.

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Ethnobotany

Topic: Contributed Papers Ethnobotany

Title: An overview of plant poisoning trends in Virginia: domestic animal cases from 2001 - 2021

Author: ***Kiya Rahn @ Virginia Tech***

Keywords: Virginia,Toxicology,Companion Animal,plant poisonings

Abstract:

Companion animal poisoning cases resulting from exposure or suspected exposure to plant material are a common occurrence in the United States. From cultivars to native plants, outdoors and inside, many plants pose dangerous health risks to domestic pets. We examined a dataset provided by the American Society for the Prevention of Cruelty to Animals (ASPCA)'s Animal Poison Control Center (APCC), a diagnostic and treatment hotline that condenses reports of pet poisonings and details in the Antox database system. Such toxicology events are characterized by poisoning agent, animal species involved, date, and location. The original dataset consisted of 111,276 call records spanning from 2001-2021; after quality control and data filtering, plant-related poisoning records of domestic dogs and cats in Virginia accounted for 7.25% of the total call volume. Canines accounted for 73.6% of this subset, while felines accounted for 26.4%. Plant families Genera Vitis sp. (table grapes), Lilium sp. (true lilies), and Allium sp. (onion, garlic, etc.) accounted for 37.8% of plant call volume. Additionally, domestic animals exposed to harmful plant tissue were asymptomatic in 56.4% of cases. This number was markedly higher for cats than dogs; felines presented with symptoms in 57.7% of cases, while canines presented with symptoms in only 38.6% of cases. We further examined these data for trends over geography, time, and other demographics and found northern Virginia disproportionately represented the number of reports per capita as compared to central and southwest VA; we determined Falls Church City, VA to have the highest density of plant-related poisoning reports per capita. As the APCC is a paid service, we hypothesized differences in median income in the state were responsible for this bias. We utilized publicly available income data and ArcGIS Pro to assess this trend and found a significant relationship between median income and poisoning report density. Finally, we used this dataset to compile non-technical guides to toxic plants in Virginia for cat and dog owners. The guides provide a quick reference for recognizing common signs and symptoms of toxicosis in companion animals, and allow users to identify potentially toxic plant genera in and around the home. Our findings reflect the importance of educating pet owners on the plant species they may encounter in or around the home that could endanger their pets.

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Ethnobotany

Topic: Contributed Papers

Title: The role of historical ecology and redlining practices on patterns of plant community assembly in urban Los Angeles

Author: ***Anthony Baniaga @ UCLA***

Keywords: community assembly,Floristics,Los Angeles County,urban biodiversity,redlining

Abstract:

The city of Los Angeles comprises nearly 500 square miles and supports nearly four million people that reside on lands that were once composed of a diverse mosaic of wetland and upland plant community associations. On top of these historic vegetation layers are socioeconomic legacies of a redlining grading system for the city established by the Federal Housing Administration's Home Owners Loan Corporation (HOLC). Throughout neighborhoods in public parkways, the spaces between property bounds and the road, resides an often overlooked spontaneous and self-propagating community of native and introduced taxa. With an interest in documenting this flora at a time of rapid environmental and socioeconomic change in the city, I performed a series of floristic checklists for nearly 400 blocks comprising nearly 50 total miles at sixteen neighborhoods throughout the city between the end of January and middle of March 2021. Transects were walked within specific neighborhood communities chosen to represent all four HOLC codes and a combination of historic wetland and upland vegetative communities. Across all transects and sites I found a total of 168 spontaneous self-propagating plant taxa, and significant effects of both historical plant community (upland, wetland) and HOLC code on plant species richness and phylogenetic diversity. I also present and discuss patterns of community similarity and turnover between sites. This dataset of plant species presence by block, and the list of transect locations, is publicly available via dataDryad so that it may serve as a point of reference for future studies of urban ethnobiology.

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Ethnobotany

Topic: Contributed Papers

Title: The Cultural Importance of Mushrooms and Foraged Foods

Author: ***Amy Wrobleski @ The Pennsylvania State University***

Keywords: Food,Food Sovereignty ,Foraging,Mushroom,forage

Abstract:

There is a long tradition of hunting for mushrooms in the mid-Atlantic of the United States. Despite this importance very little research has been carried out on mushroom hunters in the mid-Atlantic. There has been no such examination of the demographics, sustainability practices, or economic importance of wild mushrooms in the northeast or mid Atlantic, despite anecdotal evidence that interest in mushrooms in the region has been on the rise, particularly since the start of the COVID-19 pandemic. In collaboration with mushroom hunting communities in the region, this project seeks to understand how people learn about mushrooms in the region and asks questions around which fungi are culturally and economically important and why. A survey was developed and has been distributed on a rolling basis since spring 2022; to date, more than one thousand mushroom hunters have completed the survey. Respondents report growing interest in mushroom hunting since the start of the pandemic in March 2020. Respondents self-reported the year they first began to hunt for mushrooms. From 2020 to the present there was a significant spike in new mushroom hunters compared to previous years, with 35% of respondents learning to hunt for mushrooms since the beginning of 2020. Mushroom hunters, as a group, are overall younger, with a majority of respondents being between 25 and 40 years of age. Most respondents identified as women (58%) and were white (86%). Despite many respondents expressing concerns about commercial harvesting, only 3% of respondents reported selling mushrooms, and most respondents had no interest in selling mushrooms now or in the future (78%). Wild mushrooms were reported to be used for food as well as medicine and are an integrative part of culture and identity within the region. A spike in mushroom hunting interest could have major implications for if and how mushroom hunting is regulated in the region, something that many community members expressed concerns about. This rise in interest in mushroom hunting leads to exciting potential areas for outreach programs such as extension services, community based groups, and mushroom harvesting and cultivation businesses, as well as potential avenues for community science collaboration in the future.

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Ethnobotany

Topic: Contributed Papers

Title: Understanding ethnobotanical, chemical, and genetic diversity in the edible/medicinal/toxic plant Dysphania ambrosioides in Guatemala

Author: ***Tabitha Faber @ University of Wisconsin -- Madison***

Keywords:

Abstract:

Dysphania ambrosioides (Amaranthaceae) is an aromatic, weedy herb used as a food and medicine in many cultures across the globe, especially in its native range in Latin America. Simultaneously, there are cases of toxicity and death associated with the plant’s use. Does chemical variation relate to, or potentially drive, patterns of ethnobotanical (mis)use of D. ambrosioides? This presentation will explore the chemical diversity of this species at a variety of scales, including a meta-analysis of published essential oil compositions from across the globe and preliminary examinations of the chemical profiles for plants collected throughout Guatemala, the United States, and Canada.

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Topic: Contributed Papers Ethnobotany

Title: Testing the Link Between Specialized Metabolite Profiles and Medicinal Use Across Caryophyllales

Author: ***Alex Crum @ University of Minnesota - Twin Cities***

Keywords: Carophyllales,Community Phylogenetics,phytochemistry,traditional knowledge

Abstract:

Better understanding the relationship between plant specialized metabolism and human traditional medicinal use has great potential in aiding bioprospecting and untangling cross-cultural patterns of plant use. However, given the limited information available for specialized metabolites in most plant species, and specific bioactivity for most metabolites, the ability to associate a medicinal use and a metabolite is limited. The order Caryophyllales has a unique pattern of tyrosine- or phenylalanine-dominant specialized metabolism, represented by the mutually exclusive anthocyanin and betalain pigments, making the group ideal to work around the lack of specific metabolite knowledge. In this study, we compiled a list of medicinal species in selected tyrosine- or phenylalanine-dominant families of Caryophyllales, and tested for over- and underrepresented medicinal uses in a clade using a “hot nodes" approach. We hypothesized that families with a Tyr-enriched metabolism type would see different types of medicinal use compared to the ancestral Phe-enriched metabolism. Instead, the same clades are overrepresented across types of medicinal use. To further explore this pattern, we used species occurrence records and compared medicinal clades to those with less medicinal use to see how geographic range and availability to humans may have driven species selection for medicinal use.

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Topic: Contributed Papers

Title: The importance of ethnobotany among Cherokee women: an integrated approach

Author: ***Catherine Philips @ Tennessee Technological University***

Keywords: ethnobotany

Abstract:

Ethnobotany has been an integral part of life among the Cherokee for hundreds of years before Europeans settled in North America. Using the plant species available to them, the Cherokee were able to take care of illnesses, wounds, birthing children, and conduct spiritual ceremonies. All this knowledge was learned and passed on through oral traditions, without the use of laboratories or European methods. In this presentation we will explore the ethnobotanical practices and plants used by Cherokee women in their daily life. The focus is on what plants were used, how they were used, and the scientific studies conducted on the efficacy of the plants.

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Topic: Contributed Papers

Title: Checklist of Medicinal Plants Used by Traditional Women for Maternal Health Care in Lagos State, Nigeria.

Author: ***Olubunmi Sharaibi @ Lagos State University, Lagos, Nigeria***

Keywords: ethnobotany

Abstract:

Traditional women in Lagos State, Southwest, Nigeria have been using medicinal plants for maternal health care since time immemorial. However, there is no proper documentation of medicinal plants used in maternal health care, as information is passed from generation to generation orally. This study aimed at identification and documentation of medicinal plants used in Lagos, Nigeria for maternal health care. Ethnobotanical studies were carried out in six local government areas namely, Agege, Alimosho, Badagry, Ejigbo, Mushin and Ojo. Semi-structured questionnaire was designed to obtain information from 300 respondents, 50 from each local government area. The respondents included herbal merchants, herbal medicine practitioners, mid-wives, and traditional birth attendants. Information obtained included the name of the plants, plant parts used, mode of preparation and administration and dosage of the medicinal herbs. Sixty (60) plants belonging to twenty (20) families were identified and documented in the study area. were the frequently mentioned plants in the study area. Most of the reported plants belong to the Fabaceae (22.52%), Asteraceae (7.21%) Malvaceae (5.41%) and Anacardiaceae (4.51%) families. Kigelia africana, Caliandra portoricensis and Securidata longepedunculata had the highest Relative Frequency of Citation (RFC) and Fidelity Level (FL) of 0.93; 100% and 0.92; 100%, respectively. Among the categories of ailments, headache, nausea and vomiting, easy delivery and general body wellness had the highest Informant Consensus Factor (ICF) of 1.00 each. Most of the reported plants (60.67%) were herbs and shrubs and about 76.34% of the surveyed plants were wild. Leaves were the most frequently used (62.72%) plant's part. Most of the herbs(52%) were prepared as decoctions and are mostly administered orally (74.88%).

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Topic: Contributed Papers Ethnobotany

Title: Medicinal Plants Used for the Treatment of Fibroid in Lagos Metropolis

Author: ***Monisola Fawibe @ University of Lagos***

Keywords: , herbal

Abstract:

A study was carried out to identify medicinal plants that are used to cure fibroid within the Lagos metropolis as well as the recipes for preparing them via survey method to obtain the information from herbal markets. Four herbal markets: phylarry Global Herbal Heathcare at Agege, Amudalat Herb plants at Bariga, Iya Ibeji Alagbo at Ishaga and random herb seller at Oyingbo market were visited to retrieve the information. Results revealed that a total of 17 plant species distributed into 14 families including Anacardadiaceae, Apocynaceae, Asclepiadaceae, Bignoniaceae, Curcubitaceae, Cochlospermaceae, Euphorbiaceae, Fabaceae, Gentianaceae, Hypoxidaceae, Petiveriaceae and Zingiberaceae was found to have the highest numbers of species encountered during the study with two species represented. Six (6) unique recipes were also discovered to have made use of the three to four of these stated plants into concoctions, decoctions or infusions for treatment of fribroid thereby underlining their importance in the treatment of the disease and drawing a renewed emphasis on the need to conserve these plants for future useA study was carried out to identify medicinal plants that are used to cure fibroid within the Lagos metropolis as well as the recipes for preparing them via survey method to obtain the information from herbal markets. Four herbal markets: phylarry Global Herbal Heathcare at Agege, Amudalat Herb plants at Bariga, Iya Ibeji Alagbo at Ishaga and random herb seller at Oyingbo market were visited to retrieve the information. Results revealed that a total of 17 plant species distributed into 14 families including Anacardadiaceae, Apocynaceae, Asclepiadaceae, Bignoniaceae, Curcubitaceae, Cochlospermaceae, Euphorbiaceae, Fabaceae, Gentianaceae, Hypoxidaceae, Petiveriaceae and Zingiberaceae was found to have the highest numbers of species encountered during the study with two species represented. Six (6) unique recipes were also discovered to have made use of the three to four of these stated plants into concoctions, decoctions or infusions for treatment of fribroid thereby underlining their importance in the treatment of the disease and drawing a renewed emphasis on the need to conserve these plants for future use

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Topic: Contributed Papers

Title: Bark Anatomy, Proximate, Elemental and In-vitro Anti-sickling Analysis of Bark Extracts of the Three Khaya Species found in Nigeria.

Author: ***OLOLADE Oyedapo @ Obafemi Awolowo University, Ile- Ife, Osun State, Nigeria***

Keywords: Inhibition,Khaya, In-vitro, Anti-sickling,Reversal

Abstract:

INTRODUCTION
Khaya (Family Meliaceae) is widely distributed in Africa. Its trade name is African Mahogany. Three of these Khaya species are found in Nigeria. The three species found in Nigeria are the genus Khaya senegalensis, Khaya grandifoliola and Khaya ivorensis. Khaya have been found to be very useful in the treatment of arrays of diseases in Nigeria among which are malaria and sickle cell disease.
OBJECTIVE
They are generally referred to as Oganwo by the Yoruba tribe in Nigeria. The traditional medical practitioners find it difficult to identify hence this study.
METHOD
Comparative bark anatomy and macerates of the three Khaya species was carried out to identify and describe distinctive anatomical characters that could possibly be used to delimit the taxa. Transverse section, longitudinal section and macerates of stem and root bark were made. Characteristic similarity and disparity in the tissues arrangement as well as cell inclusions were noted for description and delimitation. The anti-sickling activities of the three species Khaya bark were tested, the proximate and elemental analysis were also carried out the simple analytical procedure as described by the Association of Official Analytical Chemistry (AOAC) of 1987, 13th Edition Washington DC P1094 and Dry Ashing method of AOAC 2006 respectfully.
RESULT
The three Khaya species bark have anti-sickling properties with Khaya ivorensis having the highest activity with ethanolic extract KI 76.06 ± 2.72 > KG 63.39 ± 0.56 > KS 47.02 ± 3.63. The three Khaya species bark studied had essentially the same anatomical features. The cuticle shape and type, epidermal cell shapes and cell inclusions reveal some similarities. The study reveals that the cuticle was striated, the shape of the cuticle ranges from circular, oval, polygonal and cylindrical elongated cell. Sclereids are present and prominent. However, there were characters that seem to be species specific in the number of outer bark cell layers, cuticle thickness, numerosity of crystal druses, types of sclereids present in the cell. The presence of stylliod crystal that is in the cell of Khaya grandifoliola distinguished it from the two other species. The proximate analysis revealed that Khaya leaves are very rich in minerals, proteins and carbohydrates. The elemental analysis showed that Khaya leaves contains essential elements within the limits of dietary requirement.
CONCLUSION
This study confirms the anti-sickling (inhibitory) activities of the three Khaya species with Khaya ivorensis having the highest activities in hot extraction of ethanol solvent 76.06 ± 2.72 percentage. The microscopic study of the bark of the three species revealed that there were distinctive diagnostic features that can be used in solving the identification problem of species of Khaya studied (K. senegalensis, K. grandifoliola and K. ivorensis) from one another.

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Floristics & Taxonomy

Topic: Contributed Papers Floristics & Taxonomy

Title: A new species of Chusquea subg. Swallenochloa (Poaceae: Bambusoideae) from the high Andes of Peru

Author: ***Nancy Refulio Rodriguez @ Iowa State University***

Keywords: Anatomy,Andes,bamboo,micromorphology,Poaceae,Taxonomy

Abstract:

Chusquea, a woody bamboo genus native to the New World, consists of ca. 203 recognized species that are found mainly in Brazil and the Andes. About 33 described species of Chusquea are known from Peru, representing four of its five subgenera. Chusquea subg. Swallenochloa (McClure) L.G. Clark, characteristically inhabiting high elevation grasslands, is represented by eight species in Peru, seven of which are considered endemic. In Peru, Chusquea subg. Swallenochloa ranges in elevation from 2,800 to 3,800 m. While the number of recognized species in Chusquea has increased considerably in recent years, further substantial taxonomic work is needed to better integrate collections with uncertain placement into their appropriate taxonomic ranks, especially collections from the Peruvian Andes. After morphological and anatomical examination of specimens collected in Rio Abiseo National Park (La Libertad department, northern Peru) and the Otishi National Park (Junin department, central Peru), which were considered in a recent study as one of 11 different sets of Incertae Sedis specimens within Chusquea sect. Swallenochloa, we describe them as a new species, C. crassimarginalis. This new species resembles C. depauperata because of its fistulose culms, slightly falcate spikelets, subulate foliage leaf blades, anatomy of the foliage leaf blade with a simple midrib and absent fusoid cells, abaxial epidermis of foliage leaf blade with abundant rounded simple and branched papillae, and stomatal apparatuses obscured by abundant papillae. Chusquea crassimarginalis differs from C. depauperata in having glume I (sometimes absent) and glume II developed, culm leaf blades less than 1.5 mm long, corrugated foliage leaf blades, foliage leaf blade cross sections with a prominent, adaxially projecting rib associated with first and second order vascular bundles, and a mesophyll adjacent to the bulliform cells with five to six layers of rosette cells. If most or all of the remaining 10 sets of Incertae Sedis specimens of Chusquea subg. Swallenochloa in Peru represent new species, we can expect its known diversity to double with additional taxonomic effort.

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Floristics & Taxonomy

Topic: Contributed Papers

Title: A Checklist of the Spontaneous Plants of New York City

Author: ***Lydia Paradiso @ New York Botanical Garden***

Keywords: Checklist,New York,Urban Flora

Abstract:

The first checklist of plants of the New York City area was published by John Torrey in 1819. In the years since, NYC has undergone radical changes, and although some of these plants and habitats are now extirpated, the city continues to harbor important biodiversity. The unique geology and ecology of the city, paired with its status as a hub of human activity, creates conditions for both native and introduced plants to thrive. The NYC EcoFlora is a community science project based at the New York Botanical Garden which aims to increase awareness of plant life and to document the spontaneous flora of NYC using the iNaturalist app. The data presented here synthesizes iNaturalist observations made by our community scientists with herbarium specimens, NYC Parks data on native plants, previously published checklists of greenspaces within NYC, and personal communications, to produce a snapshot of the current state of the city’s plants. In this talk, we will discuss the checklist, which includes about 1,700 taxa from 155 families of vascular plants; the changes in flora over time; and how this data can be utilized by land managers, students, ecologists, and naturalists

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Floristics & Taxonomy

Topic: Contributed Papers

Title: Morphometric analysis and self-compatibility of species in Lilium L. sect. Leucolirion in the southeastern United States

Author: ***Cassandra Fink @ Tennessee Tech University***

Keywords: morphology,Lilium,morphometric analyses,Self-compatibility

Abstract:

Lilium L. section Leucolirion Wilson, known as trumpet lilies, consists of nine species native to Central and Southeast Asia. These species are characterized by large white flowers and can be either self-incompatible or self-compatible (the latter is rare in Lilium). Four species in this section appear to be naturalizing in the southeastern United States (US): Lilium formosanum, L. longiflorum, L. philippinense, and L. regale. The reproductive mechanisms of these species are not fully understood in native or naturalized populations. Previous studies debate whether these species are self-compatible as it varies across sites. These species alone are difficult to distinguish due to morphological similarities. Additionally, hybrids have been shown to form readily among species in this section, which may complicate identification. Therefore, pollination treatments were conducted at three sites in the southeastern US to test for self-compatibility. Buds were covered with mesh bags to exclude visitors before and throughout the duration of anthesis. Pistils were collected 48 h after pollination and visualized under UV fluorescence. We conducted a morphometric analysis using both herbarium specimens and specimens collected from field sites in the Southeast to explore differences among species and identity species present in the US. Online herbarium images were downloaded from the following data portals or herbaria: SERNEC, GBIF, NY, and US. Where possible, type specimens for each species (digitized specimens, original illustrations, and species protologues) were referenced online to aid in morphological identification. Digitized images were measured using Fiji (ImageJ) and color will be standardized using a Kodak color control chip. Analysis of morphology included measurements of plant height, length and width of leaves, floral buds, tepals, fruits, and length of pistils and stamens using digital calipers or a steel ruler. The color and surface texture of leaves, bulbs, stigmas, anthers, buds, and tepals were also recorded. Data were analyzed using principal component analyses to quantify the morphological characteristics of each species in program R. Preliminary results suggest the species present in the US are self-compatible. This study seeks to identify morphological characteristics to differentiate between Lilium formosanum, L. longiflorum, L. philippinense, and L. regale to better understand the species present in the Southeast US.

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Floristics & Taxonomy

Topic: Contributed Papers

Title: Using a floristic inventory of McInnis Canyon National Conservation Area, Colorado to train undergraduates

Author: ***Stephen Stern @ Colorado Mesa University***

Keywords: Floristics,Undergraduate Research,Undergraduate teaching

Abstract:

The McInnis Canyon National Conservation Area (MCNCA) is a BLM-managed area encompassing over 123,000 acres of high desert in western Colorado. The 2012 Science Plan for the MCNCA stated that a full list of the flora in the MCNCA was a high scientific priority. The goal of this project was to complete the first floristic inventory of the area. Between 2013-2020, four Colorado Mesa University undergraduate students each spent a summer collecting plant specimens from throughout the area. The resulting 644 plant collections were combined with previously collected and online databased specimens from SEINet to compile a species list. The results of this species list and a comparison of the flora of McInnis Canyon with the adjacent Colorado National Monument will be discussed. Additionally, the benefits to undergraduate students and collaboration between the BLM and university will be highlighted.

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Topic: Contributed Papers Floristics & Taxonomy

Title: Black Holes, White Gold: A Flora of the Silver Peak Range, Esmeralda County, NV

Author: ***Peri Lee Pipkin @ California Botanic Garden***

Keywords: biogeography,botany,conservation,Fieldwork,Floristics,natural resources,Nevada,rare plants

Abstract:

The Silver Peak Range sits in a remote corner of Esmeralda County, Nevada. It is known to have floristic influences from the White Mountains and nearby mountain ranges in Death Valley National Park, and it is a transition zone between the Great Basin and Mojave deserts. The 450 square mile study site contains a 50 square mile wilderness study area, as well as many habitats, including alkali wetlands, canyons, riparian areas, forests, and subalpine peaks that reach 2,856 meters in elevation. These peaks descend into a colorful palate of diverse geology that is home to edaphically restricted and imperiled endemic plants such as Eriogonum tiehmii and Chloropyron tecopense. Plants such as these are facing multiple existential threats including poorly sited geothermal and lithium resource extraction endeavors. Prior to this study, the Silver Peak Range was considered a botanical black hole which is reflective of the lack of botanical documentation in the state. Nevada holds the record for lowest density of herbarium specimens collected per km2 of area in the western US. Currently 1933 collections have been made representing about 66 plant families and around 440 taxa (and growing), with a second season of fieldwork projected to finish in October of 2023. Floristic inventories such as this one are essential because they provide much needed botanical data to inform conservation efforts and to guide land use planning. In addition to rare and endemic species, the area has many culturally important plants in the study area and is abundant with artifacts. This study will provide information about distribution and abundance of rare vascular and nonvascular plant species in the region, will help to describe biogeographica and floristic affinities of species, and will provide data towards critical land management decisions.

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Topic: Contributed Papers

Title: A Vascular Flora of the Sacatar Trail Wilderness, Southeastern Sierra Nevada, California

Author: ***Kimberly Schaefer @ California Botanic Garden***

Keywords: Biodiversity,California,California Floristic Province,Climate Gradients ,Floristics,Great Basin,Mojave Desert,rare plants,Sierra Nevada,Taxonomy ,elevational gradient,Vegetation

Abstract:

The Sacatar Trail Wilderness (STW) occupies a unique ecological transition zone in the southeastern Sierra Nevada at the interface of the Mojave Desert, Great Basin Floristic Province, and highly diverse California Floristic Province. This 88mi2 area encompasses a significant elevational gradient from 3,500 to nearly 9,000 feet, and supports a diverse array of vegetation communities, from creosote scrub to montane meadows. The absence of weather stations within the STW make it difficult to understand the precise microclimates its plants are subject to, especially considering that conditions vary within such a wide elevational range. This region of the Sierra Nevada on the western edge of the Mojave Desert, if more thoroughly studied, could potentially serve as a setting for future research on plant migration in response to climate change. The STW is also a "botanical black-hole," an area with little to no documentation of the plants that occur there. The most notable collector in the area was botanist Ernest C. Twisselmann, who made 36 collections from 1958 to 1971. The STW's habitat heterogeneity coupled with insufficient documentation suggests possibilities for discovering new rare plant occurrences and potentially undescribed diversity.

Research objectives are (1) to produce a comprehensive inventory and annotated species checklist to document all vascular plants within the STW, (2) to generate more precise weather data from the site, and (3) to characterize the vegetation communities through quantitative surveys.

Thirteen trips were made to the study site between March and September 2022, with an estimated fifteen additional trips anticipated for 2023 to voucher specimens of all vascular plant taxa present. To supplement the limited climate information available for the STW, 12 iButton temperature data loggers have been installed along the study site's elevational gradient at 1,000-foot intervals. The data logging points will be further analyzed with 10-meter radius plots to characterize vegetation types in conjunction with elevation. Historic collections from the site will be examined and identifications verified. All collections data, including those from historic collections, will be assimilated into an annotated species checklist. Specimen vouchers collected as part of this research will be deposited in RSA, UCR, and CAS herbaria and corresponding data shared with the Consortium of California Herbaria (CCH2) database portal.

During the first field season 827 collections were made, representing 67 plant families. Range extensions were documented, including the southernmost record of yellow-flowered wild buckwheat (Eriogonum microtheca var. ambiguum), and the first ever record of California milkweed (Asclepias californica) in Inyo County. New occurrences of several rare taxa have been located, including Charlotte's phacelia (Phacelia nashiana) and Kern bird's beak (Cordylanthus eremicus subsp. kernensis), both of which the California Native Plant Society classify as rank 1B threatened taxa. Aside from exciting plant observations, this area is inhabited by the rare and threatened Mojave desert tortoise at the very northwest reaches of its range. Preliminary findings from this research demonstrate the unique and ecologically important value of this area.

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Floristics & Taxonomy

Topic: Contributed Papers Floristics & Taxonomy

Title: Insights into the taxonomic diversity of Viola subsection Borealiamericanae of the Eastern-North American Coastal Plain

Author: ***Remington Burwell @ Ohio University***

Keywords: morphology,allopolyploidy,common garden,Taxonomy

Abstract:

The acaulescent blue violets have historically been a challenging group taxonomically due to debated species limits, unclear variation patterns, the extensive evidence of hybridization, and high allopolyploid lineage origin. Recently, the Ballard lab has placed the 40-plus currently recognized taxa in nine informal species groups on morphological and ecological grounds. To delineate species, the Ballard lab has adopted a population-level integrative approach using multiple lines of evidence, including microsatellites or (more recently) high-throughput sequencing (GBS), macromorphological and micromorphological studies of herbarium specimens and garden-cultivated wild plants, reproductive behavior from common garden studies, species distribution modeling, and niche analysis using soil samples. These integrative taxonomic studies currently focus on the Affinis and Edulis species groups, previously treated to include 1-5 and 0-2 species, respectively. Questions to be answered by these new investigations include the following. How many species are there in the two groups, and how do they differ? Are specific anomalous taxa undescribed species? What is the appropriate conservation status of narrowly distributed taxa? Recent evidence from living plants in a common garden and herbarium collections suggests as many as 12 distinct evolutionary species in the two groups combined, with two undescribed species.

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Floristics & Taxonomy

Topic: Contributed Papers

Title: Floristic Inventory of Axton Ranch Mountain Park

Author: ***Jennifer Ackerfield @ Denver Botanic Gardens***

Keywords: coefficient of conservatism,floristic quality,Floristics,flora of colorado,immersive research opportunities

Abstract:

Axton Ranch Mountain Park is a previously private property that was donated to the City and County of Denver for its Mountain Park System in 2021. No previous surveys or collections of plants have been documented from Axton Ranch, and therefore a floristic study of the property fills an important gap in biodiversity knowledge. Our goals for this project were to: 1) provide a baseline knowledge of the plant species and communities, 2) document rare plant species, 3) document all introduced plant species, and 4) identify areas of priority conservation concern. This project also allowed us to provide an immersive learning opportunity for high school students in the Denver metro area to broaden participation in STEM from underrepresented groups. A total of 319 unique plant species in 62 families were found, representing approximately 10% of the flora of Colorado. Additionally, two rare species were discovered. The most speciose plant families were Asteraceae (17%), Poaceae (13.5%), Rosaceae (5%), Cyperaceae (5%), and Fabaceae (5%). The majority (88%) of species were native, and only seven species of noxious weeds were found. The majority (31%) of introduced species were Poaceae, and were most likely brought in for hay when the property was a working ranch. Eight community types recognized by NatureServe were also documented. Axton Ranch supported wetlands consisting of three montane wet meadows as well as riparian areas along streams and lake margins in lodgepole pine forests. Together, these areas supported 34 obligate and 35 facultative wetland species. Over 72% of species at Axton Ranch had a Coefficient of Conservatism (C-value) over five, and a Floristic Quality Index of 90 was determined for the overall property. This indicates that Axton Ranch mostly consists of intact ecosystems where ecological processes, functions, composition, and structure have not been (or minimally so) degraded or altered by human stressors. Potential threats to plant communities at Axton Ranch include fire, hydrologic changes, and the spread of noxious weeds. We identified five areas of priority conservation concern that supported rare or noteworthy species. In addition to documenting all plants on the property, we also noted a pond full of neotenic western tiger salamanders. While we cannot quantify the long-term impacts of providing immersive learning opportunities for high school students yet, we do have evidence in the short-term that this opportunity helped direct the paths of at least three high school interns. Two high school interns are now majoring in the natural resources in college, while another is creating an herbarium of local plants for their high school capstone project.

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Floristics & Taxonomy

Topic: Contributed Papers

Title: One world but many countries, languages, and histories

Author: ***Mary Barkworth @ Utah State University***

Keywords:

Abstract:

For the last two decades, the United State has invested considerable resources in making specimen data from its collections freely accessible. A key product of this investment has been, and continues to be, development of data management programs that make sharing occurrence data easier. One of these, Symbiota, continues to be freely available. This availability has enabled herbaria and botanists in many of poor institutions, including some Old Word Countries, to share their data online or to aggregate data from multiple locations for their own research. Doing so has revealed impediments to providing quality data, some of which go beyond the scope of a data management system but need to be addressed if countries with a poor data infrastructure are to become active partners in increasing knowledge about their biodiversity. Some impediments reflect biases in standards such as Darwin Core, for example, use of StateProvince and County for administrative regions. Others reflect the pressures created by the multiplicity of languages that people use, different taxonomic traditions, the cost of educating rapidly growing populations, poorly developed physical and digital infrastructure, and differing cultural traditions. Adopting and adapting new developments in digital technology can assist in overcoming some impediments, but it is also essential to address other impediments such as the lack of a taxonomic tradition and the difficulty of providing quality education to people in dispersed communities as must the frequently encountered lack of understanding of the wide range of skills taxonomists need to acquire. This presentation will highlight some of the impediments we have encountered while working outside the US overseas and approaches we are using, or are proposing to use, to address them.

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Floristics & Taxonomy

Topic: Contributed Papers

Title: A Vascular Floristic Study of the Piute Mountains, Kern County, California.

Author: ***Courtney Matzke @ California Botanic Garden***

Keywords: California,California Floristic Province,conservation,Eriogonum,Field Botany,Floristics,herbaria,native plants,rare plants,Sierra Nevada

Abstract:

In California, many plant species are facing impacts due to human activities, including habitat conversion, introduction of non-native species, fire suppression, and the effects of climate change. These ongoing changes highlight the urgent need for comprehensive floristic research. This study will document the flora of The Piute Mountain Range, located at the southern terminus of the Sierra Nevada. This location is near the juncture of four ecoregions including the Mojave Desert, Great Basin Desert, Central Valley, and southern California mountains, resulting in elements of vegetation from all of these biotic provinces. The study site is approximately 200 sq. mi. with a diverse topography and elevational ranges from 2,450 to 8,440 ft. There are large spatial and temporal gaps in the collection history of the Piute Mountains, and many species collected in the past have not been recently documented. There is still very high potential to find unrecorded rare plants, range extensions, or even undescribed taxa. This project will result in voucher specimens and associated data, iNaturalist observations, a complete checklist, and updated statues of rare plants within the study site. High-quality voucher specimens allow for extended future research in phenology, range expansion and contraction, effects of climate change as well as provide a source for molecular and isotope data. Throughout this project I am simultaneously compiling a conservation plan for Eriogonum breedlovei var. breedlovei (Piute buckwheat), which is endemic to the range. The goal of the conservation plan is to provide a comprehensive overview of the most up to date scientific information on E. breedlovei var. breedlovei to inform stakeholders with recommendations for conservation of this taxon. This floristic study will span two years with the expected completion of the second field season in September of 2023. To date, I have collected 986 vouchers, with 842 corresponding iNaturalist observations, resulting in the determination of 495 minimum rank taxa.

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Floristics & Taxonomy

Topic: Contributed Papers Floristics & Taxonomy

Title: Merging the Malagasy Sphedamnocarpus Planch. ex. Benth & Hook.f. into the genus Philgamia Baill. to recognize an island lineage within the Malpighiaceae

Author: ***Jackson Kehoe @ Harvard University***

Keywords: biogeography,Madagascar,molecular phylogenetics,phylogenomics,Taxonomy

Abstract:

Malpighiaceae are an angiosperm family whose species exhibit a pantropical distribution and a rich evolutionary and biogeographic history. Our ongoing phylogenomic investigations in this clade have shed light on evolutionary relationships that necessitate associated taxonomic revisions. One such example involves the genera Sphedamnocarpus Planch. ex. Benth. & Hook.f., and Philgamia Baill., whose species are distributed in Africa and Madagascar. In the current circumscription, Philgamia is entirely confined to Madagascar, while Sphedamnocarpus has a distribution on both the island and the continent. Our investigations reveal a clear split between continental Sphedamnocarpus and the island lineages of both genera, rendering Sphedamnocarpus polyphyletic. Our current work seeks to combine these phylogenomic and biogeographic insights with morphology to redefine these genera. We propose merging the Malagasy Sphedamnocarpus into the genus Philgamia and recognize a much-reduced Sphedamnocarpus whose species are restricted to Africa. Additionally, we present putative morphological synapomorphies to accommodate these readjustments to make these genera monophyletic. Future research will integrate habitat data and deeper phylogenomic explorations to better understand the dynamics of what appears to be a within-island radiation of the newly merged genus Philgamia.

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Floristics & Taxonomy

Topic: Contributed Papers

Title: The postage stamp and beyond: The vascular flora of Marietta Sand Prairie Preserve

Author: ***Elizabeth McMurchie @ Iowa State University***

Keywords: management,tallgrass prairie,Vascular Plants,Prairies,Floristics

Abstract:

An ongoing survey of the vascular flora of the Marietta Sand Prairie Preserve in Marshall County, Iowa, was begun in the 2022 growing season. Originally purchased for protection from agriculture in 1983, the Marietta Sand Prairie Preserve initially consisted of a “postage stamp” of just 6.9 ha (17 acres) of remnant sand prairie and wet sedge meadow that was dedicated as a biological and geological Iowa state preserve the following year. Marietta Sand Prairie was expanded in 2006 with an addition of about 85.8 ha (212 acres), which, although publicly owned, is not designated as part of the state preserve. The addition contains sand prairie habitat as well as restored prairie on less sandy soil, more recently abandoned agricultural fields previously planted with Glycine max (soybean) and Sorghum bicolor (sorghum or great millet), and several wetlands, including unusual small hillside fens. Sand prairie habitat is considered globally rare; about 47 ha of this habitat type are protected in state preserves in Iowa, where over 99% of land has been converted to agriculture or otherwise developed. The existence of the sand prairie habitat is dependent upon disturbance, and management techniques such as burning are undertaken by the Marshall County Conservation Board on a regular basis to clear woody debris. As with many state preserves in Iowa, Marietta Sand Prairie is also open to hunting, hiking, and birdwatching. In the first year of this study, approximately 280 different vascular plant species, subspecies, or varieties representing 195 genera and 78 families were collected and vouchered at the Ada Hayden Herbarium at Iowa State University. Several species of interest were found within the original 6.9 ha remnant, including Carex conoidea and Platanthera clavellata, which are listed as species of special concern in Iowa, and Botrychium tenebrosum, a currently unevaluated species that is likely rare in the state. This largely student-led project will continue through the 2023 and 2024 growing seasons and is expected to locate many additional species in the preserve, including some recorded in previous work in 2014 and 2015 by plant ecologist Scott Zager. A comparison of species composition of 27 prairies protected in the Iowa State Preserves system will be presented alongside the species composition of Marietta Sand Prairie Preserve. The goal of this project is to not just document vascular plant species presence, including the addition of new and potentially invasive species and possible loss of plants previously collected at the site that we can no longer locate, but to also report these findings to land managers and other stakeholders to help inform management decisions at this dynamic, multi-use site.

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Floristics & Taxonomy

Topic: Contributed Papers

Title: Introducing a new Vascular Flora of Nevada, with notable records from recent floristic efforts

Author: ***Mathew Sharples @ Adams State University***

Keywords:

Abstract:

Nevada has long lacked a field-usable technical resource for identifying plants across the state. This reality first came into focus throughout a floristic inventory of a poorly known area of the state near the borders of the Mojave, Great Basin, and Colorado Plateau: the Clover Mountains. I first summarize current results of this inventory, which is beginning to coalesce into a final checklist, and which has turned up dozens of surprising new occurrence records. Numerous county records will be newly reported, both new to Lincoln and deriving from the Clovers, as well as new occurrences of taxa outside of Lincoln. I then report on the development of a new field-usable resource towards species identification across Nevada, which is ca. 80% complete.

Numerous contributors are involved in this new Vascular Flora of Nevada, and I will solicit a few remaining treatments of diverse and (traditionally) difficult taxa (e.g., Astragalus and Phacelia). Many other new mountain range records have also been uncovered over the course of a plethora of field expeditions made while preparing the manuscript, and these will also be briefly touched upon.

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Floristics & Taxonomy

Topic: Contributed Papers Floristics & Taxonomy

Title: Development of genome-wide SSR markers for Echinochloa and studying the cross transferability in studying genetic variability in diverse populations: Know taxonomy for easy management

Author: ***Jayani Wathukarage @ Rice Research and Development Institute, Sri Lanka***

Keywords: Echinochloa, rice weed, genetic variability, SSR, in-silico

Abstract:

Echinochloa crus-galli is a serious weed in rice crop ecosystems, and widely distributed in all climatic zones of Sri Lanka. Its management was challenging through the efforts made for decades. Global scientific evidence show presence of multiple biotypes and a Sri Lankan study explained the presence of two Echinochloa crus-galli biotypes, where one has strong resistance over most of the available grass killer herbicides, however, the gentic nature of populations were not studied thereafter. Regardless the various combinations of management options studied, the efforts were fruitless as the Echinochloa populations thrive well in the rice fields. In addition to E. crus-galli there are four other species, namely E. colona, E. frumentacea, E. glabrescens, and E. stagnina available in Sri Lanka. Except for E. frumentacea all others are reportedly serious weeds and for E. frumentacea which is introduced to the nothern part of the country a long term back, the status is still unknown. Further the similarities in the morphology among the species, made them difficult to differentiate without a proper competency in taxonomic identification thereby, these species may also present in the rice fields and misidentified as E. crus-galli. The un-noticed biotypes and incorrectly identified species may have subjected to the management options designed for an early population of E- crus-galli, which might be the reason for its poor management regardless the efforts. This study was aimed at developing genome-wide SSR markers in-silico, for E. crus-galli and was planned to utilize them in studying genetic variability of the different populations. GMATA v. 2.3 was used to identify 201,846 different SSR loci. A total of 196,616 unique primer pairs were generated targeting their amplification. Primer pairs that could amplify up to five genomic regions were extracted eliminating others to retain 50,307 pairs (100,614 primers). Each primer was then manually analysed for tthe following. Primers with GC content >60% and for melting temperature ranging between 55-65OC were selected and others were eliminated. The ability generating and the relative stability of the selected primers to form secondary structures such as hairpin structures, self-dimers and hetero dimers were analysed to remove them from downstream analyses. Further, the mismatches in melting temperatures were also examined. A total of 316 primers were retained and used in e-PCR to validate their ability in amplification of the relevant SSRs against available gene pools of five Echinochloa species (collected from various genome databases) present in Sri Lanka. After successful amplification results generated from e-PCR, 50 randomly selected SSR markers were produced through a commercial supplier and were used in amplifying related genomic regions of 107 different Echinochloa leaf samples collected from diverse localities and populations. The specimens from five different species were used to understand the cross ransferability of the markers, while E. crus-galli samples were utilised in studying the population variations. Based on the results, the selected primers are found to have successful in differntiating different species while a considerable population variations of E. crusgalli were detected.

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Floristics & Taxonomy

Topic: Contributed Papers

Title: Taxonomic, conservation, ecological, morphological, and reproductive analysis of 4500 plant species of the interior Southeast US.

Author: ***Sevyn Brothers @ University of Tennessee at Chattanooga***

Keywords: Floristics,Tennessee,Kentucky

Abstract:

Tennessee and Kentucky are centrally positioned in the interior Southeastern US and combined they contain ~3600 vascular plant species and lesser taxa. There are ~900 additional species or lesser taxa across the broader region around these two states, and these have been included to ensure inclusion of all potential species in Tennessee and Kentucky. Launched in 2020, the Tennessee-Kentucky Plant Atlas (TNKY) has become a major resource for botanists, conservation workers, students, and teachers in the region. The TNKY Atlas is one of a kind, allowing for individuals to search not just by taxonomy, but by any one of 205 characters in the database.

Underlying TNKY is a database of more than 200 taxonomic, conservation, ecological, morphological, and reproductive characters for the ~4500 taxa. In total, this makes for a database of about one million cells. While a work in progress, here we report on some characteristics of the flora, which is represented by 215 families, 1024 genera, and ~4500 species and lesser taxa. Ninety-five percent of species are angiosperms, with only 3% pteridophytes and less than 1% gymnosperms. Conservation characteristics include nativity, region of origin, invasiveness, global and state ranks, federal listings, and wetland statuses. Ecological characters range from general ecological habitats of terrestrial or aquatic, soil and moisture regimes, to level three and four ecoregions. The database has more than 20 characters related to leaf and stem morphology and about 30 reproductive characteristics. Eighty percent of the flora is native and introduced species mainly originate from Europe and Asia. Over 250 species are listed as invasive by at least one southeastern state. These invasive species tend to follow the general trends of the database. This regional flora contains sixty-seven G1 species and 36 federally listed species. Eighty-seven percent of all species are terrestrial, 7% are in mudflats and wet woods, 3% are aquatic, and 1% are strict wetland species. Fifty-six percent are forbs, 19% are graminoids, and 17% are woody. Seventy-six percent are perennials, 19% are annuals, and 4% are biennials. Fifty-two percent have alternate phyllotaxy, 26% have basal phyllotaxy, 17% have opposite phyllotaxy, and 3% have whorled phyllotaxy. Eighty-four percent have simple leaves, 15% have compound leaves, and less than 1% have absent leaves or are thalloid. The majority of species reproduce in May, June, July, or August, with 30 species reproducing in all 12 months. Research is ongoing and will continue to fill in more characteristics present within the database, hopefully with a focus on rare species.

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Floristics & Taxonomy

Topic: Contributed Papers

Title: Modeling Niche Habitats of Expected Rare Species within the Vascular Flora of the Walls of Jericho, Alabama

Author: ***Garrett Billings @ University of Tenenssee at Chattanooga***

Keywords: Floristics,habitat suitability model,Maxent ,Southeastern Flora

Abstract:

The Walls of Jericho (WOJ) is a 5,062ha tract of land located in northern Alabama within the Cumberland Plateau ecoregion. The study area is known to be highly diverse with a high number of endemic species, likely due to its high concentration of limestone compared to the predominantly sandstone Cumberland Plateau. To better document these rare species, a habitat distribution model was developed for two federally listed species, Apios priceana (Fabaceae) and Clematis morefieldii (Ranunculaceae). The two species are known to occur within or adjacent to the study area and occupy similar habitats as other rare species, such as Cotinus obovatus (Anacardiaceae). This presentation will address the methodology used to create high resolution species distribution models using MaxEnt software and will present preliminary data on the accuracy and findings of the model. To date, 502 vascular plant taxa have been documented, representing 95 families and 192 genera including thirteen rare and sensitive species.

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Floristics & Taxonomy

Topic: Contributed Papers Floristics & Taxonomy

Title: Towards a comprehensive phylogeny of North American Delphinium (Ranunculaceae)

Author: ***Jared Meek @ Columbia University***

Keywords: alpine,montane,Mountain,species diversification,larkspur

Abstract:

Delphinium (Ranunculaceae) is a globally distributed genus composed of ~300 species. Originating in eastern Asia ~32 Mya, Delphinium arrived to western North America around 3 Mya and rapidly speciated along climatic and elevational gradients. At least 61 species have been described in North America, and most of these are endemic to the western United States (e.g., Rocky Mountains, Great Basin, and California Floristic Province). The toxicity of this genus has been a large research focus for US government agencies, but very little is known about the phylogeographic history, species relationships, population genetics, or conservation status of species in this group. Here, I present the first molecular phylogeny focused solely on the Delphinium of North America. Additionally, I discuss a population genetics analysis of an unresolved species complex (D. occidentale, D. barbeyi, D. glaucum) to highlight the potential for taxonomic revision in this genus. A comprehensive molecular phylogeny for North American Delphinium will provide clarity on species relationships, enable further research into plant diversification rates within and across temperate mountain regions (e.g., Himalaya-Hengduan and North American Cordillera), and provide a unique opportunity to study how plant chemical defenses affect speciation processes.

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Functional Genetics/Genomics

Topic: Contributed Papers Functional Genetics/Genomics

Title: Draba albertina illustrates adaptive responses to stress

Author: ***Nicolette Sipperly @ Stonybrook University***

Keywords: Abiotic stress,differential gene expression,herbivory,population genetics,Lignin,Draba,albertina

Abstract:

To persist in a new or changing environment, plants must adapt to obtain resource requirements for reproduction and survival. These new traits may express as change in plant growth habit structure or morphology, as well as differences in regulatory genes or protein coding genes. Draba albertina (Brassicaceae) is a widespread species found in diverse environments including in the mountainous west United States. Phenotypic and genetic differences across local D. albertina populations reflect, at least in part, adaptation to their unique conditions. Here I explore phenotypic variation in flowering time, root shoot ratio, and lignin content as well as genetic variation in three populations of D. albertina. I also compare gene expression across the two populations that most diverge in their exposure to insect herbivores, water stress, and human disturbance. Population genetics analyses reveal protein coding differences, suggesting local adaptation to a gradient of stressors such as insect pressure, water stress and human disturbance. Differentially expressed genes in the leaves concentrated in biosynthesis of secondary metabolites pathway and in particular, in the phenylpropanoid pathway, which is responsible for biosynthesis of lignin, flavonoids and a variety of aromatic metabolites in response to biotic and abiotic stimuli. Phenotype and gene expression analyses show the population exposed the most stressors to has faster time to flower and differences in expression of cell cycle genes in bolting tissue, changes in growth patterns that can decrease the stress of insect herbivory and water scarcity. Under greater stress from insect herbivores and human disturbance, D. albertina have evolved greater resilience by decreasing lignin in its stem tissue and modifying cell wall components, possibly making the nutrient inside of their cells more mobile and readily recycled in the case of insect damage. D. albertina provides a model that illustrates genetic and expression mechanisms that allow plants to survive and reproduce in stressful conditions that include defense, escape through time of development, and resilience.

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Functional Genetics/Genomics

Topic: Contributed Papers

Title: Functional Phylogenomic of KAI2 in Bouteloua gracilis

Author: ***Yanni Chen @ Texas Tech University***

Keywords: phylogenomics,smoke,KAI2

Abstract:

Smoke-induced seed germination has been discovered on a wide range of species. KAI2 was identified as the protein coding gene for the karrikins receptor, one kind of the active compounds that regulate seed germination. Most studies assumed that KAI2 is responsible for smoke-induced seed germination traits after its identified in Arabidopsis thaliana. In this study we explored the functional phylogenomic of KAI2 in a native species, Bouteloua gracilis, which have proved smoke effects on seed germination acceleration. We used RNASeq of four pools of seeds, and de novo transcriptome assembly to identify KAI2 homologs in B. gracilis. Further, we identified the KAI2 orthologs through the One Thousand Transcriptome project to trace the gene evolution path among species. Our results showed that even though there are three copies of KAI2 homolog, including two copies of KAI2 ortholog, there is no differential gene expression among these copies in response to smoke. This result indicated that KAI2 homologs are not responsible for the smoke effects in B. gracilis.

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Functional Genetics/Genomics

Topic: Contributed Papers

Title: Using multi-omics and gene family phylogeny to investigate the evolution of betalain and associated metabolites in Caryophyllales

Author: ***Ya Yang @ University of Minnesota, Twin Cities***

Keywords: Amaranthaceae,Caryophyllaceae,Caryophyllales,Co-expression network,phytochemistry,gene family evolution

Abstract:

Many Caryophyllales species produce unusually large amounts of diverse compounds derived from the amino acid tyrosine, including the betalain pigments. Due to inherent biochemical trade-offs, the production of these tyrosine-derived compounds may come at the expense of other compounds derived from the amino acid phenylalanine, such as the pigment anthocyanins. To investigate the evolution of genes and modules underline the trade-off between tyrosine- vs. phenylalanine-enriched metabolism, we carried out high light, salt, and methyl jasmonate treatments using a betalain producing species sea beet (Beta vulgaris ssp. maritima, Amaranthaceae) and an anthocyanin-producing species Silene latifolia (Caryophyllaceae). We analyzed transcriptomes, metabolite, and evolution of gene families associated with tyrosine- vs. phenylalanine-derived compounds. Preliminary results shows differential response in both gene expression and metabolite abundance depend on the type o stress and the location in the pathway. Analyses are underway to detect additional candidate genes involved in the tyrosine-enriched metabolism evolved in Caryophyllales and their "reversal" in Caryophyllaceae.

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Functional Genetics/Genomics

Topic: Contributed Papers Functional Genetics/Genomics

Title: Phenotypic trait variation in common garden comparisons between synthetic and natural allopolyploids and their parents of the North American Tragopogon (Asteraceae).

Author: ***Ingrid Jordon-Thaden @ University of Wisconsin-Madison***

Keywords: allopolyploidy,Asteraceae,common garden,fitness,hybridization,Palouse Prairie,Phenotype,physiology,polyploidy,Tragopogon,WGD,Greenhouse

Abstract:

Recently (~ 100 years) formed allopolyploids Tragopogon mirus and T. miscellus and their diploid parental species, T. dubius, T. porrifolius, and T. pratensis, offer a rare opportunity to study the earliest stages of allopolyploidy. This study is the first large-scale common-garden experiment to assess trait variation in the entire North American Tragopogon allopolyploid complex. The allopolyploid species were resynthesized in 2009, allowing direct comparisons between the youngest possible allopolyploid lineages and their natural, established counterparts in natural populations of the Palouse Prairie in Washington and Idaho. For the first time we compare phenotypic traits on a large scale in Tragopogon in the same greenhouse study over an 18-month period. Our large common-garden experiment measured traits in growth, development, physiology, and reproductive fitness and analyzed differences between allopolyploids and their parental species and between synthetic and natural allopolyploids. As previously observed in many polyploids, the allopolyploid species had some larger physical traits and a higher capacity for photosynthesis than diploid species. Reproductive fitness traits were variable and inconsistent between the two allotetraploids, but results were clouded by insect infestations in the floral structures, ultimately reducing our sample size. Allopolyploids had intermediate phenotypes compared to their diploid parents in flowering time, petal color, and number of mature seeds per inflorescence. The three generations of resynthesized and natural allopolyploid lines generally showed minor to non-existent trait differences, therefore allowing us to conclude that any trait differences due to polyploidization were seen in the very first generation after allopolyploidy had occurred and did not change much in subsequent generations after polyploidy. It is important to note that T. dubius, one of the three possible parents in the complex, often over-produced in the traits measured, which disrupted the significance or trends of some phenotypes observed in this study. Something that might have been less of a problem if the experiment had been done on-site in a common garden experiment in the Palouse Prairie itself. In conclusion, in Tragopogon, allopolyploidy results in some predicted and expected phenotypic changes, such as gigas effects seen via increased total biomass, seed weight, number of flowers per plant, and photosynthetic capacity. Being polyploid did not produce a significant reproductive advantage, except for increased number of mature seeds per inflorescence, but did show an advantage in early seedling growth and primary vegetative growth in the first-year basal rosette. Polyploid germination was more variable than diploid, which was predicted by known meiotic aberrations already observed in this complex. We can conclude from this study that polyploidization contributes to progeny (larger seeds = larger seedlings) and establishment of the young plant, as well as the already known gigas effect observed in mature polyploid plants, resulting in increased competitive ability.

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Functional Genetics/Genomics

Topic: Contributed Papers

Title: Genetic basis of pistil length variation between monkeyflower species with different pollination syndromes

Author: ***Bianca Ferreira @ University of Connecticut***

Keywords: Mimulus,Pollination syndrome,QTL,pistil,recombination mapping

Abstract:

The evolution of floral traits associated with specialized plant-pollinator interactions (pollination syndrome) enables divergence in reproductive strategies and is key for the diversification of flowering plants. Pollination syndromes are widely observed in flowering plants with a prime example in the Mimulus genus where hummingbird-pollinated M. cardinalis flowers are larger, red in color, with exserted stamens and pistils whereas self-pollinated M. parishii have small, inconspicuous, pale pink flowers with minimal anther-stigma separation. Although the variation of some pollination syndrome traits such as flower color has been relatively well understood from a genetic perspective, very little is known about the genetic mechanisms underlying the variation of more polygenic traits such as flower size, stamen length, and pistil length. Here we report the identification of a quantitative trait locus (QTL) controlling pistil length variation between the hummingbird-pollinated M. cardinalis and self-pollinated M. parishii. Introgression of this QTL from M. cardinalis to M. parishii resulted in a near-isogenic line with increased pistil length (3 mm longer than the wild-type M. parishii). Fine-scale recombination mapping using the near-isogenic line narrowed the causal gene down to a small genomic region. Functional characterization of candidate genes in this interval is underway. These results suggest that even polygenic, dimensional traits such as pistil length can be genetically dissected through the construction of near-isogenic lines, recombination mapping, and subsequent transgenic characterization, an approach that will enable us to systematically study the pollination syndrome evolution in the monkeyflower system, gene by gene, mutation by mutation.

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Functional Genetics/Genomics

Topic: Contributed Papers

Title: Salicornia depressa: genomics of a highly salt and metal tolerant plant

Author: ***Brook Moyers @ University of Massachusetts Boston***

Keywords: genome assembly,halophyte,ploidy level,salinity tolerence,whole genome sequencing,pickleweed

Abstract:

Salicornia are globally-distributed halophyte plants that thrive in the high intertidal zone and colonize salt marsh mudflats in the first stage of succession. Salicornia hyperaccumulate metals by stabilizing them in plant tissue, potentially providing remediation services. Salicornia also can be eaten as a vegetable and used for seed oil and “green salt” in emerging industries Most research in this genus has focused on European species and comparatively little is known about North American species, including the widely-distributed S. depressa. No Salicornia genome resources are currently available.

We are assembling the S. depressa genome using a combination of long read sequencing, Hi-C mapping, and short-read polishing, and annotating the genome with transcriptome and methylome data. Our initial genome profiling indicates that S. depressa is a diploid with a genome length of approximately 1.13 Gbp and 6.87% heterozygosity, contradicting the literature reporting the species as tetraploid and primarily selfing. We confirmed our results with additional sequencing and root-tip chromosome squashes (2N = 18). We have also obtained low-coverage whole genome sequence data from 94 individuals from ten populations sampled across New England at sites ranging from pristine to metal-contaminated. Our preliminary analyses of genomic and population structure in S. depressa provide insight into the evolutionary history of this understudied species and will support future research on salinity and metal tolerance.

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Topic: Contributed Papers Functional Genetics/Genomics

Title: Gene expression, Molecular proliferation and Cellular signalling on photosynthetic activities of Piper nigrum L.

Author: ***Vasu Jayaveeran @ Postgraduate Department of Botany American College Madurai Tamilnadu India***

Keywords: (epi)genetic architecture

Abstract:

I study on Gene expression, Molecular proliferation and Cellular signallings on photosynthetic activities of Piper nigrum L. grows up for cash crops verdict importance. The vigorous campaign exercise of Photosynthetic pigmentations developments happen such as Chlorophyl a b Xanthophylls carotenoids dominance characteristics features which excited by solar energy purses with Cyper electron transport by means of Doppler effect jumpsuits movement from the Biophysics Quantum systematic approach of Photosynthetic reactivity from Hydrogen molecules which shared to Mg2+ attachment of Chlorophyll a b Xanthophylls carotenoids along with the strength of mRNA expression interests depending on rRNA decodes tRNA genetic informations codes from Polyribosomes involved in Biosynthesis of enzymic proteins activities in relation with Plant Genetics of DNA Adenine methylation used to be followed by DNA Cytosine methylation from genomic loci for the yields of Photosynthetic products using the immediate response of mitochondrial ATP production process of Glucose molecules from the rotation basis of Chloroplasts mobilization used to be enhanced by means of micronutritional ZnSO4 optimum effect which produces Zn+ and SO4- ionic equilibriums as the proper pathways of formation of Bioelectrolysis cellular activities and Bioelectricity & Biomagnetic fieldstones operations involvement in the establishment of Bioelectronics ZnSO4 optimum effect on Piper nigrum L. in the present invention attentively.

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Topic: Contributed Papers Hybrids and Hybridization

Title: Breeding Battles: Reproductive Dynamics in Mixed Apomictic and Sexual Populations

Author: ***Gracy Buckholtz @ University of British Columbia***

Keywords: apomixis,GBS,hybridization,sexual cyotype exclusion principle,reproductive dynamics

Abstract:

Species that reproduce both through apomixis, the formation of asexual seeds, and sexually present complex questions around reproductive dynamics in mixed populations. Apomicts arise from sexual plants meaning that early populations that contain apomicts are mixed populations. The sexual cytotype exclusion principle theorizes that in these mixed populations sexual plants will bear the cost of hybridization. Sexuals are diploids while apomicts are polyploid and the hybrids that form between them are inviable. The cost is unidirectional because apomicts do not require external pollen for reproduction, but sexual mothers risk the chance of producing these inviable offspring if pollinated with apomictic pollen. Townsendia hookeri is an ideal system to explore these dynamics. T. hookeri is a rocky-mountain species that has both a triploid apomictic and diploid sexual form. Both forms occur in southern Wyoming and northern Colorado, but populations are always split and composed of one cytotype type or the other. Are the dynamics outlined in the sexual cytotype exclusion principle the key to explaining why we don’t find mixed populations? The answer to that depends on the strength of those reproductive interactions and therefore on their potential to increase the cost of co-occurrence. To begin to measure these forces, we collected achenes from an open pollinated garden composed of 16 apomicts and 19 sexuals. Achenes were collected and weighed prior to germination. Germination was tracked and growth was measured after 5 weeks. We are using a genotyping by sequencing protocol to designate offspring as either hybrids, the product of sexual outcrossing, or the product of facilitated selfing (mentor effect). A proximity score was assigned to each sexual plant in the array based on their relative proximity to other sexuals. Plants scored high when they were closer to other sexuals and lower when they were further from sexuals and more surrounded by apomicts. These scores will be evaluated on their ability to act as predictors for hybrid formation, achene weight, germination, and growth. We will also be examining the correlation between the traits measured and offspring type (hybrid, outcrossed, or selfed). This, in conjunction with the proximity scores, will determine the variation in the strength of reproductive interactions at a local scale. This will provide insight into if these forces operate over small spatial scales or if at that scale spatial isolation is insignificant. From these results I will be able to determine the role of reproductive dynamics in mixed T. hookeri populations.

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Topic: Contributed Papers Hybrids and Hybridization

Title: Predictive links between petal reflectance and pigment quantities in natural Penstemon hybrids

Author: ***Josh Stevens @***

Keywords: Penstemon,Flower color,hybrid zone,pigmentation

Abstract:

Flowers have evolved remarkable diversity in flower color in response to pollinator-mediated selection. This diversity arises from specialized metabolic pathways that generate conspicuous pigments. Despite the clear link between floral reflectance spectra and floral pigment production, studies determining predictive relationships between pigmentation and petal reflectance are currently lacking. In this study, we analyze a dataset consisting of hundreds of natural Penstemon hybrids that are segregating flower color, including blue, purple, pink, and red. For each individual hybrid, we measured anthocyanin pigment production and petal reflectance. We found that floral pigment quantities are correlated with hue, chroma, and brightness as calculated from petal reflectance data: hue is related to the relative amounts of delphinidin vs. pelargonidin pigmentation, whereas brightness and chroma are correlated with the total anthocyanin pigmentation. We used a partial least squares regression approach to identify predictive relationships between pigment production and petal reflectance. We find tha pigment quantity data provide robust predictions of petal reflectance, confirming a pervasive assumption that differences in pigmentation should predictably influence floral reflectance. Moreover, we find that reflectance data enables accurate inferences of pigment quantities, although the full reflectance spectra provide much more accurate inference of pigment quantities than spectral attributes (brightness, chroma, and hue). Our predictive framework provides readily interpretable model coefficients relating spectral attributes of petal reflectance to underlying pigment quantities. These relationships represent key links between genetic changes affecting anthocyanin production and ecological functions of petal coloration.

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Topic: Contributed Papers

Title: Understanding the generation and maintenance of biodiversity within the North American Coastal Plain through hybridization in pondweeds (Potamogetonaceae)

Author: ***Zacc Ramm @ University of South Alabama***

Keywords: areas of endemism,Biodiversity hotspots,hybridization,phylogenomics,Potamogetonaceae

Abstract:

The North American Coastal Plain (NACP) in the southeastern United States was initially overlooked as a biodiversity hotspot in multiple analyses of global biodiversity because it was assumed that the NACP would not support high species diversity. As a result, the same investigative efforts to document and preserve biodiversity have not been given to this center of endemism as other hotspots. The NACP exhibits particularly high freshwater biodiversity and is home to many endemic aquatic plant species. Endemic organisms are generally understudied and under-collected due to a combination of small population sizes, occurrence in restricted locations. Aquatic plants are additionally overlooked because they are more difficult to access; thus, collection efforts are typically biased towards terrestrial species. These understudied cornerstone species in an overlooked biodiversity hotspot provide an excellent opportunity to advance our understanding of the sources and patterns of endemic diversity in the NACP. The pondweed family (Potamogetonaceae) is one of the most species-rich freshwater aquatic plant families in the world and contributes greatly to the submersed aquatic plant diversity in the northern hemisphere. Despite their dominance in freshwater ecosystems and ecological and economical importance in maintaining these systems, there is a lack of basic biological knowledge for these plants. One of the most basic barriers to further research is poor taxonomic resolution. Potamogeton has historically been one of the most difficult aquatic plant groups to describe and the genus is known to readily hybridize. It is estimated that there are as many if not more hybrids than distinct species. Hybrid species are often excluded from biodiversity assessments, either passively or explicitly. Given that hybrids greatly contribute to taxonomic diversity and taxonomic confusion, more robust identification of hybrid species and their evolutionary origins will help resolve pondweed taxonomy and provide a more accurate assessment of biodiversity in the NACP. Geological processes that fragment species distributions, such as glaciation cycles and sea level fluctuations, can facilitate speciation by reproductively isolating populations for thousands to millions of years. These processes can also bring together species that did not previously share a geographic range. In the case of Potamogeton, in which species readily hybridize where they co-occur, such events likely promoted diversification through both population fragmentation and new combinations of co-occurring species. Currently, P. floridanus is the only hybrid species recognized in the southeastern US, which seems to be more an artifact of collection bias than a biological reality. This study aims to (1) assess the factors contributing to hybridization in Potamogetonaceae, (2) resolve confusion regarding the taxonomy and phylogentic relationships within Potamogetonaceae, (3) identify other potential Potamogetonaceae hybridization events within the NACP.

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Topic: Contributed Papers Hybrids and Hybridization

Title: Notes on the Genus Chloraea (Orchidaceae): Morphological Evidence of Triad Hybridization through a Conduit Species

Author: ***Justin Scholten @ Cornell University***

Keywords: co-occurring species,hybrid zone,introgression,Orchidaceae,Patagonia,species complex

Abstract:

Introgressive hybridization is known to affect the morphological structure of a population in many key ways. It can increase standing levels of morphological variation as adaptive radiation proceeds and enhance the potential for future evolution through accelerating or decelerating speciation, alleviating inbreeding depression in small populations, and the fixation of novel traits through transgressive segregation. Although hybridization is generally regarded as a common occurrence in most major lineages, especially plants, our understanding of interspecific breeding is largely limited to the study of two species. Infrequently, an interbreeding complex may arise between three species, where one species typically acts as a conduit for gene flow between two others that may rarely hybridize otherwise. A putative zone of triad hybridization involving three species of Chloraea (Orchidaceae): C. gaudichaudii, C. magellanica, and C. speciosa, is reported from Chubut, Argentina. Morphological data comprised of eight diagnostic floral characters show phenotypic intergradation within the species triad resulting from putative hybridization where C. magellanica appears to act as a conduit species to facilitate gene flow between C. gaudichaudii and C. speciosa; these findings illustrate how gene flow between three species can change the morphological demographic of a population and enhance the potential for evolutionary change.

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Topic: Contributed Papers

Title: RAD-seq reveals widespread hybridization among species of Andean Weinmannia across elevations.

Author: ***Juan Penagos Zuluaga @ Missouri Botanical Garden***

Keywords: Andes,Species boundaries,2bRad

Abstract:

The Tropical Andes are an important hotspot for biodiversity, with one of the greatest species richness and endemism on earth. This mega diversity is partly due to a complex biogeographic history, including rapid evolutionary radiations in many plant groups, coexisting in a large elevational gradient with a variety of habitats. In such complex conditions, including a history of elevational range shifts and secondary contact between isolated populations, it is hypothesized that hybridization among related lineages is common and could be driving rapid diversification processes in some clades. Weinmannia (Cunoniaceae), an abundant and diverse clade of woody plants, is an ideal group to explore this hypothesis as numerous related species occur across the elevational gradient, have broadly overlapping geographic ranges, and display wide variation in morphology. Previous observations have shown the existence of intermediate morphological phenotypes that do not correspond to known species and could be the product of interspecific hybridization. In this study, genome-wide SNP markers were used to 1) assess whether Central Andean species of Weinmannia delimited based on morphology form cohesive genetic groups and 2) to test for the presence of hybridization. We evaluated whether morphologically described species are consistent with patterns of genetic structure and tested for the presence of interspecific hybrids in a clade of six species with partially overlapping distributions. We genotyped 126 individuals using 2bRAD along an elevational gradient from 1,900 to 3,700 m in the Madidi National Park (Bolivia). Genetic clusters and putative hybrids were identified using STRUCTURE and PCA; then, we reconstructed phylogenetic relationships among the six species. The results showed that most species of Weinmannia delimited based on morphology were genetically distinct, but fewer genetic clusters were found than morphologically described species. Several species consisted mainly of hybrids, suggesting that taxonomists likely described hybrid populations as distinct taxonomic species. Two species, W. nebularum, and W. davidsonii were often found hybridizing, indicating weak species boundaries among these two species. Therefore, the study showed a high incidence of hybrids in Weinmmania species from the Tropical Andes. These results highlight the importance of considering hybridization and its effects on taxonomic and nomenclatural issues, as well as on the study of plant evolution in species-rich groups.

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Hybrids and Hybridization

Topic: Contributed Papers Hybrids and Hybridization

Title: Functional or Fluke? Genome-wide identification of introgressed genes in naturally occurring Eucalyptus hybrids

Author: ***Kasey Pham @ University of Florida***

Keywords: introgression,Myrtaceae,Eucalyptus,whole genome resequencing

Abstract:

Adaptive introgression, the transfer of useful alleles from one species to another through hybridization and backcrossing, is hypothesized to introduce new genetic diversity which could help plants expand into new habitats and respond to environmental change. With increasing awareness that hybridization is common across the plant Tree of Life, major questions have arisen, including: which genes are most likely to be exchanged between species, and how do these affect the evolution of hybridizing lineages, especially adaptation to new environments? However, little is still known about the genomic distribution and content of introgressed regions outside of a few model systems. In this study, we aimed to determine the effects of hybridization on Eucalyptus globulus by characterizing introgressed genomic regions donated from a Tasmanian endemic species, Eucalyptus cordata. Previous work has shown that morphologically typical E. globulus trees growing in close proximity to small populations of E. cordata have captured chloroplast DNA and some nuclear markers. It is possible that these alleles have been retained for over 17,000 years because they have conferred an advantage for the introgressant Eucalyptus trees. In a first step to testing the adaptive value of hybridization in this system, we use whole-genome resequencing and admixture analysis to map the mosaic nature of the E. globulus genome. With that information, we address the following questions: 1) which genomic regions and genes are most likely to be introgressed and 2) to what extent does selection, positive or negative, play a role in introgression in comparison to neutral processes?

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Hybrids and Hybridization

Topic: Contributed Papers

Title: Genomic distribution of introgression in two hybridizing milkweeds

Author: ***Victor Andreev @ Oklahoma State University***

Keywords:

Abstract:

Two milkweed species, A. speciosa and A. syriaca, are experiencing asymmetric bidirectional introgressive hybridization on the Great Plains. The average amount of introgressed heterospecific variation per individual in this system is 4.2%, yet genomic location of introgressed loci and adaptive significance of introgression was never explored. Based on the position of these species on a strong precipitation gradient and their differences in drought-related traits, we speculate that the introgressed variation can be associated with adaptation to water deficit.

Our goals were to characterize the number, size, and distribution of introgressed regions across the genomes of the A. speciosa and A. syriaca, explore the functions of genes located in these regions, and assess whether introgression in this system is mediated by natural selection. We used a sample of 147 allopatric and sympatric individuals genotyped at 732400 SPNs.

Our analysis demonstrated that the introgressed blocks can be found on multiple chromosomes of both species. The size of the blocks is relatively small and ranges from 5 kb to 83 kb. The highest number and cumulative length of introgressed blocks was found on chromosome 9 in A. speciosa and chromosome 7 in A. syriaca. Some of the introgressed loci are under directional selection (43% in A. speciosa and 55% in A. syriaca). In A. speciosa, the introgressed genes are involved in reproduction, while in A. syriaca it is mostly stress response and response to herbivores and pathogens on the one hand, and regulation of osmotic potential and stomatal conductance on the other hand.

Our findings provide insights into the possible genetic basis of differential introgression between A. speciosa and A. syriaca, and suggest the mechanism of adaptation to arid climate in A. speciosa and other Great Plains perennial herbaceous plants.

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Hybrids and Hybridization

Topic: Contributed Papers

Title: Introgression of cultivar alleles into wild carrot populations in the United States

Author: ***johanne brunet @ USDA-ARS***

Keywords: Apiaceae,Gene editing,gene flow,genomics,introgression,population genomics,SNP,ABBA-BABA

Abstract:

Gene flow between crop species and their wild relatives has played an important role in the evolution of both wild and cultivated plants. Cultivated and wild carrots are classified as the same plant species, Daucus carota, and often occur in sympatry. Wild carrot, or Queen Anne´s lace, is strongly outcrossed and weedy, and has been declared invasives in many states in the US. Wild and cultivated carrots can hybridize and crop-wild hybrids can survive and reproduce almost as well as wild individuals in some environments. While hybridization does occur, it remains unclear whether crop alleles are maintained into the wild carrot genomes or whether they are purged out by natural selection. This is important as the development of gene editing technologies will permit introduction of genetically modified genes in carrot cultivars and some of these genes may increase the invasiveness and weediness of wild carrot populations.

We used genomic data and population genomic methods to study hybridization and introgression between cultivated and wild carrots in the United States. We genotyped, using genotypic by sequencing, 450 wild individuals from 29 wild populations in seven states, and 144 cultivars, mostly from the United States, Europe, and Asia. After filtering, 523 samples (144 cultivated + 379 wild) and 34,871 SNP were kept. Wild samples had higher genetic diversity relative to the cultivars, and we detected significant genetic differentiation between the two groups. We identified, using ABBA-BABA tests and other approaches, two areas of the United States with evidence of introgression from cultivars into wild carrot populations, California and the Nantucket Island, in Massachusetts. The introgressed genes were distributed over all nine chromosomes, making it difficult to develop genetic methods to prevent their introgression into the wild carrot genome. Admixed populations were found in environments with milder winters than unadmixed populations, suggesting an influence of the environment on crop introgression. The introgression of genetically modified cultivar genes into wild carrot populations stresses the potential impact of gene editing technologies on the risk of increasing invasiveness and weediness of sexually compatible relatives of crops.

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Hybrids and Hybridization

Topic: Contributed Papers

Title: Summary tests of introgression are highly sensitive to rate variation across lineages

Author: ***Lauren Frankel @ University of Wisconsin-Madison***

Keywords: gene flow,hybridization,phylogenomics,species network,D-statistic,ABBA-BABA

Abstract:

The evolutionary implications and frequency of hybridization and introgression are increasingly being recognized across the tree of life. To detect hybridization from multi locus and genome-wide sequence data, a popular class of methods are based on summary statistics from subsets of 3 or 4 taxa. However, these methods often carry the assumption of a constant substitution rate across lineages and genes, which is commonly broken in many groups. In this work, we quantify the effects of rate variation on the D-statistic, the D3 statistic, and HyDe. All three tests are used widely across a range of taxonomic groups, in part because they are very fast to compute. We consider rate variation across species lineages, across genes, their lineage-by-gene interaction, and rate variation across gene-tree edges. For all three methods tested, we found a marked increase in the false discovery of reticulation (type-1 error rate) when there is rate variation across species lineages. The D3 statistic was the most sensitive, with around 80% type-1 error, such that D3 appears to more sensitive to a departure from the clock than to the presence of reticulation. For all three tests, the power to detect hybridization events decreased as the number of hybridization events increased, indicating that multiple hybridization events can “hide” one another if they occur within a small subset of taxa. Our study highlights the need to consider rate variation when using site-based summary statistics.

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Topic: Contributed Papers Hybrids and Hybridization

Title: Natural hybrid zones as model systems to examine the genomic basis for climate adaptation for forest trees

Author: ***Jill Hamilton @ Pennsylvania State University***

Keywords: Populus,adaptation,common garden,phenology,whole genome sequencing

Abstract:

Hybrid zones are often viewed as active sites of evolutionary change, either as sources of new recombinant types, new species, or as regions where species’ barriers may be examined to infer mechanisms of speciation. In forest trees, hybrid zones present natural laboratories to examine the genetic and ecological interactions underlying to adaptation. Indeed, hybrid zones allow us to examine the fine-scale transfer of genetic material between species that may be important in terms of adaptation, as well as identifying regions of the genome contributing to reproductive isolation and the maintenance of species barriers. Ultimately, the genetic analysis of hybrid zones leads to a more mechanistic understanding of the processes involved in the origin of adaptations and the origin of species. In this study, we are examining the respective roles of genomic ancestry, genetic variation, environmental variation, and their interactions to tree fitness. Using wild-collected material from replicated, latitudinally differentiated, natural hybrid zones between Populus trichocarpa x P. balsamifera, in conjunction with modern sequencing, and an extensive network of replicated common gardens we are evaluating the consequences of hybridization to climatic adaptation. Populus provides an ideal model for this work with its compact genomes, rapid clonal growth, ease of vegetative propagation and extensive range of natural genomic and phenotypic variation. Preliminary data suggest that hybridization is a stimulus for novel genomic architectures, but that there is substantial variability in the direction and extent of nuclear and chloroplast introgression across replicate zones of hybridization that may be associated with environmental thresholds. Indeed, genotype response functions across replicated common gardens indicate varying influence of the environment, genomic ancestry, genetic variation, and interactions for phenotypic traits important to adaptation across environments. Overall, these results underscore the value of using natural hybrid zones in a predictive context to understand adaptation needed for forest management in a changing climate.

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Topic: Contributed Papers

Title: Development of a ddPCR Protocol for Detecting Homeolog Expression in Nicotiana Allopolyploids of Different Ages

Author: ***Trinity Tobin @ SUNY Cortland***

Keywords: Nicotiana,allopolyploidy,droplet digital PCR,Evolution,Flower color

Abstract:

Allopolyploidy is when two or more sets of chromosome sets come together due to hybridization, creating homeologs. The genus Nicotiana has a variety of allopolyploids that stem from different polyploidization events, with these events giving rise to new distinct species. For example, N. sylvestris and N. tomentosiformis are the diploid progenitors of the allopolyploid N. tabacum, which originated 0.6 million years ago. In contrast, the offspring of N. sylvestris and N. obtusifolia (section Repandae) originated 4.3 million years ago. To analyze the differences in homeolog expression in allopolyploids of different ages, the diploid progenitors N. sylvestris, N. tomentosiformis, and N. obtusifolia were studied, as well as their allopolyploid offspring. Our question tests whether the differences we see in flower color in allopolyploids are due to variation in homeolog expression of flavonoid biosynthetic pathway genes. This pathway created the pigments cyanidin (pink), delphinidin (purple), and pelargonidin (red), as well as a group of colorless pigments called flavonols. We used droplet digital PCR (ddPCR) to develop a protocol to distinguish between homeologs using a single reaction to quantify expression of both homeologs.

Droplet digital PCR separates the reaction into small droplets using oil. The PCR portion of the protocol amplifies our gene of interest in the droplets. If a droplet contains our gene of interest, it will fluoresce, allowing us to quantify the expression of a given gene based on how much transcript is present. Achieving this fluorescence would let us synchronously quantify the expression of both homeologs with a single ddPCR reaction. The goal of our ddPCR fluorescence is to have high fluorescence in the maternal homelog and lower fluorescence in the paternal homeologs. To do this, we designed primers that were more complementary to the maternal homeolog than the paternal homeolog, which will impact primer efficiency.

Initially, we capitalized on SNPs between the maternal and paternal homeologs at the 3’ end o our primers, effecting the primer’s ability to anneal to the paternal homeolog efficiently. We found in our ddPCR relatively high fluorescence for the maternal homeolog and a large variation in the fluorescence in the paternal homeolog. To troubleshoot this, we created new primers that were identical on the 3’ end but had SNPs throughout the primer that would allow us to distinguish based on differences in primer melting temperatures. We hypothesize that this new method will decrease this variation of paternal homeolog expression while also achieving our original goal of distinguishing the homeologs in a single reaction.

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Hybrids and Hybridization

Topic: Contributed Papers Hybrids and Hybridization

Title: Differential gene expression and subgenome dominance in 4 million year old allopolyploids of Nicotiana section Repandae

Author: ***Talieh Ostovar @ SDSU/UCR***

Keywords: Nicotiana,allopolyploidy,differential gene expression

Abstract:

Allopolyploidy, a common and ongoing phenomenon among angiosperms, entails hybridization coupled with whole-genome duplication, and produces new species containing two or more homoeologous subgenomes. Allopolyploidy has major effects on plant genome structure and gene expression patterns, which can cause novel phenotypes not observed in progenitors. Allopolyploids often experience subgenome dominance, the preferential expression of homeologs from one of the two progenitor genomes (subgenomes). To better understand the immediate and long-term consequences of allopolyploidy and the extent to which subgenome dominance is a legacy of the progenitors' expression patterns, we investigate global gene expression architecture and the fate of homeologs in Nicotiana (Solanaceae). Nicotiana is an ideal system for studying alloploypoid evolution because of extensive genetic and genomic resources and because half of Nicotiana species are allopolyploids of different ages. We focus on gene expression in Nicotiana section Repandae, including three allotetraploid species, N. nudicaulis, N. repanda, and N. stocktonii, derived from hybridization between N. sylvestris and N. obtusifolia ~4.3 million years ago. We identify genes with differential expression across tetraploid and diploid species, as well as across stages of corolla development within each species. Furthermore, we investigate subgenome dominance patterns to track the homeolog expression bias in allopolyploids. Finally, we explore expression patterns of potential candidate genes for underlying variation in flower size. We find clear expression differences between the two progenitor species, with all the allopolyploids intermediate between them. We observe a slight bias toward N. obtusifolia, especially in the leaf tissues. Hierarchical clustering based on differential expression across corolla developmental stages reveals similar common expression patterns and different numbers of transcripts in various species. We also see differential expression of several known flower size candidate genes across the corolla developmental stages. Collectively, these results provide a perspective on evolutionarily persistent expression alterations after allopolyploidization and hint at the underlying genetic basis of speciation events.

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Hybrids and Hybridization

Topic: Contributed Papers

Title: Post-WGD changes in neoallopolyploids [VIDEO]

Author: ***Usama Mukhtar @ Massey University***

Keywords: allopolyploidy,chloroplast,physiology,polyploid,Tragopogon,mitochondria

Abstract:

Allopolyploidy has been a significant evolutionary force across the eukaryotic tree of life, particularly in plants. Newly formed polyploids inherit traits from their progenitors but may also show transgressive characters that allow them to inhabit different areas and/or outcompete their parents in similar habitats. As part of a larger study aimed at understanding genomic changes that accompany allopolyploidization and cytonuclear coordination, we are investigating anatomical and physiological characteristics in Tragopogon miscellus, a recent, recurrent, and reciprocally formed allopolyploid. This species formed naturally in the last 100 years from hybridization between T. dubius and T. pratensis. Comparative internal leaf anatomy is being studied to document differences in tissue patterns among the reciprocally formed allopolyploid forms and their parental species. We are also studying differences in the morphology and physiology of the diploids and polyploids under different climatic conditions. Days to germination, number of leaves, shoot and root biomass among other characteristics are being documented for plants grown under three different temperature conditions (10°, 20°, 30° C) and with varying watering treatments. Data gathered thus far will be presented. Currently, our results indicate a difference in optimal climatic growth conditions among the polyploids and diploids which may be caused by differences in leaf anatomy and physiology.

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Macroevolution

Topic: Contributed Papers Macroevolution

Title: Pollination Diversity in American Justicia (Acanthaceae)

Author: ***Amanda Fisher @ California State Univ Long Beach***

Keywords: Floral traits,floral visitor,Hummingbird Pollination

Abstract:

Evolutionary transitions between different types of animal pollinators may play a role in angiosperm species diversity and select for various floral forms. The approximately 400 species of American Justicia (Acanthaceae) have a wide variety of flower shapes, sizes, and colors and are pollinated by bees, hummingbirds, butterflies, flies, bats, moths, and other animals. Previous studies have found that corolla color and size, anther form, pollen morphology, and stigma morphology correlate with pollinator groups in some Justicia clades. We sought to contextualize these findings by characterizing the extent and patterns of association between animal pollinator groups and American Justicia species. We created a database of animals observed visiting open flowers of American Justicia species that relied on observations from field work, published studies and theses, interviews with field biologists, and community science observations. The most commonly observed visitors to American Justicia are hummingbirds, bees, and butterflies. We also documented beetles, wasps, and hawkmoths as visitors. Across the American Justicia clade the most common transition is between bee and hummingbird visitors. Animal visitors were found to be associated with flower color, especially red flowers with hummingbirds, purple flowers with bees and butterflies, white flowers with bees, flies, moths, and wasps, green flowers with bats, and yellow flowers with hummingbirds.

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Macroevolution

Topic: Contributed Papers

Title: Evolution of CAM anatomy and predicting physiology from anatomy

Author: ***Ian Gilman @ Michigan State University***

Keywords: comparative methods,Machine Learning,photosynthesis,Crassulacean acid metabolism,Portullugo,asparagaceae

Abstract:

Plants with crassulacean acid metabolism (CAM) have long been associated with derived anatomy, such as succulence and thick leaves, but quantitative boundaries between C3 and CAM anatomy have yet to be established. Using newly developed computer vision software to measure anatomy, we combined new anatomical measurements with published data across flowering plants. We then used machine learning and phylogenetic comparative methods to investigate relationships between CAM and anatomy. We found significant differences in photosynthetic anatomy between plants with differing CAM phenotypes. Machine learning based classification was moderately to highly accurate in classifying photosynthetic phenotypes. PGLS regression and phylogenetic threshold analyses revealed that increased CAM activity was significantly linked to increased mesophyll cell size and leaf thickness, and decreased intercellular airspace. Significant differences in photosynthetic anatomy exist between non-CAM and CAM plants, as well as between CAM phenotypes, but more data is needed for robust prediction of photosynthetic phenotypes from anatomy alone. Our findings support the hypothesis that morphological innovations are necessary to perform CAM and to transition between CAM phenotypes.

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Macroevolution

Topic: Contributed Papers Macroevolution

Title: The Stripping of the Altars: Divergence time estimation and the stray from biological realism

Author: ***Stephen Smith @ University of Michigan***

Keywords: divergence time estimation,phylogenetics

Abstract:

Divergence time estimation analyses are nearly ubiquitous in phylogenetic manuscripts. Chronograms play a key role in placing biological systems into a broader evolutionary context by facilitating comparisons to other evolutionary lineages, geologic and geographic movements, and local and global climatological changes. They are also a vital source of information for many comparative analyses, such those that track diversity dynamics through time (interpreted from changes in rates of speciation and/or extinction) and those that attempt to uncover the tempo and mode of morphological evolution. However, it is clear that we are getting no closer to accurate divergence times for major radiations. In this talk, I will discuss several of the problems we continue to face and the challenges that lay ahead in our quest to better understand divergence times across plants.

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Macroevolution

Topic: Contributed Papers

Title: A Hidden Markov framework for estimating substitute rate heterogeneity in flowering plant divergence time estimation

Author: ***Jeremy Beaulieu @ University of Arkansas***

Keywords: divergence time,divergence time estimation,hidden states,flowering plants

Abstract:

Hidden Markov models (HMMs) are a powerful approach for discovering novel insights across a number of biological applications, from biological sequence analysis to molecular structure prediction to even phylogenetic tree construction. Recently, HMMs have become the primary framework for phylogenetic comparative biology as means for modeling lineage-specific heterogeneity in both trait evolution and diversification without vastly increasing the number of parameters. In our view, HMMs have enormous potential in divergence time applications that separate branch lengths (that are in units of raw substitution counts) into their two component parts of durations of time and substitution rates, which often exhibit lineage-specific variation. These lineage-specific rates complicate the estimation of divergence times, because we cannot assume that the substitution rate from one lineage accurately represents the substitution rates in other lineages in the tree. Many solutions exist to relax these assumptions, but are largely borne out of statistical convenience. More importantly, they violate our natural intuitions about how rates likely evolve across a tree just like any trait, especially if these rates are co-evolving with changes in life-history and/or environmental interactions. Here we describe an HMM modeling framework for examining not only substitution rates that follow the evolution of an observed focal trait of interest, but also the evolution of “hidden” states, allowing the discovery of correlations with other observed and unobserved factors. We will also show how our new scalable approach can discover underlying variation of evolutionary rates, facilitating more confidence and accuracy in divergence time estimates, particularly with regards to the age of flowering plants.

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Macroevolution

Topic: Contributed Papers

Title: The evolution of floral architecture and scent in the animal pollinated clade, Lonicera (Caprifoliaceae)

Author: ***Wendy Clement @ The College of New Jersey***

Keywords: Ancestral state reconstruction,honeysuckles,Pollination syndromes,Floral Scent,floral volatiles,spme

Abstract:

The clade Lonicera (Caprifoliaceae) comprises nearly 140 species distributed largely through the northern hemisphere. Lonicera, or honeysuckles, are well-known for having tubular, nectariferous flowers that are often fragrant. Many Lonicera also exhibit fusion of extra floral organs such as bracts and bracteoles. Across this clade, biotic pollination involving bees, hawkmoths, and hummingbirds has been recorded. The contemporary diversity of size, shape, color, and fragrance among flowers of Lonicera suggest changes in floral traits over time may be connected with shifts in pollination strategies. Additionally, the diversity of fusion observed among extra floral structures has not been considered in conjunction with floral evolution and may shed light on the possible correlated evolution with pollination. Here we describe the evolution of 15 floral traits, including discrete and continuous characters, across a phylogeny of nearly 127 species reconstructed from RAD-seq data. Floral traits were studied and scored largely from herbarium specimens supplemented with field studies and the literature. Additionally, we sampled floral scent from 16 species of Lonicera distributed across the clade using solid phase microextraction (SPME) facilitated with field-sampling SPME fibers. Flowers were sampled from the living collections of the Arnold Arboretum of Harvard University and analyzed using gas chromatography-mass spectrometry (GC-MS). Here we describe the evolutionary history of Lonicera floral morphology and floral volatile composition as we identify the suites of traits that may correspond to bee, hummingbird, and hawkmoth pollination and the evolutionary steps that mark transitions to each modality of pollination.

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Topic: Contributed Papers Macroevolution

Title: Evolutionary constraint and ecological trade-off of the phenylpropanoid pathway determine the plant diversity in the past, present, and future

Author: **Jianhua Li @ Hope College**

Keywords: bryophytes

Abstract:

Different geological periods have witnessed the origin and differential diversification of various plant lineages on the Earth from Bryophytes, Ferns and allies, Gymnosperms, and Angiosperms. For example, Gymnosperms became dominant during the Mesozoic era but have declined since the emergence of angiosperms. About 1000 species of gymnosperms exist and are mostly limited to cold, dry, and high elevational or latitudinal areas. Angiosperms have radiated explosively since the early Paleocene with over 250,000 species. The differential diversification of various lineages has been associated with innovative traits such as the vascular system in vascular plants, seed in seed plants, and flower and fruit in angiosperms. Morphological and genetic integration may have existed during the evolution of the innovations but have not been explored in a comprehensive way. Therefore, the pleiotropic relationships among traits may offer an alternative to explain the differential diversification of major lineages of plants. Furthermore, some trait(s) may also be used to predict how plants perform with global environmental changes. Lignin is an important organic compound for plant cell integrity and function, and may be pleiotropically linked with the evolution of derived traits in bryophytes, ferns, gymnosperms, and angiosperms. The evolutionary pattern of lignification may provide new insights into differential diversification of plant lineages and is likely to be informative in predicting the impact of climatic change on composition and function of ecosystems. The existing lignin data show a continuing downward trend from the early plants to angiosperms, while genetic and biochemical analyses indicate that lignification and the production of flavonoids are negatively related. The negative relationship suggests a continuing upward trend of the production of flavonoids in plants, which are associated with plant development, survival, and biomass production. Both lignification and the production of flavonoids are parts of the phenylpropanoid biochemical pathway starting from the amino acid phenylalanine and both take a large amount of energy to produce. Therefore, there exists an ecological trade-off between the two competing pathways. Meanwhile, the genes involved in the two pathways are conservative or evolutionarily constrained, which is shown by the different levels of lignin in bryophytes, ferns, gymnosperms, and angiosperms. The declining amount of lignin has left more energy for biomass production via cell division and growth, and subsequently higher genetic variation, better survival, and greater diversification. In an ecosystem with plants of differential levels of lignin production, the ones with less energy for lignin may complete better than the ones with more energy for lignin production. However, in certain ecosystems (e.g., boreal forests), plants of a higher amount of lignin are more competitive (e.g., conifers). Therefore, I hypothesize that the evolutionary constraint and ecological trade-off of the phenylpropanoid pathway may be linked with the differential diversification of plants in the past, present, and future. A large amount of data from lignification, production of flavonoids, and genomics/proteomics of various plants in nature and controlled environment are needed to test the idea. The theory may have far-reaching implications for ecological and evolutionary studies and for conservation and climatic changes.

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Topic: Contributed Papers

Title: A geometric model for floral investment and form makes evolutionarily informative predictions

Author: **Eric LoPresti @ University of South Carolina**

Keywords: Floral anatomy,floral evolution,Floral meristem,Floral Symmetry,Petal size,asters

Abstract:

The convergence of flowers with varying floral organs into a recognizable shape despite their different meristic composition suggests some benefit of this shape. This benefit may be as simple as having a generally recognizable ‘flower shape’ to pollinators, though the floral bauplan is surely shaped by many biotic and abiotic agents of selection, as well as investment costs. Here, we propose a very simple geometric model of a simple actinomorphic flower and a more complicated ‘flower’ (i.e. an aster inflorescence). Using very few assumptions about investment in tissues and pollinator attraction, we make some basic predictions of floral form, which quantitatively matches several groups of plants well, though others quite poorly. We discuss the implications of its good match to certain groups and poor match to others in light of the evolution of floral shape.

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Topic: Contributed Papers

Title: Macroevolutionary patterns in flower and fruit colors

Author: **Miranda Sinnott-Armstrong @ University of Cambridge**

Keywords: Flower color,fruit color,Pollination syndromes

Abstract:

As part of their reproductive lifecycles, many plants partner with animals to achieve pollination and/or seed dispersal. As part of this mutualism, plants produce a variety of colors in their flowers and fleshy fruits in order to attract animals. In both animal-pollinated flowers and animal-dispersed fruits, “syndromes” of traits have been suggested that link traits to particular pollinators or dispersers. Flowers have been studied in considerably greater depth than fleshy fruits, despite the importance of both flowers and fruits in the plant life cycle. Here, we examine the evolution of flower color and fruit color in 1200+ species across 43 clades of plants that are animal-pollinated and animal-dispersed. We use diversity indices and stochastic character mapping to assess whether flower or fruit colors are more diverse and to characterize patterns in their evolution. We find that, within a clade, fruit colors tend to be more diverse than flower colors, and that fruit colors evolve faster than flower colors. Additionally, our data suggest that flower colors and fruit colors tend to evolve along predictable axes of variation. Flower color transitions within the same biochemical pathway (e.g., anthocyanins) are more common than transitions across biochemical pathways. Fruit colors, on the other hand, tend to evolve within the so-called “syndromes” associated with mammal and bird dispersal. These findings suggest that, although the colors of both flowers and fruits are generally assumed to be selected by animal pollen/seed dispersers, in fact these two similar traits display very different evolutionary trajectories that are likely constrained by different factors.

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Macroevolution

Topic: Contributed Papers Macroevolution

Title: The evolutionary responses of life-history strategies to climatic variability in flowering plants

Author: ***James Boyko @ University of Michigan***

Keywords: correlated trait evolution,precipitation,seasonality,Temperature,annuals,climatic nice,perennials

Abstract:

- The evolution of annual or perennial strategies in flowering plants likely depends on a broad array of temperature and precipitation variables. Previous documented climate- life history correlations in explicit phylogenetic frameworks have been limited to certain clades and geographical regions.
- To gain insights which generalize to multiple lineages we employ a multi-clade approach analyzing 32 groups of angiosperms across 8 climatic variables. We utilize a recently developed method that accounts for the joint evolution of continuous and discrete traits to evaluate two hypotheses: (1) annuals tend to evolve in highly seasonal regions prone to extreme heat and drought, and (2) annuals tend to have faster rates of climatic niche evolution than perennials
- We find that temperature, particularly highest temperature of the warmest month, is the most consistent climatic factor influencing the evolution of annual strategy in flowering plants. Unexpectedly, we do not find significant differences in rates of climatic niche evolution between perennial and annual lineages.
- We propose that annuals are consistently favored in areas prone to extreme heat due to their ability to escape heat stress as seeds, but they tend to be outcompeted by perennials in regions where extreme heat is uncommon or nonexistent.

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Macroevolution

Topic: Contributed Papers

Title: Pattern, Timing, and Biotic Context of Diversification of Western Hemisphere Justicia

Author: ***Carrie Kiel @ California Botanic Garden***

Keywords:

Abstract:

Western Hemisphere Justicia (Acanthaceae) (400 spp.) comprises incredible diversity of corolla color, form, and size. This group also encompasses fascinating micromorphological diversity in pollen: size, shape, exine ornamentation, and even aperture number vary widely. These pollen traits have been posited to have taxonomic value in Justicia, and have been traditionally used in infrageneric classifications. However, results from our previous phylogenetic study of Justicia point to considerable homoplasy in many of these traits. Preliminary data also show that micro-structures of pollen across a clade (30 spp.) of Justicia are correlated with corolla form in a pattern that is consistent with pollination syndromes: hummingbird, Lepidopteran, and bee/fly. Here we expand this earlier work by conducting a broad-scale examination across the entire Western Hemisphere Justicia lineage using a time-calibrated phylogenetic hypothesis constructed from ddradseq data. We take an integrative and comparative approach to test the hypothesis that palynological variation is linked to pollination syndromes. We also test for patterns of convergence of these traits and assess diversification rates in this remarkably species-rich lineage.

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Macroevolution

Topic: Contributed Papers

Title: Do showy mistletoes (Loranthaceae) mimic their hosts? Field sampling and computer vision to quantify phenotypic similarity in Australian mistletoe-host pairs.

Author: ***Sarah Mathews @ Louisiana State University***

Keywords: leaf traits,Loranthaceae,macroevolution,mistletoes,mimicry

Abstract:

Showy mistletoes (Loranthaceae, Santalales) are obligate hemi-parasites, unable to survive without connecting to their host. Host use, therefore, is an important determinant of mistletoe diversity. An interesting feature of some showy mistletoes is the striking degree of phenotypic similarity between the mistletoe and its host. The similarity, which involves both vegetative and floral traits, has commonly been viewed as host mimicry. Other explanations, such as coincidence, are plausible, but the processes by which similarity is achieved remain unknown. Further, data needed to study the question have not been available. A limited amount of data have been available to characterize the degree and extent of phenotypic similarity, and species-level phylogenies currently are not available to evaluate this trait in a phylogenetic context. To characterize levels of phenotypic similarity within and among species, we collected image data from leaves of 152 mistletoe-host pairs representing 59 species pairs sampled from diverse habitats across Australia. Scanned images of approximately 9,000 individual leaves were input into a comprehensive phenotypic analysis and comparison that utilized deep learning and computer vision techniques to generate deep embedding vectors of the leaves. These vectors were then compared using cosine similarity, providing an intuitive and robust measure of similarity between mistletoes and their hosts. In this talk we will present results from our initial and current analyses.

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Macroevolution

Topic: Contributed Papers

Title: Replicated radiations in the South American Marsh Pitcher genus Heliamphora (Sarraceniaceae) lead to convergent carnivorous trap morphologies

Author: ***Sukuan Liu @ University of Colorado Boulder***

Keywords: carnivorous plant,Phylogenetic comparative methods,sarraceniacea,heliamphora,morphological evolution

Abstract:

The evolution of carnivorous pitcher traps across multiple angiosperm lineages represents a classic example of morphological convergence. Nevertheless, no comparative study to-date has examined pitcher evolution from a quantitative morphometric perspective. In the present study, we used comparative morphometric approaches to quantify the shape space occupied by Heliamphora pitchers and to trace evolutionary trajectories through this space to examine patterns of divergence and convergence within the genus. We also investigated pitcher development, and in particular, how the packing of pitchers is affected by crowding, a common condition in their natural environments. Our results showed that Heliamphora pitchers have diverged along three main axes in morphospace: pitcher curvature, nectar spoon elaboration, and pitcher stoutness. Both curvature and stoutness were correlated with pitcher size, suggesting structural constraints in pitcher morphological evolution. Among these four traits (curvature, spoon elaboration, stoutness and size), all but curvature lacked phylogenetic and showed marked convergence across the phylogeny. We also observed tighter packing of pitchers in crowded conditions, and this effect was most pronounced in curved, slender pitchers. Overall, our study demonstrates that diversification and convergent evolution of carnivory-related traits extends to finer evolutionary timescales, reinforcing the notion that ecological specialization may not necessarily be an evolutionary dead end.

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Macroevolution

Topic: Contributed Papers Macroevolution

Title: Directly testing for diversification lags after polyploidization

Author: ***Eric Hagen @ University of Arkansas***

Keywords: comparative methods,Diversification,polyploidy,whole genome duplication,SSE

Abstract:

Ever since Stebbins declared polyploid plants evolutionary "dead ends," the link between polyploidization and diversification has been controversial. While several whole genome multiplication (WGM) events seem to pre-date rapid species accumulation in many clades, the existence of long lags between WGMs and diversification make the drawing of direct links difficult. Previous work has relied on nodal or temporal distances between WGMs and diversification on phylogenies, with the difficulty that there is no a priori cut-off of how long a diversification lag should be. A more robust test of the lag hypothesis, one which does not require hypotheses of lag length, can be constructed within the framework of hidden state-dependent speciation and extinction (HiSSE) models. Specifically, the SSE framework of HiSSE allows tests of whether hypothetical "hidden," or unobserved, characters may better explain the data than observed characters under study. In the context of the lag hypothesis, we construct a lag model where observed ploidy states are labeled 0 and 1 (diploid and polyploid) and hidden states are labeled A and B (low diversification rate class and high diversification rate class). Species start in combined state 0A, and can polyploidize to transition to state 1A, but they must undergo an additional transition from state 1A to state 1B in order to diversify, with the time taken to undertake this transition simulating a lag. The lag model is also directly comparable with all other types of SSE models, such as one with diversification but no lag (transitions to polyploidy immediately cause diversification shifts, with no hidden states) and one where polyploidy is unlinked with diversification (shifts between states 0A, 0B, 1A, and 1B are all possible and equally likely). Here, we apply the lag model to test the relationship between polyploidization and diversification in the well-characterized clades of Brassicaceae and Caryophyllales. Preliminary tests suggest strong support for ploidy independent models in which ploidy states and all diversification rate classes are allowed to freely transition along the tree regardless of ploidy state. This suggests that polyploidy is not associated with diversification shifts, and that other traits associated with polyploidy, such as shifts in breeding system, identified in recent work may better explain the data.

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Macroevolution

Topic: Contributed Papers

Title: The convergent evolution of ant-guarding nectaries in ferns is linked to the Cenozoic rise of insect herbivores

Author: ***Jacob Suissa @ The University of Tennessee***

Keywords: macroevolution,ants,Ferns,Nectaries,Angiosperms,herbivores

Abstract:

Herbivory has been a major selection force over plant evolution. This co-evolutionary arms race has led to a variety of plant defense mechanisms. One of particular interest is the presence of nectar-producing glands, which attract predatory ants that defend against herbivorous insects. While commonly studied in flowering plants, nectaries also occur on ferns—a group hypothesized to have minimal biotic interactions. Using a cross-kingdom phylogenetic-based approach we reveal three major insights on the evolution of nectaries in non-flowering plants: 1. fern nectaries evolved independently in at least seven lineages of ferns; 2. the potential to develop nectaries in the common ancestor of these lineages occurred during the Cretaceous, mirroring the diversification of ants associated with plants and the origin of extrafloral nectaries in flowering plants; and 3. a lag of almost 50 million years in the diversification of nectary-bearing ferns was likely driven by the Cenozoic rise of fern herbivores. This work represents a significant step towards understanding the evolution of nectaries, shedding new light on the intricacies of biotic interactions in ferns.

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Molecular Ecology

Topic: Contributed Papers Molecular Ecology

Title: Integrative analyses of variation in fully mycoheterotrophic, North American orchids

Author: ***Craig Barrett @ West Virginia University***

Keywords: morphology,_{conservation biology},genomics,physiology,Taxonomy ,Evolution,Symbiosis

Abstract:

Mycoheterotrophic plants frequently display drastic reduction in genomic and morphological features, making them attractive and charismatic subjects for systematic and evolutionary study. These same attributes have historically presented challenges for their taxonomic placement, which has complicated conservation efforts in these often rare or endangered species. Further, mycoheterotrophs may serve as useful models for testing more general hypotheses on the evolution of parasitism; specifically, of interest are potential tradeoffs between extreme fungal host specificity, morphology and reproductive biology, physiology, anc the maintenance of genomic variation and stability. Combining data from morphology, genomics, physiology, and ecology provides a holistic representation of variation for evolutionary biology, integrative taxonomy, and defining conservation units of these species. Here I use two leafless, fully mycoheterotrophic species—Cephalanthera austiniae (Epidendroideae: Neottieae) and Corallorhiza striata (Epidendroideae: Epidendreae: Calypsoinae)—as models for implementing such integrative analyses. The Corallorhiza striata species complex (loosely, the striped coralroots) comprises three species: the rare Mexican and eastern North American endemics Corallorhiza involuta and C. bentleyi (respectively), and the widespread, highly variable C. striata. The latter is distributed from southern Mexico to Canada, and comprises two named varieties: striata, in the northern Rocky Mountains east to Newfoundland; and vreelandii, from Mexico to the southern Rocky Mountains, with outliers as far north as Montana, USA. Cephalanthera austiniae (the phantom orchid) is distributed through the Coast Ranges and Sierra Nevada of California north to southwestern Canada, witl disjunct populations in southeastern Washington and western Idaho, USA. In the Corallorhiza striata complex, integrative analysis of complete plastid genomes, nuclear SNPs, fungal host ITS sequences, and abiotic niche data clearly differentiate C. bentleyi, C. involuta, and the widespread C. striata. Further analyses within the latter reveal divergence among four entities: 1) C. striata var. striata, 2) C. striata var. vreelandii, 3) populations from the Sierra Nevada (California, USA), and 4) populations from the Coast Ranges and Cascades (California, Oregon, USA). Each comprises a strongly supported clade based on >27,000 SNPs generatec via ISSRseq. However, there is a lack of fixed differences in “extended phenotype” data (i.e. morphology, niche, fungal associates) among these four entities, as required by the “lineage + role” species concept applied here, so they are best described at the infraspecific level. Similar integrative analyses of plastid genomes, nuclear SNPs, morphology, and fungal associates are being conducted in Cephalanthera austiniae, which is considered imperiled in British Columbia, vulnerable in ID, but has no current status in CA, OR, or WA. By analyzing multiple data streams for both species, with emphasis on potential adaptive variation, I hope to deepen our understanding of the conservation status in both species, and extend this framework more broadly in other mycoheterotrophs.

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Molecular Ecology

Topic: Contributed Papers Molecular Ecology

Title: To Hear Without an Ear: Mechanosensation in Plants.

Author: ***taylor paret @ University of Toledo***

Keywords: Arabidopsis thaliana,phenolics,MSL,mechanosensation,Insect feeding vibraiton

Abstract:

Plants respond to herbivory with an increase in chemical defenses. Early defense signaling depends on a plant's ability to detect, identify and respond to these attacks quickly and appropriately. Plants receive multiple cues at the site of insect attack, including insect oral secretions, tissue damage, and vibrations caused by insect feeding, triggering signaling pathways that generate local and systemic defense responses. All three cues have been been shown to contribute to plant defense, but chewing vibrations is the only one that can directly generate systemic responses because of the speed of vibration transmission within a plant.

Previous work in our lab has established that insect-feeding vibrations can cause plants to increase the production of chemical defenses without predator oral secretions or tissue damage. Playback of feeding vibrations produced by the White Cabbage caterpillar (Pieris rapae) on the plant Arabidopsis thaliana can directly induce or prime the induction of chemical defenses. The way in which plants detect feeding vibrations is unknown, although mechanosensors are likely to be involved. Plants contain multiple families of mechanoreceptors, including Mechanosenstive channels of Small Conductance-Like (MSL), Two Pore Potassium channels (TPK), and Mid1-complementing activity (MCA).

In this study, we focused on Mechanosensitive conductance Small (MscS) channels located between the cell wall and the plasma membrane in higher plants and respond to many of the same stimuli as the Mechanosensitive (MS) channels in animals, including temperature, salinity, osmotic pressure, and cell wall damage.

To identify channels in the MSL family that may be responsible for the perception of insect feeding vibration, A. thaliana wildtype-plants (col-0) and MSL lack-of-function mutants received either caterpillar feeding vibrations or a silent sham along with a second stimulus of Methyl Jasmonate (MeJA) or water. When treated with insect feeding vibrations, the triple mutant containing non-functional genes for MSL4, MSL5, and MSL6 showed diminished or no response to vibrations in levels of plant chemical defenses in contrast to the wildtype and the double mutant containing non-functional genes for MSL9 and MSL10. This indicated that one i not all of the channels from the triple mutants are responsible for plant perception of insect feeding vibrations.

To determine if MSL4, MSL5, or MSL6 played a role in plant perception of insect feeding vibrations, wildtype and individual lack-of-function MSL mutants were subjected to the same treatments as the first experiment. Each of the individual lack-of-function mutants failed to inhibit chemical defense responses to insect feeding vibrations. Therefore, all three channels are likely involved in plant perception of insect feeding vibrations.

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Molecular Ecology

Topic: Contributed Papers

Title: A long strange trip: Asarum caudatum and its migration from the Coast to the Rocky Mountains

Author: ***Daniel Turck @ University of Idaho***

Keywords: Pacific Northwest,Phylogeography,Pleistocene glaciation,temperate rainforest,western wild ginger

Abstract:

Asarum caudatum is among the many coastal disjunct species exclusively inhabiting temperate rainforest habitats in the Pacific Northwest of North America. The distribution of rainforest species inhabiting coastal regions west of the Cascades and Coast Ranges with disjunct populations in Northern Idaho, Montana, and Southeast British Columbia has long interested biogeographers. Phylogeographic work on other coastal disjunct species has concentrated thus far on overstory trees (Thuja plicata, Tsuga heterophylla, Alnus rubra) along with amphibians and mollusks. Results from the overstory trees reveal a complex phylogeographic history with species surviving glaciation in both the Southern Cascades and unglaciated regions in Northern Idaho, with secondary gene flow post glaciation. Our null expectation for Asarum caudatum, given that it is ant pollinated and dispersed, along with other life history traits, was that it too had populations surviving in the Cascades and Rocky Mountains during glaciation, but with no secondary gene flow. Preliminary results using a ddRAD approach, however, indicate that this species recently dispersed from Southwestern Oregon north and across the Okanogan Mountains post-glaciation, proceeding to separate intc northern and southern interior clades. This unexpected result gives us a clearer understanding of interior rainforest history and will inform future investigations on other understory coastal disjunct taxa.

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Molecular Ecology

Topic: Contributed Papers

Title: Seed survival, germination, and fungal communities: testing the Janzen-Connell hypothesis with seeds of tropical pioneer trees

Author: ***Daniela Varon Garcia @ University of South Florida***

Keywords: Biodiversity,seeds,plant-fungal interactions,pioneer trees,seed-associated fungi

Abstract:

Understanding how tropical tree diversity is maintained has challenged ecologists for decades. Growing literature provides evidence consistent with the Janzen-Connell (JC) hypothesis, where specialist natural enemies maintain plant diversity by reducing the survival of seeds and seedlings of conspecifics near adults favoring heterospecific recruitment, and ultimately increasing local diversity. Several studies have documented low survival rates of seedlings transplanted near conspecific adult trees, for example, a pattern explained by the action of specific enemies such as fungal pathogens. Although such studies are consistent with the JC hypothesis, their focus at the seedling level has the potential to miss massive demographic effects at the level of seeds, which may themselves be acted upon by natural enemies. We conducted a common garden experiment in which we buried fresh seeds of four species of tropical pioneer trees (Jacaranda copaia, Cecropia insignis, C. peltata, and C. longipes) below and away from the crown of adult trees of C. insignis and J. copaia at Barro Colorado Island, Panama. We retrieved seeds 3 and 12 months after burial and evaluated both seed viability and the composition and diversity of seed-associated fungi, which we characterized via amplicon metabarcoding on the Illumina MiSeq platform. Fresh seeds (not buried) were assessed equally. Fresh seeds had significantly lower fungal infection rates than seeds that were buried for 3 or 12 months, suggesting fungal infection occurs in the soil. The fungal species richness and diversity varied with burial duration and seed viability. Fungal communities associated with J. copaia had 19% more species richness and 42% more diversity when buried under the crown of conspecific trees. After 12 months of burial, seed mortality was higher under the crown of conspecific trees for J. copaia, which suggests that JC effects may be selectively modulating seed survival in J. copaia. These results provide insights into the role of seed-associated fungal communities in maintaining plant diversity in the tropics. Furthermore, our results highlight the importance of studying seed-fungal interactions as driving factors shaping plant communities.

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Topic: Contributed Papers Molecular Ecology

Title: Incorporating natural history collections and low-coverage genome sequencing in evolutionary ecology of the invasive Miscrostegium vimineum.

Author: ***Craig Barrett @ West Virginia University***

Keywords: biological invasions,Dispersal,Herbarium,Japanese stiltgrass,population genomics,genotype

Abstract:

Invasive species threaten biodiversity, cause environmental damage, and negatively impact society. While invasion genetics has a history spanning several decades, recent advances in genomics and bioinformatics have enabled an unprecedented toolkit for studies of invasion biology. Natural history collections, including herbaria, allow comparisons of genomic diversity, phenology, and trait variation over both space and time for invasive species, allowing researchers to track population dynamics, genetic diversity, and evidence for adaptive evolution. Recent methodological progress in low-coverage genome analysis is providing genome-scale resolution in myriad organisms, including invasive species, and is quickly becoming a feasible reality for researchers globally. Here we used such an approach to characterize the evolutionary history of stiltgrass (Microstegium vimineum), one of the most damaging invasive grass species in North America. Previous examination of over 1,100 digitized herbarium records indicated that stiltgrass, first collected in Tennessee, USA in 1919 (specimen included here), spread rapidly throughout the southeastern USA. All specimens examined in the USA were awnless, until in the late 1930s an awned form appeared in the northeastern USA followed by subsequent regional spread, possibly revealing a second successful invasion. To test hypotheses of multiple invasions and spatiotemporal changes in population structure, we sequenced 139 contemporary and 126 historical stiltgrass samples from the native and invasive ranges (n = 121 for Asia and 144 for the USA, respectively). Mean coverage depth per sample of the 1.12 Gb genome was 4.76 ×, with a standard deviation of 2.94. Analysis of total population structure applying genotype likelihood methods and stringent filters, using all specimens, revealed two genetically distinct clusters of stiltgrass in the USA, corresponding to each hypothesized invasion, and further corresponding to two distinct awn phenotypes: predominantly awnless in the southeastern USA and awned in the northeastern USA, with evidence of admixture and a short-awned form at mid-latitudes. For example, “southern” genotypes are observed as far north as New York, while “northern” genotypes are observed as far south as Tennessee, including at the original site where stiltgrass was first collected over a century ago. Though sampling is not as comprehensive for earlier historical specimens from Asia relative to that in the US due to limited access to material, we observed a subset of the native-range variation in the invasive range overall, but a surprisingly high amount of diversity in the latter. Lastly, we quantified patterns of population structure in the invasive range across distinct time slices, documenting the spread of genotypes, subsequent secondary contact emanating from points of origin, admixture, and evidence of long-distance dispersal, likely due to anthropogenic causes. Our findings demonstrate the utility of studying widespread, established invaders for predicting patterns and invasion routes of more recently established species, such that we may be better equipped to predict and prevent potential problems caused by future invasions.

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Topic: Contributed Papers Mycology & Phycology

Title: Fungal host diversity across the geographic range of the mycoheterotrophic

Author: ***Hana Thixton-Nolan @ West Virginia University***

Keywords: Orchid mycorrhizal fungi,Orchidaceae,Orchids

Abstract:

Mycoheterotrophic plants parasitize fungi for most to all their nutritional needs, and often have reduced genomic and morphological features. The relationship between the plants and their fungal hosts provides a compelling system to address questions of how host specificity may limit plant distribution, abundance, and diversity across multiple populations. However, the evolutionary consequences of mycoheterotrophy across a broad geographic region and fungal host specificity remain poorly understood. We are using the widespread Corallorhiza maculata complex to address questions of fungal host specificity across the broad geographic range. The complex contains C. mertensiana, C. maculata var. maculata, C. maculata var. occidentalis, C. bulbosa, C. maculata var. mexicana, and C. macrantha. Members of the C. maculata species complex vary in flowering time, floral morphology, geographic distribution, and fungal associations, with the predominant hosts belonging to the family Russulaceae (Basidiomycota). Previous work identified a pattern of high orchid-fungal host specificity based on orchid-fungal ITS genotypes and geography, but the reliance on Sanger sequencing of fungal hosts and ITS-RFLP in the orchids may not reveal the full extent of orchid-fungal associations. Our goal is to determine fungal host diversity and specificity of the C. maculata complex from populations across North America. To address host diversity, we are using fungal metabarcoding, targeting the ITS2 region to quantify the range of fungal hosts used by the C. maculata complex. We sequenced 229 rhizome samples comprising all North American members of the complex, with deeper sampling from C. maculata vars. maculata and occidentalis in Oregon, California, and Colorado. We found evidence of associations with multiple fungal families within the complex, with the predominant family being Russulaceae, followed by Thelephoraceae and Ceratobasidiaceae. We also identified that the primary trophic mode of fungi associated with the C. maculata complex to be ‘symbiotrophic,’ comprising fungi that receive nutrients in a mutualistic relationship with another plant host (e.g. ectomycorrhizal). Previous work has identified the C. maculata complex to be exclusive to Russulaceae; however this study may have implications for conservation research due to the identification of other potential hosts, including some that may be able to be cultured easily (e.g. Ceratobasidium). Our finding that there are additional fungal families targeted by the C. maculata complex suggests that fungal host identification via Sanger sequencing does not give a complete picture of fungal host diversity and may be biased towards the most abundant taxa. Further, alternative sequencing approaches are being explored such as PacBio long-read sequencing to provide species-level resolution of fungal host identity, as ITS2 Illumina sequencing appears to lack this level of resolution. The outcomes of this study will allow for the identification of host diversity and plant-fungal associations across a broad geographic range, and greatly expand what is currently known for fully mycoheterotrophic orchids and their fungal hosts.

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Mycology & Phycology

Topic: Contributed Papers Mycology & Phycology

Title: Phylogenomic investigation into the metabolic diversification of the genus Botrytis

Author: ***Jordan Dowell @ Louisiana State University***

Keywords: Generalists vs Specialists ,Metabolism,Pathogen,phylogenomics,botrytis

Abstract:

Metabolic responses to dynamic conditions drive intraspecific variation and shape species' interactions. Among metabolic responses, the use and allocation of energetic resources are critical to host-pathogen interactions. Among plant fungal pathogens, small effector proteins and metabolites are associated with variation in host-specificity. However, efficiently leveraging a host as an energy resource is critical to pathogen fitness. Here we leverage the genus Botrytis as a model to investigate the relationship between host-generalism and metabolic variation using combinations of phylogenomic and genome-scale metabolic modeling approaches. We assessed 20 species of Botrytis, identifying over >5000 single-copy orthologs to produce a maximum likelihood phylogeny with over 99% bootstrap support of all nodes. We reconstructed genome-scale models of metabolism for each species and assessed variation in metabolic flux in silico. The evolution of host-specificity was correlated with the simulated growth rate. Among species, we corroborate evidence of horizontal gene transfer of effector genes. However, we find no evidence of horizontal gene transfer of primary metabolic enzymes. Our results indicate the potential decoupling of host-energetic use from genes associated with combating host-immune responses in the evolution of host-specificity in Botrytis.

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Mycology & Phycology

Topic: Contributed Papers

Title: Morphological and molecular evidences revealed new species of Mallocybe (Agaricales, Inocybaceae) from Himalayan forests of Pakistan.

Author: ***malka saba @ Quaid-i-Azam University***

Keywords: phylogeny,Mallocybe,Himalayan forest,Taxonomy

Abstract:

The Inocybaceae is a monophyletic family encompassing ectomycorrhizal fungi with worldwide distribution and is estimated to contain 1050 species. Mallocybe belonging to Inocybaceaea was given the status of genus in 2020 by Matheny and co-authors. Macroscopically, Mallocybe species are recognized by a fibrous or scaly often flattened pileus, a short stipe, ocher, brown, or red brown coloration, a cortina, adnate lamellae and absence of a spermatic odor. Microscopically, distinctive characters of this genus include; smooth spores, absence of pleurocystidia, thin-walled without crystals cheilocystidia and necropigment in basidia of fresh and dried specimens. The genus is monophyletic and about 58 species of Mallocybe have been recorded in Index Fungorum (www.indexfungorum.org) from different regions of Africa, Asia, Australia, Europe, New Zealand, and North America. However, only two species of this genus are yet known from Pakistan.

During the exploration of ectomycorrhizal fungi of Pakistan, we have encountered eight different collections of Mallocybe which have been described using morphological and molecular analysis. Morphological analysis was performed using an Olympus Bx40 light microscope with Olympus XC50 digital camera and Microsuite special edition software 3.1. Phylogenetic analyses based on sequence data from two different loci (ITS and LSU) using maximum likelihood and maximum parsimony methods was performed to infer species relationships within Mallocybe. Results indicated that these eight collections encompass three new species of Mallocybe i.e. M. ahmadii, M. pakistanica and M. pinicola, from Pakistan. Their detailed morphological descriptions and illustration are provided. In addition, comparison with morphologically closely related taxa is also discussed. A key to the described taxa of Mallocybe from Pakistan is also provided.

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Mycology & Phycology

Topic: Contributed Papers

Title: IN VITRO EVALUATION OF SOIL AMENDMENTS ON GROWTH OF Fusarium oxysporum of pepper.

Author: ***Iyabode Kehinde @ Federal University of Agriculture, Abeokuta***

Keywords: Fungi,pepper,In Vitro,soil amendments,Fusarium oxysporum

Abstract:

Pepper is a widely grown food and spice crop in the world, in many households, pepper provides variety of needs, such as enhancing intake of dull diets, mild drugs and making stew and some local dishes. Although the types and quantities utilized vary in different areas. Pepper is faced with many challenges, one of which is fungal diseases especially Fusarium wilt. However, synthetic chemicals has been used for a long time to control this disease but they are highly detrimental both to the soil and consumers of the crop. The study therefore evaluated the effect of organic soil amendments (SA) on suppression of Fusarium wilt of pepper caused by Fusarium oxysporum. The experiment was carried out at the laboratory of Pure and Applied Botany, Federal University of Agriculture Abeokuta (FUNAAB). Sawdust was collected from a sawmill in Abeokuta, while Spent Mushroom Compost (SMC) from Forestry Research Institute of Nigeria, Ibadan and biochar was produced in FUNAAB. Fungi were isolated and identified from SA using standard microbiological methods. The in-vitro anti-fungal activities of aqueous SA at different concentrations of 0.1 g/ml, 0.15 g/ml, 0.2 g/ml and 0.25 g/ml were conducted on F. oxysporum and percentage inhibition was calculated. The data were analyzed using one way ANOVA at $p < 0.05$. The fungi isolates found in the SA were Aspergillus flavus, A. niger, Mucor sp. and Trichoderma sp. The in-vitro antifungal activities against F. oxysporum (percentage inhibition) ranged between 42.20 and 87.10 %. SMC had the highest percentage inhibition on F. oxysporum in-vitro.

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Mycology & Phycology

Topic: Contributed Papers

Title: Pharmacological intervention of Russula sp. BRF 5 on Carbon tetrachloride induced hepatocellular carcinoma in Balb C mice

Author: ***Muhammad Hanif @ GC University, Lahore, PAKISTAN***

Keywords: Anticancer,Carbon tetrachloride,Hepatotoxicity,Mushroom,Russula sp. BRF 5

Abstract:

Mushrooms possess therapeutic effects since ages due to biologically active compounds. Objective: Present research aimed to assess the protective effect of a mushroom Russula sp. BRF 5 on carbon tetrachloride-induced hepatocellular carcinoma in Balb C mice. Biochemical parameters from blood like total protein, total bilirubin content along with some enzymatic activities viz; alanine aminotransferase (ALAT), aspartate aminotransferase (ASAT), lactate dehydrogenase (LDH), alkaline phosphatase (ALP), malondialdehyde (MDA), glutathione (GSH) and catalase in blood plasma were analysed. Results: The induction of carbon tetrachloride CCl4 induced hepatotoxicity caused a highly significant surge ($p \leq 0.001$) in the activity of ALAT, ASAT, ALP, MDA and LDH while a significant decrease ($p \leq 0.001$) in GSH and Catalase level of plasma was observed. Mice were treated with CCl4 at a dose of 1ml/kg b.w for disease induction and Russula sp. BRF 5 extract at three different concentrations (1, 2 and 4 mg/ml) to check their effect on some biochemical components as well as enzymatic activities. Russula sp. BRF 5 proved to eradicate the CCl4-induced changes in the enzyme level. The mushroom caused a highly significant rise ($p \leq 0.001$) in total protein content (6.16±0.4 g/dl) which was lowered to 2.94±0.1 g/dl as compared to control (8.42±0.4 g/dl) after CCl4 administration. Moreover, ALAT, ASAT, ALP, LDH and MDA activity was restored to normal while a decline in bilirubin content (3.34±0.1 mg/dl) was also observed. Hepatic damage caused by CCl4 was obliterated by Russula sp. pre-treatment on mice. Best anticancer potential was recorded for the highest concentration of mushroom extracts at 4 mg/ml. Conclusion: These outcomes revealed that Russula sp. BRF 5 extract ameliorated the damage caused by CCl4 in the mice model, which confirms its protective effects against hepatic damage caused by oxidative as well as non-oxidative mechanisms.

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Paleobotany

Topic: Contributed Papers Paleobotany

Title: Grasses: Can we tell Bamboos in the Fossil Record?

Author: ***Melanie DeVore @ Georgia College and State University***

Keywords: bamboo,Eocene,Grasses,Okanagan Highlands

Abstract:

Bamboos are challenging to identify in fossil floras. Because they are predominantly monocarpic and many flower rarely, it is difficult to encounter the diagnostic reproductive features which would permit definitive identification. Delimiting Bambusoideae taxa in the fossil record requires identifying distinctive vegetative morphologies and definitive anatomical features such as epidermal patterns. Furthermore, fossils representative of bamboos may be misidentified as another taxon (e.g. Equisetum, leaves of cycads, or remains of conifers). Rare occurrences of bamboo megafossils are known from the Miocene of China and Strömberg has documented phytoliths which can be confidently assigned to Bambusoideae grasses from the late Eocene of North America. This is intriguing, since if there are phytoliths present, then there should be remains of bamboo in the Paleogene megafossil record. We discovered Eocene fossil specimens which could potentially represent the morphology indicative of Bambusoideae. These include at least one specimen that shows branches which are apparently branching off from the sheath. Also present are culms of a monocot which appear to have branch scars, comparable to those seen in modern bamboo. Although we are unable to assign these remains to any modern genera, we believe it is significant to describe specimens showing such features as morphotypes. Because bamboo is a defining taxon in modern communities, we believe that at least knowing that some grasses had this habit would be helpful in paleoecological reconstructions.

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Paleobotany

Topic: Contributed Papers

Title: Late Triassic floras from Guangdong, South China: biostratigraphical context and palaeoenvironmental implications

Author: ***Xiaoqing Zhang @ Wesleyan University***

Keywords: Late Triassic flora,Phytostratigraphy,Palaeoenvironment,South China

Abstract:

Triassic-Jurassic deposits are well developed in Guangdong Province, South China. In particular, the Upper Triassic marine and terrestrial alternating coal-bearing strata yield diverse and abundant plant, ammonite and bivalve fossils. These strata provide a significant reference for the study of palaeoenvironmental variations across the T-J transition and extinction event in the lower latitude regions. In this paper, we review the major progress on Late Triassic floral studies in this area. Specifically, we compare plant assemblages from different fossil sites in central and northern Guangdong which have been dated with marine fauna such as ammonites and bivalves. To date, about 155 species belonging to 57 genera of fossil plants have been reported. In ascending order, four plant assemblages can be recognized in the Late Triassic deposits from the Guangdong area, including the Pachypteris-Lindleycladus assemblage (Early Carnian), the Pterophyllum first common occurrence assemblage (Early-Late Carnian), the Clathropteris-Otozamites assemblage (Late Carnian) and the Danaeopsis first occurrence assemblage (Rhaetian). These assemblages show coordinated taxonomic variation with regards to sea level changes. The Late Triassic flora in Guangdong demonstrats a predominance of Bennettitales and ferns, followed by horsetails, seed ferns, cycads, ginkgos and conifers. In general, the Late Triassic climate in the Guangdong region was mainly humid and warm, either tropical or subtropical. The fossil plant and palaeomagnetic evidence prove that the central and northern Guangdong region was located at approximately the same latitude as it is today and formed the southern coastline of the South China Block during the Late Triassic. Palaeogeographically, the transgression started at the end of early Carnian and the south coastal terrane consisted of a western bay, a peninsula and an eastern bay. During the regression period, post-Rhaetian, the bays evolved into a gulf coastal plain.

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Paleobotany

Topic: Contributed Papers

Title: A siphonostelic euphyllophyte of cladoxylopsid affinities from the Lower Devonian of Gaspé (Quebec, Canada)

Author: ***Ellie Frazier @ Cal Poly Humboldt***

Keywords: Devonian,euphyllophyte,fossil,paleobotany,pith,Anatomy,Phloem,cladoxylop id,siphonostele

Abstract:

The Battery Point formation of the Gaspé Peninsula in Quebec (Canada) hosts a diverse assemblage of Early Devonian (Emsian, c. 395 Ma) permineralized plant fossils. One of these fossils is a previously unidentified type of euphyllophyte represented by a small axis fragment c. 1 mm in diameter. The axis has a highly irregular cross-sectional outline, due to both emission of lateral appendages and taphonomic distortion. The epidermis consists of rectangular cells 37 µm in size containing dark bodies. Abrupt indentations with rectangular to U-shaped profile or irregular profile (up to 129 µm deep and 119 µm wide) affect the epidermi and outer cortical layers all along the axis. The parenchymatous cortex is up to 140 µm wide. A thin layer of phloem with narrow, thin-walled cells is variably preserved around the primary xylem, which forms a five-lobed actinostele. The xylem lobes protrude up to 360 µm from the central core of xylem, which is c. 390 µm wide. Metaxylem tracheids, angular to oval in shape and up to 50 µm in diameter, have densely distributed circular bordered pits with large oval apertures. Each lobe of xylem has a conspicuous mesarch protoxylem strand located approximately midway between its tip and base. Lacunae are present in the position of protoxylem strands in undistorted portions of the axis. At the center of the xylem, an area up to 200 µm wide is occupied by large thin-walled parenchyma cells. At the contact between this central area and the innermost xylem tracheids, a fine layer of cells have features consistent with those of the phloem cells external to the xylem. Terete traces (c. 140 µm diameter) to lateral appendages possessing a central protoxylem strand (lacuna), diverge radially from the tips of the xylem lobes. The appendages follow a 2/5 helical taxis, are filiform (c. 250-300 µm wide in basal portions and 300-400 µm distally), extensive (>9 mm long), and branch dichotomously several times. This new Gaspé plant is similar to the cladoxylopsid Adelocladoxis praecox (described from the same strata), from which it differs in the single protoxylem strand of its appendage traces (and, possibly, the taxis of appendages) and its central parenchyma. This is a, thus, new species closely related to Adelocladoxis praecox and possibly belonging to the same genus. Importantly, the parenchymatous area at the center of the stele is a true pith, as the layer of phloem bordering it demonstrates that the new plant possesses a bona fide siphonostele with amphiphloic organization (rather than a medullated protostele). The oldest previously documented euphyllophytes with parenchyma at the center of steles are Middle Devonian (Givetian): the cladoxylopsid Arachnoxylon and the putative progymnosperm Actinoxylon. However, it is unclear whether either of these plants had true siphonosteles or if those were amphiphloic. Therefore, this new Gaspé plant represents the oldest siphonostele occurrence among euphyllophytes, pre-dating by at least 10 million-years previously known occurrences and demonstrating much deeper origins of this structural feature in the clade.

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Topic: Contributed Papers Paleobotany

Title: Phylogenetic assessment of Cretaceous fossils compared to Magnoliales: problematic cases.

Author: ***James Doyle @ University of California Davis***

Keywords: Angiosperms,Cretaceous,paleobotany,phylogenetics,Magnoliales

Abstract:

Phylogenetic analyses that use a morphological data set of living and fossil angiosperms and constrain the arrangement of extant taxa to backbone trees inferred from molecular data have strongly associated several mid-Cretaceous fossils with the order Magnoliales. These include Archaeanthus (late Albian, Kansas), which is either nested in or sister to crown group Magnoliaceae; Endressinia and Schenkeriphyllum (Aptian, Brazil), attached lower on the stem lineage of Magnoliaceae, which have a combination of magnoliaceous apomorphies such as sheathing leaf bases and plesiomorphies such as inner staminodes and a short receptacle; and Futabanthus (Coniacian, Japan), most likely a near-basal member of crown group Annonaceae. However, other putative fossil Magnoliales are weakly associated with the order, or not at all. Serialis and Riaselis, represented by isolated carpels and seeds from the Aptian-early Albian of Portugal, was assigned to Magnoliales based on seed anatomical characters. When both fossils are included in the analysis, their best arrangement is as two successive branches from the stem lineage of Magnoliaceae, but other positions near the base of Magnoliales and in the near-basal order Austrobaileyales are only one step less parsimonious. When Riaselis is added alone to the analysis, it has equally parsimonious positions in both Magnoliales and Austrobaileyales; when Serialis is added alone, its single most parsimonious position is in Austrobaileyales. These results reflect the independent origin of seed feaures in the two orders. Pecinovia, a staminate flower from the middle Cenomanian of Bohemia, was originally compared with Annonaceae. It has several most parsimonious positions, including three around the basal node of angiosperms, but none in Magnoliales; its best position in Magnoliales, sister to Myristicaceae, is one step worse. Cronquistiflora and Detrusandra, from the late Turonian-Coniacian of New Jersey, are bisexual flowers with numerous parts and a hypanthium. Depending on the backbone tree, Cronquistiflora has one most parsimonious position, sister to Eupomatia in Magnoliales, or this and additional positions in Magnoliales and Laurales. The best positions of Detrusandra are in Austrobaileyales and Laurales. These differing results are influenced by pollen characters: a continuous tectum and granular infratectum in Cronquistiflora, a reticulate tectum and columellae in Detrusandra. Another multiparted bisexual flower, Cecilanthus from the lower Cenomanian of Maryland, has equally parsimonious positions in Magnoliales and Nymphaeales. Although these results may seem discouraging, they do greatly restrict the number of potential systematic positions of the fossils. Furthermore, they are of evolutionary interest in highlighting morphological convergences between Magnoliales and the basal ANITA lines, as well as the presence in the mid-Cretaceous of extinct lines with character combinations no longer found in the living flora. Depending on the fossil in question, association with vegetative parts, complete flowers, pollen, or mature seeds could resolve these ambiguities.

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Topic: Contributed Papers

Title: Expanding the diversity of early woody euphyllophytes: new specimens from the Early Devonian of Gaspé (Quebec, Canada)

Author: ***Emma Casselman @ Cal Poly Humboldt***

Keywords: Devonian,euphyllophyte,fossil,paleobotany,secondary growth,secondary xylem,wood

Abstract:

Vascular cambial growth (woody growth) can be traced back to the Middle and Late Devonian in multiple distinct tracheophyte lineages (cladoxylopsids, sphenophytes, rhacophytaleans, zygopterids, progymnosperms, stenokolealeans, and seed plants). Recent recognition of several different Early Devonian euphyllophytes producing secondary xylem demonstrates an unexpected diversity of species that had evolved woody growth by c. 400 Ma ago, indicating that this major developmental innovation arose earlier than previously recognized. Understanding patterns and relationships in the evolution of woody growth requires detailed characterization of these earliest occurrences and development of quantitative methods for meaningful comparisons. With one exception, Early Devonian woody euphyllophytes have been described in Emsian strata (c. 405-395 Ma) from the Gaspé Peninsula (Quebec, Canada): eight formally described taxa and two additional unnamed plant types. We analyze a set of eight previously undescribed Early Devonian specimens from Gaspé that share secondary xylem of a relatively dense aspect, with tracheids of relatively small size, suggesting they may all represent the same type of woody plant. The new specimens are fragments of woody axes that range 1.4-7.3 mm in xylem diameter and 2-12 mm in length. Their central primary xylem, scarce and crushed, was probably terete. The thickness of the secondary xylem ranges from 21 to 81 tracheids (counted along radial files). To explore the implications of these specimens for the diversity of Early Devonian woody plants, we compare them to previously documented coeval woody taxa - Armoricaphyton, Franhueberia, Gmujij - and to Psilophyton dawsonii. These comparisons suggest that the eight specimens represent single plant type characterized by Psilophyton-type tracheids with sizes ranges of 37-57 µm (radial) x 25-62 µm (tangential) and rare uniseriate rays. One of the specimens that preserves extraxylary tissues shows that the plant had a wide parenchymatous inner cortex and a sclerenchymatous outer cortex a few cells thick. This plant belonging to the euphyllophyte clade (as indicated by its Psilophyton-type tracheids) is different from all coeval woody taxa: it lacks the relatively large four lobed primary xylem seen in Gmuiji and the large frequent rays o Franhueberia, and its tracheids are roughly half the size of the wood tracheids of Armoricaphyton and of the radially aligned tracheids documented in Psilophyton dawsonii. This putative new type of euphyllophyte adds another member to the growing diversity of woody plants documented from Early Devonian strata. Using the wealth of woody plant types documented in the Early Devonian, we are currently exploring quantitative methods of characterizing and comparing cambial growth dynamics in these plants, as a way to better delineate taxa and characterize their development.

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Topic: Contributed Papers Paleobotany

Title: The first Patagonian icehouse conifers: new fossil species of Austrocedrus (Cupressaceae) and Araucaria (Araucariaceae) from the earliest Oligocene of Argentina

Author: **Gabriella Rossetto-Harris @ Penn State University**

Keywords: Conifers,Cupressaceae,Evolution,fossil,Oligocene,paleobotany,Patagonia,systematics,Taxonomy ,Argentina,Araucaria

Abstract:

During the Eocene greenhouse, northern Patagonian vegetation included abundant Gondwanan rainforest-conifer lineages that are mostly endemic today to the West Pacific region, including Araucaria Sect. Eutacta, Agathis, Papuacedrus, and Dacrycarpus. The Eocene-Oligocene transition and the final breakup of Gondwana led to the earliest Oligocene (Oi-1) glaciation and an icehouse climate state ever since. However, little is known about how and when the extant conifer assemblages of northern Patagonia evolved. For example, Araucaria araucana (Sect. Araucaria) and Austrocedrus chilensis are dominant conifers in the mesic forests to xeric woodlands of the southern Andes, but the sparse and poorly dated late Paleogene record from southern Patagonia provides no information on their origins. We analyzed new fossil conifers from the Prem fossil site, the first known earliest Oligocene (33.5 Ma, U-Pb) macroflora of South America, contemporaneous with the Oi-1 glaciation. Prem is a small volcaniclastic lake deposit just 1.6 km east of the famous, highly diverse earliest middle Eocene (47.7 Ma) Río Pichileufú site in Río Negro, northern Patagonian Argentina, but remarkably different in composition. The Prem flora has low diversity and is dominated by Nothofagus, apparently showing a shift to a cooler climate. Conifers at the Prem site represent at least four species of Araucariaceae, Cupressaseae, and Podocarpaceae. We here present two of the species with leafy branches and associated reproductive structures, which provide new fossil links to the extant, endemic Andean flora. One species represents the first reliable fossil Austrocedrus from South America. We differentiate the Austrocedrus foliage from morphologically similar Cupressaceae by its small leaves with blunt apices and lateral leaves that are unfused, with concave/decurrent margins. The fossil ovulate cones, some of which are attached to leafy branches, are also consistent with Austrocedrus in having four bract-scales with valvate arrangement, two pairs being enlarged and striated longitudinally, and non-spinose bract tips extending to subtend the scale apex. Previously, fossil Austrocedrus was only reliably known from the early Oligocene of Tasmania, and thus the new species shows by this time a vast range for the genus, now restricted to South America. The second conifer species is a new species of Araucaria with broad, multi-veined leaves that resemble Sect. Araucaria and isolated ovuliferous complexes with reduced lateral extensions (wings) that resemble those of Sect. Eutacta more than the wingless seeds of living Sect. Araucaria. We used an affinity analysis to evaluate the influence of the isolated organs on the Araucaria species' phylogenetic position. The results indicate mosaic character evolution, suggesting that the wingless complexes of the living South American species evolved more recently.

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Topic: Contributed Papers

Title: Newly recognized fossils of Tetramelaceae: A biogeographically dispersed clade

Author: **Sarah Allen @ Penn State Altoona**

Keywords: Cucurbitales,fossil fruits,fossil leaves,Octomeles,Tetrameles

Abstract:

Tetramelaceae is a small family of two extant monotypic genera (Octomeles and Tetrameles, formerly in Datiscaceae) in Cucurbitales. Octomeles sumatrana and Tetrameles nudiflora are large, buttressed trees found in the tropics and subtropics of the Eastern Hemisphere. The evergreen Octomeles sumatrana can be found on most of the islands of the Malesia region. By contrast, Tetrameles nudiflora, which has a larger range than Octomeles sumatrana, is deciduous during the dry season.

Leaf and infructescence fossils of Tetramelaceae have been identified from Eocene sediments in Wyoming (Bridger and Aycross Formations), Colorado (Parachute Creek Member of the Green River Formation, PCM-GRF), and Utah (PCM-GRF). Although these organs have not been found in attachment, their co-occurrence at the same fossil sites, along with having characters consistent with Tetramelaceae, indicates that they probably represent the same extinct tree.

The fossil leaves share characters including long petioles, perimarginal veins, and glands on the laminar surface with extant Tetramelaceae. The fossil infructescences are long spikes of small, sessile, helically arranged, capsular fruits. Most fruits typically bear four small styles and four sepals, although the merosity can be obscured in the compression/impression preservation of the fossils and is more readily observed by micro-CT imagery.

The leaves and fruits were previously attributed to other families, but after careful review the prior assignments to Aleurites (Euphorbiaceae) and Clethra (Clethraceae) could not be substantiated. The fossils were identified to Tetramelaceae by using multi-entry keys and comparing the leaf architecture and morphology of the fruit capsules to extant herbarium specimens. The leaf and infructescence fossils have a combination of characters distinct from the two extant species, leading us to place each fossil organ in a new genus, Punctaphyllum and Parvispicula.

At some sites, infructescence specimens are quite common. For example, at Blue Rim (Bridger Formation, southwestern Wyoming) more than 25 infructescences have been recovered. There are some minor differences in the spikes between localities with the Blue Rim specimens having more widely spaced and less tightly packed fruits than the Parachute Creek Member specimens. The Blue Rim specimens are also noticeably smaller in fruit size than specimens from other localities, but other morphological features are consistent.

The recognition of Tetramelaceae in the Eocene of the Rocky Mountains of North America is interesting given that the family is restricted to hot, monsoon regions of the Eastern Hemisphere today. This is another example of a clade that was more widely distributed in the past. The warm climate of the early to middle Eocene appears to have allowed what is now a tropical clade to flourish at higher latitudes.

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Paleobotany

Topic: Contributed Papers Paleobotany

Title: Paleoecological implications of a new species of Pseudofrenelopsis (Cheirolepidiaceae) from the Hauterivian (Lower Cretaceous) of western Portugal.

Author: ***James Doyle @ University of California Davis***

Keywords: Cheirolepidiaceae,Conifers,Early Cretaceous,Paleoecology,Portugal

Abstract:

The extinct conifer family Cheirolepidiaceae is notable for its distinctive Classopollis pollen and its dominance over vast areas in the Jurassic and Early Cretaceous, particularly regions that show evidence of hot and dry climate (e.g., Southern Laurasia in the Late Jurassic, Northern Gondwana in the Early Cretaceous). Most Jurassic members have short, scalelike leaves of the Brachyphyllum type; these are joined in the Early Cretaceous by frenelopsids, including Frenelopsis (usually three leaves per node) and Pseudofrenelopsis (usually one leaf per node), which are even more xeromorphic than Brachyphyllum in having jointed shoots with highly reduced leaves, photosynthetic internodes, unusually thick cuticle, and sunken stomata with a ring of papillate subsidiary cells. There were early indications that the two genera occupied different parts of a salinity gradient. Pseudofrenelopsis varians is dominant in the lagoonal Glen Rose Formation of Texas (lower Albian), while Pseudofrenelopsis parceramosa occurs in brackish facies in the Potomac Group of Virginia (Aptian). By contrast, at the Fredericksburg locality in Virginia (lower Albian), Frenelopsis ramosissima is associated with diverse ferns, gymnosperms, and angiosperms in sediments that show no evidence of marine influence. However, F. ramosissima also occurs in the Glen Rose, and younger Frenelopsis species are dominant in lagoonal and saltmarsh facies, such as Frenelopsis alata in the Cenomanian of Bohemia and France. Here we report a much older frenelopsid species, Pseudofrenelopsis sp. nov., from the lower Hauterivian of the Santa Susana Formation at the Vale Cortiço clay pit complex in the Lusitanian Basin of western Portugal. It has leaves on mature shoots with a sheathing base, attenuate apex, and marginal trichomes, terminal branches with Brachyphyllum-type foliage, and only moderately thick cuticle. Although the Santa Susana environment has been interpreted as estuarine to upper deltaic, the palynoflora shows no evidence of marine influence. The mesofossil flora is dominated by the previously described species Frenelopsis teixeirae and Pseudofrenelopsis sp. nov., but Classopollis makes up only ca. 20% of the palynoflora, and spores are diverse and abundant (45%). These observations suggest that both frenelopsid species may have grown in non-saline sites in the upper part of a delta system, where most of the palynoflora was derived from upstream forests of diverse gymnosperms and ferns. Pseudofrenelopsis parceramosa dominated such environments in the Barremian of England, where its xeromorphic features have been interpreted as adaptations to occasional periods of severe drought and forest fires in a generally wet climate. These observations indicate that both Frenelopsis and Pseudofrenelopsis showed a trend from freshwater and brackish environments before the Albian to drier and more saline environments in the Albian and Cenomanian, possibly due to competitive replacement by angiosperms in inland vegetation.

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Paleobotany

Topic: Contributed Papers

Title: First Nothofagus fossil cupules and fruits from South America, earliest Oligocene of northern Patagonia

Author: ***Ari Iglesias @ INIBIOMA (Comahue University-CONICET National Scientific and Technical Research Council)***

Keywords: Glaciation,Oligocene,Nothofagaceae,reproductive,Argentina

Abstract:

Nothofagus fossil pollen, leaves, and woods are abundant in Patagonia, but until now, no reproductive macrofossils have been known, obscuring information about the histories of the subgenera and the appearances of the many types of Nothofagus-dominated forests. Globally, fossil Nothofagus fruiting structures are only known from the Oligocene and Miocene of Tasmania, representing subgenus Lophozonia and two other subgenera. The cooling trend during the late Eocene - early Oligocene transition in southern South America generally correlates with a northward expansion of micro- and mesothermal taxa, but the timing of Nothofagus-dominated forests reaching northern Patagonia remains poorly understood. A new fossil macroflora, informally the “Prem site,” found in northern Patagonia (41° south latitude) is U-Pb dated to ~33.5 Ma, the first from South America that correlates precisely to the first half million years of the Oligocene and the Oi-1 glaciation. The assemblage is dominated by Nothofagus leaves (70 % of ~1000 leaf specimens), along with a low-diversity angiosperm and conifer flora. Abundant Nothofagus cupules and fruits (nuts) were found (20 cupules and 30 nut specimens). Three winged fruits are present (two trimerous and one dimerous) on some closed cupules. Many cupules show four well-developed valves, each with several rows of prominent ramified lamellae with multiple-tipped glands, and three fruit scars are visible on the inner cupule base. These features are diagnostic of the subgenus Lophozonia, which is currently distributed in northern Patagonia, Tasmania, New Zealand, and Australia. Other cupules from the Prem site have entire lamellae and different sizes and shapes, which may indicate the presence of other Nothofagus subgenera. The new fossils represent the first record for Nothofagus reproductive structures from South America. Furthermore, the abundant leaves indicate the earliest macrofossil record of a Nothofagus-dominated forest in northern Patagonia, supporting a northward expansion of the genus associated with global cooling and the Oi-1 glaciation.

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Paleobotany

Topic: Contributed Papers

Title: Palm fruits from the Oligocene of west coastal Peru

Author: ***Ashley Hamersma @ University of Florida***

Keywords: fossil fruits,Oligocene,paleobotany,Arecaceae,Peru,palms

Abstract:

Palms are one of the most diverse and dominant plant groups in the tropical and subtropical areas of South America today, but their macrofossil record in the region is relatively limited. The Belen paleobotanical flora of western Peru was introduced by Berry and is important as one of the most diverse fruit and seed floras from South America. Dating to the early Oligocene based on diatoms, this assemblage provides insight to vegetation of northwestern Peru prior to the full uplift of Andes and establishment of the Humboldt current. This flora dates to prior to the close of the Central American Seaway and the Great American Interchange, providing vegetational insights into the flora and climate in the area prior to these paleobiogeographic events. Berry recognized three palms in his investigation of the Belen flora. Two are based on a single specimen and remain questionable because they lack diagnostic pores and other characters, but the specimens assigned to Palmocarpon bravoi show distinctive features confirming their identity as palms. Here, we revisit P. bravoi as based on original collections and supplemented by new specimens collected in 2010, concluding that the original taxon concept includes what we now consider to be two separate species.

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Topic: Contributed Papers Paleobotany

Title: Probing the origin and evolution of periderm: what can extant plants and the fossil record tell us?

Author: ***Madison Lalica @ Cal Poly Humboldt***

Keywords: Devonian,Evo-Devo,Evolution,fossil,paleobotany,periderm,secondary growth,wound response,Development

Abstract:

Secondary growth arises from the activity of lateral meristems - the vascular cambium and the cork cambium. The latter, and the tissues it produces, are collectively referred to as periderm. Periderm occurs as a typical ontogenetic phase forming protective outer tissues (canonical or native periderm), or in association with abscission areas, or as a self repair process that seals wounds (wound periderm). We review wound periderm in the broader context of periderm-type secondary growth and update the scarce data on occurrences of wound periderm outside the spermatophyte clade. In extant plants, periderm (wound and canonical) has been documented and studied extensively in spermatophytes but is exceedingly rare among the seed-free plants. The rarity of canonical periderm among the latter is nevertheless belied by occurrences of wound periderm across a broader taxonomic range of seed-free plants. Sparse published records and our own wounding experiments demonstrate that wound periderm is produced by ophioglossalean, marattialean, and filicalean ferns. In the fossil record, canonical periderm was documented in several seed-free lineages - isoetalean lycophytes, cladoxylopsids, sphenopsids, progymnosperms. Its oldest documented occurrence (Middle Devonian; Givetian) is pre-dated by that of wound periderm in the Early Devonian, 15 million years prior. This suggests that periderm evolved as a wound response mechanism that was subsequently co-opted in canonical developmental pathways to seal off outer tissues that were put under tensional stress due to significant vascular cambial growth; and that wound periderm is a conserved feature, whereas canonical periderm may have been gained and lost throughout evolutionary history. Along with its murky origins, an incompletely explored aspect of periderm regards developmental mechanisms as related to canonical vs wound periderm in seed-free vs seed plants. Namely while some periderms show consistent organization - regular layering, a well-defined cambial layer, and clear bifacial polarity (cork/phelloderm) - others are less organized, lacking consistent layering as well as a conspicuous cambial layer and bifacial polarity. Therefore, what has been considered as a single type of tissue and referred to as periderm may include two distinct types of tissue significantly different in their development and anatomy. While both types develop by periclinal divisions, in one type these divisions are spatially coordinated (organized periclinal growth), whereas in the other type they occur concurrently at several depths in the tissue of origin (diffuse periclinal growth). A preliminary survey suggests that wound periderm develops exclusively by diffuse periclinal growth outside the seed plants, whereas in seed plants it may form mostly by organized periclinal growth. Because the oldest wound periderms of the Early Devonian were produced by diffuse periclinal growth, it is possible that this periderm development mode preceded and gave rise to organized periclinal growth. Testing these hypotheses about periderm evolution will require broadening the taxonomic scope of wounding experiments in seed-free plants, in parallel with application of methods (histological staining, UV autofluorescence) to characterize the organization and assess developmental bifaciality in wound and canonical periderm in both seed-free plants and spermatophytes, and will benefit from additional discoveries of periderm in the Devonian fossil record.

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Topic: Contributed Papers

Title: Fossil Syzygium leaves with in-situ cuticles from the Pliocene of central Vietnam

Author: ***Tengxiang Wang @ Penn State***

Keywords: fossil,Myrtaceae,Pliocene,pollen,Southeast Asia,Vietnam,Syzygium,cuticle

Abstract:

Syzygium Gaertn. (Myrtaceae) is the most diverse tree genus, having ca. 1200 species distributed in tropical and subtropical regions of the Old World. Its diversity center is in Malesia, but the genus is generally thought to have an austral origin. As one of the most common forest elements, Syzygium inhabits a variety of vegetation types such as lowland to montane rainforests, swamps, savannahs, and limestone forests. Its fleshy fruits (cultivated as rose apples) are an important food source for forest animals. Syzygium leaves usually display typical myrtaceous architecture, including pinnate brochidodromous venation with the secondary veins connecting to form intramarginal veins. However, this venation pattern is also observed in most other families in Myrtales and in many distantly related families, e.g., Apocynaceae. Thus, leaf architecture alone is unreliable to infer myrtaceous affinity and generic assignment of fossil leaves. Nearly all previous ‘Syzygium’ leaf fossils require reexamination, and perhaps the only unequivocal leaf record is from the early Miocene of southern Australia. Recent studies have revealed characteristic micromorphology on modern Myrtaceae leaves and their infrafamilial patterns, allowing for the identification of myrtaceous fossil leaves using cuticular analysis. Here, we report fossil leaves of Syzygium with in-situ cuticles from a Pliocene site in the Kon Tum Formation in Central Highlands Region of Vietnam. Overall, the Kon Tum flora is characterized by relatively small-sized and predominantly entire-margined leaves, with more than 40 morphotypes recognized so far, also including Ficus, Dipterocarpaceae, Fabaceae, Lauraceae, and others that suggest a tropical monsoonal forest similar to modern regional floras. The myrtaceous leaves are mostly preserved as dark or brown compressions that are easily detached from the matrix. They are elliptic-narrowly elliptic to obovate in shape, having an acute and acuminate apex and a decurrent to cuneate base. The venation is brochidodromous, with intersecondary veins common and more than five pairs of secondary veins forming distinctive intramarginal veins, but the tertiary and higher venation is not clear. The leaves are hypostomatic, with cavity-like structures on the abaxial side interpreted as lid-cells, a characteristic feature of Myrtaceae. Both leaf surfaces completely lack trichomes, suggesting the tribe Syzygieae. The stomatal complex is paracytic or anisocytic, scattered evenly and densely, which is consistent with Subg. Syzygium. The epidermal cell flange is straight. Syzygium leaves are the most abundant element in the Kon Tum flora, accounting for over 30% of the specimens (ca. 186 out of 572), implying either proximal deposition or high abundance in the flora. A possible Syzygium pollen grain was also recovered from the same outcrop, exhibiting the characteristic triangular polar view and apocolpial field of the genus. This study provides the first Syzygium leaves with in-situ cuticles in the Northern Hemisphere. Earlier records are the early Miocene leaves from Australia and a Miocene wood attributed to the genus from South China, indicating that the dispersal from Australia to Asia occurred no later than the Miocene. The new leaf fossils show that forests with abundant Syzygium have already been established in central Vietnam since a least the Pliocene.

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Topic: Contributed Papers Paleobotany

Title: Biogeographic affinities of fossil hickory nuts (Juglandaceae: Carya) from the Tertiary (Paleogene and Neogene) of Europe

Biogeographic affinities of fossil hickory nuts (Juglandaceae: Carya) from the Tertiary (Paleogene and Neogene) of Europe

Author: ***Steven Manchester @ Florida Museum of Natural History***

Keywords: Eastern Asia – Eastern North America floristic disjunction,Miocene,Oligocene,Tertiary,micro-CT scanning

Abstract:

Fossil nuts of Carya from the Oligocene and Miocene of Europe have been studied by micro-CT scanning to augment traditional morphological and anatomical methods to assess their relationships relative to extant Carya species of North America and Asia. The course of vascular bundles within the nutshell and primary septum, the presence or absence of lacunae, the degree of development of secondary septum, the extent of development of internal longitudinal nutshell ribs, as well thickness and anatomy of the nutshell and ornamentation on the exterior of the nutshell provide characters suitable for distinguishing clades that are also recognized from molecular characters. We found that two of the European fossils, namely the Czech Oligocene species C. costata (C.Presl ex Unger) Unger and the widespread eastern European Miocene species Carya ventricosa (Sternb. ex Brongn.) Unger correspond closely to extant east Asian tropical species, C. kweichowensis Kuang & A.M.Lu and C. poilanei (A. Chev.) Leroy, but with some specific differences. On the other hand, the German Miocene fossil, C. hauffei Kirchh., has features indicating closest relations to the eastern North American species C. aquatica (F.Michx.) Elliott. These findings implicate the southern Turgai route as well as the North Atlantic land bridge as likely corridors for the spread of Carya throughout the northern hemisphere prior to its Plio-Pleistocene extinction from Europe that led to the current eastern North American-eastern Asian disjunct distribution of the genus.

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Topic: Contributed Papers

Title: Estimates of the late Early Cretaceous atmospheric CO2 based on stomatal and isotopic analysis of Pseudotorellia from Mongolia

Author: ***Xiaoqing Zhang @ Wesleyan University***

Keywords: Leaf cuticle,carbon isotope,leaf-gas exchange model,paleo-CO2 proxy,late Early Cretaceous

Abstract:

The Aptian-Albian (121.4-100.5 Ma) is a known greenhouse period, with global temperatures 10-15°C warmer than pre-industrial conditions. Given this warmth, it is surprising that the most reliable CO2 estimates from this time (from https://paleo-co2.org/) max out at about 1500 ppm. This implies a very high climate sensitivity (>>4 °C per CO2 doubling). We sought to address this discrepancy with a well-vetted paleo-CO2 proxy based on leaf gas-exchange principles (the Franks model) that requires measurements of stomatal density, stomatal size, and leaf δ13C. We applied this proxy to two species of Pseudotorellia Florin (ginkgoalean) from a single stratigraphic level (PSH261) in the Tevshiin Govi Formation at Tevshiin Govi lignite mine in central Mongolia. Dated as 119.7-100.5 Ma based on U-Pb age from coeval Khukhteeg Formation biostratigraphic constraints accommodate an age as young as the end of the Albian (100.5 Ma).

Our median estimated CO2 concentration from 42 leaves of P. resinosa is 3375 ppm (1920-6436 at 95% confidence); estimates from 9 leaves of P. palustris are lower but overlapping (median = 1878 ppm; 1321-3827 at 95% confidence). The primary reason for the high yet variable CO2 from P. resinosa is its very low stomatal density (mean = 13.4 mm-2); when stomatal densities are this low, small variations propagate to large changes in estimated CO2. Indeed, we find that at least 15 leaves are required before the aggregate estimated CO2 approaches that of the full data set (42 leaves); this is more leaves than the conventional recommendation for minimum sampling (5 leaves).

Despite the variability within and between species, we can exclude CO2 concentrations below 1300 ppm at high confidence. Analysis of how the individual inputs to the Franks model affect estimated CO2 are consistent with this view. Overall, a CO2 concentration >1300 ppm (and potentially much higher) during a greenhouse time is much more in keeping with our current understanding of climate sensitivity.

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Topic: Contributed Papers Paleobotany

Title: Revisiting early polysporangiophyte relationships with a focus on the zosterophylls

Author: ***Pénélope Claisse @ Université de Lille***

Keywords: euphyllophyte,paleobotany,phylogeny,zosterophyll ,Early Devonian,early land plants,lycopsid,Zosterophyllopsida

Abstract:

The Silurian-Devonian transition is a critical moment in early land plant evolution. During this interval, plants invaded the continent, exploring different types of morphologies, and diversifying into multiple lineages, some of which have direct living representatives. One of these lineages, in particular, plays a central role in the understanding of these evolutionary events: the zosterophylls. This group reached highest diversity during the Early Devonian and is thought to include the ancestors of lycopsids. Found in floras all over the world, they are considered a dominant component of Early Devonian vegetation. Since the definition of the group in 1968 based on a small number of genera, numerous new fossils were discovered and today more than 40 genera of zosterophylls s.l. are known. They encompass a wide range of morphological diversity, a subset of which has been included in a formally defined Zosterophyllopsida. To date, two studies have probed with large datasets the relationships among zosterophylls and between the latter and other polysporangiophytes, obtaining conflicting results. Kenrick and Crane (1997) recovered the euphyllophytes sister to a clade within which Zosterophyllopsida and Lycopsida are sister to each other. Additionally, they recovered lycopsids in a polytomy with a Zosterophyllopsida clade and other zosterophylls s.l. In the other major analysis, Hao and Xue (2013) focusing on taxa of the Posongchong flora of China, recovered zosterophylls and lycopsids in separate clades that are part of a paraphyletic grade to the euphyllophytes,or a polytomy between these three main groups. Here, we presen results based on the most comprehensive phylogenetic matrix of zosterophylls to date (56 taxa, 49 characters; parsimony-based). Results show a polytomy with rhyniophytes, protracheophytes, and a large clade including all other polysporangiophytes. Within this clade, zosterophylls are not monophyletic, because the lycopsids and euphyllophytes are nested among them. This is, thus, a third hypothesis of general phylogenetic relationships among early polysporangiophytes, based on a large dataset. Some of the conflict between the results of the three studies is due to differences in taxon sampling, especially with respect to the representation of the different main groups. However, conflict is certainly also resulting from homoplasy among the simple morphologies of different early polysporangiophytes, specifically since this increases with denser taxon sampling. This pattern is consistent with a rapid Early Devonian evolutionary radiation in several polysporangiophyte lineages. Our results question the monophyly of Zosterophyllopsida, suggesting that zosterophylls s.l. are stem group tracheophytes, and Lycopsida and Euphyllophytina the crown groups with extant representatives. Together, these results show that we have not reached consensus yet regarding the relationships among zosterophylls and between them and other groups of early tracheophytes. The current conflicting relationships may indicate that our exploration of the fossil record has yet to reach the minimum thresholds of taxon sampling density and character construction required for stable resolution of these major phylogenetic nodes.

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Topic: Contributed Papers

Title: Early Miocene evidence of abundant C4 grasses and habitat heterogeneity in eastern Africa

Author: ***Caroline Strömberg @ University of Washington***

Keywords: Africa,Kenya,Paleoecology,Poaceae,stable isotopes,phytoliths,savanna,grasslands,Uganda

Abstract:

The origins of Africa's iconic C4 grassland and savanna ecosystems is key for understanding the evolution of many mammals on the continent, not least our own lineage. Current evidence from primarily pollen, biomarkers, and stable carbon isotopic data has suggested that C4 grasses became ecologically dominant in Africa only after 10 Ma. However, the paucity of paleobotanical records older than 10 Ma prevents a full evaluation of the timing and nature of C4 grass expansion. We used a multi-proxy approach, combining analyses of plant silica microfossils (phytoliths) with stable carbon isotopic data from soil organic matter, plant waxes, and pedogenic carbonates to document vegetation structure at ten Early Miocene fossil hominoid sites across eastern Africa (Kenya and Uganda). Although not every source of data was available for all sites, there is sufficient overlap at multiple sites to provide a detailed and robust view of Early Miocene vegetation. Taken together, our results demonstrate that, between 21 and 17 Ma, C4 grasses were locally abundant in vegetation at all sites, but not for every sample from those sites. This pattern points to habitat heterogeneity during the Early Miocene, ranging from closed forests to wooded grasslands, both within sites (locally) and among sites (regionally). It also pushes back the oldest fossil evidence of C4 grass-dominated habitats in Africa – and globally – by over 10 million years, suggesting that the paleoecological context for mammalian evolution in Africa, including that of hominins, needs to be reevaluated.

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Topic: Contributed Papers Paleobotany

Title: Where are we in understanding leaf evolution?

Author: ***MIHAI Tomescu @ Cal Poly Humboldt***

Keywords: Devonian,euphyllophyte,Evo-Devo,fossil,leaf,paleobotany,Evolution,Development,lycophyte,leaf evolution

Abstract:

The Siluro-Devonian fossil record provides unequivocal evidence for independent origins of leaves in lycophytes and euphyllophytes, and in several lineages among the latter. In each lineage, leaf-bearing members are stratigraphically younger and more derived, compared to those with plesiomorphic organization lacking stem-leaf differentiation. However, the evolutionary processes underpinning each independent leaf origin have remained largely unresolved. Lycophyte leaves arose in the earliest Devonian (possibly latest Silurian). Among euphyllophytes, leaves appear 30 million-years later, toward the end of the Middle Devonian. Evolving under the same physiological and developmental-structural constraints– maximizing photosynthetic yield and arising as appendages from a meristem required to maintain indeterminacy –, leaves have converged toward the same defining features: vascularization, bilateral symmetry and adaxial-abaxial polarity, regular arrangement, and determinate growth. These structural features are underpinned by regulatory mechanisms such as auxin-mediated primordium positioning (regular arrangement), KNOX/ARP interactions (leaf determinacy), and HD-ZIPIII/KANADI interactions (adaxial-abaxial polarity). Leaf evolution can be addressed by deconstructing leaves into their defining structural features – that can be observed in living plants and traced back in the fossil record – and developmental regulatory mechanisms – that can be studied in living representatives of different lineages. Lycophyte leaves likely have a single origin, having evolved either by vascularization of enations or by sterilization of sporangia. Consistent with an independent origin, lycophyte leaves seem to lack the adaxial-abaxial patterning function that HD-ZIPIII/KANADI interactions have in euphyllophytes. The ancestral role of this regulatory pathway in the differentiation of sporangia and vascular tissue is more consistent with the sporangium sterilization hypothesis. Given the scarcity of anatomically-preserved fossils in the key interval for lycophyte leaf evolution (Silurian – earliest Devonian), understanding lycophyte leaf origins will require new and substantial fossil discoveries. The traditional view that euphyllophyte leaves evolved from lateral branching systems has supported a single origin of leaves in the clade. However, developmental regulation data show differences between ferns and seed plants in the deployment and roles o KNOX/ARP and HDZIPIII/KANADI pathways, supporting multiple origins. Additionally, the better fossil coverage of the Early-Middle Devonian interval renders the fossil record more tractable for addressing euphyllophyte leaf origins. A close look at the lateral branching systems of Early-Middle Devonian euphyllophytes shows a breadth of structural diversity that belies their apparent simplicity and morphological similarity, supports multiple leaf origins, and may offer clues on tempo and mode of leaf evolution in the different lineages. By the end of the Early Devonian, at least two euphyllophyte lineages had evolved lateral appendages with regular arrangement and possessing (one of them) bilateral symmetry. A major hurdle is the lack of phylogenetic connection between these Early Devonian plants and Middle and Late Devonian plants in which we recognize bona fide leaves. Better resolved phylogenies of Early through Late Devonian plants are needed to provide a framework for tracing the appearance o different leaf-defining features in each lineage. Significant advances will also come from functional studies in different extant seed-free lineages where such information is currently minimal, to understand the developmental mechanisms of parallel evolution of leaves.

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Paleobotany

Topic: Contributed Papers

Title: A complex megasporophyll from the Late Cretaceous of North America reveals a novel type of seed enclosure in gymnosperms

Author: ***Andres Elgorriaga @ University of Kansas***

Keywords: Cretaceous,Gymnosperms,Mesozoic,North America,phylogenetics,Campanian,seed-plants,Megasporophyll,Cupules,Homology,Angiospermy,Gymnospermy

Abstract:

A considerable diversity of exceptionally-well preserved Cretaceous gymnosperms has recently been characterized by several research groups across the world. Many of these fossils have ovules/seeds enclosed in extraintegumentary structures and the information they provide has initiated vigorous discussion and hypotheses on Mesozoic seed plant evolution and structural homologies. Here we contribute to this research focus by characterizing a permineralized seed-bearing structure from the Campanian Holz Shale Member of the Ladd Formation, California, USA. The specimen was studied via the cellulose acetate peel technique and a 3D reconstruction rendered in Avizo. Additionally, we assessed the affinities of this fossil with systematic comparisons and phylogenetic analyses using multiple seed-plant matrices. The studied fossil is a cylindrical, yet complex ovuliferous structure that we interpret as a highly modified megasporophyll. The proximal third of the megasporophyll is longitudinally folded (plicate) towards its abaxial side, in which the opposite margins are fused to one another (via secretion) forming an cup-like base. Just distal to this region, the megasporophyll divides into two free lateral lobes that run parallel to one another and form the outer wall of the cylindrical megasporophyll. The corresponding opposite margins of both lateral lobes abaxially fold towards one another, but do not fuse, and run adjacent to the fused margins of the cup-like base. Within the interior of the megasporophyll and near the junction of the lateral lobe divergences, three smaller, yet fertile, lobes diverge and form a single row. The center lobe diverges from the inner surface of the cup-like base while the other two fertile lobes diverge from the inner surface of each lateral lobe. Each lobe has a single abaxially located inverted ovule and laminar tissue that partially covers each ovule. The distal end of the megasporophyll is missing from the saw cut that exposed the specimen. The vascular pattern in the megasporophyll is pinnate, with a main bundle that extends into the central fertile lobe. Proximal to the central lobe, the main bundle produces two successive daughter bundles that supply the lateral sterile lobes. Within the lateral lobes a single trace diverges inwards from the daughter bundles and enter the respective fertile lobes. Well defined phloem gaps indicate abaxial position of the inverted ovules. The integument is vascularized by a single bundle that runs the length of the ovule. The phylogenetic position of this fossil is recovered in alternative placements in each analyzed matrix, a phenomenon that also occurs with other cupulate gymnosperms from the Mesozoic. Thus, its relationships are currently unresolved. Our preliminary systematic comparisons indicate that this fossil is most likely distinct at the ordinal level, highlighting a striking level of potential convergence of ovule enclosing structures and strategies across Mesozoic cupulate gymnosperms, Gnetales, and angiosperms. While there are outstanding issues regarding the homology of seed enclosing structures, this work highlights that there still are novel gymnosperm clades that have yet to be recognized, some of which may continue to blur the lines between gymnospermy and angiospermy.

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Topic: Contributed Papers Paleobotany

Title: A fossil moss from the Late Cretaceous (Campanian) James Ross Island, Antarctica

Author: ***Gar Rothwell @ Ohio University; Oregon State University***

Keywords: Cretaceous,fossil,moss,Anatomy,Orthotrichales,Pottiales,rheophyte

Abstract:

Several specimens of an anatomically preserved moss gametophyte have been discovered in a calcium carbonate concretion from the “Baculites Hill” locality, James Ross Island, Antarctica. The concretion is derived from the Late Cretaceous, Beta Member of the Santa Marta Formation, dated as early to middle Campanian (ca. 80 Ma). These specimens have actinomorphic stems with alternate branching, spiral, patent leaf arrangement and large numbers of attached rhizoids. Stems are 210 µm in diameter with the largest branch measuring up to 3.7 mm long and 90-100 µm wide. Most stems and branches appear to lack a distinct conducting strand and cell walls are thinner toward the center of the axis; but one specimen shows a central strand in several consecutive peels. Cross sections show that the leaves are plicate with a simple D-shaped costal anatomy and unistratose intercostal area with a bistratose border. Stem leaves range from 650-700 µm wide and more than 700 µm long. The costa is percurrent, 90 µm wide and 55 µm thick. Intercostal cells are elongate, rhomboidal, L/W= 5:1. No ornamentation or papillae have been observed on the upper medial cells of the leaf. These fossils show morphological similarities to several taxa of acrocarpus mosses, including rheophytic species of the Pottiales and some Orthotrichiales with respect to costal anatomy. Cretaceous bryophytes are underreported from Gondwana; thus, this fossil contributes meaningful data on moss diversity in Antarctic forests during late Cretaceous.

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Topic: Contributed Papers

Title: A new type of microscopic reproductive structures of unknown affinity from plant tissues in the Early Devonian (Emsian) Battery Point Formation (Gaspé, Quebec, Canada)

Author: ***Victoria Durazo @ Cal Poly Humboldt***

Keywords: Devonian,fossil,Fungi,paleobotany,sporocarp,coprolite

Abstract:

Abundant specimens of a new type of microscopic reproductive structures are present in a lateral branching system of the Early Devonian euphyllophyte Kenrickia bivena. The fossils are preserved by calcium carbonate permineralization in fluvial deposits of the Emsian (c. 400-395 Ma) Battery Point Formation, exposed along Gaspé Bay (Quebec, Canada). The reproductive structures, termed sporocarps hereafter (pending elucidation of their taxonomic affinities) are roughly isodiametric and up to 200 µm in size. They appear spheroidal but may exhibit flat sides and small papillate protrusions in some planes of section; some are compressed or distorted taphonomically into less regular shapes. The sporocarp wall consists of two layers: a dark, dense inner layer of relatively even thickness (5 µm), and a lighter colored outer layer with agglutinated structure that can look at times granular or vermicular. The outer layer, up to 25 µm thick, is denser toward the contact with the inner layer and grades into looser packing toward the sporocarp surface, which has an irregular relief and where cells (4-9 µm) are sometimes visible. The sporocarps are filled with c. 300-400 tightly packed thin-walled spherical bodies 17-25 µm in diameter, most of which preserve inside one spheroidal inclusion c. 6 µm in diameter. The sporocarps are distributed throughout the spaces formerly occupied by parenchymatous tissues of the K. bivena axis; here, they are associated with coprolites 62-100 µm in size. Given the state of preservation of the host plant, it is impossible to know whether the sporocarps developed during the plant’s life or after its death. Some of the sporocarps are immediately adjacent to cells of the sclerenchymatous plant tissues (xylem and outer cortex) and seem to affect their walls, which are conspicuously thinner at the contact with the sporocarps. At least one sporocarp is attached to a coprolite. The taxonomic affinities of the sporocarps are unclear. They are morphologically comparable to reproductive structures produced by some fungi (Ascomycota, Mucoromycota), or could alternatively represent animal (arthropod, nematode) egg masses. Both fungi and animals can produce reproductive structures inside plant tissues. Such foreign bodies are often isolated by the plant host, which produces barriers (consisting of secondary metabolites or remains of necrotized cells); the structure of the sporocarp walls, with their consistent well-differentiated layering, precludes interpretation as a host response product. If the spheroidal inclusions inside the thin-walled bodies are nuclei rather than conglobated cell content, as suggested by their consistent shape and size, a fungal interpretation is less likely because fungal nuclei are typically smaller. Additionally, the coprolites indicate that animals were present in the host plant. However, the cellular structure of the outer sporocarp walls is inconsistent with animal origin. A thinning of the plant cell walls at the contact with the sporocarps suggests enzymatic activity of the latter, which would be expected from fungal structures but cannot exclude animal egg sacs.

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Topic: Contributed Papers Paleobotany

Title: A rare anatomically-preserved lycopod macrofossil from the Triassic of Antarctica

Author: ***Meg Nibbelink @ University of Kansas***

Keywords: morphology,Anatomy,fossil,Isoetes,Lycopods,lycopods anatomy,macroevolution,Mesozoic,paleobotany,Triassic

Abstract:

The rhizomorphic lycopod lineage (Isoetales herein) has a history that extends over 400 million years into the Devonian and persists still today. During the Carboniferous, arborescent lycopods dominated the Earth's landscape and left an abundant fossil record, placing the Carboniferous Isoetales among the best characterized groups of fossil plants. However, climatic and geologic changes triggered a shift in the ecological role of Isoetales, diminished their diversity in terrestrial ecosystems, and created conditions unfavorable to plant fossilization (e.g., Permian-Triassic coal gap). Together, these events obscure key data on the last 320-million-years of their evolutionary history, including pivotal evidence on the origins of modern Isoetes. Only a small fraction of isoetalean macrofossils are known from the Triassic, and an even smaller portion of these are anatomically preserved. Similarly, a few isoetalean macrofossils are known from Antarctica but none are Triassic permineralizations. Here we report a new lycopod fossil from the Triassic Fremouw Formation of Antarctica. This specimen is permineralized in a silicified peat and was studied using the cellulose acetate peel technique. The fragment is partially compressed and incompletely preserved. Anatomical details of this specimen can only be observed when peels are attached to the slab surface, making many details of their morphology and anatomy challenging to reconstruct. Nevertheless, the anatomy that is preserved indicates the specimen has an isoetalean affinity. The primary vascular tissues are not preserved but the secondary xylem cylinder is present, measuring approximately 15-20 cells (3.2 mm) thick. To the outside of the secondary xylem is a multilayered cortex composed of homogenous, parenchymatous cells. These layers create a rippling pattern, although it is unclear whether this is a taphonomic artifact or true to the specimen, and regularly arranged isoetalean rootlet traces are found on one side of this axis. Owing to the rarity of permineralized Triassic isoetaleans, this specimen provides crucial data on the anatomy and diversity of Mesozoic Isoetales and will advance our understanding of the evolutionary history of rhizomorphic lycopods.

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Topic: Contributed Papers

Title: The Middle Miocene Clarkia flora and associated biomolecules: 50 years of multi-disciplinary research

Author: ***Hong Yang @ Bryant University***

Keywords: Paleoclimate,Clarkia,middle Miocene,fossil flora,biomolecules

Abstract:

Created and shaped by the Columbia River Basalt (CRB) Group volcanism, the Clarkia Miocene lake in northern Idaho renders an exceptional ancient archive of a terrestrial ecosystem formed during the warming period of the Miocene Climate Optimum (MCO). Among different fossil taxonomic groups, the plant mega-fossil Lagerstätten stands out with its high diversity, extreme abundance, and extraordinary preservation of cellular details, in situ biomolecules, and the fidelity of stable isotope signatures. Along with organic geochemistry data derived from its organic rich sediments, the Clarkia deposit offers an unparalleled window into the Earth's warm past that can be compared with the near future Earth under a high CO2 concentration that doubles the pre-industrial CO2 level.

Discovered more than 50 years ago, the Clarkia flora has been the subject of multi-disciplinary research, from paleobotany to paleoliminology during the early phase, to the recovery of biomolecules and stable isotope signatures in the 1990s, and to the recent paleoclimate focused studies. Representing a warm temperate vegetation, the Clarkia flora has yielded more than 150 recognized species for studies of phytogeography, paleo-physiology, phylogenetic, plant-insect interactions, and fossil taphonomy. A suite of new biological and organic geochemical technologies, ranging from the Polymerase Chain Reactions (PCR) to the compound-specific isotope analysis, was first applied to pre-Quaternary plant fossil material in Clarkia. Recently-improved leaf epidermis preparation technique using Clarkia plant material has enabled precise measurements of stomatal apparatus which are critical parameters for the reconstruction of ancient CO2 by the newly developed leaf-gas exchange models.

We recently radiometrically dated the interbedded volcanic ash layers at its type locality, P-33, yielding 15.78 ± 0.039 Ma U-Pb zircon ages. The establishment of annually-resolved Clarkia sediments using micro X-Ray fluorescence, petrographic and spectral analyses constrains the P-33 sequence under a millennium human societal timeframe during the peak of the MCO associated with major carbon-cycle perturbations. CO2 reconstructions using the Franks model (one of the leaf-gas exchange models) yielded median middle Miocene CO2 levels above 500 ppm based upon different Clarkia plant fossils of both angiosperm and gymnosperm species. Interdisciplinary research at Clarkia revealed molecular level diagenetic process controlled by the change of paleolimnological conditions, pointing toward the critical role of different microbial communities in mediating key fossilization processes within a clay mineral-rich environment.

We review the scientific achievements made based upon Clarkia plant fossils and associated biomolecules and explore new directions of research that the Clarkia plant fossils can potentially offer. The high quality of fossil preservation with precise determination of geochronology, well-constrained sedimentation rates, and demonstrated multiple proxies of climate signals warrant Clarkia plant fossils as desirable material to paleobotany, paleolimnology, and high-resolution paleoclimate research for years to come.

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Paleobotany

Topic: Contributed Papers Paleobotany

Title: Ovulate cone from the Late Cretaceous of Antarctica with close affinities to Wollemia

Author: ***Selena Smith @ University of Michigan***

Keywords: conifer,permineralized,Araucariaceae,Campanian

Abstract:

Elucidating the evolution and biogeographic affinities of Cretaceous Antarctic rainforests will help us piece together how these extinct forests served as a center for diversification and/or corridor for dispersal in the assembly of Southern Hemisphere floras. To date, pollen, wood and leaf records have pointed to the presence of Araucariaceae, Podocarpaceae, and Cupressaceae as canopy components in these temperate rainforests, with angiosperms, ferns and bryophytes forming the understory. New data from permineralized Late Cretaceous (Campanian) plants recovered from marine calcareous concretions from the Baculites Hill locality, James Ross Island (Beta Member, Santa Marta Formation), offer an opportunity to contribute insights in the biodiversity of these extinct forests based on anatomically preserved reproductive structures. One ovulate cone was identified and studied using serial cellulose acetate peels. The cone is complete, about 7 mm long and 6 mm wide, and ellipsoid in shape. There are about 50 helically-arranged cone scale complexes that are attached to the cone axis at right angles and distally expand, thicken, and bend upwards. Cone scales are asymmetric and are comprised of a narrow sclerotic proximal stalk and an expanded distal half that is slightly fleshy. Each cone scale contains a single vascular bundle and an abaxial resin canal. The vascular bundle divides vertically, providing a small ovular trace to the seed that later divides within their integuments. Each cone scale has a single seed oriented with the micropyle facing towards the cone axis and attached to the scale at the chalazal end by a shor stalk on an elevated pad of tissue. Seeds have symmetric integumentary lateral wings and a chalazal wing. Spheroidal pollen grains with granular sculpturing were observed in or near the micropyle of several seeds. The presence of fungal hyphae within the cone axis, perithecia on some cone scales, and cyanobacterial filaments between the cone scales suggests an ecosystem rich with microorganisms. Cone scale morphology and the single stalked winged seed per scale indicate affinities within agathioid Araucariaceae. Bayesian and parsimony phylogenetic analyses were performed using a matrix of 57 characters and 49 taxa of living and extinct Araucariaceae. In both analyses, the new cone forms a monophyletic group with the extinct Wairarapaia and Emwadea and the extant Wollemia. This clade is sister to Agathis. The fossil described here adds to the diversity of Cretaceous agathioids, which are not as well-known as extinct Araucaria, and provides strong support that conifers closely allied with Wollemia were components of Cretaceous Antarctic rainforests.

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Paleobotany

Topic: Contributed Papers

Title: Seed cones of Callitroideae (Cupressaceae) from the Late Cretaceous of Antarctica

Author: ***Kelly Pfeiler @ University of Kansas***

Keywords: Antarctica ,Cupressaceae,fossil,Anatomy,Late Cretaceous,seed cone,ovulate cone,Callitroideae

Abstract:

The Callitroideae is a subfamily of Cupressaceae that comprises eight exclusively Southern Hemisphere genera. These conifers occupy a diverse range of ecological habits including arid and rainforest ecosystems, and are typically trees or shrubs bearing woody seed cones with decussate to whorled ovuliferous complexes. The Cretaceous was likely a pivotal time of diversification for this group following the separation of Gondwana and Laurasia. However, the Cretaceous record of Callitroideae is sparse and is known from a single occurrence in Australia. Most Callitroideae fossils are vegetative, assigned to modern genera, and are found in the Cenozoic of Australia, Tasmania, and South America. Thus, the distribution and diversity of Callitroideae during the Mesozoic are poorly understood. Herein, we characterize callitroid seed cones from the Late Cretaceous of Antarctica. There are two seed cones attached to vegetive shoots permineralized within a calcium carbonate concretion from the Santa Marta Formation, Beta Member (Campanian; 83-72 Ma) of James Ross Island, Antarctica. The seed cones measure ca. 1.7–2.0 mm in diameter and ca. 3.3 mm in length anc consist of two alternating whorls of three ovuliferous complexes, which are keeled and ovoid-spatulate in shape. These ovuliferous complexes are composed of parenchymatous tissues, a uniseriate hypodermis, and one central resin canal. An elongate trilobed columella, ca. 2.4 mm in length, is present at the cone’s center. Between the larger ovuliferous complexes and the columella are several scale-like structures that are thin and composed of collapsed cells. We interpret these structures as vestigial ovuliferous complexes similar to what is seen in ovulate cones of Fitzroya. The cones are subtended by several transition scales and a vegetative shoot with tricussate awl-shaped leaves that are triangular in cross-section and have decurrent leaf bases. These Antarctic fossils have diagnostic characters of the Callitroideae, such as valvate ovuliferous complexes, a columella, and tricussate phyllotaxis, and share similarities with Fitzroya and Callitris. The unique combination of characters of the new fossils indicates they belong to a new genus. These Antarctic fossils add to a depauperate Cretaceous record of Callitroideae and provide additional evidence that these conifers were present in Antarctica, which was an important corridor for Gondwanan floras during the Late Cretaceous.

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Paleobotany

Topic: Contributed Papers

Title: A new hypothesis about the relationships among cycads and other seed plants

Author: ***Leandro Martinez @ CONICET***

Keywords: morphology,Anatomy,Cycadales,phylogeny,axillary buds,Spermatophytas

Abstract:

Cycads are an ancient gymnosperm lineage distinct from all other living Spermatophytes. They are considered the most primitive living seed plants, but their relationships to other early fossil spermatophytes remain uncertain. The cycads are a unique group of living seed plants lacking axillary buds and axillary branching. In this communication, we proposed at least two distinct earlier lineages of seed plants are recognized, based on the presence or absence of axillary buds: Axillaryospermae and Cycadospermae. Both lineages are mainly distinguished by the presence/absence of axillary buds, which determine a proper mode of branching, which was a key to the evolution of some groups of plants because they enabled the development of structurally and functionally different branch systems, leaves and reproductive structures. To test this new hypothesis a cladistic analysis was made using morphological and anatomical characters. The results of the new interpretation support and explain the diversity of leaves, branching, and architectural patterns in other seed plants. Studying the evolution of shoot systems and leaves in cycads and comparing them to other fossil and extant spermatophytes is crucial for understanding how seed plants have changed and diversified over time.

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Topic: Contributed Papers Paleobotany

Title: Early Diversification of Southern Cypresses: Permineralized Fitzroya from the Late Cretaceous of Antarctica.

Author: ***Brian Atkinson @ University of Kansas***

Keywords: Anatomy,conifer,Cupressaceae,fossil,Gondwana

Abstract:

Antarctica played a central role in the assembly and distribution of Gondwanan plant lineages during the Late Cretaceous and Paleogene. This is particularly true for the subfamily Callitroideae (Cupressaceae). Today these conifers are important components of arid and rainforest environments and have a disjunct distribution across the Southern Hemisphere. Their extensive Cenozoic fossil record in Australia, South America, and Antarctica have made them an ideal study system for biogeographical studies. However, while molecular divergence time estimates indicate that crown-group Callitroideae originated and diversified by the Early Cretaceous, there has only been a single Cretaceous report (ovulate cones from Australia) to support this. Thus, the early evolution of these conifers is poorly understood. As part of an initiative to better understand Antarctica's role in the evolution of Southern Hemisphere plant lineages, we report permineralized callitroid seed cones attached to an articulated branching system of leafy shoots from the Late Cretaceous of Antarctica. More specifically, the fossil was recovered from the Beta Member of the Santa Marta Formation, which is early Campanian (~80 Ma) in age and exposed on James Ross Island in West Antarctica. The cellulose acetate peel technique was used to prepare and study the specimen. In addition, a Bayesian total evidence phylogenetic analysis using five chloroplast loci and a preliminary morphological matrix of 35 characters was conducted to infer relationships of the fossil. The shoot branches at least four times and bears elongate leaves arranged in whorls of three. Leaves have a keel and midrib and are amphistomatic. Four ovulate cones terminating the ultimate shoots have been identified. Each cone is open and roughly discoid with six fertile cone scales arranged in alternating whorls of three. Cone scales are spathulate with a distal adaxial swelling. There is a conspicuous abaxial umbo near the tip of each cone scale. A conspicuous columella is present and all seeds have dispersed. In addition to the six fertile cone scales, there is an uppermost whorl of vestigial cone scales that are weakly developed and considerably smaller than the fertile ones. This combination of characters is diagnostic of the extant and monotypic Fitzroya, which is an ecologically important and emergent conifer restricted to temperate rainforests in Patagonia. Preliminary phylogenetic analysis recovers the Antarctic fossil as sister to Fitzroya; thus, we assign the fossil to the genus. The Antarctic Fitzroya differs from its extant counterpart by lacking resinous bodies in the vestigial cone scales and having a more robust columella. Our findings indicate that Fitzroya diverged from its sister genus Diselma well before their previously hypothesized Eocene-Oligocene divergence and supports a Cretaceous diversification for the Callitrioideae. Moreover, the Fitzroya fossil characterized here (and an additional taxon from the same locality described at this conference) reveals that, by the Campanian, the callitroids were established in Antarctica, which was an important corridor for the distribution of Gondwanan plant lineages. This work provides valuable data for understanding the turnover and distribution of these ecologically important conifers in deep time.

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Topic: Contributed Papers

Title: Reconstruction and systematics of the enigmatic Pennsylvanian strobilus Tetraphyllostrobus from the Mazon Creek lagerstätte using computed tomography

Author: ***Michael D'Antonio @ Field Museum of Natural History***

Keywords: Evolution,Paleozoic,spores,Strobilus

Abstract:

The enigmatic Pennsylvanian-age (~307 million years ago) fossil strobilus Tetraphyllostrobus is known from just thirty specimens preserved as compressions from the Sydney Coal Basin in Nova Scotia, Canada, and several recently recognized permineralized specimens from the Mazon Creek lagerstätte in Illinois, USA. The characters and relationships of the genus have remained problematic since it was first described as a strobilus with an unusual decussate arrangement of sporophylls thirty years ago. Here, we investigate four Tetraphyllostrobus specimens from the Mazon Creek flora preserved three-dimensionally as partial permineralizations in iron carbonate nodules. We applied x-ray micro-computed tomography and visualization techniques, combined with peels, super-resolution confocal and scanning electron microscopy, to reconstruct and characterize the three-dimensional (3D) form of the strobilus and its in-situ spores. The specimens reveal exquisite morphological and anatomical details, and clearly show that rather than pairs of decussate bracts there are whorls of six bracts at each node that have numerous sporangia in their axils. The in-situ spores are assignable to Columinisporites, a spore genus largely associated with Sphenophyllales. The new morphological assessment of the cone and its spores unequivocally indicates assignment to the Sphenophyllales. Together this work illustrates the value of combining standard approaches with advanced imagery techniques for the 3D reconstruction and systematic placement of long-extinct enigmatic fossil plants.

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Topic: Contributed Papers Paleobotany

Title: A Nothofagus-like fruit from the Campanian of Western North America

Kate Morrison, Selena Smith, Brian Atkinson

Author: ***Kate Morrison @ University of Michigan***

Keywords: Cretaceous,fossil fruits,Gondwana,North America,Nothofagaceae

Abstract:

The genus Nothofagus Blume (southern beech; Nothofagaceae, Fagales) has a substantial fossil record across the Southern Hemisphere. Its first appearance in the fossil record is represented by pollen grains preserved in late Campanian to Maastrictian deposits from Antarctica. Due to its extensive fossil record and southern distribution, Nothofagus remains an important group for understanding the evolution and biogeographical history of Gondwanan floras. While the reported fossil record of Nothofagus is restricted to Gondwanan landmasses, there are a number of Nothofagus-like fossils from North America. These fossils have been important for understanding the early evolution of Fagales, mainly the phylogenetic and morphological divergence between Nothofagaceae and all other Faglaes. Here we presen a fagalean fossil fruit with similarities to Nothofagus. The specimen is a single trimerous fruit recovered from EV Henry Point, Sucia Island State Park, Washington. Deposits at this locality belong to the Cedar District Fm, which is early Campanian (~80 Ma) in age. Serial acetate peels were made, followed by light microscopy and a 3D reconstruction, allowing the characterization of morphological and anatomical characteristics. The fruit is about 8.8 mm in cross sectional length and is missing the basal portion. It has three longitudinally elongated wings and three glabrous locules separated by thin septa that are ruptured in some areas. The pericarp is differentiated into epicarp, mesocarp, and endocarp. The epicarp includes thick-walled cells and idioblasts. The mesocarp comprises fibers and parenchyma while the endocarp comprises small, thick-walled sclereids. The mesocarp and epicarp extend to form the fruit wings, in which case it becomes parenchymatous with scattered sclereids. The wings are up to 3.9 mm in length. There are two ovules per locule, with axile placentation attached to an apical placental column. A parenchymatous tissue fills the locule cavity below the level of the ovules. There is a single whorl of three persistent tepals at the apex of the fruit. This combination of characters is highly diagnostic of Fagales, especially Nothofagaceae. A number of Nothofagus-like fruit containing cupules and isolated fruits have been previously described from the Late Cretaceous of North America; however, these fossils differ from the extant genus by key characters such as the number of tepal whorls and tomentose locules, which has precluded them from being assigned to Nothofagaceae. Conversely, the fossil described here has fruit characters diagnostic of Nothofagus, but important cupule characters are missing. Thus, we refrain from assigning the fossil to the genus at this time. Nonetheless, this fossil adds to the diversity of Nothofagus-like fossils from the Cretaceous of North America and we assign it to Nothofagaceae. This systematic assignment is further supported by the presence of permineralized nothofagaceous fruits with similar anatomy from coeval deposits in Antarctica. This new occurrence of a nothofagaceous fruit from the Late Cretaceous of North America suggests a wider distribution of the family than previously thought and supports a hypothesized biotic exchange between North America and Gondwana that occurred during this time.

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Topic: Contributed Papers

Title: Nothofagaceae fruits from the Campanian of Antarctica.

Author: ***Eva Silva Bandeira @ Instituto de Investigaciones en Biodiversidad y Medioambiente (Consejo Nacional de Investigaciones Científicas y Técnicas - Universidad Nacional del Comahue)***

Keywords:

Abstract:

Exquisitely preserved plant remains were identified from calcareous concretions recovered from the Beta Member (lower-mid Campanian) of the Santa Marta Formation, James Ross Island, Antarctic Peninsula. Plant remains were originally transported by estuarine currents from the east continental margin of the Peninsula and deposited in a shallow-marine environment. Several permineralized fruits were studied via serial acetate peels and from details exposed along the surface of concretions. Two small (4-8 mm) morphotypes were identified: dimerous (bilocular) and trimerous (trilocular) winged fruits, including a range of developmental stages. The pericarp of each morphotype is differentiated into three zones: exocarp, mesocarp, and endocarp. The fruits have two (dimerous) to three (trimerous) wings that are longitudinally elongate and formed by the outer layer. Two ovules with axile placentation are present in each locule. The locules lack trichomes. No distinct vascular bundles are seen in the mesocarp or in the central axis. There are, however, several vascular bundles running from the base of the fruit through the outer layer and toward the apex. Permineralized mature trimerous fruits are four times the size of the immature ones, with more developed sclerenchymatous mesocarp. The fruit symmetry, wings, general fruit shape, axile placentation, two ovules per locule, sclerenchymatous mesocarp, and glabrous inner locule wall are indicative of Nothofagaceae. The dimerous and trimerous fruits have the same tissue organization, indicating that both of these fruit types likely belong to the same taxon and were borne within a three flowered cupule (two trimerous flowers and one middle dimerous flower), as seen in most extant Nothofagus species. The fruits reported here are the first Cretaceous record for reproductive structures of the family, and are contemporaneous with the oldest pollen records (also from Santa Marta Formation) of Nothofagaceae that are assigned to ancestral pollen groups. In overlying Late Campanian-Maastrichtian deposits in Antarctica, the three extant Nothofagus subgenera are well represented by pollen, leaves, and wood. The structure of the fossil fruits studied here share all of the diagnostic characters of extant Nothofagus. Our findings support that three flowered cupule (with a middle dimerous flower) evolved early in the evolutionary history of the family.

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Paleobotany

Topic: Contributed Papers Paleobotany

Title: Permineralized cornalean fossil fruits from the Late Cretaceous of North America

Author: ***Austin Nguyen @ University of Kansas***

Keywords: Cornales,Cretaceous,fossil fruits,total evidence phylogeny

Abstract:

The Cornales is an asterid order that includes dogwoods, hydrangeas, and tupelos. Molecular divergence time estimates and paleobotanical studies indicate that the order underwent a rapic diversification during the Late Cretaceous (100-66 Ma). Thus, fossil cornaleans from this important interval have much potential for shedding light on the early evolutionary history of the order. Here, we report a new genus represented by two permineralized endocarps from the Cedar District Formation (Campanian, 82-80 Ma), which is principally exposed on Sucia Island, Washington state, USA. The fossils were sectioned with the cellulose acetate peel technique and studied with light microscopy. To determine the fruits' relationship to other cornalean taxa, a Bayesian phylogenetic analysis including living and fossil taxa was conducted in MrBayes using two chloroplast genes, 28S rDNA, and 71 morphological characters. The endocarps are thick-walled and woody with apically opening dorsal germination valves, one apically attached seed per locule, and transseptal vascular bundles located within the septal peripheries rather than in the central axis. This combination of characters is highly diagnostic of Cornales. Additionally, the endocarps measure 2.3-3.1 mm wide and at least 2.9 mm long. The endocarps have three to four locules that are ellipsoidal to subtriangular in cross section. Each locule is associated with a dorsal germination valve that extends less than half the endocarp length. The endocarps have smooth external surfaces, lacking ridges, grooves, and pits. Anatomically, the germination valves are composed of isodiametric sclereids, the septa and central axis are comprised of isodiametric and elongated sclereids, and there is multiseriate layer of circum-locular fibers. The seeds have copious endosperm, membranous seed coats, and ventral raphes. The combination of characters seen in these fruits precludes assignment to any extant family within the order and indicates that they represent a new genus. Phylogenetic analysis recovers this extinct genus within a clade with other extinct genera, all of which are closely related to the extant families Curtisiaceae and Grubbiaceae. Our findings provide additional evidence that the early diversification of Cornales not only resulted in the rapid divergences of major clades, but also a considerable diversity of extinct genera that most likely belong to extinct families.

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Paleobotany

Topic: Contributed Papers

Title: Neotropical fossil grapes challenge biogeography of Vitaceae

Author: ***Fabiany Herrera @ Field Museum***

Keywords: Cenozoic,Evolution,end-Cretaceous event,Andean orogeny,Paleobiogeography,Panamanian Seaway

Abstract:

Extant distributions and molecular data are commonly used to elucidate the evolutionary history of plant lineages, such as the direction and timing of long-distance dispersal and diversification events. Such reconstructions fail to account for the vast portions of biogeographic histories that are lost to extinction and are only seen in the fossil record. We show a case example based on Paleocene to Miocene (60 to 19 Ma) Neotropical seeds of Vitaceae that extend beyond their current distribution range and demonstrate the need for paleobotanical data for understanding the biogeographical history of plants. We also show hov the end-Cretaceous event, the initial rise of the proto-Central American islands during the Eocene, the Oligocene Andean orogeny, and the Miocene Panamanian Seaway, have likely played the most critical roles in Vitaceae origination, dispersal, and extinction in this part of the world.

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Paleobotany

Topic: Contributed Papers

Title: An exclusive look at a diverse coal swamp flora from the Pennsylvanian of Lawrence, Kansas

Author: ***Rudolph Serbet @ University of Kansas***

Keywords: flora,Pennsylvanian,Kansas

Abstract:

A Pennsylvanian flora from the Lawrence Shale (Virgilian) of Kansas provides an opportunity to characterize a rich and diverse coal swamp flora. The material is preserved as compression/impressions within fine grained sediments that indicate the plant parts were deposited during a low energy episode close to their original habitat. Due to this preservational event, numerous articulated remains were recovered. The composition of this flora includes sphenophytes, lycophytes, pteridophytes and pteridosperms. Within this assemblage sphenophyte foliage morphotypes Annularia, Asterophyllites, Sphenophyllum, Daubreeia, Paleostachys/Calamostachys-type cones and axes of Calamites are documented. Several types of lycopod axes are also present, including Lepidophylloides, Stigmaria and an unusual abundance of Lepidostrobus, with some cones being up to 25 cm long. Pteridophytes such as Asterotheca, Dicksonites, Pecopteris, Alloiopteris, Acitheca are a major component of this flora with many of them being fertile. Pteridosperms are well represented and several morphotypes of foliage and reproductive structures reveal their diversity. These include Neuropteris, Alethopteris, Aphlebia and Trigonocarpus up to 8 cm in length. The lyginopterids, although somewhat scarce, are characterized by minute delicate Sphenopteris, Telangiopsis-like pollen organs and small ovoid lyginopterid-type ovules. Cordaites leaves and Cordaitanthus are also present. Interactions between plants and arthropods are indicated by gall-like structures on leaves and marginal feeding scars. The Pennsylvanian coal swamp flora of Kansas was previously characterized using compression/impressions plant fossils from 77 different localities (Cridland et al., 1963). The flora presented here allows for further interpretation of this Late Pennsylvanian coal swamp forest. Some components of the Lawrence Shale flora differ from what was previously documented for the Carboniferous of Kansas, providing a more detailed regional reconstruction of a swamp flora during a time of a glacial-interglacial cycle.

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Paleobotany

Topic: Contributed Papers

Title: Update on the paleobotany of the Upper Pennsylvanian Dennis Formation in Missouri and Kansas, USA

Author: ***Nathan Jud @ William Jewell College***

Keywords: fossil wood,Fossils

Abstract:

Plant fossil assemblages from the Upper Pennsylvanian Dennis Formation in Missouri and Kansas are dominated by remains of cordaitaleans and medullosan pteridosperms, but the flora has never been treated in detail. Description of these fossils helps to fill a geographic gap between the Illinois Basin (Bond Formation) to the east and the early Missourian of New Mexico (Tinajas Member, Atrasado Formation) to the west. Locally, they also fill a temporal gap between the wetter Desmoinesian coal floras of Missouri and Kansas and the drier, later Late Pennsylvanian conifer-dominated floras at Garnett and Hamilton, Kansas. Macrofossils include Cordaites spp. “Neuropteris” lindahli, Neuropteris hastata, Macroneuropteris scheuchzeri, Cyclopteris sp., and permineralized wood. The wood has the following combination of characters: tracheids with closely spaced alternate circular bordered pits in 1–2(3) series on the radial walls, rays 1–21 cells high and uniseriate with local biseriate portions, cross-fields with 1–2 cupressoid oculipores, and little to no axial parenchyma. One specimen with primary tissues preserved has a wide (~18 mm by 8 mm) hollow pith without septae surrounded by >46 mesarch cauline bundles. The palynoflora includes monosaccate and bisaccate grains typical of cordaitaleans and early conifers, monolete spores typical of sphenophytes, and trilete spores of ferns and lycophytes. These fossils provide direct evidence of colonization of the region by drought-tolerant (dryland) Cordaites-pteridosperm forests during the early Missourian when the sea level was low.

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Topic: Contributed Papers Paleobotany

Title: Cyclocarya brownii (Juglandaceae): an update on what we know about this plant.

Author: ***Kathleen Pigg @ Arizona State University***

Keywords: fossil fruits,paleobotany,Juglandaceae,Almont,Beicegel Creek

Abstract:

Cyclocarya brownii Manchester & Dilcher was described in 1982 from the Late Paleocene Almont locality, Morton County, North Dakota, USA. Additional specimens from Almont, including infructescences with attached fruits were discovered in the early 2000s along with exquisite anatomically preserved material at Beicegel Creek, McKenzie County, North Dakota. Witt Taylor's dissertation in 2011 comprised this material, and since then we have updated and broadened the study to review new occurrences of fossils and new developmental studies of extant Cyclocarya. We can now recognize several interesting details: 1) in contrast to extant C. paliurus which has relatively few (around 5), widely spaced sessile fruits in a catkin, C. brownii's fruits are crowded, numerous (around 23) and borne on elongate pedicels; 2) fruits are pyramidal with basally attached wings in contrast to equatorial attachment of oblate to lenticular fruits in C. paliurus, and this may correlate with being attached at the broadest part of the fruit; 3) fruit wall anatomy is distinct and more complex than that of extant and related fossil species; 4) triporate (vs tetraporate) pollen of the Momipites triorbicularis (Leffingwell) Nichols type occurs both in typical pollen catkins and in stamens borne on fruits. Fruits bearing stamens also occur on occasion in extant Cyclocarya paliurus and may be a plesiomorphic character in the clade. Lastly, 5) individual fruits of Cyclocarya brownii serve as the major disseminule, accounting for the rare occurrence of infructescences in the fossil record. The lignified, persistent infructescence remains on the tree and serves as the platform from which fruits can be dispersed. We interpret the abundance of individual Cyclocarya fruits at the Almont locality to represent sites where the buoyant fruits were carried to relatively low energy environments such as the distal edges of overflow deposits into abandoned channels. The bedforms and more fragmentary fossils recovered at Beicegel Creek suggest a higher energy environment such as fluvial deposition. Clearly, the combination of wind dispersal and hydrochory played a role in dispersal in fossil Cyclocarya, as it does within the genus today.

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Topic: Contributed Papers

Title: Investigating relationships among leaf functional traits and paleoclimate variables: a case study using fossil ginger (Zingiberaceae) leaves from the Cretaceous and Paleogene of North America

Author: ***Zack Quirk @ University of Michigan***

Keywords: Cretaceous,Eocene,leaf traits,Zingiberaceae,ginger,Paleocene,Paleogene

Abstract:

Flowering plants have persisted through many climate shifts across the last 100 million years. Fossil leaf traits can provide valuable insight into plant adaptation in response to severe ecological changes, as they relate to plant functions (e.g., photosynthesis) and can correlate with their local ecosystem. While leaf functional traits, such as leaf mass area, have been empirically and extensively tested in extant and extinct woody dicots, monocot flowering plants are understudied in how functional leaf traits correlate with other environmental, physiological, and climatic variables. However, because monocots are highly diverse (~60,000 species), contribute significantly to global agriculture, and represent large carbon sinks in both terrestrial and marine ecosystems, they are worth studying further. Here, we focused on one family within monocots, Zingiberaceae (the gingers) because they have a good temporal and spatial fossil distribution and can potentially provide valuable information on how they adapted to shifts in climate. First, we first tested the validity of applying fossil dicot leaf area estimation (LAE) and leaf mass area (LMA) on living Zingiberaceae leaves. Neither the LAE nor LMA methods were applicable to living Zingiberaceae leaves, pointing to fundamental developmental differences in monocot and dicot leaves. Second, we measured leaf traits of 58 fossil Zingiberopsis specimens from the Cretaceous-Paleogene of North America; the leaf traits measured were vein length per area (VLA) of parallel, cross, and all venation (parallel, cross, and total VLA), leaf width, leaf vein packing, and average vein thickness. We compared the leaf trait data with paleoclimate data (mean annual temperature, mean annual precipitation and [CO2]) to determine any statistically significant relationships and whether these leaf characteristics could be classified as leaf functional traits. Many mean values of the paleoclimate and fossil trait data (except for leaf width) were statistically and significantly different within each time period (Cretaceous-Paleocene-Eocene). In general, parallel vein traits had negative correlations with mean annual temperature and precipitation, while cross vein traits had positive correlations with those climate variables. All vein traits had statistically significant differences between time bins representing distinct [CO2]. Our findings suggest monocot venation is responding to local climate, with parallel vein architecture increasing in cool/dry climates in order to decrease the distance water needs to travel. Our study also illustrates the possible application of using monocot leaf traits for past plant-climate interactions, especially when fossil leaf material is fragmentary.

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Paleobotany

Topic: Contributed Papers Paleobotany

Title: Tracing the fossil diversity of the conifer family Podocarpaceae through the ages

Author: ***Ana Andruchow-Colombo @ University of Kansas***

Keywords: Podocarpaceae,fossil record,Rissikia,Mataia,Nothodacrium,leaf morphology,seed cone morphology

Abstract:

The Podocarpaceae are a morphologically diverse conifer family that have a cryptic fossil record, reported since the Permian. We reviewed the fossil record of Podocarpaceae, tested the affinities of the oldest records using phylogenetic analyses, compiled macrofossil occurrence records, and investigated the diversity, distribution, and morphology of Podocarpaceae through time. We found that Permian, Triassic, and some Jurassic fossils referred to Podocarpaceae should not be placed in the family. We performed total-evidence phylogenetic analyses, sampling all major conifer lineages, to analyze the positions of three genera previously assigned to Podocarpaceae that have been used as calibration points for the family —the Triassic Rissikia, and the Jurassic Nothodacrium and Mataia. We recover Rissikia and Nothodacrium as stem-group conifers, and the Jurassic Mataia as part of the stem group of the order Araucariales (Podocarpaceae + Araucariaceae). We conclude that the earliest reliable Podocarpaceae occurrences are from the Jurassic of both hemispheres, have scale-like leaves, belonging exclusively to extinct genera. The majority of living genera appear in the record between the Late Cretaceous and early Cenozoic. Most extant leaf morphologies appear in the Early Cretaceous, coeval with angiosperm diversification, consistent with the hypothesis that expanded leaves in Podocarpaceae are adaptive responses for light harvesting in today's angiosperm-dominated environments.

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Paleobotany

Topic: Contributed Papers

Title: Early South American grasses (Paleocene-Eocene) occupied forested ecosystems

Author: ***Elena Stiles @ University of Washington***

Keywords: Grasses,Paleoecology,Patagonia,Poaceae,South America,phytoliths

Abstract:

Grasses (Poaceae) exhibit exceptional taxonomic and ecological diversity, with grassland-dominated habitats around the world covering about 40% of Earth's land surface. Modern grasslands occur in temperate to tropical ecosystems spanning low to high altitudes, a wide range of temperatures, and wet to arid climates. However, the ecology of early grasses and their environmental affinities remain poorly understood because of the scant fossil record of grasses before the global Oligocene-Miocene spread of grasslands. We analyze phytolith assemblages extracted from sediment samples collected in Paleocene-Eocene Rio Chico Group sites along the San Jorge Basin of Argentine Patagonia to reconstruct the ecosystems early grasses occurred in. The coastal lowland deposits of the Las Violetas up to the base of Las Flores formations of the Rio Chico Group are preliminarily dated between 60.01±0.58 Ma to 50.93±0.40 Ma (unpublished information). These deposits produced phytolith assemblages comprising among the oldest occurrences of grass phytoliths in the fossil record of South America. Preliminary results of traditional phytolith assemblage analysis and reconstructed canopy structure using epidermal phytolith shape suggest that early grasses in the Paleocene and Eocene of the San Jorge Basin occurred in low abundances in palm and woody dicot-dominated forests of moderately open canopies. These results support the hypothesis that early grasses emerged as rare understory components in non-analog shrublands dominated by palms, or forests dominated by woody angiosperms, before expanding to open habitats later in the Cenozoic, where they would become dominant elements of terrestrial landscapes during the mid-late Miocene. Continuing to build the phytolith record in the Cretaceous and early Cenozoic of South America will be necessary to fully understand the habitats that early grasses occurred in, which will, in turn, shed light on the timing and possible mechanisms that drove the global expansion of grasses and grasslands over the last 60 million years. Furthermore, the studied records capture the critical Paleocene-Eocene transition in southern South America, contributing to our understanding of the impact of this period of extreme global warming on terrestrial ecosystems in the Southern Hemisphere.

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Paleobotany

Topic: Contributed Papers

Title: Reexamination Of Arthmiocarpus Hesperus From The Late Cretaceous Of South Dakota: Expanding The Fossil Record Of Bisexual Climbers In Araceae

Author: ***Jeronimo Morales Toledo @ University of Michigan***

Keywords: Araceae,fossil fruits,paleobotany,Late Cretaceous,Monsteroideae

Abstract:

The study and re-evaluation of Cretaceous plant fossils is an opportunity to understand the early evolution of angiosperms, prior to the establishment of modern ecosystems. The most diverse family within Alismatales, Araceae, are the sister group of all other extant monocots (other than Acorales) and have a fossil record that can be traced back to the Early Cretaceous (110 to 120 Ma). However, the only confidently assigned aroid fossils prior to the Cretaceous-Paleogene (K-Pg) mass extinction come from the early divergent lineages (i.e., Orontioideae and Lemnoideae), obscuring our complete understanding of the historical evolution of the aroid subfamilies in deep time. In this study, we investigated the morphology, anatomy, and taxonomy of Arthmiocarpus hesperus (Wieland) Delevoryas, a permineralized fossil from the Late Cretaceous Fox Hills Sandstone, Cottonwood Creek, South Dakota. This specimen was previously interpreted as a drupe from the fig family (Moraceae), but shows features consistent with Araceae. Thus, reinvestigating the morphology and classification of this fossil could provide greater understanding of the aroid evolutionary history. Thin sectioning and X-ray micro-computed tomography (μCT) were used to re-examine this species' type material, resulting in 3D reconstructions of the seed and characterization of structures in multiple planes of section. This allowed us to resolve conflicting interpretations of fruit-seed morphology and anatomy, and to identify additional characters useful in refining potential taxonomic affinities. The helically arranged sessile berries on a central spadix confirm affinities to Araceae, and features of the fruits and seeds such as berries that are hexagonal in cross section, fibrous pericarp, a smooth seed coat, and a monocotyledonous L-shaped embryo suggest it is most closely related to members within the subfamily Monsteroideae. However, Arthmiocarpus presents a unique set of characters that differentiate it from extant and extinct members of Araceae. This study is an example of how the subfamilies of extant angiosperms were constituents of Cretaceous ecosystems prior to the K-Pg mass extinction and the establishment of modern ecosystems.

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Paleobotany

Topic: Contributed Papers Paleobotany

Title: Paleogene evidence for anatomically preserved gleicheniaceous pinnules with sori in marine carbonate concretions from Vancouver Island, B.C., Canada

Author: ***Gar Rothwell @ Ohio University; Oregon State University***

Keywords: Anatomy,Fossils,Appian Way,Gleichenia,Gleicheniaceae,Paleocene-Eocene

Abstract:

Gleicheniaceae has what may be the longest fossil record of all leptosporangiate families with living representatives. Nevertheless, anatomically preserved fertile structures are extremely rare from Cenozoic deposits. Fertile frond fragments with abaxially attached radial sori recently have been recognized in a diverse assemblage of plant remains preserved in carbonate marine concretions at the Paleocene-Eocene Appian Way collecting locality along the eastern margin of Vancouver Island, British Columbia, Canada. Pinnule fragments with a lamina ~70 µm thick and relatively homogeneous mesophyll anatomy bear sori of seven to nine annulate sporangia. Sori are positioned below a vein, and are exindusiate with a receptacle that bears sporangia both laterally and terminally. Each sporangium has an ovoid capsule up 120 µm in maximum diameter and 155 µm long, and an extremely short, broad stalk. An oblique, uniseriate annulus makes up much of the capsule wall, but there are thin-walled cells along one side that form a stomium. Most sporangia are senescent, but one contains oval-radial trilete spores 13 - 18 µm in diameter with a thin wall that appears psilate under light microscopy. These fertile structures accompany vegetative organs at the Appian Way locality that have been described as Gleichenia appianensis. Rhizomes of G. appianensis have a marginally mesarch stolid protostele and attached adventitious roots, and the frond segments have pseudo-dichotomous branching and C-shaped traces with infolded adaxial hooks. Because only one type of gleicheniaceous rhizome, vegetative frond, and fertile pinnule have been discovered within the extensively sampled and studied floral assemblage at the Appian Way locality, it is reasonable to suspect that all of those organs were produced by a single species of gleicheniacous ferns. If correct, this material represents the most complete gleicheniaceous plant in post Mesozoic fossil record. These fossils also document that essentially modern species of Gleicheniaceae evolved no later than the base of the Cenozoic.

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Paleobotany

Topic: Contributed Papers

Title: Ovuliferous complexes of Wollemia nobilis and the dual bundle system of conifer seed cones

Author: ***Kelly Matsunaga @ University of Kansas***

Keywords: Anatomy,conifer,Araucariaceae,Wollemia

Abstract:

The relationship between the anatomy of modern conifer seed cones and the organization of axillary ovuliferous shoots of fossil conifers was central to Rudolph Florin's foundational model of seed cone homology. In particular, the presence of two series of vascular bundles within the ovuliferous (bract-scale) complexes of modern seed cones was of special significance. In cones with clear differentiation of bract and ovuliferous scale, one set of bundles supplies the bract and have adaxial-abaxial polarity consistent with leaf homology (adaxial xylem, abaxial phloem). The second set of bundles supplies the ovuliferous scale but is inverted relative to the bract bundles: polarity is reversed and phloem is adaxial. Importantly, this dual bundle system is also present in taxa without clear differentiation of bract and scale (e.g., Cupressaceae, Araucariaceae), an observation central to the hypothesis that ovuliferous complexes in modern conifers are homologous and evolved through modification of an axillary shoot and its subtending bract. However, it remains unclear what these bundles correspond to structurally and their evolutionary significance, and thus further study of the development and variation of the dual bundle system is essential for understanding the homology and evolution of conifer seed cones. Here we describe the anatomy and vascular architecture of ovuliferous complexes in Wollemia nobilis, for which these traits have never been formally documented. Individual ovuliferous complexes were fixed, embedded in paraffin, serially sectioned, and stained using a modified triple-stain protocol derived from Sam (1983, Ann. Bot. vol. 51). Ovuliferous complexes are broad and parenchymatous basally, becoming narrow and more sclerotic distally. In the specimen studied, they are vascularized by a single bundle, which branches continuously to form a row of ~9-10 bundles distally. The seed is vascularized by 4 inverted bundles that are adaxial to the main bundle system. Two of these bundles branch from lateral bundles near the base of the ovuliferous complex and the other two diverge from medial bundles. The inverted bundles initially diverge laterally but subsequently rotate to produce the inverted orientation, resulting in phloem that points towards the adaxial side of the ovuliferous complex. The vasculature entering the seed appears to contain only phloem. Vascular anatomy of Wollemia ovuliferous complexes is similar to that
of Agathis and Araucaria and falls within the range of variation documented for these genera. The inverted bundle system is more complex than that of Agathis australis and is more similar to A. macrophylla and some species of Araucaria. Unlike most Araucaria, the upper bundle system does not persist beyond the seed. Study of additional specimens will be necessary to understand intraspecific variation of these traits in Wollemia nobilis, but the pattern is nevertheless consistent with the presence of an ovuliferous scale that is reduced, fully fused to the bract, and does not extend beyond the seed. This study fills a conspicuous gap in our knowledge of the anatomy of Araucariaceae, providing data necessary for understanding the evolution, homology, and fossil record of conifer seed cones.

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Topic: Contributed Papers Paleobotany

Title: New floral diversity of Lauraceae in the Late Cretaceous

Author: ***Keana Tang @ University of Kansas***

Keywords: flowers,fossil,phylogenetics,Cinnamomeae,permineralized

Abstract:

Lauraceae comprises up to 3,500 species within about 50 genera and has an exceptional fossil record extending into the Albian of the Early Cretaceous (113-100 Ma). Numerous fossil flowers have been assigned to Lauraceae but their phylogenetic relationships among extant species are poorly understood. Thus, our understanding of the early evolutionary history of this diverse family is limited. Previously, we analyzed phylogenetic relationships of lauraceous fossil flowers using a preliminary genus-level morphological dataset of floral characters, which we revised and used to infer relationships of a new fossil flower. The new fossil is permineralized in a calcium carbonate concretion from Coniacian (89.8-86.3 Ma) deposits of the Eden Main locality in British Columbia, Canada. The specimen was serial sectioned using the cellulose acetate peel technique. The serial sections were studied with light microscopy, imaged, and used to render a 3D reconstruction in Avizo. We analyzed the phylogenetic relationships of the Eden Main flower using a Bayesian total-evidence approach. This dataset was further evaluated by conducting phylogenetic pseudofossilization analyses of living species, which test whether a morphological dataset can accurately recover the positions of living taxa. The new fossil flower is trimerous with two whorls of tepals, two outer whorls of tepaloid stamens, one whorl of fertile stamens, an inner whorl of staminodes, and a superior ovary. The tepal whorls are unequal in size with the outer tepal whorl significantly smaller than the inner whorl. The two outer whorls of the androecium consist of tepaloid stamens with two latrorse anther locules. The third androecial whorl comprises three extrorse bisporangiate stamens with broad filaments that are flanked by paired, peltate staminal appendages. The third whorl alternates with an innermost whorl of sagittate staminodes. The gynoecium consists of a unilocular ovary. Trichomes are present throughout the androecium and inside the hypanthium. These characters indicate the Eden Main flower belongs to Lauraceae and is a new genus based on the combination of unequal tepal whorl sizes, tepaloid stamens, bisporangiate anthers, and peltate staminal appendages. Pseudofossilization analyses recover most extant taxa in their respective tribes with the exception of several taxa that were incorrectly recovered in the morphologically diverse and species-rich tribe Cinnamomeae. This indicates that the current dataset is able to identify crown-group members of Lauraceae and many of its tribes, but that any recovered relationships with tribe Cinnamomeae must be treated cautiously. The Bayesian phylogenetic analysis recovered the Eden Main flower within crown group Lauraceae, but relationships with extant tribes remain uncertain, consistent with the distribution of key traits of the fossil within Lauraceae. While precise systematic relationships of the Eden Main fossil within crown group Lauraceae are yet to be determined, this fossil provides further evidence of the diversification of the family in the Cretaceous.

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Topic: Contributed Papers

Title: The CuticleTrace workflow: An ImageJ toolset for capturing cell outlines of leaf cuticle — implications for paleoecology and paleoclimatology

Author: ***Ben Lloyd @ University of Washington***

Keywords: Cuticle morphology,paleobotany,Paleoclimate,Paleoecology,Leaf cuticle,imageJ,LAI

Abstract:

Fossilized leaf cuticle - the waxy surface of leaves common to geologic sediments from the last 400 million years - remains an underutilized data source for reconstructing paleoclimate and paleovegetation assemblages. The morphology of a leaf's upper epidermal pavement cells reflects the environmental conditions of its growth. Traditionally, cell morphology was determined by hand-tracing cell walls using digital tools. This is a slow and tedious process, with cell-outline quality highly dependent upon both the tracing setup used and the experience level and attention to detail of the tracer. To avoid the issues associated with hand-tracing cell outlines, we developed the CuticleTrace workflow: a user-friendly automated image analysis workflow using the freeware programs 'ImageJ' and 'R'. Our easily tunable code allows for the generation of large cell-shape datasets from images of leaf epidermis, with options for different measurement parameters and levels of automation. Use of this method results in a higher degree of cell-tracing consistency, while allowing for increased sample sizes by drastically decreasing the time required to generate these data.

We applied this method to an image set of 130 vouchered herbarium specimens extracted from The Cuticle Database (cuticledb.eesi.psu.edu), representing 127 species in 87 genera from 36 families. Images were chosen to maximize taxonomic breadth and span the range of cell shapes and sizes, utilizing the specimens with the highest quality image of the upper cuticle. For each image, our workflow produced a set of vectorized cell outlines, with associated shape parameters. 50 of these images were additionally traced by an expert in the field and by undergraduate researchers. Across this subset, CuticleTrace measurements are statistically similar to expert measurements >85% of the time (average p-value of 0.63), while student measurements are only statistically similar to expert measurements ~66% of the time (average p-value of 0.43).This workflow can now be used to reconstruct parameters such as Leaf Area Index, and thus the canopy structure of forests in deep time, more effectively utilizing the vast repository of leaf cuticle in the fossil record.

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Paleobotany

Topic: Contributed Papers Paleobotany

Title: An anatomically preserved monocot from the Eocene Appian Way locality of Vancouver Island, British Columbia, Canada

Author: ***Gar Rothwell @ Ohio University; Oregon State University***

Keywords: Anatomy,Eocene,Appian Way,monocot stem

Abstract:

The biota of Appian Way on the east coast of Vancouver Island contains permineralized fossil plants, gastropods, echinoderms, decapods, bivalves and shark teeth in calcareous concretions that are embedded in a silty mudstone matrix representing a shallow marine environment. The fossil beds unconformably overlie the Late Cretaceous Nanaimo Group strata and are most probably Eocene (ca. 50 Ma) in age. Among the flowering plant remains yet to be described from the locality is a distinctive branching monocot axis with clearly defined tissue zones, leaf bases, and attached roots. The preserved stem segment is at least 5 cm long and ca. 1.5 cm in diameter, with a pith and cortex composed primarily of compact parenchyma and scattered sclereid nests. Lateral branches and adventitious roots diverge from the stem at a wide angle. The pith is surrounded by a vascular cylinder of numerous scattered vascular bundles. Stelar bundles are collateral near the stem center, circular to ovoid, and surrounded by a distinct bundle sheath of smaller cells. Clasping leaf bases in the outer cortex encircle the stem and show several vascular bundles of two distinct sizes. Conducting elements of the xylem, probably narrow diameter vessels, have multiseriate circular bordered pitting and horizontal end walls. Branches have vascular bundles and a pith that are similar to those of the main stem. Roots are vascularized by bundles that extend around the periphery of the vascular cylinder before entering the diverging root. Each root has a polyarch stele that consists of radiating rays of xylem and phloem that surround a parenchymatous pith. Differentiation of an endodermis and an outer rhizodermis are not evident, but roots do have a well-defined zone of sclerotic cortex that shows no evidence of aerenchyma. Intact anatomically preserved monocot stems, like the Appian Way specimen, are rarely encountered as fossils. The most well-known of these are from the Middle Eocene Princeton Chert of British Columbia including, Soleredera rhizomorpha, Ethela sargantiana, and a coryphoid palm, Uhlia allenbyensis all of which are clearly distinct from the Appian Way monocot. Spadices of an aroid, Appaniospadix bogneri, recently described from Appian Way, show sclereid clusters similar to those seen in the new stem. However, the inflorescence axis lacks the scattered bundles seen in the new stem, and we cannot link this reproductive structure to the stem at this time with our current level of knowledge of the anatomy.

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Paleobotany

Topic: Contributed Papers

Title: A new species of Acmopyle (Podocarpaceae) with preserved accessory transfusion tissue from the early Eocene of Argentinean Patagonia

Author: ***Ana Andruchow-Colombo @ University of Kansas***

Keywords: Acmopyle,Early Eocene climatic optimum,Podocarpaceae,Accessory transfusion tissue,Reproductive bud

Abstract:

Acmopyle is one of the 18–20 genera with extant representatives of the conifer family Podocarpaceae. The genus comprises two extant species with restricted rainforest ranges, A. pancheri (New Caledonia, Near Threatened) and A. sahniana (Fiji, Critically Endangered), along with a rich fossil record in Australia since the Paleocene and a few prior reports from Antarctica and South America. Here, we report a new Acmopyle fossil species from the early Eocene (52.2 Ma) Laguna del Hunco locality, Chubut, Argentina, based on 42 compression specimens of leafy shoots (expanded photosynthetic units). As the extant species of the genus, the new fossil taxon is heterophyllous, being characterized by three distinct leaf types: (1) scale-like leaves that are mostly bifacially flattened; (2) transitional leaves that are tetragonal in cross-section to bilaterally flattened; and (3) mature, highly coriaceous, robust and expanded leaves that are bilaterally flattened and show a two-ranked secondary arrangement over their branches. The new species uniquely preserves coalified but distinctive remains of accessory transfusion tissue (ATT, an extra-venous water conducting tissue), an important physiological adaptation of extant Acmopyle. Some fossil specimens also have possible reproductive buds. To test the placement of the new Patagonian Acmopyle, we included it in a total evidence phylogenetic analysis, together with extant and extinct members of the Podocarpaceae and Araucariaceae families and recovered it in a polytomy with the two extant Acmopyle species. Additionally, we report herbivory damage, including margin feeding (DT12), apex feeding (DT13), hole feeding (DT01), and circular punctures (DT47). The presence of Acmopyle in the early Eocene of Argentina is significant because of the previously demonstrated drought intolerance of the genus, which stems from the high collapse risk of the ATT. Thus, the new fossils provide direct physiological evidence of ever-wet rainforest environments in Patagonia during the early Eocene Climatic Optimum and the final stages of Gondwana.

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Phylogenomics

Topic: Contributed Papers Phylogenomics

Title: Phylogenetics and species delimitation of the Pinus Oocarpae clade using low copy nuclear genes

Author: ***David Gernandt @ Universidad Nacional Autonoma de Mexico***

Keywords: Incomplete Lineage Sorting,Multispecies coalescent,nuclear DNA,Reticulation,pine

Abstract:

Pinus is a wind-pollinated, long-lived genus that includes many species long generation times, weak reproductive barriers, and large population sizes. Several North American pine clades have evolved since the Oligocene or Miocene. Consequently, slow coalescence and high interspecific gene flow have been important in shaping their genomes. The Oocarpae clade (Pinus subgenus Pinus, section Trifoliae) comprises 18 taxa classified in 16 species distributed from the southwestern United States to Central America, with its main diversity in Mexico. We inferred phylogenetic relationships for multiple individuals per taxon of the Oocarpae based on >500 low copy nuclear loci recovered using target enrichment. Maximum likelihood and the coalescent method ASTRAL gave results that were largely congruent, although there were important points of discordance with plastid-based trees and a phylogenetic study of Pinus based on transcriptome sequences. We explored the levels of nuclear discordance, evidence for reticulation, and the use of the multispecies coalescent to delimit species.

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Phylogenomics

Topic: Contributed Papers Phylogenomics

Title: Bringing light into the darkness – resolving the complex evolutionary history of North American shrub willows (Salix L.)

Author: ***Natascha Wagner @ University of Goettingen***

Keywords: Salix L.,biogeography,hybridization,molecular phylogenetics,RADseq

Abstract:

Willows are distributed in the Northern Hemisphere and comprise about 450 species. In North America about 140 Salix species occur, more than 100 belong to the so-called “shrub willows” (Chamaetia/Vetrix clade). The huge diversity of Salix subgenus Vetrix in North America and the lack of phylogenetic resolution within this clade was a challenging, however fascinating mystery for decades. The taxonomy is still under debate and complicated by measures of ancient and recent hybridization as well as polyploidization. In this study, about 50 species representing 19 described sections (sensu Argus 1999) from the USA and Canada were included and combined with about 100 species from Europe and Asia. With a RAD sequencing approach it was possible to produce a well-resolved phylogeny of 145 shrub willow species (235 accessions) based on ten thousands of RAD loci. The resulting tree showed an exclusively “North American clade” containing the majority of included species from this region in sister position to a “Eurasian clade”. The latter included samples of worldwide distributed species as well as some North American endemics. Most species were monophyletic, however, several North American species were polyphyletic. The results revealed that the diversity of subgenus Vetrix in North America was shaped by a radiation as well as several migration and long distance dispersal events.

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Phylogenomics

Topic: Contributed Papers

Title: Resolving taxonomic uncertainty and clarifying species boundaries in the Cymopterus terebinthinus species complex.

Author: ***Annie Taylor @ Boise State University***

Keywords: Angiosperms353 Hyb-Seq,Apiaceae,species complex,species delimitation

Abstract:

Speciation processes in vascular plants are frequently not well resolved or agreed upon. They are however essential to our general understanding of the evolutionary processes that lead to diversification. Determining the juncture at which a genetically and/or morphologically divergent population becomes a unique species can be challenging, especially with respect to recent divergences and closely related taxa where issues such as incomplete lineage sorting may bring about confounding results. To complicate our theoretical disagreements on species definitions, different models inferring species boundaries may accordingly lump or split species. Using multiple lines of evidence to define species boundaries can greatly improve species inference and preclude erroneous taxonomic groupings. Taxa in the Cymopterus terebinthinus (Apiaceae) species complex have long puzzled botanists owing to their similar yet diverse, consistently recognizable morphotypes. These morphotypes are often found in generally well-defined geographical subregions of varying habitat types. To further complicate taxonomic groupings in this species complex, previous phylogenetic studies are interpreted to show that varieties in Cymopterus terebinthinus are not monophyletic. We aim to clarify species boundaries and infer evolutionary relationships in the Cymopterus terebinthinus species complex using phylogenetic inference paired with ecological parameters, morphology, and biogeography. We apply the genealogical species concept to guide our interpretations of species boundaries in this group. To test this, we used target capture with the angiosperms353 bait kit and next generation sequencing. We performed phylogenetic analysis with maximum likelihood and coalescent based species delimitation models. We also used corroborating evidence based on analysis of ecological variables to better understand factors related to phylogenetic groupings. We find that Cymopterus terebinthinus and its varietal infrataxa comprise a monophyletic clade that includes Cymopterus petraeus. We also find that geographical location is typically the best predictor of phylogenetic placement, meaning that in the large majority of samples analyzed, defined clades largely correspond to previous varietal assignments. Our findings argue that gene flow is likely actively occurring amongst populations in peripatric and sympatric proximity. Additionally, species differentiation processes are likely actively producing divergence within biogeographical regions.

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Phylogenomics

Topic: Contributed Papers

Title: Phylogenetic and biogeographic patterns in sequencing deficiency across vascular plants

Author: ***Daniel Spalink @ Texas A&M University***

Keywords: biogeography,DNA Sequencing,rare species,prioritization

Abstract:

Producing a useful tree of life is a data-intensive process that relies heavily on the DNA sequences assembled over the past few decades. Critical gaps in taxonomic sampling of sequence data remain despite ongoing efforts, both in terms of the per taxon quantity (i.e., number of individuals, number of genes) and quality (i.e., barcode markers, transcriptomes, genomes). Arguably, not all newly generated sequence data are of equal value in terms of information gained with respect to the identification of new genes, alleles, lineages, or relationships. Establishing priorities to fill data gaps more efficiently may therefore be fruitful. Here we present a new statistic, SeqDef (Sequencing Deficiency), which incorporates cophenetic distances in calculating the data deficiency and thus the priority for additional sequencing efforts in each tip of a phylogeny. SeqDef can be tailored to the needs or priorities of each user. To demonstrate this flexibility, we used SeqDef to answer three questions. 1) How is data deficiency distributed across the vascular plant tree of life? 2) How is data deficiency distributed across the globe? 3) Which rare species should be priorities for additional sequencing before they go extinct?

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Phylogenomics

Topic: Contributed Papers

Title: Rampant chloroplast capture in Sarracenia revealed by plastome phylogeny

Author: ***Ethan Baldwin @ University of Georgia***

Keywords: carnivory,chloroplast capture,Chloroplast genome,hybridization,introgression,phylogenomics

Abstract:

Sarracenia is a genus of carnivorous plants endemic to North America. The ~10 species in the genus hybridize with one another readily in sympatric populations, and all hybrids are fertile with no obvious intrinsic fitness loss. With frequently observed fertile hybrids in natural populations, the opportunity for interspecific gene flow is high. Phylogenetic analysis of 199 nuclear genes resolved most species relationships within the genus, but a whole chloroplast genome (plastome) phylogeny is strongly discordant with the nuclear species tree. This discordance between the plastome tree and the species tree could be due to introgression of the chloroplast due to frequent hybridization and backcrossing, or it could be due to incomplete lineage sorting. To determine whether the level of discordance between the two trees could be caused by incomplete lineage sorting, 1000 gene trees are simulated under the multispecies coalescent assuming no hybridization. The simulated gene trees are compared to the species tree and plastome tree using an information theoretic generalized tree distance metric. The tree distances between the species tree and the simulated gene trees are consistently significantly lower than the distances between the plastome tree and the simulated trees. Similarly, the distance between the plastome tree and the species tree is significantly greater than the distance between the simulated gene tree set and the species tree. These results indicate that the plastome tree is more discordant with the species tree than would be expected under incomplete lineage sorting alone, implying that introgressive hybridization has happened within the genus multiple times.

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Topic: Contributed Papers Phylogenomics

Title: Phylogenomic insights into the evolution, biogeography, and taxonomy of Andean Weinmannia (Cunoniaceae)

Author: ***Eduardo Aguirre-Mazzi @ Missouri Botanical Garden***

Keywords: Diversification,molecular phylogenetics,phylogenomics,Plant Biogeography,Taxonomy ,systematics,Weinmannia

Abstract:

The Andes Mountains of South America are one of the most biodiverse regions on the planet and are home to many large plant radiations. One example of an important Andean plant radiation is Weinmannia section Weinmannia (Cunoniaceae), a clade of evergreen trees and shrubs that are prominent members of Andean forests. Most of the diversity in the group (> 90 Species) is distributed mainly in the Andean region, but some species are found in Atlantic forests, the Tepuis formations of the Guyana shield, the mountains of Central America and the Caribbean islands, and in temperate forests from Southern South America. Despite high levels of diversity found in Andean forests, the evolution of this group is poorly understood, and many species limits are unclear. The aim of this study was to elucidate the phylogenetic relationships among Andean Weinmannia species and to test the monophyly of morphologically described species. We estimated a maximum likelihood phylogeny of the genus based on 2b-RAD sequence data of Weinmannia species distributed across the Andes spanning Chile, Bolivia, Peru, Ecuador, and Colombia. Whenever it was possible, we included at least three individuals of each species and location, and we excluded all putative hybrids identified morphologically or through preliminary molecular data analysis (i.e., STRUCTURE). The results of the study showed that phylogenetic relationships exhibited a strong geographic structure, with species from Ecuador and Colombia forming distinct clades nested within a larger clade consisting of species from the southern Andes and Bolivia. Additionally, there was a clear pattern in which specimens collected from southern latitudes (Chile) grouped closer to the root of the phylogeny, whereas those from northern latitudes (Colombia and Ecuador) were placed closer to the crown of the tree. This phylogenetic pattern suggests that the lineage diversified as it dispersed from south to north, tracking cool environments that originated with the Andean uplift. In addition, we did not find all morphologically described species to be monophyletic; for example, specimens identified as W. pinnata and W. balbisiana were assigned to different clades along with several different species. In addition, clades often contained species with disparate morphologies, ranging from pinnate leaves to simple leaves. Altogether, these findings suggest either that these species may have experienced hybridization and introgression with relatives or that the genus has repeatedly evolved similar morphologies in different locations. Weinmannia promises to be an important model for understanding the ecology and evolution of plants that occupy a broad range of elevations in the Andes, and further research will continue to explore the main processes driving the diversification of the genus in the Andes from an integrative taxonomy perspective.

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Topic: Contributed Papers

Title: Caught in the Act: Incipient Speciation at the Southern limit of Viburnum in the Central Andes

Author: ***Carlos Maya-Lastra @ Yale University***

Keywords: RADseq,speciation,Andes,Tucuman-Bolivian Forest,leaf ecomorphs,neotropical cloud forest,Yungas ecoregion,Oreinotinus

Abstract:

Several species and infraspecific taxa of Viburnum have been recognized at the southern edge of its geographic range in the neotropics, from central Peru through Bolivia to northern Argentina. Using multiple lines of evidence and analytical approaches, we support the recognition of just a single species, V. seemenii, which we infer to have recently moved southward through the central Andes. We highlight the ongoing evolution of leaf ecomorphs in the region and a case of incipient speciation. We show that what has previously been recognized as V. seemenii f. minor has recently occupied the drier Tucuman-Bolivian forest region from Samaipata in Bolivia to Salta in northern Argentina. Plants in these populations form a well supported clade with a distinctive genetic signature and they have evolved smaller, narrower leaves. We interpret this as the start of a within-species divergence process that has given rise to the different leaf ecomorphs described by Donoghue et al. (2022) for the entire neotropical Oreinotinus clade. Specifically, the southern populations are in the process of evolving the small, glabrous, and entire leaf ecomorph that has evolved in four other montane areas of endemism. As expected based on our studies of leaf ecomorphs in Chiapas, Mexico, these southern populations experience generally drier conditions, with large diurnal temperature fluctuations. A population in Central Peru is noteworthy in also showing a tendency towards smaller leaves. In a central portion of the range of V. seemenii, characterized by wetter climatic conditions, we may also be seeing the beginnings of the differentiation of the leaf ecomorph with larger, pubescent, and toothy leaves. Within this region, the initial stages of the evolution of the leaf forms appear to be associated with geographic separation, whereas in other regions, it may initially have been driven by differentiation along elevational gradients, with corresponding differences in flowering times.

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Topic: Contributed Papers Phylogenomics

Title: Evolution, Diversification, and Conservation Implications in the Pantropical Clade Barlerieae (Acanthaceae)

Author: ***Robert Comito @ California Botanic Garden***

Keywords: Acanthaceae,conservation,phylogenomics,Phylogeography

Abstract:

Among Acanthaceae (ca. 4,000 spp.), Barlerieae (ca. 440 spp.) is a tribe that needs considerable further study. Barlerieae contain 13 genera, the two largest and most widespread of which are Barleria (ca. 300 spp., primarily paleotropical), and the pantropical Lepidagathis (ca. 100 spp.). Sub-Saharan Crabbea includes 14 species. The remaining ten genera, with ~25 species in all, are distributed across Latin America, South Asia, Africa, and Madagascar. Barlerieae present several taxonomic problems, and some species have intriguing biogeographic patterns (e.g., a few species, such as Lepidagathis alopecuroides, have amphi-Atlantic distributions). Many species in this group are important to tropical ecosystems and support a wide range of pollinators. In a recent reclassification of Acanthaceae, three subtribes have been proposed based on corolla and calyx characters: (1) Barleria, (2) Crabbea and allies, and (3) Lepidagathis and allies. Using a next-generation sequencing (NGS) approach (ddRADseq), I will: (1) estimate a well-sampled phylogeny of the tribe to test current taxonomy as well as proposed classifications, (2) test genera and sub-generic groups for monophyly, (3) identify morphological characters that support monophyletic groups, (4) examine patterns of biogeography and diversification, and (5) address conservation concerns and prospects in a phylogenetic context. A Maximum Likelihood phylogeny of 153 taxa was estimated in IQ-TREE with 1000 Ultrafast Bootstraps, using GTR+F+I+G4 model, based on an alignment of ddRAD 59,304 loci, resolving relationship among all thirteen currently recognized genera in Barlerieae This group, which can be recognized by the developmental character quincuncial corolla aestivation, is monophyletic with our sampling. In addition, data suggest a major taxonomic revision of Lepidagathis is necessary. Species of Lepidagathis are found in three clades: Lepidagathis s.s., including species with bithecous posticous anthers, species formerly recognized as Lophostachys + Lepidagathis with monothecous posticous anthers; and the widespread species Lepidagathis aloepecuroides. The phylogenetic relationships recovered here suggest each of the three clades may merit recognition at the generic level. In addition, L. aloepecuroides is found to be monophyletic with sampling across its range in Africa and South America. Multiple transcontinental disjunctions across the tribe have also been illuminated. This research will contribute to taxonomic revisions and updated keys that will aid in conservation efforts and provide insight into the evolutionary processes that shape biodiversity in this remarkable lineage.

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Topic: Contributed Papers

Title: Preliminary phylogenomic and morphometric analyses fail to find support for the taxonomic circumscription of the Endangered Kern mallow

Author: ***C. Matt Guilliams @ Santa Barbara Botanic Garden***

Keywords: morphology,breeding system,ddradseq,endangered species,Gynodioecy,Malvaceae,conservation,Eremalche

Abstract:

Eremalche parryi (Greene) Greene is an annual herb endemic to Central California, USA. It has two subspecies – parryi and kernensis – which are reported to differ in breeding system and morphology. The circumscriptions of the E. parryi subspecies have never been quantified and tested, which is of critical concern as subsp. kernensis is listed as Endangered under the Federal Endangered Species Act. Here, we present the preliminary results of a study aimed at examining the circumscriptions of the subspecies using phylogenomics and morphology. For the phylogenomic analyses, we developed and analyzed a SNP dataset for Eremalche taxa and close relatives in the Malvaceae using the reduced representation ddRADseq approach. To examine the circumscription of the subspecies using morphology, we gathered morphometric and color data from ca. 200 field-collected samples of E. parryi, focusing on taxonomically important flower features. Preliminary maximum likelihood phylogenetic analyses recover a well-supported tree. Eremalche is monophyletic with strong support. Samples of E. rotundifolia form a clade with strong support sister to all other samples of Eremalche. Samples of E. exilis and E. parryi are reciprocally monophyletic, each clade with maximum statistical support. Samples of the E. parryi subspecies are interdigitated, with support values low to moderate throughout the E. parryi clade. Morphometric analyses suggest that plants assigned to the two E. parryi subspecies are not statistically different from one another. However, it does seem clear that the pistillate flowers produced by some E. parryi plants are distinctive, with perianths smaller in all measured dimensions. Furthermore, plants of E. parryi subsp. kernensis with bisexual flowers are statistically different from subsp. parryi and pistillate-flowered subsp. kernensis in having fewer carpels. A similar pattern was reported by Bates, who suggested that plants of subsp. kernensis with bisexual flowers may have undergone a reduction in carpel number to allocate greater resources to anther/pollen production. This hypothesis – then limited to subsp. kernensis – may work equally well at the species rank in explaining the evolution of gynodioecy in E. parryi. Should our preliminary findings continue to hold in further analyses using expanded datasets, abandoning the E. parryi subspecies may be warranted.

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Phylogenomics

Topic: Contributed Papers Phylogenomics

Title: Disentangling the Relationships between Paleopolyploidy Events and Arctic-Alpine Adaptations in the Caryophyllaceae

Author: ***Keyi Feng @ University of Michigan***

Keywords: alpine,arctic,Caryophyllaceae,Gene duplication,phylotranscriptomics,Paleopolyploidy

Abstract:

The Caryophyllaceae (the carnation family) is one of two flowering plant families with a cosmopolitan distribution spanning all seven continents. Previous systematic work on the Caryophyllaceae demonstrated multiple transitions into arctic-alpine climates, indicating that they may provide a natural model for understanding how plants adapt to changing climates. Arctic-alpine is a stressful environment and outside of the optimum temperature range for most angiosperms. Surviving these stressful conditions requires several adaptive changes. Several species within the Caryophyllaceae have converged on the cushion plant adaptation, which is often associated with plants surviving in cold temperatures. Previous research has shown that paleopolyploidy events are correlated with climatic shifts in Caryophyllales. In this study, we investigate whether paleopolyploidy events and gene duplications are associated with arctic-alpine adaptations in the Caryophyllaceae, specifically identifying genes that may have contributed to these processes. Utilizing 26 newly collected transcriptomic data with increased cushion plant sampling, along with 45 previously published transcriptomes, we inferred a species tree for the Caryophyllaceae. The species tree was mostly congruent with the current consensus within the family with the exception of the genus Dianthus (carnations) that had a high level of dominant alternative gene tree conflicts. Additionally, we inferred five new paleopolyploidy events that have not been previously published. Paleopolyploidy events mostly do not directly correspond to a shift to an arctic-alpine climate at the same or adjacent nodes though they are a major source of gene duplications. We identified overlapping gene duplications for arctic-alpine clades, in which some are involved in stress tolerance based upon the GO annotations indicating the potential for convergent evolution in cold-tolerant Caryophyllaceae species. We further explore the correlation between climatic niche shifts and gene duplications in this family and conduct positive selection tests on genes potentially involved in cold adaptation.

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Phylogenomics

Topic: Contributed Papers

Title: Eukaryotic metagenomic identification: "off label" bioinformatics for mixed botanical samples

Author: ***Liz Hunter @ US Food and Drug Administration***

Keywords: bioinformatics,genomics,Metagenomics,Food safety

Abstract:

Even as the cost of genomic sequencing decreases dramatically, and the technology for longer and more accurate data improves, reliable metagenomic identification of unknown plants remains challenging. Identification of mixed samples is highly relevant for food safety questions that arise at the U.S. Food and Drug Administration for a variety of consumer products, including botanical dietary supplements. These products continue to rise in popularity, with more and more Americans purchasing and consuming them each year. They are typically ground, processed, or otherwise devoid of morphological characters, making visual methods of identification difficult. Historically, both the methods and the analysis pipelines have focused on barcodes, organellar genomes, or targeted assays for specific groups, all of which pose their own limitations. Here, we attempt to optimize and adapt some o the numerous popular workflows available for prokaryotic metagenomics to mixed botanical samples. Some of these modifications include expanded database representation for Viridiplantae using NCBI WGS, tiered identification, and enhanced filtering metrics to reduce background noise. We are also incorporating recent innovations in the field of metagenomics such as DNA sketching algorithms for taxonomic classification. Additionally, we are exploring the application of long read data to improve both the reference databases available, and the methodology used to make identifications. We hope this research will inform future studies on the best ways to leverage existing tools for prokaryotic metagenomics "off label" for mixed botanical samples.

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Phylogenomics

Topic: Contributed Papers

Title: The next phase of Angiosperms353: improved targets, mixed DNA, and bioinformatics resources

Author: ***Matt Johnson @ Texas Tech University***

Keywords: Angiosperms353,bioinformatics,Target Enrichment,DNA Metabarcoding

Abstract:

Angiosperms353 has gained popularity both as informative single copy genes and universal probes for cost-effective target capture in high-throughput sequencing. Wide adoption of the loci by the phylogenetics systematics community provides an opportunity to revisit applications of DNA sequence data for the identification of plant tissues in mixed DNA samples. We describe ongoing efforts to improve Angiosperms353 as a resource for DNA sequencing in flowering plants by 1) using expanded genomic resources to refine the representative sequences for Angiosperms353 target capture, 2) developing new computational resources to support the assembly of Angiosperms353 sequences from mixed DNA sources, and 3) leveraging a large growing reference database of Angiosperms353 sequences from over 10,000 species (maintained by RBG-Kew, treeoflife.kew.org) to identify unknown plant samples. We provide proof of concept of our work flow using targeted sequence from adulterated plant tissue and from soil seed banks.

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Phylogenomics

Topic: Contributed Papers

Title: The correlation of mating system and polyploidy on discordance and reticulation in Droseraceae

Author: ***Rebekah Mohn @ University of Minnesota - Twin Cities***

Keywords:

Abstract:

Using transcriptomic data, we explored six chromosome number duplications inferred in Drosera. We found evidence for four of the six and found evidence for two additional polyploid events. This uneven distribution of discordance and reticulation provides an interesting comparison to mating system which we will discuss further.

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Phylogenomics

Topic: Contributed Papers Phylogenomics

Title: The evolution of petaloidy in Caryophyllaceae

Author: ***Riley Rees @ Ohio University***

Keywords: morphology,Caryophyllaceae,Caryophyllales,floral evolution,flower,Phylogenetic comparative methods,phylogenetics,staminode

Abstract:

Floral evolution across angiosperms has been quite dynamic, where even structures like petals have evolved and been lost multiple times. Contradictory studies have suggested that, in Caryophyllaceae, flowers were either ancestrally apetalous but regained petals later in the phylogeny, or petals were ancestrally present and lost in some early clades. Further convoluting our understanding of the evolution of petals in the family are staminodes, which are present in many of the early apetalous lineages, but we currently do not understand the relationships of staminodes to that of petals. To date, no study has combined dense sampling of taxa with robust phylogenetic comparative methods of well characterized structures based on homology that includes petaloids, staminodes, and differences in their development and positions. Caryophyllaceae, therefore, is an ideal system to study how attractive structures evolve and could provide insights across angiosperms. To provide an evolutionary framework, we reconstructed a phylogeny from two chloroplast regions (maturase-K and the trnL–F intergenic regions) and a nuclear ribosomal marker (intergenic spacer regions 1 and 2). Samples were acquired either from GenBank or from herbarium tissues that were Sanger sequenced, to sample nearly all genera while sampling proportionally at the species level. Phylogenies were reconstructed with maximum likelihood analyses. Flowers were characterized by measuring herbarium specimens of mature flowers and comparing them to scanning electron microscope images of developing flowers to assess structural and developmental homology. We discuss patterns of floral evolution across the family to determine the origin of petals and how they relate to staminodes.

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Phylogenomics

Topic: Contributed Papers

Title: Examining points of phylogenetic conflict between organelles across the plant tree of life

Author: ***Karolis Ramanauskas @ University of Illinois, Chicago***

Keywords: mitogenome,molecular phylogenetics,plastome,phylogenetic conflict

Abstract:

The chloroplast and mitochondrion are often uniparentally inherited, so the inferred relationships between the organelles should be concordant. However, several recent studies have found that some plant clades exhibit biparental inheritance of the organelles. Therefore, the two organelles have the potential to exhibit conflicting topologies. This study examines four cases where phylogenetic conflict between organelles has been reported. Using a series of phylogenetic tests, we investigate whether this conflict reflects evolutionary history or results from limitations in phylogenetic methods.

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Phylogenomics

Topic: Contributed Papers

Title: Phylogenomic and species delimitation of a Polygonatum odoratum complex

Author: ***Tae-Young Choi @ Chosun University***

Keywords: Angiosperms-353,phylogenomics,East Asia,Polygonatum

Abstract:

Genus Polygonatum Mill. (Asparagaceae) comprises 70 taxa and most are particularly well appreciated in East Asia for the various commercial uses. Despite the increased recognition for its commercial value, the taxonomy and phylogenetic relationships among congeners remain elusive. Polygonatum odoratum complex is a great example of the taxonomic conflicts in the genus. The complex consists of 7 taxa with high morphological diversity (P. odoratum var. odoratum, P. odoratum var. pluriflorum, P. thunbergii, P. robustum, P.grandicaule, P. lasianthum, P. infundiflorum), however species boundaries and the taxonomic identities of the taxa are ambiguous. In the present study, we aim to delimit species boundaries and understand the phylogenetic relationships among P. odoratum complex. First, we carefully examined the key morphological characters of P. odoratum complex from ~2,000 herbarium specimens. Genome-scale phylogeny of P. odoratum complex taxa was inferred by targeted gene capture with publicly available 353-angiosperm single copy gene probe sets. We also reconstruct chloroplast phylogeny using off-target sequences obtained from target capture sequencing. Maximum likelihood algorithm with 1000 bootstrap replicates and multi-species coalescent model were used for tree building and node support evaluation respectively in RAxML v8.2.12 and Astral v5.7.1. To investigate admixture proportion among the taxa, we performed ADMIXTURE analysis with 813 SNPs identified from the target capture data. 32 morphological characters measured failed to discriminate most taxa in the complex except for Polygonatum lasianthum from the rest. Overall, phylogenies of nuclear and chloroplast genes showed discrepancy on several clades. In the nuclear gene tree, we found three major clades representing three species previously recognized as Polygonatum odoratum, Polygonatum lasianthum and P. infundiflorum. Our result suggests that 7 taxa in the P. odoratum complex should be re-arranged to three species P. odoratum, P. infundiflorum, and P. lasianthum although additional samples collected outside of East Asia may improve the results.

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Phylogenomics

Topic: Contributed Papers

Title: New Compositae specific probe set tackles paralog issues in the complex genus Packera (Senecioneae; Asteraceae)

Author: ***Erika Moore-Pollard @ University of Memphis***

Keywords: phylogenomics,polyploidy,MarkerMiner,discordance

Abstract:

Probe sets have been designed to broadly target gymnosperms, angiosperms, or specific plan families (i.e., Asteraceae, Fabaceae, Ochnaceae, etc.), enabling great advances in our understanding of evolutionary relationships in large plant groups. The Asteraceae specific probe set, Compositae-1061, has become popular among researchers studying members of Asteraceae, and has helped pave the way for investigations at lower taxonomic levels and non model organisms. Though Compositae-1061 has shown to be highly efficient at higher- and some lower-taxonomic levels within the family, it generally lacks resolution at the genus to species level. In this study, we collected 48 transcriptomes spanning Asterales to generate an improved probe set designed specifically for Asteraceae using the software MarkerMiner. Using this new probe set, we sequenced 17 Packera Á. Löve & D. Löve and two outgroup Senecioneae taxa that have previously been sequenced using the Compositae-1061 probe set. Sequences from both probe sets were then used to generate phylogenetic trees, compare their topologies, and assess node support to determine whether this new probe set provided greater resolution at the genus/species level compared to Compositae-1061. We found that the newer probe set recovered drastically less paralogous sequences than Compositae-1061, with only about 5% of the recovered loci reporting as paralogous with the new probe set, and 59% with the 1061 probe set. Additionally, we found that discordance was lower and species relationships more closely followed previous studies when utilizing the new probe set. Alternatively, we found that Compositae-1061 produced less missing data and was more parsimony informative than the newly designed probe set. We anticipate that further testing wil provide additional support for the utility of this probe set in complex groups in the sunflower family.

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Phylogenomics

Topic: Contributed Papers Phylogenomics

Title: Phylogenetics of the Perennial Endemic North American Clade of Apiaceae (PENA)

Author: ***Phebian Odufuwa @ Boise State University***

Keywords: Apiaceae,Diversification,Endemic Species,Geophyte,Incomplete Lineage Sorting,molecular phylogenetics,Reconstruction,speciation

Abstract:

The Perennial Endemic North American clade of Apiaceae (PENA) is the second largest plant group endemic to North America. The large majority of diversity within PENA – 16 genera - is west of the Rocky Mountains, with three genera east of the Mississippi River. The largest genus of the 19 genera within the group, Lomatium, has over 100 species. Some of its widespread taxa lack clear boundaries due to cryptic speciation, convergent evolution, and incomplete lineage sorting – phenomena not uncommon in young lineages such as the PENA clade (molecular dating studies showed that diversification of the clade happened around 2mya). A comprehensive and conclusive phylogenetic hypothesis for the entire clade (containing ~230 taxa) is thus needed. Through intensive collaborative efforts and thorough sampling of every named taxon, in addition to numerous suspected undescribed taxa within PENA and using the next-generation hyb-seq technique, we have been able to sample >300 genes from 400 samples (including all PENA species and multiple individuals from widespread taxa). The concatenated dataset, using maximum likelihood analysis, yielded results that were somewhat congruent with previous analyses. Several clades that were recovered with Sanger sequencing did come out as monophyletic in our analysis, such as the Vesper clade, and the clade we are referring to as the eastern clade (Zizia, Polytaenia, and Thaspium). However, there was poor support at the backbone. Further analyses were done using phased accessions as we suspected high levels of polyploidy within PENA; this second analysis boosted support to a greater extent, especially support at the tips, whereas support at the backbone showed better improvement over non-phased accessions. Efforts are ongoing to construct the multispecies coalescent phylogenetic tree using phased accessions. These efforts will help reconstruct the evolutionary history of this large species-rich clade, resolve where generic and species boundaries may be best drawn, and form the basis for future biogeographic studies.

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Phylogenomics

Topic: Contributed Papers

Title: Untangling relationships within Chaetogastra DC. (Melastomateae, Melastomataceae) and among closely related genera.

Author: ***Malu Ore-Rengifo @ University of Florida***

Keywords: Melastomataceae,phylogenomics,South America,Chaetogastra,Andean clad

Abstract:

The pantropical family Melastomataceae is one of the top 10 families worldwide in terms of species richness, demonstrating some of the highest speciation rates within the angiosperms. Within the Neotropics, generic limits and species relationships are still unclear across many different clades. The genus Chaetogastra DC., with ca. 120 species, represents a significant Neotropical radiation where generic limits and species relationships remain problematic. Most species of Chaetogastra and close relatives were formerly treated as Tibouchina s.l., which in turn are closely related to the genera Andesanthus, Heterocentron, Monochaetum, and Pleroma. Chaetogastra has a wide distribution from Mexico to Central America, the West Indies, northern South America, across the Andes, Paraguay, Uruguay, and a great number of species occur in Brazil. We carried out a phylogenomic analysis using both plastome and HybSeq data to try to resolve species relationships within Chaetogastra and generic relationships among close relatives. We sampled broadly across Chaetogastra and closely-related genera and likewise we added publicly available sequences from Genbank. We performed Maximum likelihood inference and Bayesian analysis for the plastome data and the pseudo-coalescence method ASTRAL for species using our nuclear dataset to test our hypothesis of patterns of speciation and divergence in both genomes. Comparative phylogenomic analyses using both the plastome and nuclear probe set allowed us to test topological differences among species and generic relationships. Furthermore, we were able to gain insights about the evolution of Chaetogastra as it relates to the Andean uplift in South America, as compared with other radiations in that region.

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Phylogenomics

Topic: Contributed Papers

Title: Phylogenetic relationship and phenotypic evolution in the carnivorous plant Pinguicula L.

Author: ***Yunjia Liu @ The Pennsylvania State University***

Keywords: morphology,Pinguicula,carnivorous plant,Phylogenetic comparative methods,phylogenomics,phylogenetic

Abstract:

Pinguicula L. (Lentibulariaceae) is a genus of carnivorous plants known as the butterworts. Members of the genus forms a rosette of carnivorous leaves with mucilage glands from which the floral scape arises and produces one to multiple bilabiate, tubular flowers. Three subgenera comprise Pinguicula (Isoloba, Temnoceras, and Pinguicula) and 115 species are currently recognized [1, 2]. Morphological characters vary greatly among species and were once used to assign taxonomic groupings. Molecular marker-based phylogenetic reconstruction have refined Pinguiculamorphological-based taxonomy, however, infrageneric classification remains incongruent among different markers, especially for subgenus Temnoceras sect. Temnoceras [3, 4]. Meanwhile, this subgenus also displays great diversity in floral morphology. To resolve the tangled relationship, 34 representative species from section Temnoceras and section Isoloba for phylogenetic reconstruction were selected for Illumina whole genome sequencing (30Gb for each species) and assembled with MaSuRCA. Following assembly, genome completeness was estimated using BUSCO based on the eudicots_odb10 database [5]. All assemblies were found to be above 88% completeness. The phylogenetic reconstruction was generated using ASTRAL, a coalescence-based approach that incorporated over 2,000 individual gene (BUSCOs) trees into species tree estimation [6]. A robust phylogeny has been reconstructed, with posterior probabilities high for most branches (1). Pinguicula morphological characters have also been comprehensively collected from publications [7]. The phylogenetic reconstruction will serve as the basis for following comparative phylogenetic methods and statistical analyses to investigate Pinguicula infrageneric classification and phenotypic trait evolution.

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Phylogenomics

Topic: Contributed Papers Phylogenomics

Title: Strong phylogenetic signal despite high phylogenomic complexity in the Andean tree genus Freziera (Pentaphylacaceae)

Author: ***Laura Frost @ University of South Alabama***

Keywords: Andes,Angiosperms353,herbariomics,introgression,paralogy,discordance,gene tree - species tree,locus filtering

Abstract:

The Andes mountains of western South America are a globally important biodiversity hotspot, yet there is a paucity of resolved phylogenies for plant clades from this region. Filling an important gap to our understanding of the World's richest flora, we present the first phylogeny of Freziera (Pentaphylacaceae), an Andean-centered, cloud forest radiation. Our dataset was obtained via hybrid-enriched target sequence capture of Angiosperms353 universal loci for 50 of the ca. 75 spp., obtained almost entirely from herbarium specimens. We identify high phylogenomic complexity in Freziera, including a significant proportion of paralogous loci and a high degree of gene tree discordance. Via gene tree filtering, by-eye observation of gene trees, and detailed examination of warnings from recently improved assembly pipelines, we identified that cryptic paralogs (i.e., the presence of only one copy of a multi-copy gene due to assembly errors) were a major source of gene tree heterogeneity that had a negative impact on phylogenetic inference and support. These cryptic paralogs likely result from limitations in data collection that are common in museomics, combined with a history of genome duplication; they may be common in plant phylogenomic datasets. After accounting for cryptic paralogs as source of gene tree error, we identified a significant, but non-specific signal of introgression using Patterson's D and f4 statistics. Despite phylogenomic complexity, we were able to resolve Freziera into nine well-supported subclades whose histories have been shaped by myriad evolutionary processes, including incomplete lineage sorting, historical gene flow, and gene duplication. Our results highlight the complexities of plant phylogenomics, and point to the need to test for multiple sources of gene tree discordance via careful examination of empirical datasets.

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Phylogenomics

Topic: Contributed Papers

Title: Phylogenomic and Phylotranscriptomic Analyses of Whole Genome Duplications in Large Angiosperm Groups and Families with Implication on Functional Evolution

Author: ***Taikui Zhang @ Pennsylvania State University***

Keywords: phylogenomics,WGD,genome evolution

Abstract:

Phylogenomic and Phylotranscriptomic Analyses of Whole Genome Duplications in Large Angiosperm Groups and Families with Implication on Functional Evolution.

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Abstract

Whole genome duplications (WGDs) have been reported in early angiosperm history and for many groups and are considered as an evolutionary force for angiosperm diversification, in partly due to the raw genetic materials for evolutionary innovation from WGD-derived gene duplicates. WGDs can be identified by strong evidence in genome sequences and are supported by clusters of large number of gene duplications (GDs) of nuclear genes at specific nodes in the angiosperm phylogeny from phylogenomic/phylotranscriptomic analyses. Specifically, a recently developed tool Tree2GD provides an efficient mean for detecting WGD. We have performed phylogenomic/phylotranscriptomic analyses for large angiosperm groups, such as the Asterids, and large families, including Asteraceae, Cucurbitaceae, Fabaceae, and Solanaceae. These analyses have yielded strong evidence for WGDs, including phylogenetic placements of WGDs supported by genome sequences. These results and likely roles of WGD derived duplicates on functional and morphological evolution will be presented and discussed.

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Phylogenomics

Topic: Contributed Papers

Title: Dealing with paralogs: what a phylogenomic dataset contains for the high-Andean Brachyotum

Author: ***Diego Paredes-Burneo @ Louisiana State University***

Keywords: macroevolution,polyploidy,target-capture,Andean clade

Abstract:

Assuring the usage of orthologs is crucial for phylogenetic inference. Despite its role in plant evolution, gene and whole genome duplication pose a challenge when using genomic data du to the presence of paralogous sequences. It has been a common practice to drop these paralogous loci when they were identified, but this may mean that a significant portion of our data is being discarded. When analyzing our target-capture dataset for understanding the evolution of the high-Andean genus Brachyotum (Melastomataceae), we found a high content of putative paralogs (near 90% of our total dataset). To obtain the most of our dataset, we applied filters and inferred orthologs from putative paralogs under a phylogenetically aware framework. We were able to implement 66% of the data flagged as putative paralogs to our dataset, which were later used to infer both gene and species trees. We are working towards investigating if these paralogs represent ploidy in Brachyotum, which may shed light into understanding the colonization of this genus into high-Andean ecosystems.

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Phylogenomics

Topic: Contributed Papers Phylogenomics

Title: Towards a complete angiosperm tree of life

Author: ***Alexandre Zuntini @ Royal Botanic Gardens, Kew***

Keywords: Angiosperm353,Classification ,Diversification,flowering plants,Museomics

Abstract:

Angiosperms dominate most land ecosystems. From shaping biomes and influencing the diversification of different organisms, to providing the base for human development, they are key elements in Earth's history. However, given its huge diversity, with more than 300.000 species organised in nearly 14.000 genera, reconstructing the phylogenetic history of angiosperms is not an easy task. Either limited by sample availability or genetic representation, the complexity of angiosperms evolution is yet poorly assessed. Thanks to advances in sequencing technologies, we are now capable of harnessing the full potential of botanical collections to obtain high quality data from centuries-old specimens. Moreover, target sequence capture enables us to dive deeper into the nuclear genome, providing hundreds of truly independent loci. Here we present a phylogenetic tree of angiosperms based on 353 nuclear loci, including almost 8.000 genera (58%). With all orders and families included here for the first time in a nuclear phylogenomic framework, couple with a dense generic sampling, our tree supports the evaluation of the current classification system, redefining major clades, orders and families. Based on more than 200 fossils, we calibrated this phylogenetic tree and used this dated framework to study the diversification of angiosperms, unveiling an intricate pattern of diversification rates shifts. With the wide taxonomic and genomic coverage of our dataset, we emphasise the advantage of nuclear data to elucidate the relationship among flowering plants, paving the way towards the tree of life of angiosperms.

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Phylogenomics

Topic: Contributed Papers

Title: Phylogenomics, historical geography, adaptive radiation, and quantitative floral convergence in lilies (Lilium)

Author: ***Thomas Givnish @ University of Wisconsin-Madison***

Keywords: adaptive radiation,convergence,Pollinators,geographic spread

Abstract:

Lilies – with ca. 125 species in Lilium and the former genus Nomocharis – are restricted to the Northern Hemisphere, with centers of diversity in East Asia, southern Europe, the Caucasus, and eastern and Western North America. Species vary widely in habitat and in floral form, orientation, color, and fragrance. To identify relationships within Lilium and reconstruct its adaptive radiation and geographic spread, we conducted the first phylogenomic analysis of relationships in the genus by sequencing, assembling, and analyzing more than 400 single-copy nuclear loci and whole plastomes of almost all extant species. The maximum-likelihood plastome phylogeny fails to resolve any of the traditional, morphology-based sections as monophyletic, with two origins for North American § Pseudolirium, two for Himalayan/Tibetan § Nomocharis, four for East Asian § Sinomartagon, two for Asian § Leucolirion, two for Asian § Archelirion, three for European and Central Asian § Martagon, two for East Asian § Daurolirion, and two for European § Liriotypus. The nuclear phylogeny, however, resolves most sections as monophyletic, except for polyphyletic § Sinomartagon and § Leucolirion, supporting most traditional sections but also pointing to widespread reticulate evolution deep within the phylogeny. Reconstructions of historical biogeography point to an origin in East Asia or Himalayas/Tibetan Plateau, with subsequent dispersals into North America, the Himalayas/Tibetan Plateau, Europe, Formosa, Japan, and the Philippines. Within the North American clade § Pseudolirium, we found strong quantitative convergence in flower shape, orientation, and color associated with pollination by hummingbirds, sphingid moths, and bees, and apparent retention of ancestral characters in species pollinated by butterflies. Hummingbird pollination is particularly common in cool and/or moist environments, as expected on functional grounds

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Phylogenomics

Topic: Contributed Papers

Title: A phylogenomic analysis of the hyperdiverse tribe Anthemideae (Asteraceae)

Author: ***Gonzalo Nieto Feliner @ Real Jardín Botánico (RJB-CSIC)***

Keywords: chloroplast capture,Classification ,herbariomics,HybSeq,phylogenomics,target-capture,Taxonomy

Abstract:

With over 1,800 species distributed across 111 genera, the marguerite daisy tribe (Anthemideae) is one of the largest within the sunflower family (Asteraceae). Mainly distributed across Eurasia and Africa, a large number of its species occur in dry environments, with the Mediterranean basin representing a diversification center for several of its lineages. Despite being the subject of numerous systematic studies, the classification of tribe Anthemideae has remained particularly unsettled for decades. In recent years, phylogenetic studies based on Sanger sequencing have provided some measure of clarity; however, doubts remain pertaining subtribe classification. With 19 subtribes (in the latest revision), Anthemideae presents one of the highest numbers of subtribes within Asteraceae. To achieve a more stable classification, we have undertaken a phylogenomic study based on target capture sequencing, using the Angiosperms353 enrichment panel, as well as publicly available transcriptome and plastome data from OA repositories. Sixty-eight species across 64 genera were sampled for DNA and 78 were bioinformatically mined (146 accessions total). Our results provide conclusive answers to several pending questions. Osmitopsis is sister to the remainder of Anthemideae. Cotulinae was recovered as monophyletic in all analyses. Glebionidinae and Santolininae were highly supported as reciprocally sister groups. Subtribes Matricariinae and Anthemidinae should be merged into a single subtribe to solve their current paraphyletic circumscription. Strong indication of chloroplast capture was also obtained, which underscores the importance of sampling genome-wide data and analyzing nuclear and plastid data independently.

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Topic: Contributed Papers Phylogenomics

Title: Integrated phylogenomic and ecological analyses of the Vitis cinerea species complex reveal geographic isolation, ecological differentiation and hybridization impacting species diversification in North America

Author: ***Alicia Talavera @ Smithsonian Institution // University of Malaga***

Keywords: North America,phylogenomics,species diversification,grapes,geographic isolation

Abstract:

In spite of the evolutionary interest and economic importance of the grape genus Vitis, the phylogenetic relationships and drivers of species diversification remain poorly understood. Previous studies on North American Vitis in the last decade have detected strong cytonuclear discordances. Further phylogenomic analyses are needed to unravel phylogenetic relationships and explore hybridization events, especially in several North American species complexes. The Vitis cinerea species complex (VCC) is morphologically highly polymorphic. Several studies recognized four varieties in the complex, and these varieties have recently been treated at the species level as V. baileyana, V. berlandieri, V. cinerea and V. simpsonii. However, integrated analyses with an enhanced sampling of the V. cinerea complex including contact zones/areas of sympatry are needed to clarify hybridization events and explore drivers of diversification in this complex.

In this study, samples of the Vitis cinerea complex across its distributional range were broadly collected with all four varieties included. Major clades and relationships of the species complex have been assessed in a broad phylogenetic framework of North American Vitis, using newly developed baits for Vitaceae with 1013 nuclear genes. Hybridization events have been tested in the species complex to aid in the species delimitations. Ecological niche modeling and principal component analysis (PCA) of the environmental variables were used to assess ecological differentiation in the diversification of VCC. Our results support the recognition of four species (V. baileyana, V. berlandieri, V. cinerea and V. simpsonii) in the VCC, and showcase the interactions of geographic isolation, ecological differentiation and hybridization in driving the processes of species differentiation.

Topic: Contributed Papers

Title: Identifying serpentine adaptation genes by tracing evolutionary-genomic history of Streptanthus, Caulanthus and their allied genera (Brassicaceae)

Author: ***Kasuni Daundasekara @ Texas A&M University***

Keywords: Brassicaceae,phylogenomics,Serpentine,Caulanthus

Abstract:

Adaptation to extreme environments is an important problem in ecology and evolutionary biology. Serpentine soil, which has high concentrations of toxic heavy metals and low concentrations of essential plant nutrients, is an excellent model environment to study plant adaptations to harsh environments. The annual mustard, Caulanthus amplexicaulis var barbarae (CAB), which is serpentine tolerant, and its sister taxon, Caulanthus amplexicaulis var amplexicaulis (CAA), which is serpentine intolerant is a superb model to study genetic mechanisms underlying serpentine tolerance. Several approaches (QTL analysis, coding sequence evolution, RNAseq) are being used in our laboratory to identify candidate genes for serpentine tolerance in CAB. In this study, we are using the gene ancestry of CAB and CAA as an additional tool to prioritize candidate genes.

To trace the ancestry of CAB and CAA, we are using ~30 species within the genera Caulanthus, Streptanthus, and related genera. Elucidation of the phylogenetic history of CAB and CAA is challenging due to at least one known episode of recent introgression. Here, we are determining the evolutionary history of CAB and CAA by comparing highly resolved phylogenies from both organellar (chloroplast and mitochondria) and nuclear genomes. Comparison of plastid genomes has led to identification of natural selection in this phylogenetic group. Results from chloroplast and mitochondrial phylogenies show that the maternal lineage of CAB and CAA clade is likely a serpentine-intolerant Caulanthus lineage. We are using gene-tree discordance between organellar and nuclear phylogenies to identify nuclear loci with paternal inheritance and explore the potential of using this information to prioritize candidate serpentine tolerance genes and test using synthetic biology and CRISPR/CAS9 mutagenesis approaches.

Topic: Contributed Papers Physiology

Title: Blue Carbon Sequestration from seagrass and mangroves in the Gulf of Mexico and Lower Caribbean basins: An Overview.

Author: ***Arthur Schwarz @ Southwestern Adventist University***

Keywords: Carbon sequestration seagrass,Carbon sequestration mangroves,Caribbean basin coastal carbon,Caribbean seagrass,Caribbean mangroves

Abstract:

Carbon sequestration for mangroves and seagrass communities is greater than that of tropical forests, representing dramatic carbon storage opportunities for climate change mitigation. Global hotspots for blue carbon sequestration have been examined for the Gulf of Mexico (GOM), the Lower Caribbean (LC) and the Indo-Pacific (IP) region of Southeast Asia have been examined. Here we estimate carbon sequestration for the whole Caribbean coastal basin by including our own and published analyses of carbon sequestration and areal extent of seagrass and mangroves. We find far fewer measurements of blue carbon in the IP than for the GOM. The Caribbean has 26% of global mangroves. The 12-month productivity cycle of both seagrass and mangroves with their high growth rates is key to understanding their high annual carbon sequestration. Often seagrass and mangroves accumulate carbon of riverine origin. Nations bordering the Caribbean basin frequently have higher extents of seagrass than mangroves. For example, the northern part of the Caribbean, the GOM, has about 1 million ha of seagrass, and about 650,000 ha of mangroves. On the other hand, mangrove carbon sequestration values in the LC far outnumbers that for seagrass. However, measurements of areal extent by satellite in the clear waters of the Eastern Caribbean have shown high areal extent of seagrass, especially in the Bahamas. The total mangrove extent in the Caribbean is estimated at 2,728,333 ha (650,000 ha in the GOM; 2,077,902 ha in the LC. The total seagrass extent in the Caribbean is 3,000,000 ha (1,000,000 ha in GOM; 2,000,000 in LC). Carbon sequestration in mangroves ranges from 282 Mg C ha-1 to 633 Mg C ha-1, leading to a total estimate of 1,276 Tg C in the combined Caribbean basins (476.13 Tg C in the GOM; 800 Tg C in the LC). Carbon sequestration in seagrass ranges from 50 Mg ha-1 to 254 Mg C ha-1, leading to a total estimate of 552 Tg C in the combined basins (184 Tg C in the GOM; 368 Tg C in the LC) . The total carbon sequestered by mangroves and seagrass communities in the Caribbean as a whole is estimated to be 1,828 Tg C. Clearly, the Caribbean basins are a carbon sequestration hotspot. Our total carbon sequestration estimate combined for mangroves and seagrass is lower than that of the IP region, which apparently is the highest in the world. We hypothesize that the shallow seas, many kilometers of island coastline, and the "flow through effect", (discovered by Klaus Wyrtke) of the IP region create ideal conditions for mangroves and seagrasses to sequester blue carbon. Such condition are not met to the same extent in the greater Caribbean.

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Topic: Contributed Papers

Title: A Plan for Large Scale Restoration of Damaged Seagrass Communities.

Author: ***Arthur Schwarz @ Southwestern Adventist University***

Keywords: Halodule wrightii restoration shorelines Texas ,seagrass restoration,seagrass extent Texas,Seagrass Matagorda Bay,seagrass services,seagrass degradation

Abstract:

The global area occupied by seagrass has been estimated at 191,000 km2 with 7% loss per year (Waycott et al, 2006). Industrialized coastal areas around the world have experienced major losses of seagrass from urbanization, dredging for navigational channels and ports, release of damaging effluent, and direct land fill. Seagrass loss has far exceeded restoration of damaged areas. In coastal Texas, large areas have experienced all such degradation in estuaries that were once rich seagrass beds. This coastline is one of the worlds' major fossil fuel refining complexes. A major study of the loss of Texas seagrass (Pulich, 1999) showed only 30% seagrass remaining, with some estuaries having far less. Small scale restoration of seagrass has occurred along the coast of Texas for three decades. We are building a systematic effort to create a Texas State plan for restoring seagrass and its services on a larger scale. The major ecological services seagrasses provided include enhanced water clarity, fisheries nursery habitat, food-webs for endangered species, shoreline stability, and mineral cycling. Various areas offer restoration of differing services. We are beginning with the third largest Texas estuary, Matagorda Bay, which has received the least attention for it's seagrass. We have begun by selecting degraded sites where critical services could potentially be restored. We next filtered these sites based on where we believe restoration will be most beneficial throughout the 1,093 km2 expanse of the bay. The precise shoreline elevation and configuration are being confirmed by coastal shoreline surveys. A series of over 1,200 plugs of seagrasses will be planted in spring. Past seagrass restorations, including our own, ranging from south (Padre Lagoon) to north (Galveston Bay) has shown that plugs of Halodule wrightii establish most successfully. Restored seagrass beds along shorelines in three locations from Galveston Bay to Corpus Christi Bay have showed high resilience and persistence of the shoreline during hurricanes, while marshes without associated seagrass along the shoreline were more likely to sustain damage or wash away. All our restorations resulted in recolonization of animal communities within months. The water clarity is improved with the presence of seagrass as sediment is trapped among the stems, rhizomes and roots. Blue carbon sequestration was higher than natural seagrass growing in the vicinity (Thorhaug, 2017). Our plan is to restore various types of sites and monitor the return ecological services. Generally, the estuaries have relatively high flow of surface water from large catchment areas flowing into the bay. The eastern sides of Texas bays have barrier islands with infrequent passes to the Gulf of Mexico. Thus, there are varying types of sites, which will be ranked for priority of restoration efforts.

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Physiology

Topic: Contributed Papers Physiology

Title: EFFICIENT METHOD FOR MASS PROPAGATION OF ORCHID (Vappodes phalaenopsis) USING POLYETHYLENE GLYCOL TO STUDY IMPACT OF INDUCED WATER STRESS ON THE RELATIVE GROWTH.

Author: ***Nusrat Jahan @ BUITEMS***

Keywords: tissue culture,PEG, drought stress,,NAA,BAP

Abstract:

Tissue culture is a fascinating tool that enables the rapid production of genetically identical, high-yielding, disease-resistant, and long-lasting plants with relatively little use of water, space, materials, and time. Drought is a major abiotic factor limiting crop production worldwide. Orchid species are considered drought sensitive species. The present research work involves the induction of shoots, leaves, callus of orchid species (Vappodes phalaenopsis), and investigated the effects of drought stress on the in vitro growth of orchids. Solid polyethylene glycol (PEG -6000) of high strength (0.5gm/L) was used for drought stress induction in MS. Shoot and leaf induction from explants (shoot tips) showed that Murashige Skoog (MS), 2ml BAP and 1ml NAA were best for shoot initiation and PEG 0.5.gm/litre Murashige Skoog (MS), 2ml BAP and 1ml NAA proved best for callus initiation. PEG reduces transpiration of orchid plants by reducing the number of leaves, shoots, and increases the number of callus. The reverse was true in the medium MS without PEG. Keywords: PEG, tissue culture, drought stress, BAP, NAA.

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Physiology

Topic: Contributed Papers

Title: Aluminum toxicity in Solanum macrocarpon

Author: ***Emmanuel Kalu @ Abia State Polytechnic***

Keywords:

Abstract:

The purpose of this work is to map out how Aluminium (Al) toxicity is expressed in plants using Solanum macrocarpon. Field and laboratory sections were performed. The field studies measured response of the plant to Al using germination and yield parameters while laboratory studies studied changes in peroxidase enzymes and chlorophyll values. The treatments were 6X10-4Mol AlCl3, 9X10-4 Mol AlCl3, 12X10-4 Mol AlCl3 and blank, which served as control. Field studies were in open field (before the rainy season) using CRBD experimental design and the following parameters were investigated: germination rate, percentage germination, day of emergence. Yield parameters include: Length of shoot (LOS), Length of root (LOR), Fresh weight of shoot (FWSh), Dry weight of shoot (DWSh), Fresh weight of roots (FWR), Root dry weight (RDW), Fresh Weight of stem (FWS), Stem dry weight (SDW), Fresh weight of leaves (FWL), Leaf Dried weight (LDW) Number of leaves (NOL) Circumference of stem (COS) Circumference of roots (COR). The parameters that was investigated on fully matured plants include Area of leaves (AOL), NOL, length of leaves (LOL), Number of Branches (NOB), Number of fruits (NOF), Number of ripe fruits (NRF), Fresh fruit weight (FFW), Fruit Dried weight (FDW). Peroxidase enzyme studies and Chlorophyll counts were performed using spectrometer (721G Spectrophotometer, Searchtech Inc, China). Data analysis and means compared by LSD ($P \leq 0.05$) mapped out model of Al toxicity in S. Macrocarpon. The plant showed some degree of tolerance which further studies can investigate how to take advantage on the genetic resources.

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Phytochemical

Topic: Contributed Papers Phytochemical

Title: Quantifying chemodiversity as a way of understanding the ecological function of phytochemicals

Author: ***Hampus Petrén @ Philipps-University Marburg***

Keywords: chemical defense,defensive metabolites,herbivory,methods,phytochemical,plant-insect ecology,plant-pollinator interactions,functional diversity

Abstract:

Plants produce a great variety of phytochemical compounds, which are important for shaping interactions between the plants and their biotic and abiotic environment. Traditionally, research has often focused on examining the function of individual compounds on specific ecological interactions, such as herbivory and pollination. However, phytochemicals occur in multicompound mixtures that form a complex phenotype, and relatively little is known about what aspects of this phenotype are most important for its function. Recently, measuring chemodiversity has attracted considerable interest as an ecologically meaningful way to quantify mixtures of phytochemical compounds. However, our understanding about how such diversity, and what components of it, are important for function has remained limited. In this talk, I go through the theoretical background of how the diversity of compounds could be linked to function, and examine evidence for such effects in the literature. Then, I introduce the R package chemodiv, which provides functions for calculating and visualizing chemical diversity, with methods that take the richness, relative abundance and – most importantly – structural and/or biosynthetic dissimilarity of compounds into account. With such new comprehensive measures, chemodiversity can be measured in ways that are suitable for different kinds of datasets and questions. We believe that these theoretical and statistical developments will increase our knowledge of how phytochemicals and their diversity varies across different levels of biological organization, and how they affect ecological interactions between plants and other organisms.

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Phytochemical

Topic: Contributed Papers

Title: Predicting enzyme functions: A case study using BAHD acyltransferases

Author: ***Gaurav Moghe @ Cornell University***

Keywords: comparative genomics,Functional genomics,phylogenomics,phytochemistry,enzyme,gene family evolution

Abstract:

Over a thousand plant genomes have been deposited in databases today. While assembling genomes and identifying genes is no longer a major bottleneck, predicting gene functions is still a major challenge. This is especially true for genes in families, such as those in metabolism, where gene duplication is highly prevalent and leads to rapid functional divergence and promiscuity. Which signals are important for functional prediction in duplicate genes is still not clear. Here, we used the large BAHD acyltransferase family as a model for addressing this question. Several dozen BAHDs are present in individual diploid angiosperm genomes but typically the functions of only 10-20% of BAHDs are meaningfully annotated. We explored whether using phylogenomic data coupled with extensive literature curation, sequence motifs, co-expression data and structural features can help in functional prediction. Using phylogenomic data, we improved the number of BAHDs associated with a substrate class in cultivated tomato from 15% to 45%. Sequence analysis also revealed enrichment of specific active site motifs in individual clades that may indicate lineage-specific selection. We found evidence of a large 110 amino acid long intrinsically disordered region in BAHDs, however, there were drastic clade-specific differences. Further analysis indicated that the flexibility of this motif plays a role in substrate specialization and/or promiscuity possibly by changing protein conformational diversity. Co-expression analysis further allowed definition of biological roles of certain BAHDs such as in pathogen defense, detoxification and stress response. Our analyses based on first principles reveal multiple features of enzymes contributing to their in planta functions. We are currently expanding this analysis to ten other enzyme families – comprising ~5% of angiosperm plant genomes – making available thousands of previously published and predicted activities for the phytochemical community to access in the future.

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Topic: Contributed Papers Phytochemical

Title: Chemical, genetic, and morphological characterization of the floral scent and scent releasing structures of Gynandropsis gynandra (Cleomaceae, Brassicales)

Author: ***Brandi Zenchyzen @ University of Alberta***

Keywords: Brassicales,Cleomaceae,Volatile Organic Compounds,Pollinator attraction,Gynandropsis gynandra,Floral Scent

Abstract:

Approximately 85% of flowering plants are pollinated by animals. As such, most flowering plants exhibit an array of features that act synergistically as signals for pollinator attraction. In conjunction with visual displays, flowers present limitless possibilities of fragrance blends consisting of different volatile compounds and ratios of components, which can be learned and recognized by pollinators. Gynandropsis gynandra (L.) Briq. (Cleomaceae, Brassicales) is an underutilized leafy vegetable native to Africa and Asia. With its extensive geographical distribution, G. gynandra exhibits intra- and inter-continental variation in morphology, phenology, and phytochemistry. In addition to the variation of the plants themselves, the reported insect visitors of G. gynandra differ between continents. These differences suggest the possibility of distinct, geographically separated G. gynandra morphs, which could be further supported with floral fragrance profiles. Therefore, we characterized the floral scent blends of African and Asian G. gynandra accessions to compare volatile compound composition between geographical regions and to pollination syndromes. As G. gynandra is ar important vegetable in some African countries and food security is a global concern, understanding the morphology and genetics of the floral features associated with pollinator interactions is vital for ensuring its reproductive success. Hence, we also described floral cell morphology and explored gene expression across floral organs for the African accession to identify possible scent releasing structures and integrate emitted floral scent compounds with volatile biosynthetic pathway expression profiles.

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Topic: Contributed Papers

Title: Towards Capturing Global Metabolic Responses through -Omics Approaches

Author: ***Elizabeth Mahood @ Corteva Agriscience***

Keywords: comparative transcriptomics,integrative method,specialized metabolism,untargeted metabolomics,brachypodium,big data

Abstract:

The functions of specialized metabolic genes remain difficult to elucidate, as they often belong to large gene families that undergo frequent gene duplication. While the most common methoc of gene function prediction -- the transfer of known gene functions through related species -- is easily implementable, it may yield inaccurate conclusions for metabolic genes. As diverse agronomic traits are controlled by metabolic pathways, the scarcity of functionally annotated metabolic genes has wide-reaching implications in agriculture and the plant sciences.

In my talk, I will describe the results of an integrated transcriptomics and metabolomics experiment in the model C3 species Brachypodium distachyon, designed to elucidate metabolic functions of genes. B. distachyon plants were grown under different conditions (heat Copper [Cu] deficiency, combined heat-Cu deficiency stress, low Phosphate [P], and Arbuscular Mycorrhizal Symbiosis [AMS]). Transcripts and metabolites were simultaneously extracted from leaves and roots, and RNA-seq and untargeted metabolomics was performed.

An Information theoretic analysis of the metabolomics data revealed that while leaves had the most complex metabolite profiles, root metabolomes were more inducible and produced more condition-specific metabolites. Differential analysis of metabolite levels coupled with deep learning techniques helped identify broadly stress-responsive metabolite classes. Many condition-specific metabolites – such as blumenols (C13 apocarotenoids) – that can potentially serve as stress biomarkers were also found. We show that while emerging algorithms for metabolite annotation can dramatically increase the interpretability of untargeted metabolomics data, the accuracy of these algorithms should be verified beforehand on in-house, gold standard data.

After determining gene expression, we quantified the correlation of both experimentally validated and predicted pathways. Next, we identified genes with conserved expression under AMS and with structurally similar, highly correlated metabolites as candidates of AMS-regulated biosynthetic pathways. This workflow successfully identified both known genes, and new candidate genes regulating plant metabolism under AMS in B. distachyon.

Associating stress-induced genes with metabolic pathways provides i) an alternative and effective method of gene function prediction in understudied species, and ii) gene targets for the breeding of more stress-tolerant plants.

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Phytochemical

Topic: Contributed Papers Phytochemical

Title: Hyperspectral prediction of volatile organic compound mediated responses across the genus Helianthus

Author: ***Jordan Dowell @ Louisiana State University***

Keywords: Biotic interaction,hyperspectral imaging,Volatile Organic Compounds

Abstract:

Constitutive production of defense metabolites supplies a continual 'blanket of safety' against natural enemies at the energetic cost of lifetime investment by the plant while increasing the likelihood of herbivore adaptation to specific defenses. In contrast, inducible defenses are more dynamic and require short-term energetic investments in response to a perceived threat. In addition, because these defenses are only around for short bursts of time, there is a lower likelihood of comparable adaptation, allowing for potential pest and pathogen susceptibility maintenance. Among plant-specialized metabolites, volatile organic compounds (VOCs) are low-carbon molecules that act directly on pests and pathogens while simultaneously inducing priming responses in neighboring plants. Therefore, breeding crops with an increased capacity for inducible defenses mediated by VOCs would increase the sustainability of agricultural systems by reducing nutrient and pesticide inputs. However, incorporation necessitates high-throughput methods to phenotype inducible plant responses in crops and wild relatives for introgression of resistance traits. For this study, we leverage the constitutive and inducible VOC and hyperspectral reflectance diversity of crop Helianthus annuus and 20 wild-relatives in the genus Helianthus to (1) assess the commonality of a signal of 'herbivore threat' across the genus and (2) describe induced qualitative and quantitative changes in VOC profiles during herbivory by a generalist lepidopteran, Vanessa cardui, and when exposed to herbivore-induced VOCs (HIPVs). Our findings suggest that herbivore- and HIPV-induced VOC responses across Helianthus are highly species-specific. However, a single classification model using hyperspectral reflectance applied across all species accurately distinguishes among controls, herbivore-, and HIPV-induced individuals with high specificity and sensitivity, corroborating patterns of delineation within each species. Our Results suggest hyperspectral reflectance can detect induction across the genus, suggesting a potential conserved signal. Further, VOC diversity highlights a wide range of induced responses to a generalist herbivore across the genus.

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Phytochemical

Topic: Contributed Papers

Title: Post-secretory synthesis of a natural analog of iron-gall ink in the black nectar of Melianthus spp.

Author: ***Evin Magner @ University of Minnesota***

Keywords: flower,nectar,nectary,pigments,plant-pollinator interactions,South Africa,Sunbirds,flowering plants,color,iron,ink,black

Abstract:

Floral nectar is a sugar-rich liquid generated by plants to attract pollinators. The critical components of nectar are sugars in varying concentrations and forms, yet many also include a range of phytochemicals that attract pollinators and deter predators1. These compounds include alkaloids, flavonoids, terpenes, and others, which have been found to affect pollinator behavior and influence their preference for the nectar. Colored nectar is a distinctive and uncommon trait of nectar. While scientists have known about colored nectar since at least 1785, it has only lately gained concerted scientific investigation2. Melianthus species produce black nectar that is believed to attract avian pollinators visually; however, the chemical identity and synthesis of the black pigment are unknown2,3. To identify the pigment responsible for the black color of Melianthus nectar and its biosynthesis mechanism, a combination of analytical biochemistry, transcriptomics, proteomics, and enzyme assays were utilized. Here, we demonstrate that the black nectar produced during anthesis contains a natural analog of iron-gall ink formed from an ellagic acid-Fe complex4. High concentrations of ellagic acid and iron give the nectar its dark black color, which may be replicated using synthetic solutions containing solely ellagic acid and iron (III). The nectar also includes a peroxidase, which oxidizes gallic acid to generate ellagic acid. In vitro processes, including nectar peroxidase, gallic acid, hydrogen peroxide, and iron (III), completely replicate the black color of the nectar. The use of visual modeling of pollinators was further employed to deduce the probable functio of the black coloration. Results indicate that within the context of the flower, the black nectar is conspicuous to avian pollinators5. While this study focused on the impact of black nectar as a visual cue to pollinators, it may also serve other non-exclusive functions. As the pH and polyphenol content of nectar vary with the flowering stage, stage-specific filtering of floral visitors may occur6. Comparing Melianthus nectar to dark-colored nectars from Schiedea, Leucosceptrum, and Aloe species may help explain how chemistry and color influence fitness6–8.

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Phytochemical

Topic: Contributed Papers

Title: Variation in glucosinolate content in clubroot-resistant and -susceptible rutabaga (Brassica napus) cultivars in response to clubroot disease

Author: ***Harleen Kaur @ University of Alberta***

Keywords: auxin,glucosinolates,Clubroot,Rutabaga

Abstract:

Clubroot disease is a serious soil-borne disease caused by the obligate biotrophic Plasmodiophora brassicae in roots of cruciferous crops belonging to the Brassicaceae family. Glucosinolates (GSLs) are defense-related secondary plant products found in cruciferous plants that have been associated with clubroot disease. We investigated changes in total and individual GSLs in roots of rutabaga (Brassica napus subsp. rapifera Metzg) resistant ('Wilhelmsburger') and susceptible ('Laurentian') cultivars at an early stage of clubroot infection [7 days after inoculation (dai) with P. brassicae]. GSLs belonging to three major GSL groups, the aliphatic, aromatic, and indolic, were found in roots of both cultivars, with progoitrin being the most abundant GSL in both cultivars. Distinct patterns of various GSLs were observed in the roots of resistant compared to the susceptible cultivar. In general, the roots of the resistant cultivar had higher levels of aliphatic and aromatic GSLs than that observed in the susceptible cultivar. Indolis GSLs also can be precursors for the auxin indole-3-acetic acid (IAA), an auxin implicated in clubroot gall development. Roots of the clubroot-inoculated resistant cultivar showed a 17 % reduction in free IAA levels along with a 1.9-fold increase in the transcript abundance of BnIAGLU (codes for an enzyme that converts free IAA auxin to an inactive glucose eater conjugate) compared to its non-inoculated control at 7dai, suggesting that increased conjugation of free IAA to an inactive IAA-glucose ester could be associated with P. brassicae resistance. Overall, our current analysis suggests that GSLs play a role in inducing enhanced plant defense against the clubroot pathogen.

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Phytochemical

Topic: Contributed Papers Phytochemical

Title: Optimization of extrusion treatments, quality assessments, and kinetics degradation of enzyme activities during storage of rice bran

Author: ***Muhammad Rashid @***

Keywords: Lipid peroxidation,Rice,extrusion,Storage

Abstract:

Over the years, extrusion has been a multi-step thermal technique that has proven to be the most effective process to stabilize rice bran (RB). This study aimed to investigate the effects of extrusion treatment and temperature (15, 25, and 40°C) on the storage stability, lipid oxidation peroxidase and peroxide values, free fatty acids, fatty acid composition, and protein variations of RB over 60 days. The study offers novel insights into the changes in RB's protein and amino acid compositions during extrusion and storage, which has not been extensively explored in prior research. After extrusion processing, peroxidase activity (POD) and lipase activity (LPS) were significantly reduced. However, peroxide value (PV), free fatty acids (FFA), and malondialdehyde content (MDA) observed a significantly increased by 0.64 mEqO2/kg, 8.3 mg/100g, and 0.0005 µmol/L respectively. The storage stability of RB after extrusion shows that the POD, LPS, FFA, PV, and MDA were positively correlated with storage duration and temperature. The oleic acid/linoleic acid ratio in processed RB by extrusion had no significant changes during storage. The total and essential /non-essential amino acid ratios showed a downward trend of 5.26% and 8.76%, respectively. The first-order kinetics was the best-fitting model to describe the enzymatic inactivation and degradation of extruded RB during storage. The extrusion treatment did not affect the crude protein and the essential subunits of protein. Overall, the optimized extrusion procedure exhibited promising results in stabilizing the RB.

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Population Genetics/Genomics

Topic: Contributed Papers Population Genetics/Genomics

Title: Population genetics and fruit adaptation in Astragalus lentiginosus, the most taxonomically diverse species in North America.

Author: ***Michael Grillo @ Loyola University of Chicago***

Keywords: Astragalus,adaptation,California Floristic Province,dd RAD,ddradseq,Fabaceae,Fruits,population genetics,pod,pst-fst

Abstract:

Astragalus lentiginosus is the most taxonomically diverse species in the North American flora with over 40 named taxonomic varieties. However, these varieties are delineated somewhat arbitrarily and the number of varieties depends on the systematist. Thus, it remains unclear if varieties represent distinct population genetic entities. Many varieties are distinguished based upon variation in fruit morphology. The adaptive and functional significance of fruit morphological differentiation is unknown and it is possible that fruit variation is shaped largely by neutral genetic processes as populations of A. lentiginosus are often small and isolated. The goals of this study were to 1) characterize population genetic structure use ddRADseq among 16 taxonomic varieties from the southwest portion of distribution; and 2) to determine if fruit morphological variation exhibits a signature of being shaped by natural selection through a PST-FST analysis. Sequencing using ddRAD resulted in approximately 5000 SNPs for 400 plants that were collected from 79 sites among 16 taxonomic varieties. Population genetic analysis using STRUCTURE and PCA identified 3-4 major genetic groupings with significant isolation by distance and a single large genetic cluster in northern sites and 3 distinct clusters in the south. AMOVA revealed that a majority of the genetic variation occurred among varieties. Several taxonomic varieties represented unique genetic entities particularly narrow ranged taxa, whereas others exhibited considerable admixture and are not distinct. Morphometric geometric analysis of over 2,000 fruit images with a procrustes estimation of fruit shape was used to characterize fruit morphological variation. PST-FST analysis indicated that fruit morphological differentiation far exceeded underlying levels of population genetic differentiation suggesting that fruit morphological variation is likely adaptive. The selective force driving fruit morphological variation is uncertain. Fruits of A. lentiginosus are wind-dispersed and it is unlikely that wind dispersal generates spatially divergent natural selection across the landscape that might drive fruit adaptation. Defense against pre-dispersal seed predation by beetles is suspected to be shaping fruit morphological variation. Astragalus lentiginosus is an important study system given that many, but not all specimens, are toxic to grazing livestock, warranting the common name "locoweed". Additionally, several varieties are of conservation concern and receive some form of protective status.

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Population Genetics/Genomics

Topic: Contributed Papers

Title: Defining gene flow within Sabal minor to understand trunk diversity

Author: ***Ayress Grinage @ Cornell University***

Keywords: population genetics,Southeast US,systematics,Arecaceae

Abstract:

Sabal minor (Dwarf Palmetto) is considered one of a handful of cold tolerant palms with the ability to withstand winters as far north as Virginia. Across its native range, S. minor can be found across three different climatic zones: tropical, subtropical, and subtropical/temperate. Unlike other species of Sabal, most populations of S. minor do not form a trunk which may serve

as an adaptation to living in extreme habitats. Across the central US Gulf Coast, however, the species becomes variable for trunk type where individuals within populations can be either trunkless or trunked. The trunked phenotype is strongly heritable, and the trunked growth form of S. minor is horticulturally known as ‘Sabal louisiana’. For my dissertation research, I am adopting a population genetic approach to characterize the genetic diversity of S. minor and investigate the evolutionary and ecological processes associated with the geographically restricted trunk polymorphism (trunked/trunkless).

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Topic: Contributed Papers Population Genetics/Genomics

Title: Evolutionary history and population genetics of an endangered plant species (Amsonia tharpii) across a fragmented landscape

Author: ***Dylan Cohen @ Chicago Botanic Garden***

Keywords: Apocynaceae,ddradseq,Endangered Species Act,population genetics,conservation

Abstract:

Habitat fragmentation can lead to a cascade of negative effects such as reduced fitness, population decline, or extinction. Narrowly distributed species occurring in small populations across a fragmented landscape are strong candidates for conservation assessment. Small, isolated populations are more likely to be inbred and contain less genetic variation than widespread, panmictic populations. Inbreeding depression leads to loss of genetic variation and to less adaptability. Amsonia tharpii (Apocynaceae) is listed as rare and endangered by the states of New Mexico and Texas and consists of five populations occurring on limestone and gypsum substrates across the Permian Basin in eastern New Mexico and western Texas. The Permian basin is a natural resource rich region and produces more crude oil than the rest of the United States. It is suspected that land use and climate changes have led to demographic decline for all A. tharpii populations and field surveys to find seedlings have been unsuccessful. In addition, there are taxonomic uncertainties surrounding A. tharpii and A. fugatei. We generated two double digest Restriction site associated DNA sequence data (ddRADSeq) sets to address phylogenetic and population genetic questions for conservation assessment. The phylogenetic dataset was used to elucidate evolutionary relationships across the western North American Amsonia, and to determine if A. fugatei and A. tharpii are conspecifics. We then used a comparative phylogenetic framework to investigate genetic diversity, population structure, and effective population size for A. longiflora (widespread), A. fugatei (narrow endemic), and A. tharpii (threatened, narrow endemic). Phylogenetic results indicated that A. fugatei and A. tharpii are sister species to a clade containing A. tomentosa and A. arenaria. Population genetics of all three species revealed similar genetic diversities, suggesting that inbreeding and low genetic variation is not a concern for A. tharpii. However, populations of A. tharpii were found to be highly structured (K = 5) which suggests low interpopulation gene flow, genetic drift, and divergence. Flowers of Amsonia are white to blue, produce a sweet-smelling scent and nectar, open in the evening, and have elongated floral tubes. These traits are consistent with moth pollination and large bodied moths such as Hyles lineata (hawkmoths) are capable of transferring pollen long distances. Population structure for A. longiflora and A. fugatei suggest hawkmoth pollination as these were panmictic. Populations of A. fugatei are geographically closer together and are not interspersed with oil and gas wells like A. tharpii. The lack of gene flow among A. tharpii populations has created distinct population segments or ESU's (evolutionary significant units) with unique genetic variation (and evolutionary potential). We therefore recommend that all populations of A. tharpii be treated as distinct population segments and protected.

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Topic: Contributed Papers

Title: Mating system and life history: estimating selfing rates in annual and perennial species

Author: ***Anri Chomentowska @ Yale University***

Keywords: comparative genomics,ddradseq,life history,Mating system,population genomics,selfing,selfing syndrome,conservation genetics

Abstract:

Increased rates of self-fertilization (“selfing”) in sexual systems are tightly associated with an annual life history in flowering plants; we expect an increased selfing rate and morphological traits associated with selfing (“selfing syndrome”) to evolve in annual lineages.

One key trait to measure here, of course, is the level of selfing. Selfing rates, however, are difficult to estimate––large progeny arrays are often unattainable for natural populations, and population genetic studies using the Inbreeding Coefficient to calculate selfing rates can be unreliable. To circumvent this problem, selfing rates can also be estimated from a population genomic value called the Identity Disequilibrium (g2), defined as the variance in inbreeding levels as measured by how much multilocus heterozygosity deviates from expectation under random assortment.

Here, we test whether life history would give rise to differences in selfing rates among closely related annual and perennial, self-compatible species of genus Calyptridium Nutt. in the Montiaceae family. We sample 20-30 individuals from around 10 populations for two annual Calyptridium species and two perennial species across western North America. We utilize ddRAD sequencing and assemble the resulting reads using a closely-related whole genome reference to identify a large number of SNPs. The assembled ddRAD loci are then used to calculate g2 to estimate average population selfing rate, such that we can compare the values among populations, and importantly, between annual and perennial species.

This is one of few examples utilizing high-throughput sequencing to comparatively and concurrently study selfing rates and plant life history. Furthermore, this provides an excellent population genomic dataset for ongoing conservation efforts in the genus Calyptridium.

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Topic: Contributed Papers Population Genetics/Genomics

Title: Ecological Bastion and Iconic Cultural Food: Conservation Genomics of the Argan Tree

Author: ***Madeline Slimp @ University of California***

Keywords: _{conservation biology},Angiosperms353,Argan

Abstract:

The Argan tree (Sideroxylon spinosum, Family: Sapotaceae), is an iconic keystone species endemic to Morocco, where it serves as one of the only ecological barriers to the encroaching Sahara desert. A number of local livelihoods, predominantly those of Moroccan women, depend on the tree for producing edible oil used in Moroccan cuisine. This cultural significance is recognized worldwide, with the Argan tree being added to UNESCO's Representative List of the Intangible Cultural Heritage of Humanity in 2014. Additionally, Argan oil is being exported out of Morocco for global use as an ingredient in cosmetic and personal care products, with the Argan oil market estimated at nearly 300 Million USD.

In the past century, forest cover has halved, with some areas seeing a 66% reduction in argan tree density. In 1998, UNESCO erected the Arganeraie Biosphere Reserve, designed around the declining argan tree and its reliant rural communities. Sideroxylon spinosum has been recently categorized as 'Vulnerable' on the IUCN Red List, with major threats reported as overgrazing, logging, land clearing for agriculture and urban development, and increased aridity. Despite being at evidenced risk, the Argan tree has been overlooked for broad genome approach research, which could be beneficial for conservation, management, and improvement.

In this presentation we describe our recent effort to characterize the population genomics of Sideroxylon spinosum using the Angiosperms353 target capture kit. This study will be the first large-scale within species population genomics study using Angiosperms353. The outcome of this project is to quantify and map genetic qualities of current Argan tree populations across Morocco for the purpose of informing future biobanking efforts to preserve current genetic diversity. The information generated by this project could inform land managers about sources of genetic variability to integrate into current argan forests based on ancestral population data paired with existing ecotype identifications. We determine the number of ancestral genetic populations across the country of Morocco and compare this with previous microsatellite and ISSR marker papers. We calculate 'Genetic health' metrics such as Tajima's D, heterozygosity, inbreeding coefficient and used to identify regions of Morocco that are at the greatest need for conservation effort for the Argan tree.

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Topic: Contributed Papers

Title: Conservation genomics of an endangered Asteraceae (Deinandra increscens subsp. villosa) native to the Central Coast of California

Author: ***Susan McEvoy @ Santa Barbara Botanic Garden***

Keywords: Asteraceae,conservation,landscape genomics,population genomics,Reference genome,Deinandra,endemic,endangered

Abstract:

California is one of the most biodiverse regions in the world, but more than 30% of its species are at risk of extinction. One such taxon is Deinandra increscens subsp. villosa (Gaviota tarplant), endemic to Santa Barbara County, where it exists in small and fragmented populations of the coastal and inland areas. Deinandra increscens subsp. villosa is a small, yellow, insect-pollinated, annual with disk and ray florets common to most Asteraceae. The Asteraceae family is large, comprising 10% of angiosperm species, but not well-represented in genomic studies. Deinandra increscens subsp. villosa is listed as Endangered under both the Federal and State Endangered Species Act. Since 2016, the Strauss Wind Project has been constructing a large turbine wind farm within the core of the distribution of D. increscens subsp. villosa. While this project will provide clean energy to 44,000 homes, turbine construction will directly impact some number of plants within the construction footprint and may impact ongoing biological processes (e.g., pollen transfer) through normal turbine operation. potentially eliminating sources of adaptive genetic diversity. As part of the permitting requirements, regulatory agencies require a detailed genetic study of D. increscens subsp. villosa. As such, we are applying conservation genomics approaches to understand the genetic impact of development among the Strauss population and the broader native range. This will include population genetics, landscape genetics, and time-to-extinction modeling. Samples from almost 1,000 individuals were collected from across the range over the course of three years: 384 in year 1, and 288 in years 2 and 3. Ninety-six from each year will be sequenced at 30x with the remainder at 4x. Reference genome sequencing includes 40x of Pacific Biosciences HiFi, 60x of Oxford Nanopore Technologies PromethION, and 70x Dovetail OMNI-C for scaffolding. Initial estimates based on flow cytometry and k-mer profiling indicate that the plant is a diploid around 1.7-2.3 Gbp in length. We are currently testing assemblies with Verkko, Canu, and Flye, and this will be followed by scaffolding with 3D-DNA, and gene annotation with both de novo and homology methods. For the transcriptome, root and shoot tissue was collected from 3 seedlings plus stem and leaf from the adult reference individual. From these eight samples, we generated 150 bp PE Illumina sequencing which will be assembled using the Oyster River Protocol. We will conduct population genetics analyses to discern population structure, effective population size, and demographic history; levels of inbreeding and runs of homozygosity; and amounts of admixture and gene flow between populations. We will incorporate environmental metadata to examine the effects of landscape and climate on populations, and we will integrate genetics and life history traits to model time-to-extinction. Together, these analyses encompass a three-year plan of evaluation which will be followed by additional assessments in 10 years. Results will help inform ongoing development within the Strauss project footprint. This study will also have broader impacts on policies regarding endangered species in California by providing an exemplary study of implementing genomic analysis for conservation planning.

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Topic: Contributed Papers Population Genetics/Genomics

Title: Does size really matter? Implications of small population size for rare plants

Author: ***Andrew Davies @ Northwestern University and Chicago Botanic Garden***

Keywords:

Abstract:

Theory states that for populations that are small the risk of extinction is large. The small population paradigm was theorized to describe how demographic dynamics and population genetics contribute to increasing small populations' susceptibility to stochastic events. However, numerous species have always persisted at low numbers with minimal impact, suggesting that this idea might be an over generalization. Population extinction from stochastic events is inherently unpredictable, and uncoupling the demographic drivers from the impacts of limited genetic diversity and inbreeding on small population size is a major challenge. This study aims to examine the predictions of the small population paradigm and importantly attempt to untangle the demographic effects from the genetic ones to improve our ability to predict extinction risk and better manage small, rare plant populations. This study aims to 1) assess the demographic consequences of population size, 2) assess the genetic differences by populations size, and 3) finally determine if demographic factors, genetic parameters, or the interaction of both are best at predicting population fitness. To address these objectives, censuses of a rare midwestern endemic plant were conducted to identify a gradient of small to large populations. Plant size and reproductive fitness data were collected from each population, and genetics metrics were calculated from sequence data. To determine further fitness differences, we conducted a drought experiment on plants grown from seed collected in small and large populations and that had high and low genetic diversity, and different combination of both. This experiment aimed to assess each population's ability to cope with an ecologically relevant event. We found a positive correlation between population size and reproductive fitness and genetic diversity, but not plant size. There were population level differences between other fitness metrics, including response in plant growth and survival under experimental drought conditions. These results hint at genetic and demographic outcomes of increased stress placed on small populations. While some small populations may persist through stochastic events, if inbreeding increases and genetic diversity is lost, fitness reductions may hinder the populations' ability to adapt. It may be prudent to consider pathways for preventing the loss of genetic diversity and minimize inbreeding when managing small populations. Future work should address how isolation, gene flow, and potential genetic rescue can aid in decreasing the susceptibility of certain small populations to stochastic events such as drought.

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Topic: Contributed Papers

Title: Pitcher sages in peril? A conservation genomics study of Lepechinia rossii (Ross's pitcher sage)

Author: ***Robert Comito @ California Botanic Garden***

Keywords: _{conservation biology},conservation,population genomics,rare plants

Abstract:

Lepechinia rossii (Ross's pitcher sage) is a highly aromatic shrub narrowly endemic to southern California. It occurs in chaparral communities at two locations in the Western Transverse Ranges of Los Angeles and Ventura counties. It is listed by the California Native Plant Society (CNPS) with a Rare Plant Rank of 1B.2, rare or endangered in California and elsewhere, and fairly endangered in California. It is considered "Critically Imperiled" both statewide (S1) and globally (G1; NatureServe 2020). It faces a range of threats from invasive species; changes in fire regimes; and human activities including off highway vehicle use, power line maintenance, and petroleum exploration. Conserving the handful of occurrences that are known to be extant is crucial to ensuring the future of this species. Conservation actions include resurveying known occurrences, searching for new occurrences and potential habitats, updating threat assessments, and studying the natural history of the species and genetic structure of known populations.

Field work was conducted on in the Angeles National Forest (ANF) and Los Padres National Forest (LPNF) to sample leaf tissue from Lepechinia rossii populations across its range. Seventy-three samples were collected from the ANF and forty-five samples were collected from the LPNF. Many plants, especially in LPNF, had begun to lose their mature leaves due to drought conditions, so tissue for DNA extraction was taken from young leaves and protected buds. DNA has been extracted from 132 samples of L. rossii and outgroups including: L. hastata, L. calycina, L. fragrans, L. ganderi, and two samples of wild collected L. cardiophylla from the Santa Ana mountains. DNA was extracted using Qiagen DNeasy kits, and DNA concentrations were standardized to 20 ng/ul. A maximum likelihood phylogeny has been estimated with 1000 ultrafast bootstraps in IQtree on alignment of ddradseq 74,898 loci generated through an ipyrad pipeline. The preliminary phylogeny of sect. Calycinae of Lepechinia (Lamiaceae), with five sampled species from California (L. calycina, L. cardiophylla, L. fragrans, L. ganderi, and L. rossii) show a monophyletic group containing all sampled L. rossii as sister to a clade containing the remaining four California species. Furthermore, specimens from the two sampled localities (Ventura and Los Angeles counties) form reciprocally monophyletic groups. Population genomic analyses sampled the entire L. rossii range and nearby populations of L. fragrans and revealed highly differentiated populations that show little sign of admixture. Genetic structure of L. rossii populations in uncovered in this study will inform future conservation management and possible restoration efforts.

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Topic: Contributed Papers Population Genetics/Genomics

Title: Reconstructing the invasion history of Microstegium vimineum using plastid genome sequencing and herbariomics

Author: ***Cameron Corbett @ West Virginia University***

Keywords: biological invasions,genomics,plastome,Poaceae,population genomics,seed dispersal,grass

Abstract:

The study of invasive species is a critical area of research due to negative impacts on biodiversity and economies globally. The ecological impacts of invasive species have been the focus of a significant number of studies in recent years, however, less is known about how they adapt and spread in new environments. Stiltgrass (Microstegium vimineum) is an invasive species that was first discovered in the United States approximately 100 years ago near Knoxville, Tennessee. Based on a previous study using digitized herbarium records, it is hypothesized that there were at least two introductions from genetically distinct source populations in Asia. However, few genomic studies across space and time for invasive species have been conducted, including stiltgrass. I hypothesize that multiple introductions have occurred leading to the genetic diversity present in the invasive range. Illumina sequencing via genome skimming was focused on plastomes, which are highly conserved in land plants and uniparentally inherited. They can therefore be used to track seed dispersal between the native and invasive ranges, and within the invasive range post-establishment. DNA was extracted from over 200 contemporary field collections and historical herbarium samples, and Illumina libraries were generated from all sampling locales collected and sequenced on an Illumina NextSeq2000. Plastomes were assembled with GetOrganelle and aligned with MAFFT, maximum likelihood trees were constructed using IQtree, and haplotype networks were drawn using PopArt. Plastome data were used to reconstruct the pattern of invasion history and specifically seed dispersal by using the uniparentally inherited plastome as a proxy for seed dispersal. Plastid genomic relationships were used to characterize geographic patterns of important traits (e.g. awn presence/absence) across space and time in the eastern USA and Asia and determine how genetic diversity differs from the native to invasive range. Constructed haplotype networks were used to trace the ancestry of individuals in the invasive range, using the native-range samples as a comparative reference for total plastome diversity. Historical samples are split into seven time slices of approximately fifteen years. Slices were studied to reconstruct the invasion history and track patterns of genetic diversity in the invasive range over time. All southern US accessions appeared to initially comprise the same haplotype, indicating a single introduction, possibly from Japan. Northern US accessions revealed multiple haplotypes that are most closely related to accessions in China, Japan, and Taiwan. Additionally, new haplotypes occurred over time, suggesting multiple introductions or a more diverse initial introduction than would be expected under a severe genetic bottleneck resulting from a single introduction. Furthermore, there is evidence for long distance seed dispersal as new haplotypes are found in increasingly large areas over time. Evidence for long distance seed dispersal and multiple introductions sheds light on a more complicated invasion history than previously thought, and illustrates how stiltgrass has spread since its initial discovery in the US over 100 years ago. The invasion pattern of stiltgrass can be used as a model to determine how other potentially invasive species might become established and spread to better contain and manage them.

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Topic: Contributed Papers

Title: It’s A Small World After All: Applying library miniaturization and “microhaplotypes” to plant population genomic research

Author: ***Madison Bullock @ Texas Tech University***

Keywords: Angiosperms353,bioinformatics,high-throughput sequencing ,target-capture,relationship inference,congeneric species

Abstract:

The evolution of high-throughput targeted sequencing using universal markers has allowed for the generation of substantial sequence data pools from non-model organisms at cost-effective rates. These methods target areas of interest such as highly conserved regions and functional genes under the assumption of containing enough genetic variability to differentiate between species or even individuals. However, despite the relatively low cost when compared to whole-genome sequencing methods and subsequent feasibility for multi-sample population research, there is room for improvement. Recent population genomic studies using Angiosperms353, a universal probe set for 353 protein-coding genes found in flowering plants, found little gene recovery bias based on taxon, high recovery in segregating sites representing both between- and within-species distinction, and hitchhiking recovery of flanking non-coding regions. It is therefore possible to genotype multiple SNPs occurring in both coding and their flanking non-coding regions together as a multi-allelic “microhaplotype” for use in relationship inference of individuals and populations. In order to conduct relationship inference, we require large sample sizes and new methods for high-throughput targeted sequencing analysis. We describe our use of low-volume automated liquid handlers to prepare target-capture libraries from herbarium specimens at ⅒ volumes and compare recovery results to ½ volume library sequences. We also propose a “microhaplotype” bioinformatics pipeline through examples of results from two congeneric species pairs with a special focus on core-edge range and widespread-endemic population demographics.

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Population Genetics/Genomics

Topic: Contributed Papers Population Genetics/Genomics

Title: Chloroplast diversity and relationships between Johnsongrass (Sorghum halepense) and sorghum (Sorghum bicolor)

Author: ***Michael McKain @ The University of Alabama***

Keywords: chloroplast capture,chloroplast sequencing,hybridization,invasive species,Johnsongrass,Sorghum,chloroplast haplotype

Abstract:

Johnsongrass (Sorghum halepense (L.) Pers.) is an invasive, polyploid grass found throughou disturbed and agriculture areas of temperature, subtropical, and tropical regions. This species is thought to be an allotetraploid formed through the hybridization of sorghum (Sorghum bicolor (L.) Moench) and Sorghum propinquum (Kunth) Hitchc. Subsequent hybridization back to S. bicolor followed by introgression into Johnsongrass populations has led to the introduction of weedier traits in some germplasm. Since its introduction into the United States in the early 1800s and secondary introduction into Arizona sometime later, Johnsongrass has spread throughout much of the Southeast, lower Great Plains, portions of the Midwest, Southwest, and California. The movement of this invasive has been facilitated by the transport of agricultural products and the development of major railway and highway systems where Johnsongrass thrives in the disturbed areas surrounding fields, railroads, and highways. In this study, we sampled and isolated whole genomic DNA from approximately 300 individuals from more than 50 populations across the United States. Using low-coverage whole genome shotgun Illumina sequencing, we assembled whole chloroplast genomes for each sample. We also assembled whole chloroplast genomes from similar data found in the NCBI SRA for multiple Sorghum species including over 50 S. bicolor lines. Using these data, we reconstructed a maximum likelihood phylogeny using other members of the Andropogoneae as outgroups. We also constructed a chloroplast haplotype map focusing on S. arundinaceum (S. bicolor var. arundinaceum), S. bicolor, S. halepense, and S. propinquum chloroplast genomes to identify patterns of similarity across US populations. We found that the chloroplast diversity of US Johnsongrass falls into two main groups: one allied with S. bicolor and S. propinquum and the other with unique haplotypes and no clear relationship to putative parenta haplotypes. There was no clear relationship between geographic origin of specimens and their chloroplast haplotypes. In some cases, identical or nearly identical haplotypes were found in populations from across the country, suggesting potential long-distance dispersal. Similarly, chloroplast haplotypes were found to be identical to those seen in improved sorghum lines, suggesting recent hybridization and chloroplast capture of these sorghum haplotypes into US Johnsongrass populations. This works demonstrates that though widespread dispersal and hybridization to sorghum have likely shaped the genetic variation across populations of Johnsongrass, there remains a subset of chloroplast haplotypes that may represent unique genetic diversity. Future work will investigate the nuclear genomes of these samples to better describe this diversity and how variation in diploidization may drive adaptation into new environments.

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Population Genetics/Genomics

Topic: Contributed Papers

Title: Analysis of Populations of Bromus tectorum from Cyprus, Greece, and Turkey: Circumscribing its Center of Genetic Diversity

Author: ***Stephen Novak @ Boise State University***

Keywords: Cheatgrass,Bromus tectorum,native range,Central-Marginal Hypothesis

Abstract:

The “Central-Marginal Hypothesis” posits that centrally located core populations would have higher genetic diversity compared to populations at the margin of a species’ distribution. To test the predictions of this hypothesis, comprehensive sampling, and genetic analysis of many populations are necessary to circumscribe a species' center of genetic diversity. Bromus tectorum L. (cheatgrass, Poaceae) is a diploid annual grass that is broadly distributed across much of Eurasia. As part of our long-term analysis of native populations of B. tectorum, we previously analyzed the genetic diversity of 93 populations from across Eurasia, using allozymes. By far, populations from the Middle East display the greatest genetic diversity, 4.35 multilocus genotypes (MLGs) per population, with 11 populations from Israel displaying the most diversity (31 MLGs and 5.4 MLGs/population). To circumscribe further the center of genetic diversity of B. tectorum in its native range, we report here the analysis of 51 populations from Cyprus (12 populations), Greece (20 populations), and Turkey (19 populations). Among these 51 populations, 40 MLGs were detected, with populations from Greece (24 MLGs and 3.1 MLGs/population) and Turkey (26 MLGs and 3.4 MLGs/population) having the greatest diversity. Populations bordering the Aegean Sea in Greece and Turkey display the highest diversity, compared to other populations (i.e., from eastern Turkey and Cyprus). For instance, 10 populations from western Turkey have 24 MLGs and 5.0 MLGs/population. Values for western Turkey populations are similar to those previously reported for populations from Israel. Taken together, these results indicate that the center of genetic diversity for B. tectorum in its native range occurs in the eastern Mediterranean region (including areas surrounding the Aegean Sea). These findings likely reflect the long history of human occupation, transport, and commerce throughout this region.

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Population Genetics/Genomics

Topic: Contributed Papers

Title: Possible cryptic species in widespread Abronia fragrans complex species

Author: ***Sherese Price @ Texas Tech University***

Keywords: Angiosperm 353,Angiosperms,Cryptic Species,population genetics,high-throughput sequencing

Abstract:

The sand verbenas in Abronia (Nyctaginaceae) have had an extensive history of inconsistent classification, possibly due to overlapping regions among species. Abronia fragrans is the most widespread species within the Abronia genus that also has the lowest support in genetic relationships to other species. In our previous phylogenetic analysis, we found that although Abronia fragrans is in a clade with high support it remains indistinct from several range-restricted taxa including the gypsum endemic Abronia angustifolia. We sampled over 200 herbarium specimens of Abronia fragrans to identify genetic structure in the range, especially related to a color morph variation found in west and central Texas. By using population genetic methods, we investigate further whether A. fragrans has a history of gene flow associated with color morphology and introgression with other species that have restricted distributions.

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Population Genetics/Genomics

Topic: Contributed Papers Population Genetics/Genomics

Title: Capricious chromosomes: Influence of polyploidy on morphology, reproductive strategies and genetic differentiation amongst varieties of Rhodohypoxis baurii (Hypoxidaceae).

Author: ***Bianca Ferreira @ University of Connecticut***

Keywords: gene flow,polyploid,clonal reproduction,Rhodohypoxis,reproductive strategie

Abstract:

Evolutionary mechanisms, such as whole genome duplication (polyploidy) has been noted to alter morphology and reproductive strategies of plant species, leading to the generation or the loss of species. Rhodohypoxis (Hypoxidaceae) is a small Drakensberg near endemic genus containing six species, one of which is Rhodohypoxis baurii. Rhodohypoxis baurii contains three morphologically distinct varieties, each with varying ploidy-levels (2x, 3x and 4x). Gene flow has been noted to occur between varieties as well as ploidy levels making R. baurii an ideal system to evaluate whether polyploidy can lead to lineage divergence or homogenization via shifts in reproductive strategies. To evaluate potential reproductive barriers, a total of 231 crosses were performed both between and within varieties and ploidy-levels, of which 113 produced 1530 seeds. Pollen viability was compared among varieties and ploidy levels to assess if reproductive barriers were pre-zygotic. Genetic differentiation and gene flow were quantified both among the varieties and ploidy-levels across 11 populations using 12 microsatellite markers. Thirty vegetative, floral, and reproductive traits were measured across 124 herbarium specimens and 43 individuals housed in the greenhouse. Ploidy levels were estimated using flow cytometry and compared to morphology, genetic differentiation and reproductive strategies. Rhodohypoxis baurii polyploid individuals show a shift away from sexual reproduction to asexual reproduction as polyploid intra-ploidy crosses showed lower seed sets and germination rates than diploid intra-ploidy crosses. Furthermore, all polyploid R. baurii individuals showed higher rates of clonal reproduction than diploid individuals. A latitudinal ploidy gradient was found across sampled populations that correspond with shifts in reproductive strategy, and changes in the extent of gene flow. Population genetic structure coincided primarily with geographic localities, with diploid Northern Drakensberg populations comprising similar allelic diversity to each other, but differed from the tetraploid Southern Drakensberg populations. Conclusively, decreased gene flow facilitated by polyploidy, shifts in breeding systems and geographic isolation are likely contributing to both species diversification and homogenization in this lineage.

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Population Genetics/Genomics

Topic: Contributed Papers

Title: 2 does not equal 4: Variance dissimilarities in mixed-ploidy genomic data cause irregular patterns in PCA and other clustering analyses

Author: ***Trevor Faske @ University of Nevada, Reno***

Keywords: Diploid and polyploid ,heteroploid dataset,polyploid,simulation,STRUCTURE,PCA,mixed-ploidy,Ordination

Abstract:

The formation of polyploids, individuals with multiple sets of chromosomes, has played a major role in the diversification of plants and can have pronounced evolutionary consequences with extended ecological effects. A history of polyploidization events is evident within roughly 50% of plant species and has been shown to vary across latitude, elevation, and environmental stressors. Moreover, it is estimated that 16% of all plant taxa are mixed-ploidy systems, where a single species has multiple known ploidal levels that can vary either between populations across geographic and environment gradients, or within a single population. While high-throughput sequencing has made it possible to generate a genome-wide perspective easily and affordably for thousands of individuals across the landscape, there are still many statistical and bioinformatic uncertainties arising from ploidal variation. In recent years, a plethora of statistical software has been published to appropriately call genotypes and incorporate uncertainty in mixed-ploidy systems, but proper assessment of how mixed-ploidal variation affects widely used downstream population genetic analyses is lacking. To address this, we evaluated outcomes of principal components analysis (PCA) and other clustering analyses (e.g., Structure, neighbor-joining, UMAP, etc.) across a range of common variant calling and genomic standardization approaches. We simulated multiple mixed-ploidy systems that varied by the extent of genetic differentiation as well as number of demes, individuals, and loci. Our results show that currently accepted practices for variant calling and standardization can have vastly different effects on clustering outcomes and interpretations. Alarmingly, the effect of ploidal variation on clustering is more pronounced that of true genetic differentiation, which is the goal of these analyses. We identify the cause to be dissimilar variance across ploidy levels, which influence clustering results in analyses that rely on forms of variance partitioning or maximization. We also highlight the evolutionary scenarios in which this issue is more pronounced and offer suggestions to better handle and interpret mixed-ploidy variation in clustering analyses. This research builds on recent advances in mixed-ploidy population genetics and provides researchers with an improved framework to handle and interpret results from various population and landscape genomic analyses.

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Pteridology

Topic: Contributed Papers Pteridology

Title: A systematic revision of the Athyrium filix-femina species complex in the Americas

Author: ***Bertrand Black @ University of Vermont***

Keywords: fern diversity,phylogenomics,target-capture,Taxonomy

Abstract:

Athyrium filix-femina (L.) Roth is a terrestrial fern that is widespread in forest regions across the Northern Hemisphere and South America. Despite its prevalence, its taxonomy in the Americas remains unresolved and the evolutionary relationships between taxa remain poorly understood. Uncertainty about whether to recognize a single widespread A. filix-femina or several endemic American species has persisted to the present day due to unclear morphological differences between regional varieties and a lack of a comprehensive study across its range. To address this uncertainty, we sampled herbarium specimens from four continents and employed an integrative methodology that combined molecular, morphological, and biogeographic data to examine evidence for speciation, hybridization, and cryptic diversity in this species complex. Our results indicate that there are at least five monophyletic lineages in North America with diagnosable morphology, habitat preferences, and discreet geographic ranges. In spite of many documented hybrids in Asia, we found no evidence for widespread hybridization or reticulation among North American species. In South America, we did not find clear species boundaries defined by morphology, geography or molecular evidence to recognize more than a single species. Allele phasing identified a single putative hybrid from Queretaro, Mexico of unknown origin. Research such as this enhances our capacity to recognize and document American floristic diversity that may be concealed in plain sight and highlights the value of utilizing integrative molecular methods to facilitate biologically accurate classification of plant species.

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Pteridology

Topic: Contributed Papers Pteridology

Title: A morphometric analysis of western sword fern (Polystichum munitum) pinnae and pinnae scales across the coast redwood forest ecological gradient

Author: ***Lacey Benson @ San Jose State University***

Keywords: ecological gradient,foliar water uptake,pinnae scales,Polystichum munitum,summer fog,coast redwood,Polystichum

Abstract:

Ferns are an integral component of biodiversity and productivity in the coast redwood understory and canopy. Given that summer fog is expected to decrease and winter precipitation patterns are predicted to change it is vital to understand the role of microclimates and adaptation strategies utilized by ferns in the coast redwood ecosystem in order to gauge how the distribution, community dynamics, and reproductive success of ferns will be affected in the coming decades. Researchers have found ferns display signs of shifting climate patterns through leaf traits such as number of fronds, size of fronds, foliar uptake capacity and leaf water retention. By studying morphological and physiological changes to ferns scientists can get a more rapid understanding of how community dynamics and slower growing species such as the coast redwood will be affected by future changes to climate. The aims of this study are (1) to compare western sword fern (Polystichum munitum or POMU) pinnae size traits (length, width, and length:width ratio) to environmental variables such as precipitation, fog frequency, and temperature; (2) to quantify pinnae scale density to compare with in situ climate data; and lastly (3) to collect, mount, and enter POMU specimens and redwood associate species into the Carl W. Sharsmith Herbarium at SJSU. To achieve these objectives, we will utilize digitized herbarium accessions as well as personal collections to measure pinnae in ImageJ and count scales on both pinna surfaces. Data will then be compared to latitude and in situ environmental variables. The results of this study will greatly inform our understanding of the landscape scale variety of morphological and physiological traits within POMU and add to previous research on POMU foliar water uptake capacity and leaf water retention abilities.

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Pteridology

Topic: Contributed Papers

Title: An updated phylogeny of athyriid ferns (Athyriaceae: Polypodiales) focused on recalcitrant species

Author: ***Julia Hobbie @ Utah State University***

Keywords: Chloroplast genome,Ferns,phylogenetics,Athyriaceae

Abstract:

Athyrium and allied species (the “athyriid” ferns) form a clade of mostly terrestrial ferns that are distributed worldwide with most diversity represented in Asia. The treatment of this group has been inconsistent, with some workers recognizing one genus, Athyrium, and others splitting the clade into multiple genera including Anisocampium, Cornopteris, Ephemeropteris, and Pseudoathyrium. Most studies have focused on particular clades or geographical regions, which has limited the resolution of generic ambiguity. We used four chloroplast genes to infer a phylogeny of the athyriids focusing on non-core-Athyrium species that have been difficult to place. Our updated phylogeny will help resolve uncertainty in the generic circumscriptions of athyriid ferns.

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Pteridology

Topic: Contributed Papers

Title: Phased HybSeq Data Provides Further Support for Reticulate Allopolyploid Evolution within the Notholaenid Desert Fern clade (Pteridaceae).

Author: ***David Adelhelm @ Utah State University***

Keywords: Ferns,HybSeq,nuclear DNA,phylogenetics,polyploidy

Abstract:

Phylogenetic analysis of plants has historically been hindered by the paucity of low- or single-copy nuclear markers available for amplification and sequencing. As a result, plastid markers dominated phylogenetic workflows due to their relative abundance and applicability across many taxa. However, as a consequence of their uniparental inheritance, plastid markers are unable to fully reflect the evolutionary history of individuals that have experienced recent hybridization, a defining feature of allopolyploids. Hybseq and the release of the GoFlag451 probe set represent a prime opportunity to augment existing phylogenetic knowledge through the inclusion of numerous single- to low-copy nuclear loci. Here we demonstrate the effectiveness of multi-locus hybseq data in inferring the phylogeny of a group with allopolyploids, with a pipeline incorporating recently available methods in polyploid read assembly (PATÉ) and locus phasing (homologizer), applied to the notholaenid ferns of Mexico and the US southwest. In addition to providing evidence of allopolyploid evolution within the clade, our well-supported multi-locus phylogeny provides a strong framework for a subsequent taxonomic treatment of Notholaena and its relatives.

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Pteridology

Topic: Contributed Papers

Title: The ferns and lycophytes of Honey Island, Paraná, Brazil

Author: ***Fernando Matos @ CRIA (Centro de Referência em Informação Ambiental)***

Keywords: Education,Floristics,Pteridology,Taxonomy,field guide,pteridophytes

Abstract:

Honey Island is located at the entrance of Paranaguá Bay, 2,800 meters offshore from Pontal do Sul, Paraná, Brazil. With an area of about 3,000 hectares and elevations ranging from sea level to 150 meters, this subtropical island harbors a great diversity of plants, including 131 pteridophytes. An earlier publication, from 2005, reported 109 species, including 103 ferns and six lycophytes. During the COVID-19 pandemic, I started visiting that island with the goal of photographing as many species as I could find. From May 2021 to March 2023, I went on 32 field trips and took more than 10,000 photographs of landscapes, animals, and plants. So far, I have found 118 species of pteridophytes, including 96 species from that previous list and 22 new records. My goal now is to find the remaining 13 species from that list, and once they are all photographed, I would like to produce a nice book about them. In this field guide, each species would have two facing pages, one with text and the other with photos. The text would be bilingual (English and Portuguese) and the photographs would be standardized to show features of the stems, leaves, and sori. An identification key for all the species will also be provided. The target audience for this book would be local residents, visitors (national and foreign), students (from elementary to university level), botanists (amateurs and professionals), and other researchers alike. My idea is to educate people about ferns and lycophytes based on my field observations and my knowledge acquired during the past 20 years working as a pteridologist. In this Oral Paper, I will give a preview of this book.

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Pteridology

Topic: Contributed Papers Pteridology

Title: Frond dimorphism in Tectaria ferns: trends of their foliar characteristics and spore investment

Author: ***You-Wun Hwang @ National Tsing Hua University***

Keywords: Frond Dimorphism,Tectaria,Reproductive Investment

Abstract:

Balancing between reproductive and vegetative investment help maximize plants’ fitness and their long-term adaptation. This question can be interesting in a group of plants, ferns, that utilize the same organ, fronds, to carry out both reproductive and vegetative missions. Bearing sporangia for reproduction or not, fern fronds can be categorized as either fertile or sterile. In many ferns, two kinds of fronds are monomorphic in their appearance. By contrast, dimorphic fern species produce the two fronds in distinct morphologies. This dimorphism has long been assumed to enhance spore dispersal, but less attention looks deep into their reproductive investment at the organismal level. Our aim was to study (1) what foliar traits contribute most to the frond dimorphism of Tectaria ferns and (2) whether the degrees of frond dimorphism also correlate with their reproductive investment of spores. Nine Tectaria species with varied dimorphism levels were sampled, and size-independent parameters derived from quantitative foliar traits were used to infer the dimorphism degree through linear regression analysis (LDA). Leaf mass per area (LMA), spore production, and total mass of frond production were also calculated to estimate their annual spore production per foliar mass as their reproductive investment. We found that frond area and perimeter are the two main factors contributing to the dimorphism degree. A negative correlation was discovered between frond dimorphism and reproductive investment. The reproductive investment itself is size-dependent in most sampled species and rises as body size increases.

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Pteridology

Topic: Contributed Papers

Title: Is Hawaiian Doryopteris (Pteridaceae) an incipient adaptive radiation?

Author: ***Carrie Tribble @ University of Hawaii at Manoa***

Keywords: evolutionary radiation,Hawaiian Islands,Tropical Botany,Cheilanthoid ferns

Abstract:

Doryopteris J. Sm. includes roughly 20 species of pantropical cheilanthoid ferns. Four species of Doryopteris are endemic to the Hawaiian Islands, including two widespread species found across all major islands and two narrow endemics known from small, isolated populations. The two widespread endemics are thought to hybridize, producing Doryopteris x subdecipiens. The evolutionary origins of these Hawaiian species, and their relationships to each other, are still unknown. Using a dataset of 316 nuclear loci generated by target enrichment from a sample of 69 individuals of Doryopteris and outgroups, we investigate the evolutionary relationships between the four endemic Hawaiian species of Doryopteris and the status of the putative hybrid. We find that while most Hawaiian Doryopteris samples fall together in a single clade (suggesting a single colonization of Hawai’i), one individual of Hawaiian D. cf. decipiens falls instead with a clade of the broadly-distributed species, Doryopteris concolor. This pattern suggests that while one dispersal event and subsequent radiation led to the current distribution of most Doryopteris across the Hawaiian islands, a second migration event contributed to previously undescribed diversity in Hawaiian Doryopteris. Furthermore, all Hawaiian species appear nested within the widely-distributed D. concolor complex, which occurs across the Americas, Pacific islands, and tropical Africa. However, our molecular data fail to recover the individual Hawaiian species as reciprocally monophyletic clades. Complex population dynamics, such as ongoing/ incipient speciation, hybridization, or extensive gene flow, may be contributing to the lack of monophyly within most Hawaiian species, and further population genetic analyses may be needed to untangle relationships within the Hawaiian clade.

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Pteridology

Topic: Contributed Papers

Title: A phylogenomic study of Elaphoglossum provide new insights and highlight persistent challenges in the study of diverse tropical fern groups

Author: ***Weston Testo @ Field Museum of Natural History***

Keywords: alpine,Andes,Colombia,hybridization,Neotropics,phylogenomics

Abstract:

With more than 600 recognized species, Elaphoglossum (Dryopteridaceae) is one of the most species-rich and taxonomically complex genera of ferns in the world. Despite being the focus of extensive taxonomic and systematic study, many species groups of Elaphoglossum remain taxonomically intractable and several important evolutionary relationships within the genus are still unresolved. Improving our understanding of Elaphoglossum diversity is important because the genus is one of the most species-rich, dominant, and frequently collected vascular plant genera in many areas of tropical America, where ca. 500 species of Elaphoglossum occur. In this talk, we present the first phylogenomic study of Elaphoglossum, including more than 230 accessions and target-capture data from ca. 400 nuclear loci. We infer a phylogeny that is largely congruent with those reported previously, but with improved support and the recovery of novel clades and previously unsampled taxa. Our phylogenomic analyses also reveal, for the first time, the importance and frequency of reticulate evolution in Elaphoglossum. By integrating our phylogenomic data with information extracted from floristic accounts and herbarium specimens, we are able to present a data-driven assessment of the current state of knowledge for Elaphoglossum for the first time. From this, we highlight persistent challenges impeding the study of Elaphoglossum today and identify priorities and opportunities for research looking forward.

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Pteridology

Topic: Contributed Papers

Title: All Tangled Up: Unraveling reticulation and karyotype evolution in the vining ferns Lygodium

Author: ***Jessie Pelosi @ University of Florida***

Keywords: Aneuploidy,fern,polyploidy,reticulate evolution,phylogenomics

Abstract:

Reticulation has long been recognized as an important mechanism in the evolution of plants. These non-bifurcating evolutionary histories can arise from hybridization and polyploidy, which are prevalent throughout vascular plants. This is particularly evident in ferns with nearly one-third of speciation events in ferns accompanied by a change in ploidy in comparison to just 15% in angiosperms. The use of genome-wide data (e.g., phylogenomics) has been instrumental in resolving non-bifurcating evolutionary histories. Polyploidy is abundant in the vining ferns, Lygodium, which comprise a small clade of ferns with current classifications recognizing between 20 and 40 with a unique habit as the only group of vining ferns. Despite having relatively few species, Lygodium spp. have substantial ecological and economic impacts across their range; there are several ethnobotanical uses in their native ranges, while other taxa are highly successful invasive species. Here, we use a target-capture dataset to explore the phylogeny of Lygodium to 1) reconstruct the evolutionary relationships of Lygodium globally, 2) identify polyploid taxa and their putative diploid progenitors, and 3) asses the roles of autopolyploidy, allopolyploidy, aneuploidy in the evolution of this clade. Using the GoFlag408 probes, we assembled a dataset of 380 nuclear loci and developed the largest and most well-resolved phylogeny for the clade to date. Together with existing and newly generated genome size estimates, chromosome counts, and spore size measurements, we used alleleic phasing to explore hypotheses about the origin of several polyploid and hybrid taxa in Lygodium.

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Pteridology

Topic: Contributed Papers Pteridology

Title: Finding the hidden quillwort: identifying cryptic species in Isoëtes L. using an integrative systematic approach.

Author: **Forrest Freund @ Great Basin Institute**

Keywords: morphology,Californina,Cryptic Species,Isoetes,molecular phylogenetics,population genetics,Oregon

Abstract:

One of the greatest puzzles in taxonomy and conservation is the question of cryptic species. A cryptic species is one that is difficult to differentiate from others, be they close or distantly related. The genus Isoëtes has a high potential for crypsis: it is morphologically simple, difficult to find in the field, and generally not very well known. When studying the Californian members of the genus, I found indications that there were cryptic taxa treated under the widespread species I. nuttallii and I. orcuttii. To test my hypothesis that both species harbored cryptic taxa, I used a combination of molecular phylogenetics, population genetics, and morphological observations to test if all of the individuals identified as either speicies formed natural, monophyletic clades that matched the described species. As a result, I found that there were not two, but six species represented by the collections identified as I. nuttallii and I. orcuttii. My results show that not only is there potentially greater taxonomic diversity in Isoëtes than previously recognized, but the use of integrated phylogenetic, population genetic, and morphological evaluation, while time consuming, is capable of parsing out cryptic species.

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Pteridology

Topic: Contributed Papers

Title: Multiscale drivers of polyploid plant ecology

Author: **christopher krieg @ University of Wisconsin-Madison**

Keywords: ecological niche,ecology,ecophysiology,polyploidy

Abstract:

Polyploidy (or whole genome duplication) is common in vascular plants and is thought to be an important driver of evolution by facilitating species diversification. Classic theoretical models of polyploid establishment and persistence make clear predictions that polyploid ecological success is strongly impacted by organismal and ecological traits of polyploids. However, the empirical patterns of polyploid organismal and ecological traits are diverse and mixed; thus, the mechanisms that underlie the ecological success of wild polyploid individuals remain poorly understood. Here, I use a powerful model to intuitively interpret ecological and functional patterns in polyploid biology, which I call the Transgression Index (TI). I use this simple model to test classic polyploid ecology theoretical predictions across scales including the population, landscape, and global scales, using case studies and a large set of polyploid complexes. I show that the function and physiology of polyploids can predict co-occurrence patterns, range-wide niche occupancy, and the global distribution of polyploids when using the TI framework. The results of my analyses and using the TI framework represent a new tool to reconcile patterns of polyploid ecological niche and trait patterns observed in the wild polyploid taxa.

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Pteridology

Topic: Contributed Papers

Title: Genetic Mechanisms of Sex Determination in Ceratopteris richardii

Author: **Katelin Burow @ Purdue University**

Keywords: sex determination,SNP,Ceratopteris,Bulk Segregant Analysis,antheridiogen

Abstract:

Ceratopteris richardii is an aquatic, homosporous fern that produces both male and hermaphrodite haploid gametophytes. Spores developing on their own will develop into hermaphrodites which produce a pheromone called Ceratopteris antheridiogen (ACE) that is secreted into its surroundings. Spores developing in the presence of ACE will develop as male. Previous work has identified 32 mutants of C. richardii that are defective in their sexual development, making it an ideal model for studying sex determination in plants. Ten of these mutants are hermaphroditic (her) mutants which all produce an identical phenotype that has been mapped to four separate loci. These her mutants are insensitive to the ACE pheromone. To identify the underlying mutations for this phenotype, three mutants were selected for bulk segregation analysis. Using a SNP analysis, we identified regions of the genome on chromosomes 28 and 29 that are linked to the mutant phenotype. Ongoing work will identify the causal SNP and identify genes involved in the sex determination pathway of C. richardii and plants in general.

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Pteridology

Topic: Contributed Papers

Title: Dispersal of ferns by mountain gorillas (Gorilla beringei beringei)

Author: **Melanie DeVore @ Georgia College and State University**

Keywords: Dispersal,Ferns,Mountain gorillas

Abstract:

Biogeographical analyses and the establishment of homosporous fern populations have overwhelmingly been based on assuming spores are dispersed by wind and water. We rarely assess if, besides spores, whether sporangia and actual fronds (complete or fragmental) serve as dispersal units. However, recent studies indicate epi- and endozoochory are also important dispersal modes. Fern epizoochory was documented during a more comprehensive study of the role of epizoochory in dispersal of mountain gorilla (Gorilla beringei beringei) food plants in Volcanoes National Park, Rwanda. Field data were collected using focal sampling method for age classes of gorillas including immature, sub-adult, and adult individuals. Video footage obtained permitted the documentation of plant parts attached on six gorilla body parts includin back head, legs, arms, shoulders and front part/stomach. Climbing and playing by juveniles was associated with the adhesion of frond fragments of epiphytes to the gorilla body. All age classes, during feeding activities, had frond fragments of terrestrial taxa become attached to their body. It is apparent that besides wind dispersal and previously documented endozoochorous dispersal, epizoochory also likely plays a role in fern dispersal. These results also indicate that spores, sporangia and even entire frond segments can potentially serve as diaspores for ferns. Clearly, the ecological role of mammals as dispersal agents, including the viability of spores after transport, needs to be evaluated in future studies.

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Pteridology

Topic: Contributed Papers Pteridology

Title: Evolution and hybridization in the endemic Hawaiian fern Polypodium pellucidum

Author: ***Jonas Mendez-Reneau @ University of Louisiana Lafayette***

Keywords: morphology,biogeography,Ecological divergence,Ferns,Hawaiian Islands,hybridization,phylogenetic methods,target-capture

Abstract:

Closely related taxa having undergone rapid evolution and hybridization are often difficult to delimit. Next generation molecular methods combined with bioinformatic tools provide unprecedented opportunities to discern among cryptic taxa and study the complex evolutionary processes underlying the divergence of independent lineages as well as secondary hybridization or gene-flow among them. Having radiated across the Hawaiian archipelago within the past five million years, Polypodium pellucidum encompasses a complex of endemic ferns exhibiting substantial morphological and ecological variation. Using a set of 400 universal fern baits with target-capture, admixture analyses, and phylogenetic methods, we show that P. pellucidum lineages have undergone rapid divergences structured by morphology, ecological niche and island biogeography. We also present evidence for hybridization among lineages, clarifying previous morphological ambiguities and overlap between taxa. Our results offer insights into the co-occurring evolutionary factors structuring divergence and hybridization in P. pellucidum as well as inform conservation of these endemic taxa.

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Pteridology

Topic: Contributed Papers

Title: Seed-free Synteny: A history of genomic stasis in homosporous ferns and lycophytes

Author: ***David Wickell @ Cornell University***

Keywords: comparative genomics,genomics,Huperzia,polyploidy,tree ferns,WGD,Ferns,Lycophytes,lycopodiaceae,Diphasiastrum,diploidization,synteny

Abstract:

Polyploidy both ancient and recent have long been seen as important drivers of plant evolution. However, a related and equally important process is that of diploidization that occurs following whole genome duplication (WGD). Diploidization is characterized by extensive changes to gene content, gene order, chromatin organization, and chromosome structure affecting multiple biological processes including cell division, gene expression, and dosage effects. While the importance of polyploidy has been extensively studied across the tree of life relatively little is known about factors driving diploidization or how it varies between groups of plants. This is especially true among seed-free lineages where a paucity of genome assemblies has hindered investigation into the genomic signatures of large-scale duplication. With the recent publication of several fern and lycophyte genomes we are beginning to be able to examine the downstream effects of WGD on genomic organization in these deeply diverged and evolutionarily important lineages. Our analyses of the tree fern Alsophila spinulosa as well as lycophytes Huperzia asiatica and Diphasiastrum complanatum in the family Lycopodiaceae have provided evidence that genomic rearrangement following WGD occurs at a much slower rate in certain homosporous groups of ferns and lycophytes with syntenic relationships being preserved over hundreds of millions of years. Furthermore, this genomic stasis appears to be accompanied by significantly lower substitution rates in both lineages. While the mechanisms for this evolutionary slow-down remain elusive our characterization of diploidization in seed free plants provides an interesting counterpoint to similar studies in angiosperms that have found rapid rates of gene loss and rearrangement immediately following polyploidization.

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Reproductive Processes

Topic: Contributed Papers Reproductive Processes

Title: Pollination niche partitioning in buzz-pollinated Melastomataceae

Author: ***Agnes Dellinger @ University of Vienna***

Keywords: Bumblebee pollination,buzz pollination,Melastomataceae,Niche Partitioning,flower traits

Abstract:

Closely related plant species frequently co-occur and overlap in ecological characters. This overlap may lead to resource competition (i.e., for pollinators) and result in character displacement (i.e., divergence in floral phenotype or phenology) or reproductive interference (i.e., hybridization). Shared ecological characters may, on the other hand, also promote facilitation among co-occurring species and increase reproductive success. We use the North American plant genus Rhexia (Melastomataceae) as model to test whether co-flowering species share pollinators and whether co-flowering leads to subtle divergence in floral phenotypic traits as expected when flowers compete for pollinators. Rhexia further presents a functionally highly specialized pollination system, buzz-pollination, where pollen may only be released from flowers when specific vibrations are applied. Bees are the only major group of pollinators capable of producing such vibrations, but to date, we know little about how the niche of buzzing bee pollinators is partitioned. From preliminary field studies in Florida, the genus' diversity hotspot, we know that Rhexia share pollinators, and largely overlap in floral trait space. Subtle temporal differences in activity patterns of different bee species may contribute to reproductive isolation, as well as differences in floral traits mediating fit with pollinators. We will draw references to first insights into buzz-pollination niche partitioning also from tropical Melastomataceae communities, where the family is most diverse in terms of species richness and floral disparity.

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Reproductive Processes

Topic: Contributed Papers Reproductive Processes

Title: Annual chasmogamous and cleistogamous reproductive contributions in four mixed-breeding violets

Author: ***Samuel Lockhart @ Ohio University***

Keywords: Cleistogamy,reproductive biology,selfing,Viola

Abstract:

Plant breeding systems are characterized by the mechanism by which offspring are produced. Endpoints of the continuum of sexual reproduction are represented by outcrossing, where two genetically distinct plants contribute hereditary material to offspring, and selfing, where one organism acts as both pollen and seed parent. A specialized form of selfing exhibited by many plants is cleistogamy, a mechanically enforced self-pollination strategy involving closed, bud-like flowers. This breeding system contrasts with chasmogamy, which involves open, showy flowers with the potential to cross-pollinate. The plant species that maintain both breeding systems display a chasmogamous/cleistogamous mixed breeding. Most species of Viola (violets) exhibit the chasmogamous/cleistogamous mixed breeding system; however, many are understudied, and basic life history traits, such as reproductive contributions of floral forms, are not well understood. In addition, the impact of environmental factors, including light, temperature, water availability, and soil characters, on the breeding system has only recently been examined in violets. The present study addresses the previous gaps in knowledge in the taxonomically complex high polyploid stemless blue violet lineage, Viola subsect. Borealiamericanae, in central and southeastern Ohio.

To answer these questions, a total of 12 populations of four mixed-breeding stemless blue violets were surveyed for the entirety of their reproductive season in 2022. Total reproduction in flowers, capsules, seeds, and seed viability were recorded for 12 to 15 plants per population. Environmental variables including light level at ground, soil water content, soil temperature, and soil pH, were regularly measured over the course of the growing season. Generalized linear mixed models were applied to analyze the effect of environmental factors on chasmogamous to cleistogamous reproduction.

Our analysis found that chasmogamous flowers successfully produced capsules and dispersed seeds only half as often as cleistogamous flowers did across all species. However, we found that chasmogamous to cleistogamous ratio differed widely among species, populations, and individuals within plots. Further, no environmental characters were found to be significant to these ratios across or within species. We suspect that age or stored nutrients strongly impacts the breeding system of the stemless blue violets.

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Reproductive Processes

Topic: Contributed Papers

Title: The evolutionary history and morphological basis of Penstemon’s personate flowers

Author: ***Trinity Depatie @ University of South Carolina***

Keywords: Penstemon,flower shape,morphology,personate flowers,phylogenomics

Abstract:

Personate flowers are a novel floral type within Penstemon. These flowers are characterized by an upward bulge in the lower lip of the corolla tube that seals off the floral passageway. Personate flowers have evolved at least two times within Penstemon (sect. Penstemon and sect. Dasanthera) and exist in other species in the family Plantaginaceae (e.g., Antirrhinum and Linaria). Despite the repeated evolution of this floral trait, little is known about its morphological basis, evolutionary history, or ecological function. The eastern North American Penstemon group (sect. Penstemon) provides an opportunity to address these research areas. In this group, personate flowers result from morphological changes arising from ventral petal pleats. A phylogenomic analysis based on whole genome resequencing data suggests that personate flowers may have arisen more than once within this focal clade. To determine whether this unexpected pattern is due to historic introgression, rather than two separate origins of personate flowers, we have conducted several analyses to estimate introgression between the personate taxa. This talk will discuss the results from both morphological and phylogenomic analyses and aims to provide information regarding the mechanisms underlying the evolution of this novel floral trait in Eastern Penstemon wildflowers. I will also discuss future plans to determine the genetic basis and ecological function of personate flowers in this system.

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Reproductive Processes

Topic: Contributed Papers

Title: Developmental evidence for parental conflict in driving Mimulus species barriers

Author: ***Gabrielle Sandstedt @ Utah State University***

Keywords: endosperm,reproductive isolation,seed development,speciation,hybrid incompatibility

Abstract:

The disruption of the endosperm, a tissue responsible for nourishing the embryo in the seeds of flowering plants, is a common occurrence in inviable hybrid seeds of closely related species. A key question is whether parental conflict plays a significant role in this type of reproductive isolation. To explore this question, we conducted reciprocal crosses between pairs of three species of monkeyflowers (Mimulus caespitosa, M. tilingii, and M. guttatus) and observed varying degrees of hybrid seed inviability, which we attributed to differences in species divergence in effective ploidy. A time series of seed development led us to identify parent-of-origin phenotypes that strongly indicate the role of parental conflict in shaping the evolution of the endosperm. Specifically, we discovered pronounced differences in the growth of the chalazal haustorium, a tissue within the endosperm that develops at the maternal-filial boundary, between reciprocal hybrid seeds formed from Mimulus species that differ in effective ploidy. These parent-of-origin effects suggest that the chalazal haustorium may act as a mediator of parental conflict, possibly by regulating the movement of sucrose from the maternal parent into the endosperm. Our findings imply that parental conflict in the endosperm may function as a driver for speciation by targeting critical developmental stages and regions essential for resource allocation and proper seed development.

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Reproductive Processes

Topic: Contributed Papers Reproductive Processes

Title: **Pollinator shifts and geographic range evolution in the origin of Aeschynanthus acuminatus (Gesneriaceae)**

Author: ***Jing-Yi Lu @ University of Chicago***

Keywords: Ornithophily,RADseq,Range expansion,Pollinator shift,Generalization

Abstract:

How do plants evolve under a geographic mosaic of pollinators? The Grant-Stebbins model predicts that a plant species encountering different pollinators across its range may undergo local adaptation and, subsequently, ecological speciation. We test this theory in the SE Asian genus Aeschynanthus, whose 160 species mostly overlap with their putative pollinators, nectar specialist sunbirds. A conspicuous exception is A. acuminatus, a species widespread across mainland East Asia that also occurs in Taiwan, beyond the range of sunbirds. Previous studies of A. acuminatus in Taiwan have shown it to be exclusively pollinated by a group of uncommon avian pollinators, generalist passerines. However, comparable data are lacking in mainland Asia, where both sunbirds and generalist passerines are available. In this study, we integrate population genetics with pollination studies to investigate the roles of pollinator shifts and range expansion in the origin of A. acuminatus. Genome-wide SNPs acquired by restriction-site associated DNA (RAD) sequencing revealed a mainland origin, preceding range expansion to Taiwan. Pollinator observations at 14 populations of A. acuminatus across its range showed varied visitation by both sunbirds and generalist passerines on mainland Asia. The origin of A. acuminatus was thus likely coincident with a shift from ancestral sunbird pollination to a more generalized pollination system, possibly driven by selection for reproductive assurance in an unpredictable pollinator climate. This ecological shift then allowed A. acuminatus to expand its range beyond that of sunbirds. Our research sheds light on how the evolution of pollination systems can influence the origin and range dynamics of species.

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Reproductive Processes

Topic: Contributed Papers

Title: **Heading for a breakdown: Assessing evolution through the hybridization of two sexual systems**

Author: ***Diamanda Zizis @ Bucknell University***

Keywords: Solanaceae,Solanum,Australia,Dioecy,hybridization,hybrids,morphometrics,pollen,reproductive biology,Undergraduate Research,andromonoecy,fluorescence microscopy

Abstract:

Hybridization is an important evolutionary pathway that has contributed to the world’s vast biodiversity. In plants, hybridization is known to be an important mechanism for speciation, phenotypic divergence, and changes in reproductive systems. Solanum species present an ideal system to investigate how hybridization between two different sexual systems impacts the reproductive and phenotypic biology of the hybrid progeny. Hybrid seeds were acquired from crosses between Australian Solanum species Solanum dioicum (dioecious) and S. ultraspinosum (andromonoecious) in order to track what happens when you cross two plants with different sexual systems. Morphological measurements were conducted and the data was analyzed using R to conduct 18 analysis of variance (ANOVA) and a principal component analysis (PCA). Hybrid crossing failure was evaluated under a microscope using fluorescent microscopy technique. The only successful hybrids from the original crosses were those derived from S. dioicum as the pollen donor and S. ultraspinosum as the pollen recipient. Due to strong maternal effects, all F1 hybrids resembled S. ultraspinosum, thus all F1 plants were andromonoecious. The F2 and F3 hybrids demonstrate variability in inflorescence architecture, specifically the persistence of cosexual flowers in the staminate position of an andromonoecious inflorescence and the abortion of staminate buds, which may be suggestive of a change in sexual system. The PCA suggested that the F1 and F2 hybrids were distinct from both parents, but were most similar to S. ultraspinosum, the pollen recipient, while the F3 hybrids clustered independently. In attempts to create an F3 and F4 hybrid generation, nearly all of our crosses have failed—suggesting that a hybrid breakdown is occurring. The observation of pollen germinating but failing to reach the ovary suggests that pollen tube abortion in the style is contributing to hybrid breakdown. This study should promote a better understanding of hybridization—a driving force in plant diversification—among Australian Solanum, a group in which hybridization is known to be widely possible but rarely confirmed in nature. Likewise, hybridization between taxa with two distinct sexual forms may shed light on the evolution of reproductive strategies in this clade.

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Reproductive Processes

Topic: Contributed Papers

Title: **Combining citizen science and field survey approaches to study floral color variation across a species' geographic range**

Author: ***Shu-Mei Chang @ University of Georgia***

Keywords:

Abstract:

Coloration of the floral organs, including petal, anthers, and stigam, is an ecologically important trait and uncovering color variation over a geographic range, particularly in species with large distributions and/or short bloom times, requires extensive fieldwork that can sometime fall short on collecting a thorough coverage of the entire range. Using a recently developed method, we supplemented the field survey data by including images from citizen science repositories such as iNaturliast. Using a recently developed automated method, we characterize a large dataset of photographs from across the distribution range of the wild geranium, Geranium maculatum, to enhance our survey of floral color variation from the entire geographic range of this species. We analyze the color data against Bioclim data to determine whether trait variation is associated with any abiotic environmental factors. Our results showed that pigmentation of G. maculatum is correlated with precipitation, annual mean temperature, and UV level. We discuss the added value and caveates of using citizen science data in this study.

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Reproductive Processes

Topic: Contributed Papers

Title: **Sex-based physiological differences in a native sex-changing tree species**

Author: ***Jennifer Blake-Mahmud @ Hope College***

Keywords: Acer,demography,ecophysiology,sex determination,sex expression,sexual dimorphism

Abstract:

Approximately 6% of plant species have sexes separated by individual. A small fraction of those may change sex during their lifetimes based on environmental cues. While the presence of reproductive structures such as gynoecia and androecia determine sex, there may be sex-based differences in physiology or life-history traits. This variation may result from natural selection optimizing traits in diverging ways for females and males. Spatial segregation of sexes or nonconformity in microclimate can further complicate studies of sex-based dimorphism and physiology. Here we report preliminary data on physiological differences in the sexually labile tree, Acer Pensylvanicum, a native understory tree. Individuals in this species may switch sex throughout their lives based on environmental cues and therefore offer a unique chance to investigate differences in sex-based physiology. We present field data on demography (size, flowering sex, health, growth, and mortality) and physiology (photosynthetic rate, stoichiometric ratios, and fluorescence). We show that both season and sex impact physiological and demographic parameters and that the patterns persist across seasons.

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Topic: Contributed Papers Reproductive Processes

Title: Pollen tube growth as a barrier to hybridization in Schiedea (Caryophyllaceae)

Author: ***John Powers @ University of California, Irvine***

Keywords: adaptive radiation,Hawaii,pollen competition,pollen tube growth,reproductive isolation,Dioecy,post-pollination prezygotic barriers

Abstract:

Dioecy is an uncommon reproductive strategy with a higher prevalence on oceanic islands. While alleles required for forming solely staminate or pistillate flowers can be transmitted vertically from ancestral species during island radiations, horizontal transfer among plant species through gene flow is also possible. Reproductive barriers may determine which species can interbreed and transmit sex-determining alleles. We investigated these isolating mechanisms in five reproductively diverse pairs of sympatric species of Schiedea that are endemic to the Hawaiian Islands and either show evidence of past hybridization or share a pollinator. We characterized post-pollination, prezygotic barriers such as pollen tube growth, as well as capsule formation, seed production, germination, and survival. We hypothesized that these barriers would increase with phylogenetic distance, and with style length. To directly measure pollen tube growth, we made reciprocal interspecific crosses and intraspecific crosses and counted stained pollen tubes at the middle and bottom of the style at 4 and 24 hr. To measure pollen competition, we pollinated each species with a mix of equal numbers of conspecific and heterospecific pollen grains and scored the proportion of hybrid offspring. Compared with conspecific pollen tubes, the number of heterospecific pollen tubes at the bottom and middle of the style at 24 hr decreased with phylogenetic distance, but this effect was not evident after 4 hr. In distantly related species, heterospecific pollen tubes had a lower growth rate than conspecific pollen tubes at 24 hr. All measured stages of early acting reproductive isolation increased with phylogenetic distance, with hybrids among closely related species showing heterosis in survival. The proportion of surviving hybrids from mixed pollinations decreased with phylogenetic distance and with maternal style length. Low pre- and post-zygotic reproductive barriers in closely related sympatric Schiedea species could potentially facilitate the transfer of sex-determining alleles across species boundaries during the evolution of this island lineage, although hybridization is impeded in species with different style lengths. Ongoing genomic studies may unearth the evolution and transmission of dioecy in Schiedea.

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Topic: Contributed Papers

Title: A War Within: Modeling gene conflict between life stages in land plants with shadie

Author: ***Elissa Sorojsrisom @ Columbia University***

Keywords: alternation of generations,gametophyte,simulation,genome evolution,gene conflict

Abstract:

The life cycle of land plants alternates between multicellular gametophyte (1N) and sporophyte (2N) life stages. Land plants vary widely in the degree to which one life stage is dominant over the other. In homosporous ferns, both stages are free-living (i.e. the lifecycle is biphasic) and therefore both stages are subjected to environmental conditions that exert selection pressure on the genome. Transcriptome data suggests a high degree of overlap in the identity of genes expressed in haploid and diploid life stages, which introduces many gene interactions between life stages. In theory, there is a high potential for gene conflict, as beneficial mutations in one life stage are likely to be deleterious in the other. Such conflicts can alter predicted patterns of genome evolution, but little is known about how variation in life history traits among biphasic stages affects evolutionary phenomena, such as the fixation rates of beneficial alleles. Emerging data suggests that haploid selection in primarily diploid organisms is more prevalent than previously thought, even in organisms which have a reduced or ephemeral haploid stage (e.g. animals, seed plants). Studying the dynamics of genome evolution in organisms with more balanced biphasic life cycles (e.g. ferns), where gene conflict should be more extreme, may provide insights that are applicable to many sexually reproducing organisms.

Here, we use the Python program shadie to simulate genome evolution in the presence of gene conflict under models of fern-like life cycles and contrast our findings with traditional theoretical expectations. We characterize the effects of gene conflict on rates of fixation of beneficial alleles, purging of deleterious alleles, and the effects of linked selection on genome diversity. We also examine how differences in demographic parameters (e.g., population size, cloning, selfing) among diploid and haploid life stages affects these patterns. Finally, we search for signatures in simulated genomes characteristic of genetic conflict which may be used to identify conflicts in empirical data.

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Reproductive Processes

Topic: Contributed Papers Reproductive Processes

Title: Reproductive effort and reproductive success in dwarf bilberry in the Superior National Forest

Author: ***David Hainlen @ University of Minnesota Duluth***

Keywords: Vaccinium,conservation,genetics,reproductive effort,Reproductive Success,seeds,clonal,Vaccinium cespitosum,land management,clonality,berries

Abstract:

The forests of northeastern Minnesota are home to many native species of Vaccinium, all of which are wild and produce edible fruit. Flower and fruit production of many species of Vaccinium are influenced by factors such as canopy cover (open, partially open, or closed), the clonality level of the population (as some of these species are partially clonal), and climatic conditions. Traditionally, tribes have used fire to promote fruit production, and current land management techniques involve controlled burns as part of the timber harvest regime to promote vegetative recovery. While the relationship between active land management and an increase in berry production is well documented in the literature, the underlying mechanisms that lead to this increase are unknown. In areas that have been recently managed, or where there is an open canopy, sexual reproductive effort (i.e., flowers) has been shown to be higher than in unmanaged/closed canopy populations. However, very little is known about how sexua reproductive success (e.g., the % fruit set) is affected by land management. In addition, the degree of clonality of a population is expected to influence sexual reproductive success, with highly clonal populations showing reduced reproductive success stemming from the impacts of geitonogamous inbreeding. In this study, we used standardized measures of sexual reproductive effort and success in multiple populations of Vaccinium cespitosum (the dwarf bilberry) with contrasting land management histories to investigate the relationship between these two variables, land management, and clonality. Clonality was assessed from genotyping-by-sequence data from 12 populations of V. cespitosum and compared to measures of reproductive success. Sexual reproductive effort was measured as the number of flowering ramets and the number of flowers per ramet in selected plots. We found that reproductive effort differed significantly between populations, but not between different land management types, which is in contrast with previous findings based in the literature. We measured sexual reproductive success based on the percent fruit set for each population and the number of viable or inviable seeds per berry. We found that both of these measures of sexual reproductive success differed significantly between populations with contrasting land management histories. Our findings suggest that land management impacts sexual reproductive success, but that it may not play as important a role in sexual reproductive effort as previously thought.

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Reproductive Processes

Topic: Contributed Papers

Title: Floral scent differences within Nyctaginaceae correlate with shifts in mating system and pollination

Author: ***Evan Hilpman @ Oberlin College***

Keywords: Abronia,plant-pollinator interactions,pollinator,trait evolution,Volatile Organic Compounds,Floral Scent,scent,Tripterocalyx,autogamy

Abstract:

The evolution of autogamy is hypothesized to correlate with a reduction in traits associated with pollinator attraction. Floral scent represents a complex trait with ecological consequences and strong potential for rapid evolution. However, few studies have broadly tested the hypothesis that floral scent emissions differ between selfing and outcrossing lineages. Here, we present a glimpse into the complexity of floral volatiles across a monophyletic clade of Nyctaginaceae (Abronia and Tripterocalyx) and provide the first phylogenetically replicated study of floral scent emission in the context of mating system evolution. We measured floral volatile and morphological traits in a common garden including 24 of around 30 taxa in this largely self-incompatible, monophyletic clade. Across two independent transitions to autogamy, lineages experienced parallel reductions in total floral volatiles, and transitions to smaller and fewer flowers. We also found that species which close their flowers during the day, characteristic of moth pollination, emit distinct volatile profiles. Our results may support pollination syndromes within this clade, provide macroevolutionary snapshots of transitions between mating systems and suggest a predictable, multi-trait reduction of investment in autogamous lineages.

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Reproductive Processes

Topic: Contributed Papers

Title: Pollinators’ Flower Color Selection is Influenced by Sexual Dichromatism in Rare Cacti Species

Author: ***Scarlet Steele @ San Diego State University***

Keywords: Cactaceae,Evolution,Flower color,plant ecology,Plant-pollinator Interaction,sexual dimorphism ,sexual dichromatism

Abstract:

Pollinators’ Flower Color Selection is Influenced by Sexual Dichromatism in Rare Cacti Species
Scarlet Steele, Niveditha Ramadoss, Lluvia Flores-Renteria
The reproductive success of all animal-pollinated plants depends on their ability to attract pollinators. This is especially important in dioecious species that have their sexes separate because they cannot self-fertilize. Dioecious plants usually express sexual dimorphism which is the differences in morphological characteristics between male and female individuals. Sexual dimorphism in plants’ floral traits, is a critical factor for pollinators’ attraction to those flowers. It is imperative that we further understand sexual dimorphism and its effect on pollinator visitation, which ultimately affects their reproductive success. A great model to study sexual dimorphism and its impact is Cylindropuntia wolfii, commonly known as ‘ Wolf’s cholla’. This is because this species has a functionally dioecious sexual system that possesses six different flower morphs within the same location. We have also observed the flowers to have sexually dimorphic traits that are attractive to pollinators. The goal of our current study is to determine if there is a difference in pollinator visitation rate between male and female flowers and to understand pollinator flower color choice. To achieve this we first observed whether there are any potential pollinators to the species by manual survey in the field. Then we manually observed the pollinator visitation for different male and female individuals of different flower colors by observing them for 10 mins each. Finally, to track the pollinator color preference we used the fluorescent dye that dyes the pollen and can be transported by the pollinator to other flowers. We manually noted the presence or absence of fluorescent dye spread in the flowers of the neighboring plants. Our preliminary results showed that males attract more pollinators than females and that the pollinators are attracted to green/yellow flower colors more than orange or red. This suggests that when the pollinator density is low, the female flowers will hardly be visited leading to low seed production which has previously been reported in C. wolfii. This study has important implications for the management of rare dioecious cacti.

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Topic: Contributed Papers Symbioses: Plant, Animal, and Microbe Interactions

Title: Legacy effects of precipitation and land use impact maize growth and microbiome assembly under drought stress

Author: ***Joel Swift @ University of Kansas***

Keywords: Microbiome,plant-microbe interactions,drought

Abstract:

As climates change, plants and their associated microbiomes must contend with water limitation and increased frequency of drought. Natural precipitation gradients provide an opportunity to assess the legacy effects of precipitation on soil microbiomes and how these microbiomes influence the performance of future generations of plants. We collected six soil microbiomes across an east-west precipitation gradient in Kansas, which spans the temperate Great Plains region. Soil microbiomes encompassed two land use types, agricultural fields with conventional management practices and native prairies. Seedlings of two Zea Mays (maize) genotypes were inoculated with each soil microbiome in a factorial drought experiment, assessing maize phenotypic and root-associated microbiome responses (bacteria and fungi) to drought stress. Changes in maize resource allocation were apparent, with droughted plants exhibiting decreased shoot mass accumulation rates and greater root mass relative to shoot mass. Restructuring of the bacterial root-associated microbiome was also apparent, with depletion observed in Pseudomonadota and enrichment in Actinomycetota, while the fungal root-associated microbiome was largely unaffected by drought. We detected a legacy effect of historical precipitation exposure on soil microbiomes' interactions with plant hosts during drought treatment, but only among prairie soils. Whereby maize growth under drought was maximized when seedlings were inoculated with prairie soil microbiomes from historically wetter soils. Our results demonstrate links between soil microbiomes and plant performance under drought and provide a foundation to further dissect plant-microbiome interactions towards improving drought tolerance in maize.

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Topic: Contributed Papers

Title: The genetic basis of adaptive partner choice in the Medicago truncatula -Ensifer spp. symbiosis

Author: ***Andres Gutierrez @ Loyola University of Chicago***

Keywords: GWAS,legume-rhizobia symbiosis,next generation sequencing,nitrogen fixation,SNP

Abstract:

The legume-rhizobia symbiosis is considered one of the most important plant-microbe interactions in the biosphere. The relevance of this symbiosis lies in the possibility of replenishing the soil with fixed-nitrogen, action that can contribute to the development of sustainable agriculture and reduce the use of fertilizers. Understanding of the molecular events underlying the symbiosis is key to enhance the nitrogen-fixation efficiency. Medicago truncatula has been used as model plant for studying plant-microbe interaction in legumes due to the several resources available (genome sequence, gene expression data and mutant collections). The advent of new resources in molecular biology, has made possible to obtain new data to elucidate the underlying molecular mechanisms in different biological processes. Genome-wide association studies (GWAS) has been an important tool that combines newer resources available in molecular biology (next generation sequencing), to produce genome-wide single nucleotide polymorphisms SNPs, and complex statistical analysis to search for the genetic architecture of complex traits. A GWAS analysis was performed to identify the genetic basis of the mutualism variation in M. truncatula – Ensifer spp. complex. Based on Batstone, et al. 2021, two Ensifer spp. strains were selected and used as inoculum source in a subset of 149 accessions of the M. truncatula hapmap population to identify genes associated with the partner choice selection of M. truncatula for a specific Ensifer spp. strain

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Topic: Contributed Papers

Title: Phylogenetic and spatial determinants of leaf endophyte microbiomes in the flowering plant Heuchera

Author: ***Dexcem Pantinople @ Mississippi State University***

Keywords: Heuchera,abiotic drivers,Community composition,endophyte,Microbiome,plant-microbe interactions,symbioses,leaf endophyte,host phylogenetic drivers

Abstract:

Endophytic plant-microbe interactions, universal across the land plants, range from mutualistic relationships that confer important ecological and agricultural traits to neutral or quasi-parasitic relationships. In contrast to substantial research on root and rhizosphere endophyte interactions, the role of environmental and host-related factors responsible for acquiring leaf endophyte communities remains relatively unexplored. In our research, we explore a novel approach using broad geographic coverage of North America within the restricted phylogenetic scope of the genus, Heuchera (Saxifragaceae), a recent plant host radiation. Heuchera has well-characterized phylogenetic relationships and diverse habitat specializations. We used strong host species and population sampling to assess microbial diversity at multiple host evolutionary levels, from phylogenetic to within-population diversity. Here we assess leaf endophyte diversity to test the hypothesis that membership of these microbial communities is driven primarily by abiotic environment and host phylogeny. Bacterial and fungal communities were characterized with 16S and ITS amplicon sequencing, using QIIME2 to call OTUs (operational taxonomic units) and calculate standard diversity metrics (species richness, Shannon diversity, phylogenetic diversity). We assembled a series of environmental predictors for bacterial and fungal diversity at collection sites including latitude, elevation, temperature, precipitation, and soil parameters. To account for spatial autocorrelation, a geographic distance matrix among sites was also calculated. Surprisingly, we find differing assembly patterns for bacterial and fungal endophytes. Using UniFrac distances to investigate community composition, we found that only host phylogeny is significantly associated with bacterial endophytes, while geography alone was the best predictor of fungal community composition. Species richness and phylogenetic diversity are very similar across sites and species, with only fungi showing a response to aridity and precipitation for some metrics. Unlike what has been observed with rhizosphere and root endophyte communities, in this system microbes show no relationship with pH or other soil factors. Our results indicate the importance of detailed clade-based investigation of microbiomes and the complexity of microbiome assembly within specific plant organs.

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Symbioses: Plant, Animal, and Microbe Interactions

Topic: Contributed Papers Symbioses: Plant, Animal, and Microbe Interactions

Title: Primary bacterial symbionts of creosote bush (Larrea tridentata)

Author: ***Abigail Ferson-Mitchell @ University of Idaho***

Keywords: bacteria,Competition,Larrea tridentata,primary symbionts,creosote,seed endophyte,heterospecific interactions,conspecific interactions,Bromus tectorum

Abstract:

The primary symbionts of a plant are seedborne microbes that strongly influence the next generation of both the plant and its microbiome. According to our hypothesis, the primary symbionts of creosote bush (Larrea tridentata, family Zygophyllaceae) should contribute to the prominence of this species in desert plant communities of the American Southwest. In particular, primary symbionts might explain the absence of both conspecific and heterospecific plants in close proximity to creosote bush. In this exploratory investigation, we have isolated bacteria and fungi from seeds of L. tridentata. Over 80% of the microbes isolated were fungal. A representative of each morphotype was sent off for ITS sequencing and screened for pathogenicity against lettuce seedlings (Lactuca sativa, family Asteraceae). Two bacterial symbionts reduced emergence when seeds came into direct contact with the microbe prior to sowing. Seedling emergence of heterospecifics (i.e., Achillea millefolium, Lactuca serriola, Bromus tectorum, Layia platyglossa, Lens culinaris, etc.) was further tested with the two bacterial symbionts from L. tridentata seed. The first symbiont had either a positive or negative effect on the germination, emergence, growth, and reproductive potential of heterospecific species. In contrast, the other symbiont had either a neutral or negative effect when compared to the control groups. Neither symbiont demonstrated pathogenicity as a foliar application. Additionally, the symbionts had both direct and indirect effects on fungi (e.g., powdery mildew of Lactuca serriola). In ongoing testing, seedborne bacteria appear to act as primary symbionts of creosote bush; its seedborne fungi have yet to be tested.

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Symbioses: Plant, Animal, and Microbe Interactions

Topic: Contributed Papers

Title: The effects of plant inbreeding on mutualisms

Author: ***Isabela Lima Borges @ Michigan State University***

Keywords: ecology,inbreeding,legume-rhizobia symbiosis,mutualism

Abstract:

One of the major concerns for the persistence of small isolated populations is inbreeding depression. When investigated in plants, the severity of inbreeding depression often depends on the environment in which it fitness is assessed. Here, I use the legume Chamaecrista fasciculata to explore how plant inbreeding combines with mutualistic interactions to affect plant fitness. I conducted two generations of experimental crosses to obtain C. fasciculata that differ in their extent of inbreeding, then planted the resulting seeds in a common garden where they were exposed to mutualist soil bacteria (rhizobia) and ants. I assessed how plants at different inbreeding levels interacted with rhizobia by observing root nodules, and did ant and extra-floral nectary surveys to assess plants' mutualism with bodyguard ants. Throughout the experiment, I measured different plant fitness metrics, including total seed count. I found that plant inbreeding decreased plants' investment in the mutualism with ants and with rhizobia. Plant fitness also decreased with inbreeding, yet the slope of that decline varied by trait and was different for plants that did or did not interact with rhizobia. Overall, I find that mutualisms are affected by plant inbreeding, and that mutualist presence or absence can change the severity of fitness losses in inbred populations.

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Symbioses: Plant, Animal, and Microbe Interactions

Topic: Contributed Papers

Title: Do wet and dry ecotypes of a dominant grass grow better with their native soil microbes?

Author: ***Eli Hartung @ Kansas State University***

Keywords: Andropogon gerardii,intraspecific variation,Local adaptation,plant-microbe interactions,Prairies

Abstract:

Big bluestem (Andropogon gerardii) is a dominant grass of the Great Plains that accounts for roughly 70% of the biomass of tallgrass prairies. Its distribution across a steep rainfall gradient in the Great Plains has given ample time for the rise of locally adapted wet and dry ecotypes. Abiotic factors, such as rainfall, in the formation of ecotypes has been well-studied. However, we know little about the role of biotic factors influences, such as soil microbiomes, in local adaptation. Soil microbiomes are reported to play fundamental roles in drought resistance and nutrient uptake and are expected to vary like A. gerardii along the Midwest precipitation gradient. We investigated how local soil microbes affect A. gerardiigrowth and whether specific plant ecotypes are matched to local soil microbes. We predicted that each ecotype would grow better when grown with its native microbes. We collected seed and soil samples from six A. gerardii populations from western KS (500 mm rainfall) and Illinois (1200 mm per year). We isolated microbes from roots and native soil, cultured them in R2A agar broth, and reciprocally inoculated wet and dry microbes (plus mock control) weekly into garden soil where plants were grown for 12 weeks with 6 replicates per treatment. Plant form and function were measured weekly for a variety of responses. Preliminary genetic results showed distinct differences between ecotypes and soil microbe composition. Population markers show that ecotypes are genetic differentiated and that wet ecotypes are more variable than dry ecotypes. Metabarcode sequencing (v4 of the 16s) showed overlap among the wet and dry soil inocula as well as some notable differences among them. Clostridium, Paenibacillus, and Lysinibacillus were abundant in the dry soil inoculum but almost entirely absent from the wet inoculum. Repeat sequencing over time indicated that inocula were compositionally stable over time. We found that ecotypes differed in biomass, leaf area and width, and height. Wet ecotypes produced more biomass, greater leaf area, and were taller than the dry ecotype. For inoculation effects, physiological traits, such as chlorophyll absorbance, a proxy for photosynthesis, were enhanced in ecotypes growing with their local microbes. Even more notable, the dry ecotype produced ~30% more biomass when it was matched with its local microbiome. Taken together, these results suggest effects of ecotype specific and microbe-mediated effects on nutrient availability. These results provide insight into how plants interact with their native microbiomes and suggest they play an important role in nutrient availability and uptake for A. gerardii. Because A. gerardii is widely used in prairie restoration and as forage for the cattle industry, understanding how A. gerardii interacts with its local soil microbes is crucial. Millions of acres of agricultural land have been restored throughout the plains and cattle grazing is a multi-billion-dollar industry throughout the Midwest. These results will help to inform range managers and land conservationists to optimize forage production and restoration through use of and matching with beneficial microbes.

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Topic: Contributed Papers Symbioses: Plant, Animal, and Microbe Interactions

Title: Variation in synthetic floral microbiome composition is largely ignored by foraging bumblebees

Author: ***Nevin Cullen @ University of Pittsburgh***

Keywords: Bumblebee pollination,Floral Constancy,Hyperaccumulation,plant-microbe interactions,Plant-pollinator Interaction

Abstract:

Most flowers are occupied by diverse communities of microbes, which can alter floral attractiveness to key pollinators and floral fitness by interacting with floral traits. Different species of flower often acquire unique communities of microbes. Consequently, pollinators are frequently forced to choose between two flowers with distinct floral microbiomes while foraging. However, it is currently unknown whether pollinators have an inherent preference for flowers containing one floral microbiome over another, and whether microbial preference is modified by variation in floral traits. We investigated this knowledge gap using distinct bacteria and yeasts cultured from a nickel-hyperaccumulating plant (Streptanthus polygaloides) and its non-accumulating relative (S. tortuosus). Specifically, we hypothesized that 1) bumblebee foraging preference (initial, overall and over time) depends on the interaction of microbiome origin (hyperaccumulator vs non-accumulator isolated) and nectar metal content, and 2) that bumblebees exhibit the greatest floral fidelity (successive visits to the same kind of flower) when flowers vary in both microbiome composition and nectar metal concentration. To test these hypotheses, we observed foraging patterns of lab-reared eastern bumblebees on arrays of artificial flowers containing nectar treatments of nickel/no-nickel, hyperaccumulator microbes/non-accumulator microbes or a cross of metal-by-microbe treatments. Microbial community treatments were synthetic and assembled from the most abundant bacterial and fungal taxa found on wild hyperaccumulator and non-accumulator flowers. Bumblebees initially had a preference against nectar containing nickel and non-accumulator microbes. Across all visits in the trial, bumblebees expressed no variation in preference among nectar treatments and preference did not shift over the course of each trial. Bees also did not exhibit variation in constancy when presented with different kinds of treatments. Together our results suggest that variation in floral microbiome composition does not drive strong foraging patterns in bumblebees. More broadly our suggest that the simple presence or absence of microbes living in a flower may be a stronger component of pollinator foraging patterns than variation among existing microbiomes.

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Topic: Contributed Papers

Title: Impacts of temperature and fur texture on the adherence of mucilaginous seeds

Author: ***Elizabeth Waring @ Northeastern State University***

Keywords: seeds,Temperature,mucilage,epizoochory

Abstract:

Within the epidermal tissues of some species of seeds, a polysaccharide substance called mucilage is formed. In mature seeds this mucilage often remains dehydrated. However, mucilage is readily rehydrated when it encounters water. Although nonvisible when dehydrated, mucilage that is water imbibed becomes a sticky, gel like substance. Not only is hydrated mucilage sticky and adhesive but as mucilage dehydrates it cements the seed to its current surface. As a result of adhering to surfaces, mucilaginous seeds often attach to animals and are dispersed over various distances. Dispersal of seeds to sites where they are able to germinate is an important process in continuing ecological succession because it brings plant growth to new areas. Zoochrous dispersal of seeds is directly related to the different traits of both plants and animals. Seed morphology has an effect on the adhesivenes to fur and feathers but fur types and feather types also has an effect on the adhesiveness of seeds. Additionally, the temperature of the surface can affect how strongly the now-dried mucilage attaches the seed to the surface. This talk will address two experiments. One looking at how mucilaginous seeds, from 5 different plant families, attachment is impacted by the temperature of the surface and one looking at the force needed to remove attached seeds fron animals. In the first experiment, we hypothesized that the seeds on hotter tiles would require less force to remove because the mucilage would dry quicker. This was done using white and black tiles were placed in the shade or sun and the temperature of the tiles was measured. The seeds were then imbibed, placed on the tiles and positioned back into the sun or shade. After the seeds dried, the force to remove them was measured. The findings revealed the hotter surfaces required a lower amount of force to remove the seeds than the cooler tiles, which corresponds to our hypothesis. The data shows that the mucilage drying too rapidly causes the seeds to attach with less strength. In the second experiment, we investigated: (1) The effect of different mucilaginous seeds adhering to animals. (2) How mucilaginous seeds adhere to different species of animals. This study contributes to a better understanding of how mucilage contributes to epizoochory dispersal by showing how mucilage attaches seeds to animals. To determine if the type of mucilaginous seed affected the force needed to remove the seed from animal feathers and fur,we chose multiple different species of seeds. We also chose five different species of animal, including mammals and waterfowl, to place the seeds upon. We used animal pelts and feathers for each type of specimen. The seeds were left to dr on the animal specimens for at least two hours and the amount of force to remove them was measured. Our research indicates that mucilage enhances seed's ability to adhere to animals, particularly mammals. These results suggest that mucilage plays a key role in epizoochory seed dispersal.

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Symbioses: Plant, Animal, and Microbe Interactions

Topic: Contributed Papers Symbioses: Plant, Animal, and Microbe Interactions

Title: **The impacts of florivorous fruit flies on Asteraceae in Capitol Reef National Park and its implications for restoration efforts**

Author: ***Jenna Miladin @ Capitol Reef National Park***

Keywords: climate change,phenology,plant-animal interaction,restoration,seed viability

Abstract:

Vegetation restoration in arid areas is imperative for maintaining biodiversity, but the influences of climate change must be accounted for in restoration efforts. Climate impacts often focus on the effects of temperature fluctuations, shifting water availability and plant phenological shifts, but combinations of these can result in unexpected outcomes. Asteraceae are crucial plants to include as restoration species given their ability to sustain pollinator communities, reduce erosion, and compete well with invasives. During seed collection for revegetation on road resurfacing project at Capitol Reef National park a native florivorous fruit fly Trupanea radifera (Tephritidae) was detected on the flowerheads of Gaillardia spathulata using genetic sequencing techniques. Various species of Asteraceae were tracked across the park for both fruit fly presence and flower head infestation rate. A second fruit fly species of the genus Neaspilota was detected, and fruit fly presence was further found on six different Asteraceae species. A parasitoid (Pteromalidae) wasp was also found in the pupae of the same tephritid fruit flies. Previous seed collection activities in the park have not detected these tephritid fruit flies. Phenological shifts and ground disturbance, caused by heavy monsoonal flows, could be impacting tephritid occurrence rates. There was an apparent disparity in infestation rates of tephritids on flower heads between disturbed and undisturbed sites, where disturbed sites had higher rates of fruit fly infestation on flower heads. Additionally, plants in Capitol Reef appear to be shifting back phenologically due to shifts in precipitation. Early winter months show a trend towards increasing precipitation over a period of 56 years, and the growing season has been extended later in the season. As a result, late-season blooms line up with tephritid activity in the fall, allowing them to produce two generations a year. Multiple tephritid generations a year due to plant phenological shifts may result in a reduction of Asteraceae seed production contributing to the higher infestation rates seen parkwide. However, parasitoid presence may help curb Asteraceae seed production decline. Multiple climate change induced trends bundled together can disrupt the normal oscillation of fruit fly and parasitoid cycles, resulting in lower seed production in restoration plant species. Less collectable seed material, reduced seed viability and established plants survival in disturbed areas as a result of infestation could negatively impact restoration success at Capitol Reef National Park and other arid landscapes.

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Symbioses: Plant, Animal, and Microbe Interactions

Topic: Contributed Papers

Title: **P-LDH/BC as a controlled-release fertilizer: Effects on plant growth and the soil microbiome**

Author: ***Tajinder Singh @ Mississippi State University***

Keywords: agriculture,nodule microbiome,fertilizer,eutrophication

Abstract:

Layered Double Hydroxide (LDH) has been recently established as an effective means to remedy nutrient-polluted water. As an efficient low-cost alternative to established remediation methods that is easy to produce and scale, its application as a water treatment relies on the potential for nutrient pollution to be recycled as a controlled-release fertilizer. In this project, Mg-Al LDH was synthesized, dispersed on biochar, and adsorbed with phosphorous to obtain a P-LDH/BC complex. The P-LDH/BC complex was characterized for chemical properties including stability, surface area, and available nutrient content. The P-LDH/BC complex was studied for its efficiency as a controlled-release fertilizer in green beans (Phaseolus vulgaris) and compared to standard industry fertilizer in a greenhouse experimental study. Based on preliminary analysis, the synergy of biochar and LDH resulted in an improvement in the key growth indicators in green beans compared to standard fertilizer, including yield, nutrient content, height, dry weight, and chlorophyll index. Furthermore, the effects of the P-LDH/BC complex on the rhizosphere and nodule microbiome was studied using molecular DNA extraction methods and related to the key growth indicators. The P-LDH/BC complex is predicted to show an improved microbial activity in the rhizosphere and contribute to an improved soil microbial health in comparison to standard industry fertilizer.

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Symbioses: Plant, Animal, and Microbe Interactions

Topic: Contributed Papers

Title: **Response of maize seedlings and their root-associated fungal communities to water deficit stress and water recovery**

Author: ***Gregory Pec @ University of Nebraska at Kearney***

Keywords: arbuscular mycorrhizal fungi,drought,Maize,roots

Abstract:

Water deficit stress is considered one of the most important factors limiting maize production. Exposure to longer-term water deficit stress conditions inhibits growth and leads to yield loss. Less understood is the response of maize roots and their associated microbial communities to water deficit stress and water recovery. Toward this goal, a growth chamber experiment was conducted to characterize the response of maize seedlings under water deficit and recovery conditions. We specifically focused on maize seedling response following the V3-V4 growth stages as upon reaching these stages, maize seedlings shift their nutritional dependence from kernel reserves to the nodal root system for development, and water stress during this vegetative phase can significantly reduce overall grain yield. Furthermore, as root-associated microbes, particularly fungi, play vital roles in enhancing the water and nutrient uptake and overall seedling performance of their hosts, a secondary objective was to explore any relationships between root-associated fungal communities (i.e., inoculated vs. non-inoculated) and maize growth under both water deficit and water recovery conditions. Overall, water deficit stress reduced stomatal conductance, shoot and root growth, specific leaf area, leaf N concentration, and specific root length in maize seedlings. However, under water recovery conditions, growth of seedlings in the presence of root-associated fungi were similar to well-watered conditions over time. Changes in the composition of root-associated fungal communities under water recovery conditions resulted in increased above- and below-ground tissues and leaf N concentration of seedlings. Taken together, our results provide insight into the water deficit stress response of maize and suggest that under water recovery conditions, beneficial outcomes on maize seedlings are mediated through the effects of belowground fungal mutualists.

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Symbioses: Plant, Animal, and Microbe Interactions

Topic: Contributed Papers

Title: **Partial mycoheterotrophy and fungal associations of Triphora trianthophoros, a rare North American orchid**

Author: ***Brandon Corder @ University of Wisconsin-Madison***

Keywords: Microbiome,mycoheterotrophs,Mycoheterotrophy,Orchid mycorrhizal fungi,Orchidaceae,Orchids,stable isotopes,Orchid,mixotrophy

Abstract:

Orchids, one of the largest families of flowering plants, contain the highest abundance of mycoheterotrophs, or plants that obtain carbon and other nutrients through fungal parasitism. In addition to the presence of over 250 species of fully mycoheterotrophic, achlorophyllous species, a growing number of green orchids are known to combine fungal parasitism and photosynthesis in a strategy known as partial mycoheterotrophy. Our knowledge about the breadth and identity of fungal hosts of partial mycoheterotrophs is still developing, but recent findings have shown that partial mycoheterotrophs associate with broad functional groups of fungi including both mycorrhizal fungi and free-living saprotrophic fungi. Here, we investigate Triphora trianthophoros (Epidendroideae, Triphoreae), or three birds orchid, an enigmatic North American terrestrial orchid of conservation concern, for its fungal relationships, host preference, and trophic mode. Triphora trianthophoros has a suite of features that suggest it has a strong relationship with soil fungi including a long underground transit time, presence in shaded forest understories during the late summer when irradiance is the lowest, and the persistence of achlorophyllous mutant individuals. Using comparative stable isotope analysis and two-source mixing models, we determined that green T. trianthophoros plants derive approximately 50-100% of its C from fungal parasitism, indicating a strongly partially mycoheterotrophic strategy. Next, we extracted, amplified, and sequenced ITS loci from fungi within T. trianthophoros roots from sites across its North American range to uncover the identity of its fungal symbiont. Future steps, in progress, will further increase sampling across different forest types and ecological contexts that T. trianthophoros occurs in. We expect this study to contribute to our understanding of the particular fungal requirements of this rare orchid species, advance in-situ and ex-situ conservation efforts, and give further insight into partial mycoheterotrophs in the North American orchid flora.

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Symbioses: Plant, Animal, and Microbe Interactions

Topic: Contributed Papers Symbioses: Plant, Animal, and Microbe Interactions

Title:

Future directions for plant microbiome research

Author: ***Anna Scharnagl @ UC Berkeley***

Keywords: Global change,Literature Review,Microbiome

Abstract:

The study of plant microbiomes has skyrocketed in the last fifteen years and from this it is clear that microbiomes play crucial roles in many biogeochemical processes from immune function to development, but they are also sensitive to environmental change. While there has been a plethora of studies on plant microbiomes, they remain limited by a short list of plant host species and geographic area. Here I will present on what plant groups and habitats have been studied and what areas are still in need of more research. I propose the need for a repository of information to tackle patterns and changes in plant microbiomes on a global scale. Such a repository will engender further microbiome studies, and help to address the urgent need for setting a baseline across plant hosts and ecosystems. My assessment of the studies conducted thus far will lead to a discussion on designing future plant microbiome studies that capture the necessary metadata to make sense of these patterns on a global scale

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Symbioses: Plant, Animal, and Microbe Interactions

Topic: Contributed Papers

Title:

Distinct components of floral scent and display predict pollination and seed predation in Castilleja sessiliflora

Author: ***Evan Hilpman @ Oberlin College***

Keywords: morphology,mutualism,plant-insect ecology,Plant-pollinator Interaction,Seed Predation,Volatile Organic Compounds,antagonism

Abstract:

Angiosperm diversity stems, in part, from the complex ecological interactions in which they participate. This diversity is expressed through morphological and chemical traits that are vital in mediating the behavior of both mutualists and antagonists. Using extensive sampling of individual plants within a large population of Castilleja sessiliflora, we compared the relative importance of morphological and floral volatile traits in the attraction of mutualistic and antagonistic insects. We used structural equation modelling and multiple linear regressions to identify those plant traits that best predicted visitation by pollinators (fruit set) and seed predators (fruit predation). (Z)-β-ocimene was positively correlated with fruit set, while the related and more abundant volatile, (E)-β-ocimene, along with the number of stems per plant, were negatively correlated with fruit set. Loss of fruits to seed predators was positively correlated with corolla length and seed predator visitation was positively correlated with β-myrcene emission. Traits that predicted pollination were distinct from those that predicted seed predation. Floral volatile traits were generally stronger predictors of both pollinator and seed predator activity than were morphological traits. Indirect and direct measures of seed predator activity provided complementary corroboration of the importance of β-myrcene in influencing seed predation.

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Biogeography

Topic: Contributed Papers Systematics

Title:

Examining phylogenetic (dis)agreement with migration route hypotheses in tarflowers (Bejaria, Ericaceae)

Author: ***Senna Robeson @***

Keywords: Andean Flora,Angiosperm353,Angiosperms353,Angiosperms353 Hyb-Seq,biogeography,ericaceae,GAARlandia,herbariomics,herbarium specimen,herbarium specimens,HybSeq,Hyb-Seq,molecular phylogenetics,Neotropics,phylogenetics,phylogenomics,phylogeny,tropical mountai

Abstract:

Tarflowers (Bejaria, Ericaceae) are very common in Neotropical mountains, but exhibit notable range disjunctions across the Americas, with only a few scattered species found north of South America. A longstanding hypothesis is that the genus reached its present distribution by passage through Caribbean islands, making a subsequent secondary expansion into Central America. However, this has not been tested amid a paucity of recent work with the group. As biotic connectivity between continents via the Caribbean (such as in the GAARlandia hypothesis) has received little empirical support in recent research with other taxa, we set out to test whether any such connection is fundamentally congruent with species relationships in the group. A preliminary species tree based on target capture sequencing from herbarium specimens using Angiosperm 353 probes is presented here, representing around fifty individuals of at least 18 tarflower morphospecies from every region where the genus occurs. The tree topology suggests that a Central American over-land migration route is more likely to have led to the present-day distribution of the group. These early data also suggest that the Central American tarflowers are likely to require systematic revisions corresponding to the biogeographic entities revealed by the phylogeny. Further clarifying work is needed to pinpoint the timing of divergences, especially as there are no fossils available for the group, but this research begins to shed light on the origins of this little-studied but ecologically prominent genus.

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Systematics

Topic: Contributed Papers Systematics

Title: Chloroplast phylogenomics of the Lepanthes (Orchidaceae) backbone: a Neotropical unsolved diversification history

Author: **Tatiana Arias @ Marie Selby Botanical Gardens**

Keywords: Andes,chemotaxonomy,Orchids,phylogenomics,systematics,Lepanthes,Pleurothallidinae,Plastids

Abstract:

The subtribe Pleurothallidinae hosts the charismatic miniature orchid genus Lepanthes, one of the largest genera in the subtribe with more than 1000 species. The majority of the Lepanthes species are found in the Andean region of Colombia and Ecuador with more than 300 species in each country. Many endemics to the northern Andes. Olaf Swartz described the genus in 1799. Species share ramicauls (stems) enclosed by a series of tubular sheaths known as lepanthiform sheaths and each bears a single leaf. Also typical of the genus are racemose inflorescences, flowers with petals usually transversely lobed, and a trilobed lip with a modified mid-lobed named as the appendix. The footless column is adnate to the base of the lip and the stamen has two hard pollinia. Beginning in 1996 with species from Ecuador, the botanist Carlyle Luer suggested a taxonomic classification below the genus level using the morphological variation observed in sepals, including morphological features such as petals fused or free, and number of veins observed in each sepal, usually two or three. This taxonomical hypothesis has not been examined to date using phylogenetics to understand main evolutionary lines among Lepanthes species. Here we examined the maternal plastome evolution of ten Lepanthes species representing major taxonomic groups in Luer's taxonomic classification.Plastomes had a mean length of 156,000 bp, with L. narcissus being the species with the smallest plastome size at 155,484 bp and L. caprimulgus the largest at 156,546 bp and the GC content of all plastomes was approximately 37%. All plastomes shared the same number of genes (140) and gene content (78 coding genes). We also recovered the first resolved backbone phylogeny for the genus, taking as an initial hypothesis taxonomic groups proposed by C. Luer. All analyses support the monophyly of Lepanthes (BS = 100, PP= 1), while both subgenera are paraphyletic (Lepanthes and Marsipanthes) and sections, subsections, and series are also paraphyletic. Two main sister clades were identified. Clade 1 included two species L. narcissus(subgen. Lepanthes, subsect. Bilabiate) containing species exclusively found in Ecuador and L. caprimulgus(subgen. Marsiphantes sect. Caprimulginae) found in Ecuador and central Peru. Clade 2 includes the rest of the species representing the genus backbone. The species L. monoptera represents section Breves, which includes six species with distribution in Colombia and Ecuador, and is sister to a clade we have named core Lepanthes that includes L. manabina (series Lepanthes), L. hexapus + L. mucronata (series Mucronata) and L. eros (subsect. Breves) sister to L. felis (sect. Felinae) + L. ribes (sect. Marsipanthes). This phylogeny will accelerate evolutionary studies in this hyperdiverse genus including a large study we are developing for around 200 species. from Colombia.

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Systematics

Topic: Contributed Papers

Title: Cleaning the variable mess: a population genomics approach to understanding the evolutionary history of a complicated plant group

Author: **Claire Marino @ Bucknell University**

Keywords: Solanaceae,Australia,Dioecy,population genomics,PUI,Solanum,Undergraduate Research,Species boundaries

Abstract:

The Solanum dioicum clade, which is a group of Australian bush tomatoes consisting primarily of species native to Western Australia and the Northern Territory, is a set of taxa whose species delimitations tend to be quite unclear. Since the publication of David Symon's monograph A Revision of the Genus Solanum in Australia in 1981, little additional progress has been made in determining these relationships. In this project, a population genomics approach was used to analyze the relationships and delimitations between three species within the S. dioicum clade: Solanum dioicum, S. carduiforme, and S. ossicruentum. The use of population genomics methods is advantageous to understanding the fine-scale genetic diversity and population structures of species, especially given that phylogenetic approaches have not been successful in the past, and morphological approaches are not feasible. To complete this project, DNA extractions from different populations of the three aforementioned species were conducted prior to DNA sequencing, assembly, and data analyses that allowed the interpretation of these relationships. This project allows a continued and improved understanding of the relationships and delimitations between species within the S. dioicum clade. Our results indicate that there is a clear separation between the three studied species, and multiple genetic clusters within the S. dioicum populations, some of which may be their own independent taxa. In the context of global climate change, documenting species populations, particularly those which are rare or previously undocumented, helps regions that need extra protection get the resources they need, thereby protecting the biodiversity and stability of these habitats. It is extremely difficult to obtain the necessary resources to protect species if they have not been named or correctly described.

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Systematics

Topic: Contributed Papers

Title: Understanding the divergence of a rare California sand verbena, Abronia villosa var. aurita (Abrams) Jeps.

Author: **Eli Allen @ Cal Poly Humboldt**

Keywords: Abronia,Endemic Species,Evolution,molecular phylogenetics,rare species

Abstract:

Rare plants comprise a significant portion of biodiversity hotspots, making them paramount for preserving species-rich areas in the face of the Anthropocene. In the California Floristic Province, a global hotspot for plant diversity, nearly 1/3 of the flora is considered rare. A. villosa var. aurita (Abrams) Jeps. – the Chapparal Sand-Verbena – is a rare species endemic to California, whose taxonomic boundaries, genetics, and evolutionary origin are poorly known. Morphological taxonomy suggests that A. villosa var. aurita and A. villosa var. villosa S. Watson are two varieties of the same species. However, a recent phylogenetic analysis for the genus indicates that A. villosa var. aurita and A. villosa var. villosa may not be monophyletic and thus do not comprise a single species. Relationships and species delimitation within A. villosa and between A. villosa and its allies, A. umbellata Lam. and A. gracilis Benth. warrant further study. To define species boundaries within the clade, multiple individuals and populations will be sampled within species to infer a high-resolution phylogeny using target sequencing (Angiosperms353). This project aims to test the hypothesis of A. villosa var. aurita being a separate species and assess the placement and genetic variability of members of the group in the context of conservation.

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Systematics

Topic: Contributed Papers Systematics

Title: Morphology and placement of perennating organs play an important role in generic delimitation in subtribe Malaxidinae

Author: ***Pankaj Kumar @ Texas Tech University***

Keywords: homoblastic,heteroblastic,Liparis,UPGMA,homoplasty

Abstract:

Malaxidinae is a small subtribe of family Orchidaceae containing 14 genera that are accepted currently. However, this subtribe has a very complicated taxonomy and the taxonomic delimitations of its genera has remained unclear after multiple attempts by many experts from time to time. most of the genera do show homoplasty along a range of morphological features, however, they also show some distinct characters which adds to the confusion.

A few attempts have been made in past where functional traits of species were plotted against the phylogenetic tree obtained using combined ITS and matK sequences. One such study attempted to classify this group on the basis of species' habit (epiphytic/terrestrial), leaf morphology (shape- linear/rounded; foldings- plicate/conduplicate/compressed/unifacial) and leaf number (1, 2, >2). However, the monophylly in Liparis (contains both epiphytic and terrestrial members and leaves can be conduplicate (linear/rounded) or plicate) and Malaxis (leaves can be both plicate or conduplicate-rounded) could not be achieved.

Another attempt utilized growth habit (terrestrial/epiphytic), habitat (grassland/forest) and morphology of leaves (conduplicate/plicate/duplicate) to resolve the taxonomy. However, the monophyly was not achieved in Liparis (can be both epiphytic or terrestrial, may occur in both grassland and forest habitats; contains plicate, conduplicate and duplicate leaves) and Malaxis (occurs in both grassland and forest habitats; contains both plicate and conduplicate leaves) in this study either.

Current study emphasized the use of additional ecological, vegetative and floral characters, along with the previously used characters. Analysis of 25 morphological characters based on UPGMA generated a dendrogram, which was cross-referenced against the phylogenetic tree obtained using the combined sequences of nrITS and matK regions. While growth habit, perennating organ structure (homoblastic/heteroblastic), placement of perennating organ (above ground/below ground), leaf texture (leathery/soft) and number of leaves were able to resolve the monophyly among terrestrial members of Crepidium clade, epiphytic and terrestrial members of Liparis still remained polyphyletic. The remaining set of floral characters were able to segregate genera within the terrestrial Crepidium clade further as per current taxonomic delimitations.

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Systematics

Topic: Contributed Papers

Title: The Evolutionary History of the Silene hookeri Nutt. complex (Caryophyllaceae), Part I.

Author: ***Michael Mayer @ University of San Diego***

Keywords: Silene,chloroplast DNA,Pacific Northwest

Abstract:

The range of Silene hookeri Nutt. (Caryophyllaceae) spans the Cascades of Oregon to the Coast Ranges of Northern California. This beautiful catchfly is also the namesake of a small complex of species that has included the narrowly distributed S. bolanderi, S. salmonacea, S. serpentinicola, as well as S. nelsonii, which has only recently been described. A combination of morphological and molecular evidence revealed that S. nelsonii was not derived from within the complex, and suggested that S. hookeri served as a progenitor of the remaining members of the complex. Further analyses of non-coding chloroplast sequences have supported this hypothesis, showing separate clades for each of the species (S. bolanderi, S. salmonacea, and S. serpentinicola) that also include representatives of S. hookeri from the same region.

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Systematics

Topic: Contributed Papers

Title: Plastid phylogenomics and plastome evolution of Lithospermeae (Boraginaceae)

Author: ***James Cohen @ Weber State University***

Keywords: genome skimming,plastome,Boraginaceae,Lithospermeae

Abstract:

The tribe Lithospermeae (Boraginaceae) includes ca. 450 species, with most distributed across the Old World. The tribe houses a variety of notable speciose genera, including Onosma, Lithospermum, and Echium, as well as a variety of genera with fewer than 10 species. During the past 15 years, the tribe has been the subject of multiple phylogenetic studies, with most including only a few DNA regions. To better understand the evolutionary relationships within the tribe, we employed genome skimming to assemble the plastid genome and nuclear ribosomal cistron and reconstructed phylogenies from these genomic regions. Additionally, we investigated patterns of evolution and selection across the plastid genome. The resulting phylogenies provide evidence that, in general, relationships across the tribe are similar to those that have been previously resolved; however, the addition of greater sequence data suggests that some genera, such as Alkanna, are resolved as non-monophyletic, and other genera, such as Onosma, that were sometimes recovered as paraphyletic may, indeed, be monophyletic. Similar results are reconstructed among the two genomes. For the plastid genome, genes at the IR boundary are fairly conserved across most of the tree, but among Onosma and relatives, greater variation is identified. Most areas of the plastid genome are not under positive selection, but five genes are recognized as being under positive selection.

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Systematics

Topic: Contributed Papers

Title: Origin and Distribution of Leaf Teeth in Temperate Woody Angiosperm Flora

Author: ***Oluwatobi Oso @ Yale University***

Keywords: Biome shift,temperate forest,Leaf Teeth,Woody Angiosperms,Phylogenetic Distribution

Abstract:

Leaf margin is important taxonomic trait that has been widely used in many paleoclimatic inferences and biome studies. One of the most significant documented trends in multiple studies using leaf margins is the association between toothy-margined woody Angiosperms and temperate biomes, as well as association between entire-margined woody angiosperms and tropical biomes. Some studies suggest that this leaf-form gradient succeeds a correlation shift through time, from more toothed and tropical early-diverging angiosperm clades, while others suggest that this variation is a result of adaptive environmental convergence in temperate regions. Despite previous research identifying the need to put this global trend in an evolutionary context, not much has been done, with most works focusing on a few species from selected sites or clades. This study provides some insights into the origin and distribution of leaf toothiness in temperate woody angiosperm flora by pooling information from multiple databases, flora, and literature. We collected biome shifts, toothiness, and climate data, and used the resulting phylogenetic trees to analyze the evolution, origin, and geographic distribution of toothiness in temperate woody angiosperm flora. About 232 plant clades have undergone at least one shift between tropical and temperate biomes, and this shift correlates with leaf form. Many temperate woody angiosperm clades independently evolved leaf teeth multiple times, and the geographic distribution of toothiness in most of these clades is associated with regions of low mean annual temperature. This study presents the first documentation of woody angiosperm clades that have undergone shifts between tropical and temperate forests and the origin of toothiness in temperate forests.

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Systematics

Topic: Contributed Papers Systematics

Title: Investigating conserved pollinator attractants as a driver of hybridization in Heuchera.

Author: ***Nicholas Engle-Wrye @ Mississippi State University***

Keywords: Heuchera,Floral traits,floral visitor,hybridization,phylogenetic conservatism

Abstract:

Little is known about environmental drivers of hybridization, but its phylogenetic distribution across plants is heterogeneous, suggesting that plant traits may play an important role. Conservatism of biotic niche could explain why some plants are prone to hybridization, as conserved pollination strategies would lead to a lack of pollinator assemblage divergence and therefore opportunities for gene flow, although this hypothesis has yet to be tested. The taxonomic tribe Heuchereae (Saxifragaceae) is a well-characterized system for pollinator interactions and particularly for floral scent, the primary pollinator attractant in the group. Floral volatile organic compounds (VOCs) in this clade, characterized to date only in Asimitellaria and Lithophragma, are hypervariable at the population level and are thought to be responsible for pollination selectivity, leading to divergent pollinator assemblages. High levels of interspecific pollinator attractant divergence may be therefore responsible for the relatively low levels of hybridization observed in these groups. Heuchera flowers, by contrast, are thought to be pollination generalists and Heuchera species accordingly hybridize frequently. While floral volatiles have yet to be characterized for Heuchera, understanding variation in pollinator attractants would offer insight into whether the diversity of prezygotic isolation mechanisms across a recent radiation are predictive of hybridization rate.

Given that pollinator-mediated gene flow primarily hinges on VOCs in the relatives of Heuchera, we investigated whether high rates of hybridization observed in Heuchera may be associated with low interspecific divergence of VOCs, using as a system the hybrid zone between H. americana and H. richardsonii in the midwestern US. We optimized a closed-space collection and GC-MS (gas chromatography-mass spectrometry) protocol to characterize VOCs in Heuchera flowers. To identify floral visitation and effective pollinators, we conducted pollination observations at 47 different populations across the eastern United States, ranging from Arkansas to North Carolina, north to Minnesota, over the span of two years. GC-MS data from ~110 Heuchera representing 21 populations suggests that shared classes of VOCs, and to some extent individual compounds, are shared within the hybrid complex while other Heuchera that do not hybridize with these species have distinct species-specific compounds. Pollination observations confirm shared effective pollinators and the importance of VOCs in determining floral visitation in Heuchera.

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Systematics

Topic: Contributed Papers

Title: Non-monophyletic origins of floral phenotypes, plastome structure variation, and phylogenetic relationships of Agave subgenus Manfreda

Author: ***Bryan MacNeill @ University of Alabama***

Keywords: morphology,floral evolution,México,phylogeny

Abstract:

Agave (Asparagaceae) is a well-known genus due to several economically and culturally important species involved in alcohol, fiber, and sugar production. Apart from economic species, Agaves serve as ecological keystone species for many desert ecosystems and consists of over 250 species. Agave is divided into multiple subgenera based on morphology including Manfreda, Agave, and Littaea. Subgenus Manfreda consists of 52 herbaceous species that diverged early within Agave evolution. Manfreda exhibits highly variable floral architecture compared to other Agave lineages, attracting specialist pollinators like hummingbirds and hawkmoths as well as generalist pollinator like bees. How these floral phenotypes diversified has yet to be precisely understood, as there is little molecular evidence for phylogenetic relationships of taxa within Manfreda. Here we present a robust plastome phylogeny of taxa in Manfreda across the subgenus's distribution, integrating an extensive floral morphometric database to assess the role pollinators played in shaping the floral diversification of this group. Our phylogenetic results indicate hybridization and chloroplast capture are likely prominent in the group. Short branches of the phylogeny backbone suggest little divergence of chloroplasts during the diversification of the group. We recovered non-monophyletic origins of similar floral phenotypes, suggesting the convergent evolution of pollinator-associated syndromes. More broadly within Agave we discovered a ~1000-base pair inversion in the plastomes of non-Manfreda Agave species used in our analyses. These results directly contribute to our understanding of the origins of convergent floral phenotypes, plastome structure variation, and species diversification within Manfreda. More generally, these results will contribute to our knowledge of Agave systematics and to this system as an emerging model for studying floral evolution. Future research will incorporate nuclear genes from an Asparagaceae custom-probe set to help parse hybridization events and, hopefully, a more resolved species phylogeny for this economically and ecologically important genus.

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Systematics

Topic: Contributed Papers

Title: Phylogenomics, systematics, and biogeography of the figwort family Scrophulariaceae

Author: ***richard olmstead @ University of Washington***

Keywords: biogeography,Diversification,Lamiales,molecular dating,Buddlejeae,Limoselleae,Hemimerideae

Abstract:

We developed a probe set based on five Scrophulariaceae transcriptomes to conduct a target-sequencing approach for phylogenetic analysis of 66 species representing all recognized tribes fo Scrophulariaceae plus three genera unassigned to tribe, Androya, Camptoloma, and Phygelius. Ten tribes are recognized based on the resulting phylogeny. Diversification of crown Scrophulariaceae was inferred to have started in the southern hemisphere approximately 60 Ma. A southern African origin is estimated for most tribes with two exceptions, Leucophylleae and Myoporeae.

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Topic: Contributed Papers Systematics

Title: Resolving species relationships in the recent and rapidly evolving Mentzelia section Bartonia (Loasaceae) with Angiosperms-353 target capture

Author: ***Paige Fabre @ Ohio University***

Keywords: Angiosperms-353,Chloroplast genome,floral evolution,genome skimming,HybPiper,hybrid enrichment,HybSeq,Loasaceae,Mentzelia,phylogenetics,phylogenomics,staminode,Target Enrichment,target-capture

Abstract:

Since the sudden burst of Angiosperms in the Mid-Cretaceous, flowering plants have steadily diversified while continually evolving new and innovative structures. Staminodes are infertile stamens that are sometimes functionally co-opted to perform novel functions other than pollen production, including a variety of supportive roles in pollination or protection. Petaloid staminodes, such as those found in Mentzelia section Bartonia (Loasaceae, Cornales), for example, are likely co-opted for pollinator attraction. Mentzelia section Bartonia has emerged as a recent and rapidly evolving clade of 51 species that are distributed across western United States and northern Mexico. Approximately half of the species contain staminodes, but a fully resolved phylogeny is needed to identify the number of times staminodes have been gained or lost. Because of its recent and rapid evolution, reconstructing a fully resolved phylogeny has been hampered by low sequence divergence, high cytonuclear discordance, and cryptic morphological changes, which have impeded phylogenetic reconstruction using a limited number of plastid and nuclear markers. To better infer species relationships, we implemented a target-capture approach with the Angiosperms-353 nuclear bait set for all taxa in the section. Sequences for orthologous supercontigs (combined intron and exon regions) were assembled with HybPiper and maximum likelihood gene trees were reconstructed in 1,000 bootstrap replicates and compiled into a species tree using Astral-III. The chloroplast genome was also sequenced with genome skimming and a phylogeny was reconstructed with maximum likelihood. We discuss species relationships within the section, compare phylogenies reconstructed with Angiosperms-353 baits to those inferred with chloroplast genomes, and examine how many times staminodes have been gained and lost in the group.

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Topic: Contributed Papers

Title: A new hypothesis for the origin and species relationships of the scaly-bracted green leaf manzanitas (Arctostaphylos)

Author: ***Tito Abbo @ UC Riverside***

Keywords: Arctostaphylos,distributions,hybridization,manzanita,systematics,Taxonomy

Abstract:

Arctostaphylos (manzanitas), the most diverse woody genus within the California Floristic Province, is regarded as a taxonomically and evolutionarily complex system. High diversity and hybridization pose challenges for both species delimitation and morphological identification. A key debate in developing a classification system for manzanitas that accurately reflects evolutionary relationships is whether taxa that share morphological traits derived those traits from descent or homoplasy. The taxa that I am calling the SBGL (scaly-bracted green leaf) manzanitas all share the combined traits of scale-like inflorescence bracts and shiny green leaves. In manzanitas, bracts can be leaf-like, scale-like, or fleshy, and leaves can be green, gray-green, or glaucous. Munz and Roof considered many low-growing SBGL manzanitas to be aligned with A. uva-ursi and erect SBGL manzanitas to be aligned with A. pungens. Wells, on the other hand, considered Central Coast SBGL manzanitas as subspecies of A. hookeri. Markos et al. (1998) using nuclear ITS and 26S loci found limited but sufficient phylogenetic resolution to conclude that A. hookeri was paraphyletic without direct evidence of alignment with A. uva-ursi nor A. pungens. This suggested that the SBGL phenotype was derived multiple times independently. However, using reduced representation genomic sequencing (ddRADseq), I present evidence that SBGL manzanitas are not independent but rather are associated due to hybridization. The hybrid origin of SBGL manzanitas appears to be associated with one or more hybridization events involving two very distantly related manzanita lineages (the two ITS clades), which were thought to have sufficiently diverged to develop reproductive isolation. Herein, I present the hypothesis that the Central Coast is a large hybrid zone which has led to the origin of several narrow endemic SBGL manzanita lineages. Further, I present evidence for numerous hybrid origins of the taxa morphologically identified as A. benitoensis and A. parryana ssp. parryana.

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Systematics

Topic: Contributed Papers Systematics

Title: Evaluating the limits of Piper amalago L., a widespread Neotropical shrub

Author: ***Cara Hastings @ Boise State University***

Keywords: Angiosperm353,Piper,species complex,species delimitation

Abstract:

The delimitation of species boundaries is a question that has plagued biologists, taxonomists, and philosophers alike. Subtle and minor morphological differences in a widespread species complex makes delimiting the boundaries of the species particularly challenging. High throughput targeted sequencing of hundreds of loci has allowed researchers to gain better insight to phylogenetic processes and gain confidence in previously ambiguous relationships. Piper amalago sensu lato occurs throughout the Neotropics. Piper amalago is morphologically similar to many other Neotropical Piper species that have more restricted ranges or occur as narrow endemics. Taxonomists have debated whether the morphological differences between Piper amalago and other similar species are significant. Recent data indicates that other Neotropical Piper species are nested within the Piper amalago lineage. Using herbarium specimens of Piper amalago collected throughout its range, specimens of synonyms of Piper amalago and specimens of morphologically similar species, this study focuses on the phylogenetic relationships of Piper amalago and similar species and seeks to determine if Piper amalago forms an exclusive monophyletic lineage that includes other currently recognized species of Piper following the genealogical species concept. Alternatively, Piper amalago may be better split into a series of species each monophyletic and exclusive. For this study, the Angiosperms353 bait set is used to retrieve nuclear genes used for building maximum likelihood and multispecies coalescent phylogenetic models. This analysis will lead to a better understanding of morphological variation within the Piper amalago lineage and where species boundaries should be drawn. The delimitation of species boundaries is a question that has plagued biologists, taxonomists, and philosophers alike. Subtle and minor morphological differences in a widespread species complex makes delimiting the boundaries of the species particularly challenging. High throughput targeted sequencing of hundreds of loci has allowed researchers to gain better insight to phylogenetic processes and gain confidence in previously ambiguous relationships. Piper amalago sensu lato occurs throughout the Neotropics. Piper amalago is morphologically similar to many other Neotropical Piper species that have more restricted ranges or occur as narrow endemics. Taxonomists have debated whether the morphological differences between Piper amalago and other similar species are significant. Recent data indicates that other Neotropical Piper species are nested within the Piper amalago lineage. Using herbarium specimens of Piper amalago collected throughout its range, specimens of synonyms of Piper amalago and specimens of morphologically similar species, this study focuses on the phylogenetic relationships of Piper amalago and similar species and seeks to determine if Piper amalago forms an exclusive monophyletic lineage that includes other currently recognized species of Piper following the genealogical species concept. Alternatively, Piper amalago may be better split into a series of species each monophyletic and exclusive. For this study, the Angiosperms353 bait set is used to retrieve nuclear genes used for building maximum likelihood and multispecies coalescent phylogenetic models. This analysis will lead to a better understanding of morphological variation within the Piper amalago lineage and where species boundaries should be drawn.

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Systematics

Topic: Contributed Papers

Title: Code Red: Dissecting the evolutionary and ecological relationships of red, perennial paintbrushes, Castilleja (Orobanchaceae), along the California coast

Author: ***Adriana Hernandez @ California Academy of Sciences***

Keywords: hybridization,PacBio,polyploid,population genetics,Reference genome

Abstract:

Castilleja (the "paintbrushes") is a genus of American wildflowers with long-standing challenges in formally describing its 200+ species and their evolutionary relationships. Many co-occurring Castilleja species are difficult to distinguish in the field, in part due to their hypervariable nature, their overlapping distributions, and their potential to hybridize. This project focuses on evaluating species relationships of red, perennial Castilleja that grow mainly along the coast of California that appear to be diverging in the midst of gene flow. We use PacBio Hifi technology to assemble a high-quality, phased genome which provides a reference for comparative genomic and population genetic analyses. We have begun to collect extensive datasets across genetic, morphological, and ecological lines of evidence, in order to take a holistic approach to assessing and characterizing how these species and populations are related to each other, to characterize their ecological specializations, how to best identify species in the field, and ultimately, how they are related to other species in the genus.

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Systematics

Topic: Contributed Papers

Title: A phylogeny of Trillium subg. Trillium using nuclear capture data

Author: ***Wesley Knapp @ NatureServe***

Keywords: Endemic Species,Southern Appalachians,Trillium,conservation

Abstract:

The North American species of Trillium subgenus Trillium include some of the pedicellate species, is the only clade of Trillium that has a North American-Asian disjunction pattern. In North America, the distribution of subg. Trillium is disjunct with one species in W NA (T. hibbersonii) and the remainder in eastern North America. Most of the North American diversity is in the Southern Appalachians with several local endemics, e.g. T. simile and T. vaseyi. Here we provide updated phylogenetic analyses doubling our taxon sampling from what we discussed in 2022, using the Angiospermum 353 nuclear capture kit and genomic skimming data to discern the number of species and their relationships with a secondary focus on their apparent hybridization in the Southern Appalachians. We will discuss these results, including how they impact current species concepts and rarity. We have completed a typification of all published names in subg. Trillium that includes newly designated lectotypes for T. flexipes, T. rugelii, and T. vaseyi. We also lectotypify the name of T. rhomboideum var. album (=T. rugelii) which has been associated with T. erectum.

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Systematics

Topic: Contributed Papers Systematics

Title: Phylogenomics Resolve Species Boundaries of the Pantropical Genus Neptunia (Fabaceae: Mimosoid Clade)

Author: ***Ellie Becklund @ Ohio University***

Keywords: Angiosperms353,chloroplast,Fabaceae,Hyb-Seq,Neptunia,nuclear DNA,phylogenomics,systematics,target-capture,Mimosoid clade

Abstract:

Neptunia Lour. (Fabaceae) is a mimosoid genus of 22 species that occur worldwide in the tropics and subtropics and is the sole mimosoid genus with aquatic species, the pantropical N. oleracea and N. plena. The genus is characterized by unarmed prostrate or ascending stems, thigmonastic leaves, and heteromorphic inflorescences with distally perfect but proximally sterile or male flowers. Previous molecular studies reconstructed Neptunia as monophyletic from three chloroplast regions and nrDNA markers, but were unable to resolve inter- and infraspecific relationships. We applied a target-capture approach with the Angiosperms353 bait-set to sequence hundreds of nuclear genes and the chloroplast genome to infer species relationships of the 22 Neptunia species. DNA sequences were reassembled with HybPiper, gene trees were reconstructed with maximum likelihood, and the nuclear species tree was estimated in Astral III. Phylogenies estimated with the Angiosperms353 bait-set were more resolved than previous studies based on Sanger sequencing data. The reconstructed phylogeny identified clades of species that correlated to their geography, in particular an American clade and an Australian clade. The two aquatic species were sister to each other, indicating a single transition into an aquatic habitat. Species boundaries did not correspond to clades for some species, such as N. plena, but others formed a monophyletic group. Relationships among species and supporting morphological characters will be discussed for taxonomic considerations, with a focus on the aquatic, American, and Australian clades.

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Systematics

Topic: Contributed Papers

Title: Delving into the cryptic diversity of a holomycotroph – progress with dissecting Hypopitys monotropa (Ericaceae) across North America

Author: ***John Freudenstein @ Ohio State University***

Keywords: species delimitation,ericaceae,parasites

Abstract:

Plants with reduced morphology, such as holomycotrophs, are a particular challenge for species circumscription because of the paucity of phenotypic features. Hypopitys monotropa Crantz (formerly Monotropa hypopitys L.) is a case in point. Currently most often recognized as a single species, its distribution is vast, from central America north across North American and across Eurasia. Although segregates have at times been proposed, most in both the New and Old Worlds have been disregarded. Because of the structural reduction, a case such as this is a particularly important one for application of molecular data. Applying an integrative approach that requires evidence of phenotypic shifts coincident with lineage resolution is challenging because of structural reduction and because color, which is variable in the species, is largely lost in dried specimens. Another potentially relevant source of variation is the identity of the host fungus that Hypopitys parasitizes, yielding an extended phenotypic character. We have sequenced over 100 accessions from across the species' range in North America for a nuclear ITS-26S 1500 bp segment. Likelihood analysis resolves six well-supported groups, which are also supported by a broader genomic sampling of SNPs for a subset of these accessions. The groups have distinct geographic ranges, phenology and, to the extent of our fungal sampling thus far, may be using different groups of Tricholoma as hosts. Some of these groups are also morphologically distinct, such as a red-flowered group from the southwestern US and Mexico, and the previously-named H. lanuginosa (Michx.) Raf., a late-flowering group from the eastern US. We propose that these should be recognized as distinct species. Other groups remain challenging to diagnose morphologically, and thus from dried specimens, but citizen-science biodiversity reporting sites such as iNaturalist provide a very useful source of information on color, and to some extent structure, of fresh plants, information rapidly lost in the drying process.

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Systematics

Topic: Contributed Papers

Title: Phylogenomics and seed morphology of Cleomaceae

Author: ***Theresa Saunders @ Washington State University***

Keywords:

Abstract:

We present a revised phylogenetic hypothesis for the plant family Cleomaceae. Cleomaceae is composed of 27 genera and approximately 270 species occurring world-wide, making it difficult to sample comprehensively. Previous research has used morphology and limited genetic data to update various Cleomaceae lineages, but a stable family phylogeny has not been generated. We used herbarium vouchers and high throughput sequencing (Hyb-Seq) combined with the Angiosperms353 probe set to clarify phylogenetic relationships in Cleomaceae. We imaged seeds from a majority of the species in Cleomaceae using a Canon camera system with focus stacking functionality and microscopic objective lenses, resulting in images comparable to those generated by Scanning Electron Microscopy (SEM). In this talk, we present phylogenetic findings produced from approximately 380 specimens representing 26 genera and 236 species (~85% of the species in the family), with most samples coming from herbaria collections. Seed images revealed a wide range in variation between and within genera of Cleomaceae. We discuss inter- and intrageneric phylogenetic relationships and correlations with seed ornamentation and morphology.

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Systematics

Topic: Contributed Papers

Title: Using Targeted Sequence Capture to infer the phylogeny of Zinniinae (Asteraceae: Heliantheae)

Author: ***Samuel Skibicki @ West Virginia University***

Keywords: Asteraceae,Heliantheae alliance,herbariomics,phylogenomics,systematics

Abstract:

The evolutionary relationships within Zinniinae, a subtribe of ~54 species across seven genera, have proven difficult to elucidate due to hybridization and polyploidy. Species of Zinniinae display a variety of chromosome counts and live in a wide variety of habitats that include temperate, semiarid, and desert environments. Target Sequence Capture (TSC) of genomic libraries was used to address these challenges. Leaf tissue from 119 taxa (70 from the Zinniinae, 49 from the sister subtribe Spilanthinae, 1 from Montanoinae, a more distantly related subtribe but still in the tribe Heliantheae) were collected from herbarium specimens. Genomic DNAs were extracted using a modified CTAB procedure, and genomic libraries were built using a fragmentase-based library prep kit. A probe set specifically designed for the Asteraceae, the Compositae-1061, was chosen to perform the TSC. High-throughput sequencing was performed on the captured loci in a single lane on an Illumina HiSeq sequencer. A preliminary subset of the samples (n = 61) across the Zinniinae were analyzed in order to test the functionality of downstream analysis pipelines, focusing on genus-level relationships. Reads were adapter- and quality- trimmed with BBDuk. Trimmed reads were run through HybPiper which flagged paralogs and filtered loci with less than 40% representation. Of the 1,022 loci targeted, 441 (43.15%) were recovered and passed the 40% representation barrier. Assembled loci were aligned with MAFFT. Maximum Likelihood gene trees were created with IQTREE2 using models chosen by ModelFinder, with 100 UF bootstrap support replicates for each tree. A coalescent analysis was run with ASTRAL-III. PhyParts and PhyPartsPieCharts were run to insert pie charts showing concordant and discordant trees at each node of the species tree. Additionally, gene and site concordance factors were calculated in IQTREE2. The species tree was well supported with 58.6% of nodes receiving at least 95% bootstrap support. The genera within Zinniinae all have 100% bootstrap support as does the split between Zinniinae and Spilanthinae. Overall, the gene concordance factors were lower than the site concordance factors for the nodes of the species tree. This means the individual gene trees were not as informative when compared to the total data which is consistent with many other studies of this type. Subsequent analyses of the whole dataset will explore patterns of gene tree concordance and discordance, chromosome number evolution, and diversification/dispersal to arid environments. The findings will be used to delimit sections within the genera of Zinniinae. Taxonomic changes in the Spilanthinae will need to occur as these results point to paraphyly in Salmea. Herbariomics and the ever-lowering price of genomic tools make phylogenetics projects on these previously challenging clades easier to perform, and these methods can be used more broadly for other clades in Asteraceae.

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Systematics

Topic: Contributed Papers Systematics

Title: Phylogenomics of Eriogonum (Polygonaceae) with a Focus on Subgenus Oligogonum and Shifts to Serpentine Soils

Author: ***J. Travis Columbus @ California Botanic Garden***

Keywords: Eriogonum,phylogenomics,species delimitation,Polygonaceae,serpentine soils

Abstract:

With over 250 species, Eriogonum is one of North America's largest plant genera. Species occupy a wide range of elevations and habitats, and many occur on unusual, inhospitable soils such as serpentine. In California, over 25 species grow on serpentine, and about half are thought to be endemic to these ultramafic soils. Eriogonum subgenus Oligogonum is especially well represented. With a focus on Oligogonum, objectives of our ongoing study are to evaluate the existing classification and reveal the number of evolutionary shifts to serpentine soils. We employ a reduced-representation method, double-digest restriction site-associated DNA, for sequencing. Analysis of these data suggest the polyphyly of E. umbellatum, the presence of multiple currently unrecognized species, and multiple transitions to serpentine soils.

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Biogeography

Topic: Contributed Papers

Title: Niche overlap and differentiation in Leavenworthia, a genus of rare, glade-endemic plants

Author: ***Kyle Simpson @ Texas A&M University***

Keywords: Brassicaceae,co-occurring species,glades,Leavenworthia,niche differentiation,rare plants

Abstract:

Two species with similar niches are not expected to be able to coexist because they will compete for the same resources. Closely related species often occupy similar niches because of a recent common ancestor. Because of this, closely related species are not expected to coexist, and if they do, they may partition their niches in order to coexist. There are abundant examples of communities in natural systems that violate the competitive exclusion principle, but the reasons species with similar niches are able to coexist in these communities are often not understood. Leavenworthia, a genus of rare plants in Brassicaceae that is endemic to rock outcrops in the eastern United States, is an excellent system for studying the factors facilitating the co-occurrence of closely related species. At many sites, several Leavenworthia species can be found growing in close proximity to each other, and at some sites in Tennessee as many as four species (half the genus) can be found co-occurring. To elucidate the factors facilitating the co-occurrence of Leavenworthia species, we characterized the niche of each species using bioclimatic, geologic, and hydrologic data. Niche divergence was assessed for each species comparison considering i) the total niche space available to each species and ii) a subset of the niche space that is available to both species. The first test determined the degree to which the species overlapped in their niches. If low overlap was detected, the second test determined whether this low overlap was due to true niche divergence or if it was due to substantial differences in the niche space that is accessible to each species.

We found that the niche overlap between species depends on the niche axes being compared. Specifically, niche overlap was generally lower when geology was used to characterize the niche than when bioclimatic variables were used. Niche overlap was low even for species that are sympatric across much of their range, and several niche comparisons revealed that species had access to substantially different areas of niche space. These results demonstrate that despite frequent co-occurrence, Leavenworthia species occupy distinct regions of niche space. Two competing hypotheses could explain this paradoxical finding. One possibility is that Leavenworthia was more widespread historically, species were isolated from one another, and occupied distinct areas of niche space, and these differences are retained in the contemporary distribution of the species. Another possibility is that species co-occurred for most of their evolutionary history and have partitioned their niches in order to persist in an area where their endemic habitat is abundant.

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Systematics

Topic: Contributed Papers

Title: Goldenrod herbariomics: Hybrid-sequence capture reveals the phylogeny of Solidago (Asteraceae).

Author: ***James Beck @ Wichita State University***

Keywords: Chrysoma,Oligoneuron,Anchored Hybrid Enrichment,Asteraceae,herbarium specimens,North America,polyploidy

Abstract:

The phylogenetic relationships among the ca. 140 species of goldenrods (Solidago; Asteraceae) have been difficult to infer due to species richness, polyploidy, and shallow genetic divergence among species. We addressed these obstacles by combining aggressive sampling of diploid goldenrod herbarium specimens with the use of a custom Solidago hybrid-sequence capture probe set. A set of tissues from herbarium samples comprising ca. 90% of Solidago species was assembled and DNA was extracted. A custom hybrid-sequence capture probe set was designed using two Solidago species, and data from 854 nuclear regions was obtained and analyzed from 209 specimens. Maximum likelihood and coalescent approaches were used to estimate the species tree for 157 diploid samples. Hybrid enrichment and sequencing from goldenrod herbarium specimens was successful. Although DNAs from older specimens were both more fragmented and produced fewer sequencing reads, there was no relationship between specimen age and our ability to obtain sufficient data at the target loci. The resulting Solidago species tree was generally well supported, with 88/155 (57%) nodes receiving ≥95% bootstrap support. Solidago was strongly supported as monophyletic, with Chrysoma pauciflosculosa identified as sister. A clade comprising Solidago ericameriodes, Solidago odora, and Solidago chapmanii was identified as the earliest diverging Solidago lineage. The previously segregated genera Brintonia and Oligoneuron were identified as placed well within Solidago. These and other phylogenetic results were used to establish four subgenera and fifteen sections within the genus. The combination of expansive herbarium sampling and hybrid-sequence capture data allowed us to quickly and rigorously establish the evolutionary relationships within this difficult, species rich group. This general strategy should allow the phylogenies of similar genera to be inferred.

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Systematics

Topic: Contributed Papers

Title: Preliminary species delimitation results of Neotropical Palo Santo trees (Bursera graveolens; Burseraceae)

Author: ***Elizabeth Collins @ George Mason University***

Keywords: Cryptic Species,Neotropical biogeography,Phylogeography

Abstract:

Bursera graveolens (Kunth) Triana & Planch. (Burseraceae), or palo santo, is an economically and ecologically important tree species found throughout the seasonally dry tropical forests (SDTF) of southern Mexico south to Peru. No study to date has evaluated the relationship among the many disparate island and continental populations of B. graveolens, which are among the most widespread in the genus and rivaled only by those of B. simaruba, a distantly related species of Bursera. subg. Bursera. My research examines the population genetics and phylogeography of palo santo to test biogeographic hypotheses regarding the formation of the SDTF on a continental scale and population genetic variation across its range. I am also completing a taxonomic revision using morphological and phylogenetic data to determine if palo santo as currently described comprises a single, widespread lineage or segregate taxa. In this presentation I will share the outcomes of my field collection expeditions to Mexico, Colombia, Ecuador, and Peru and present preliminary findings from phylogenetic and morphological analyses related to species delimitation.

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Systematics

Topic: Contributed Papers Systematics

Title: Species delimitation in the Symphyotrichum subulatum group (Asteraceae) reveals a new species in central México

Author: ***Sushil Dahal @ Mississippi State University***

Keywords: Asteraceae,Central Mexico,morphometrics,phyologenomics,Symphyotrichum subgenus Astropolium,Symphyotrichum mexicanum

Abstract:

Symphyotrichum is a well-circumscribed genus within Asteraceae based on morphological and molecular data, but species boundaries remain poorly understood. Several subgeneric classifications have been proposed for the North American taxa of Symphyotrichum. Symphyotrichum subgenus Astropolium (the annual and perennial salt marsh asters), among the most geographically widespread radiations in the genus, has proven to be among the most problematic, with two primary competing classification proposals. Sundberg (1986) divided into three North American species in the Flora of North America (FNA) treatment. Nesom (2005), while consistent with Sundberg in the number of taxa recognized, presents justifications for the recognition of these taxa at the species level. The primary justification of Brouillet et al. (2006) for treatment at the varietal rank appears to be evident morphological intermediates, yet they also note that these taxa are “nearly entirely allopatric” and “mostly reproductively isolated” based on data from Sundberg (1986) that were interpreted as evidence for species-level distinctions by Nesom (2005). No newer classification framework has been proposed for subgenus Astropolium since Nesom (2005) and Brouillet et al. (2006), yet the foregoing indicates that uncertainty remains and the group merits further study. Here, I illuminate the species delimitation of the contentious S. subulatum group (S. subg. Astropolium) using morphometric, phylogenomic, and geographical analyses. Symphyotrichum mexicanum sp. nov., a new species endemic to central Mexico, is described and distinguished from Symphyotrichum expansum based on its morphometric attributes, phylogenetic placement, geographic range, and ecological specialization.

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Systematics

Topic: Contributed Papers

Title: Phylogenetic systematics of Vigna sensu stricto (Leguminosae, Fabaceae): the Old World Vigna

Author: ***Ashley Egan @ Utah Valley University***

Keywords: Fabaceae,Leguminosae,phylogeny,molecular systematics,Vigna

Abstract:

Premise of study: The evolutionary relationships between the diverse Vigna Savi species have been through many taxonomic revisions in legume systematics to reflect natural groupings. Vigna includes economic crop and wild species that sustain much of the world. Previous revisions to taxonomic organization of Vigna s.s. have presented questions about the Old World (OW) Vigna interspecific and inter-subgeneric relationships.
• Methods: A molecular phylogenetic analysis was undertaken to resolve long-standing OW Vigna taxonomic questions. Maximum likelihood and Bayesian phylogenetic analyses included cpDNA matK-trnK and nuclear ribosomal ITS/5.8S (ITS) sequence variation. African species were comprehensively sampled within the context of New World (NW) relatives and genera within Phaseolinae.
• Key results: The matK and ITS data analyses concurred in resolving five well-supported clades of Vigna s.s.: subg. Lasiospron, a reduced subg. Vigna, subg. Haydonia, subg. Ceratotropis, an enlarged subg. Plectrotropis, and a clade including V. kirkii and V. stenophylla that could be considered as new subgenus or section.
• Conclusions: Former subg. Vigna is reduced to yellow and blue flowered species and subg. Plectrotropis is enlarged to all white-pink-purple flowered species. Vigna s.s. in the Americas now includes subg. Lasiospron and a few pantropical species. Elaborate floral asymmetries are readily used to apomorphically diagnose nearly all the American genera. The age estimates of the extant diversification of the American and its Old World sister clade are approximately coeval at ca. 6 – 7 million yr.

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Systematics

Topic: Contributed Papers

Title: Investigating leaf shape variation and taxonomy in the pan-Caribbean Coccoloba diversifolia Jacq.

Author: ***Daniel Koenemann @ Claflin University***

Keywords: Bioclim variables,species complex,momocs,PCA

Abstract:

The West Indies are a biodiversity hotspot. As such, many of the plant genera growing in this region remain poorly known from a taxonomic perspective. The tree genus Coccoloba, is one of these poorly known genera. One species in particular, Coccoloba diversifolia Jacq. is distributed throughout the Caribbean and varies in morphology, particularly leaf size and shape, in different parts of its range. Additionally, the taxonomic history of C. diversifolia is complex. The present circumscription of C. diversifolia dates to the middle of the 20th Century, and is an exercise in lumping. A number of narrowly distributed or endemic Caribbean taxa were synonymized to form the present widely distributed taxon. It remains unclear, however, if C. diversifolia constitutes a single, widespread biological entity, or rather a number of more narrowly distributed biological entities. To date, taxonomic circumscription has used only classical tools, such as verbal leaf description. I here apply more contemporary tools to objectively describe and compare leaf shape in C. diversifolia specimens from across its range in order to begin the process of disentangling what is likely a species complex. I extracted leaf images from digitized herbarium specimens and described them using Elliptical Fourier Analysis in MOMOCS. The leaf shapes were then compared using PCA and clustering methods. Additionally, in order to make a primitive assessment of the impact of environmental conditions on the leaf shape in C. diversifolia, I georeferenced the specimens using GeoLocate and extracted the values of the BioClim variables at each location. This preliminary work suggests that leaf shape in C. diversifolia is systematically different in different island groups. While the majority of specimens occupy a single cluster in morphospace (consistent with the current circumscription of C. diversifolia), the subsections of this cluster correspond to major geographic regions in the west indies (roughly consistent with previous circumscriptions). In this regard the Bahamas looks like the most well defined morphological group of plants. BioClim variables did not help to explain leaf shape, except in the Bahamas. Further work is planned to incorporate DNA, better curated material for leaf tracing, and the examination of other key morphological features in Coccoloba (ochrea).

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Systematics

Topic: Contributed Papers

Title: Resolved at last? A genus-wide Arctostaphylos ddRADseq phylogeny

Author: ***Tito Abbo @ UC Riverside***

Keywords: Arctostaphylos,hybridization,manzanita,phylogeny

Abstract:

Since the early twentieth century, with the interest from botany greats such as Eastwood, Arctostaphylos (manzanitas) have challenged and captivated biologists. Although the majority of experts who have worked with the genus conclude that manzanitas are extremely diverse, the precise number of manzanita species and phylogenetic relationships among those species is both an historical and contemporary topic of debate. With its current taxonomic treatment, manzanitas form the most diverse woody genus within the California Floristic Province, and the majority of this diversity is represented by narrow endemics of conservation concern. Manzanitas are often considered difficult to identify in part because authoritative taxonomic keys reference characters unique to the genus and/or require characters from multiple phenological stages. This, compounded with limited phylogenetic resolution using traditional molecular systematics methods, poses significant challenges for conservation biologists and land managers who need to differentiate rare manzanitas from widespread ones that often occur in sympatry. Herein, I present a maximum likelihood ddRADseq phylogeny for 43 manzanita species (55 taxa including subspecies) and 3 outgroup taxa. This represents >70% coverage of currently recognized species, and taxa have been replicated to test for monophyly. The phylogeny has a high degree of resolution and the majority of narrow endemic species are supported as monophyletic. The phylogeny, however, also reveals high complexity apparently associated with hybridization. In addition to the two major clades recovered in nuclear ITS phylogenies, this study found a third early diverging clade. Here I present why this clade as well as numerous independent lineages recovered for certain taxa suggest evidence of widespread hybridization.

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Systematics

Topic: Contributed Papers Systematics

Title: Clarifying taxonomy and species delimitations within Diervilla (bush-honeysuckle, Caprifoliaceae) based on morphology and ddRAD sequence analysis

Author: ***Kathy Mathews @ Western Carolina University***

Keywords: morphology,Caprifoliaceae,molecular phylogenetics,RAD-Seq,Diervilla

Abstract:

Diervilla is an eastern North American genus sister to the eastern Asian Weigela within subfamily Diervilloideae of Caprifoliaceae. Diervilla contains two Southeastern USA endemic taxa, D. sessilifolia and D. rivularis, and one more northern taxon, D. lonicera, that also has a relictual distribution in high elevations of the Southern Appalachians. While three species of Diervilla are often accepted in floras and checklists, confusion among what constitutes the species still exists and has led to questionable identification in the field and on herbarium specimens and uncertainty about species distributions. The difficulty lies in high morphological similarity between the Southeastern endemics, as well as identification keys using adjacent quantitative character measurements and few discrete characters to distinguish among all three taxa. Previous phylogenetic analyses using sequences of the nrITS and noncoding cpDNA regions were unable to resolve relationships among the taxa or even to determine whether samples from multiple populations of each taxon were monophyletic due to lack of informative variation. To clarify the taxonomy and relationships within Diervilla, I obtained samples from multiple populations of each taxon throughout their ranges, examined and measured morphological traits on herbarium specimens, and sought new characters to aid in species identification and delimitation. I generated a ddRAD-Seq dataset from field and herbarium specimens to try to obtain a better resolved phylogeny and study the potential for incomplete lineage sorting or admixture, which might signal lack of species differentiation or post-speciation introgression. RAD sequences were assembled and aligned de novo, and resulting datasets were used in maximum likelihood and quartet sampling phylogenetic analyses, as well as Structure admixture analyses. Morphological data were subject to multivariate analyses. As a result, the three named species, D. sessilifolia, D. rivularis, and D. lonicera were resolved into clades with high bootstrap support and distinguished by a newly described, discrete morphological character, twig hair type. Other, often overlooked, qualitative traits can help distinguish taxa, while quantitative traits are often overlapping. Diervilla sessilifolia and D. rivularis are confirmed as closely-related sister species. Structure results show some admixture among all three species, either as a result of recent shared ancestry or hybridization, possibly following Pleistocene range contraction and expansion. This study demonstrates the utility of genome-wide RAD-Seq data to resolve relationships among closely related taxa and the need to critically assess morphological characters in groups with taxonomic confusion.

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Systematics

Topic: Contributed Papers

Title: Phylogenomics of African Impatiens

Author: ***Nora Gavin-Smyth @***

Keywords: Africa,Angiosperm 353,Impatiens,phylogenomics,Tanzania,Eastern Arc

Abstract:

African Impatiens (Balsaminaceae) have long been recognized as a difficult taxonomic group because of high variation within some species and suspected hybridization. Considerable Impatiens diversity is found in Africa. Previously, three African clades have been identified, suggesting multiple colonizations of the continent. A small group represents descendants of the first dispersal events from Asia around 10 mya, but the majority of African Impatiens are descended from a third dispersal event around 5 mya. The mega-diverse Malagasy Impatiens are also included within this large clade. In the monograph of African Impatiens from 1980, 110 African taxa were recorded and dozens more have been described since then. We use target capture with Angiosperm 353 baits, extensively sampling the African taxa, to investigate the phylogenetic relationships within and among the African clades.

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Systematics

Topic: Contributed Papers

Title: Using the PURC II pipeline and homologizer to infer a multi-locus reticulate phylogeny of Cystopteridaceae (Polypodiales)

Author: ***Chinedum Anajemba @ Utah State University***

Keywords: allopolyploidy,hybridization,reticulate evolution,species complex,species network,Amplicon Sequencing,Cystopteridaceae,Pipeline for Untangling Reticulate Complexes (PURC)

Abstract:

Allopolyploids present a challenge for multilocus phylogenetic inference due to their multiple distinct subgenomes, each of which may have its own evolutionary history. Generating sequence data from such lineages is challenging due to the difficulty in isolating the sequences of each of the distinct homoeologous gene copies. In addition, the phasing of gene copies into polyploid subgenomes remain another challenge even when the correct biological sequences are inferred. Recent advances in polyploid phylogenetics have made it possible to effectively undertake phylogenetic study of groups that comprise polyploids. In this study, we investigated the phylogeny of Cystopteridaceae, a fern family that contains a wide array of polyploid complexes. We used PURC II to infer the underlying sequences of three c. 1-kb-long nuclear loci from a broad sample of Cystopteridaceae accessions generated using the PacBio platform. PURC II (Pipeline for Untangling Reticulate Complexes) infers the true biological sequences (alleles, paralogs, or homeologs) from amplicon data, by using a model-based method (amplicon sequence variant inference) to correct PCR and sequencing errors. The sequences of each polyploid accession recovered by PURC II were assigned to their respective subgenomes using homologizer, a Bayesian method that uses a phylogenetic framework to phase gene copies across loci, allowing us to infer a multilocus reticulate phylogeny of the family.

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Systematics

Topic: Contributed Papers

Title: A new phylogeny of tribe Hibisceae (Malvaceae) reveals complex patterns of polyphyly in Hibiscus and Pavonia

Author: ***Maggie Hanes @ Eastern Michigan University***

Keywords: Malvaceae,Hibiscus,Hibisceae,large genera,Pavonia

Abstract:

The diverse and spectacular Hibisceae tribe comprises over 750 species. No studies, however, have broadly sampled across the dozens of genera in the tribe, leading to uncertainty in the relationships among genera. The non-monophyly of the genus Hibiscus is infamous and challenging, whereas the monophyly of most other genera in the tribe has yet to be assessed, including the large genus Pavonia. Here we significantly increase taxon sampling and assess monophyly of most currently recognized genera in the tribe. We also include many newly sampled species and sections of Hibiscus and Pavonia. Our phylogenetic trees demonstrate that Hibiscus, as traditionally defined, encompasses at least 20 additional genera. The status of Pavonia emerges as comparable in complexity to Hibiscus. We offer clarity in the phylogenetic placement of several taxa of uncertain affinity (e.g., Helicteropsis, Hibiscadelphus, Jumelleanthus, and Wercklea). This phylogenetic study paves the way for a new classification for the tribe.

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Systematics

Topic: Contributed Papers Systematics

Title: **Morphological Evolution in Viburnum: Synthesis, Surprises, and Lessons Learned**

Author: ***Michael Donoghue @ Yale University***

Keywords: morphology,Viburnum,character evolution,phylogenetic correlations

Abstract:

I used a nearly complete phylogenetic tree for Viburnum (Adoxaceae) to analyze the evolution of 20+ conspicuous morphological traits. These show various levels of homoplasy, from none at all (e.g., extrafloral nectaries, panicle inflorescences) to >20 inferred state changes (leaf teeth, leafing behavior). Most traits are in a range from 2-10 shifts, including tri-lobed leaves, naked buds, sterile marginal flowers, pollen exine sculpture, stipules, ruminant endosperm, corolla tubes, and fruit colors. There are several striking phylogenetic correlations. For example, toothed leaves are strongly correlated with the deciduous habit, both having evolved in response to colder and more seasonal climates. Other correlations arise from one character likely promoting the evolution of another character to provide a particular function. For example, tuft domatia have originated multiple times in the major lineage characterized by extrafloral nectaries, apparently to enhance protection by leaf mites. Likewise, shifts to derived branching architectures appear to have promoted the evolution of sterile marginal flowers, which increase pollinator visitation and fruit set. The independent origins of several fruit syndromes has entailed the coordinated evolution of fruit color and size, mesocarp texture, endocarp shape, and chemistry. Other cases of phylogenetic clustering are less clearly related to function. Stipules have evolved in the context of trilacunar nodal anatomy and lobed or toothed leaves. Here, developmental studies in Viburnum are consistent with the view that stipules are non-functional appendages homologous to leaf lobes or teeth that are initiated very late in the basipetally developing leaf. This case, and several others (tri-lobed leaves, yellow fruits), provide prime examples of what persecuted Russian geneticist, Nikolai Vavilov, termed “the law of homologous series in variation” — the recurrence of particular variants in closely related plants underlain by structures and developmental processes that promote their repeated emergence. Two other general findings are noteworthy. First, there are no clear cases of morphological “key innovations” in Viburnum, either in the sense of opening up a new adaptive zone or enhancing diversification. Instead, shifts in diversification rate appear mostly to have been promoted by the occupation of mountainous regions. Second, morphological traits are not misleading with respect to Viburnum phylogeny. Indeed, they collectively yield results that match those based on molecular data, though with less resolution. Changes in multiple characters provide unequivocal support for many major clades, especially for the small early-branching Pseudotinus, Tinus, and Opulus lineages. In the few cases where chloroplast and nuclear data conflict, morphological traits are more consistent with the nuclear data.

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Biogeography

Topic: Contributed Papers

Title: **Biogeography and Evolution of the Iconic and Endangered Mascarene Hibiscus**

Author: ***Brock Mashburn @ Washington University in St. Louis***

Keywords: Malvaceae,Hibiscus,Mascarenes,Island biogeography

Abstract:

The Mascarene Archipelago comprises three volcanic islands in the Indian Ocean east of Madagascar: Rodrigues, Mauritius and Réunion. Although recent studies are beginning to address long-standing questions about the origins of the Mascarene flora and biological connectivity across the islands, comparatively little research has focused on understanding the evolutionary and biogeographic histories of Mascarene plant groups. One emblematic group of plants whose evolutionary and biogeographic history in the Mascarenes is poorly known is Hibiscus section Lilibiscus. The group currently contains four described species in the Mascarenes, all of which are critically endangered: Hibiscus boryanus (Mauritius and Réunion), H. fragilis (Mauritius and Réunion), H. genevii (Mauritius), and H. liliiflorus (Rodrigues). The goals of this study were to: 1) assess the monophyly of sect. Lilibiscus in the Mascarenes and place them in relationship with other section Lilibiscus species that occur across the world; 2) assess species boundaries, particularly for species that occur in more than one island; and 3) understand biogeographic patterns within the Mascarenes, particularly how island ages and topological complexity may have contributed to patterns of colonization and speciation. We sampled 312 individuals from the four species on all three islands, including all known wild individuals in both Rodrigues and Mauritius. We also collected samples of outgroup species from across the worldwide range of sect. Lilibiscus. We genotyped these samples using a 2bRADseq genotyping approach and constructed a maximum-likelihood phylogeny of the group. Results showed that the Mascarene species of sect. Lilibiscus form a monophyletic group that is nested within a clade of species from the geographically distant Fijian Archipelago, suggesting that the Mascarene species may have originated via a dispersal event from Fiji. For the two species that occur in both Mauritius and Réunion, we found convincing genetic and morphological evidence to divide each species into two single-island endemics, resulting in one new species in each of Mauritius and Réunion and a total of six species in the Mascarenes instead of the currently described four. We found that diversification followed the progression rule, where the species endemic to the oldest island (H. liliiflorus in Rodrigues) is sister to the remainder of the species, with the other species arising through what appears to be single dispersal events from Rodrigues to the next-oldest island (Mauritius), and from there to the youngest island (Réunion). The species in Mauritius and Réunion may have diverged through adaptation to environmental variation, as they occur in different habitats (i.e., wet and dry habitats), which may have been facilitated by topographical characters unique to each island. These patterns of dispersal and speciation provide a framework for understanding the evolution of the unique biodiversity of the Mascarene Archipelago.

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Systematics

Topic: Contributed Papers

Title: **Revision of Sapindus sect. Sapindus (Sapindaceae)**

Author: ***Alan Franck @ University of Florida***

Keywords: Asia,Polynesia,Taxonomy,soapberry,Melanesia,Americas

Abstract:

Sapindus (Sapindaceae) contains about 10-20 species of trees which are well known for their soap-making properties and the utility of their hard, spheroidal endocarps for ornament or games. Section Sapindus has the most wide-ranging distrubition within the genus, probably partly due to oceanic hydrochory; this section is native to the Americas, Asia, Melanesia, and Polynesia. Most modern treatments have recognized around 3-5 species in sect. Sapindus (here provisionally including two species from Vietnam), with the name S. saponaria being applied nearly throughout the distribution of this section. Undertaking a revision of Sapindus sect. Sapindus, ca. 700 herbarium specimens were physically examined and several hundred digital images of herbarium specimens were studied. Four species were studied in cultivation and field work was conducted in Florida. Within sect. Sapindus, 13 species are recognized, including two new combinations and two newly described species. The application of Sapindus saponaria is clarified, as a primarily Neotropical speces.

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Systematics

Topic: Contributed Papers Systematics

Title: The evolution of Hawaiian blueberries (Vaccinium sp.): targeted SNP-based phylogenies reveal extraordinary diversity of a species-rich adaptive radiation

Author: ***Anna Becker @ University of Florida***

Keywords: Vaccinium,biogeography,Evolution,Hawaii,Hawaiian Islands,Historical biogeography,molecular phylogenetics,Pacific islands,SNP

Abstract:

The tropical archipelago of Hawaii is famous for fostering a high proportion of island endemic lineages that have recently evolved across relatively small geographic distances, some diversifying on a grand scale through adaptive radiation. The archipelago has been termed a “conveyor belt” of volcanic islands which reach a carrying capacity of organismal diversity and subsequently submerge. This system predisposes endemic lineages to diversify from older islands to younger (progression rule), with diversity tending to be highest on younger islands. The Hawaiian blueberries (endemic Vaccinium species) clade is a dominant keystone group that occurs at high elevations across the island chain that appears to be highly diversified. The current treatment that comprises just three species is heavily disputed, having synonymized many species previously recognized. For over a century, outstanding questions have remained: (1) how many species of Hawaiian blueberries are there, and how can we define them? and (2) from what spatiotemporal origins did Hawaiian Vaccinium colonize the islands, and can we infer anything about the historical diversification of this group using current knowledge of island biogeography? Time-calibrated biogeographic analyses of a nuclear dataset (Angiosperms353) for 10 species of Vaccinium, including the three recognized species from Hawai‘i, revealed a single dispersal from a temperate source ca. 5.1 MYA, a pattern typical of species-rich lineages and adaptive radiations in Hawai‘i. To address species diversity of Hawaiian Vaccinium, aiming to provide a genetic reference for species delimitation, we used a target capture probe set built from the blueberry genome (V. corymbosum) to genotype by sequence 179 Hawaiian specimens representing the full morphological and geographic diversity of the group. 37,000 snps were called using the bilberry genome (V. myrtillus) as a reference, a species closely related to Hawaiian Vaccinium. SNPs were used to construct a maximum likelihood, concatenated (IQTree) and coalescent (SNAPP) phylogenetic trees of Hawaiian Vaccinium. Based on these analyses, we conclude that the current taxonomy of three species of Hawaiian Vaccinium does not adequately represent patterns of phylogenetic and morphological diversity. We detected more than 20 morphologically distinct lineages that may represent an adaptive radiation. Biogeographic analyses reveal a general pattern of migration from older islands to younger, with the highest diversity concentrated on the youngest islands, in agreement with studies of other Hawaiian lineages.

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Systematics

Topic: Contributed Papers

Title: Comparative taxonomic studies on some members of Tribe Schleichereae Radlk.

Author: ***Temitope Onuminya @ University of Lagos***

Keywords: Stomata,trichomes,TETFUND,Striation,Sapindaceae,Schleichereae,Haplocoelum,Lecaniodiscus,Schleichera

Abstract:

Schleichereae Radlk. is a tribe of flowering plants in the family Sapindaceae Juss. In this study, foliar anatomical evaluation of some species in the tribe Schleichereae namely: Haplocoelum gallaense, Schleichera oleosa, Lecaniodiscus punctatus, Lecaniodiscus cupanioides was carried out, with the view to aid proper identification of the species. Both quantitative and qualitative characters were studied following standard procedures. Strips of epidermal layers were obtained from the adaxial and abaxial surfaces of the leaves and viewed under the light microscope. The number, length and width of the epidermal cells, stomata and trichomes were measured on both adaxial and abaxial surfaces. The data obtained were subjected to statistical analysis where mean, standard deviation, standard error, and range were calculated. In all the four species studied, the leaf is hypostomatic with stomata restricted to the abaxial surface of the leaf. Stomata type is typically anomocytic; sunken in S. oleosa, raised in H. gallaense and L. cupanioides and flat in L. punctatus. Cell shape is irregular on both the adaxial and abaxial surfaces, except in L. punctatus and S. oleosa where the cells are polygonal to irregular on the adaxial surface. The anticlinal wall pattern is sinuous except in S. oleosa where it is straight to undulate. Trichomes were typically absent with exception to S. oleosa where simple unicellular trichomes were observed on the adaxial surface. Striations were observed on both surfaces of the leaves of all the four species studied however all the species varied greatly in their quantitative characters. This variation in epidermal characters between the studied species is of value for taxonomic purposes. An indented dichotomous key is presented for the delimitation of the taxa.

*The authors appreciate the Tertiary Education Trust Fund, Nigeria for the conference attendance sponsorship given.

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Systematics

Topic: Contributed Papers

Title: Molecular phylogeny of the Eryngium (Apiaceae) “Pacific” clade: Geographic phylogenetic structure, morphological shifts and a reticulated history

Author: ***Ariana Padin @ Instituto de Investigaciones en Biodiversidad y Medioambiente (INIBIOMA), Universidad Nacional del Comahue-CONICET***

Keywords: Adaptive morphological novelties,Atacama Desert,Consensus network,Monocarpic plants

Abstract:

The “Pacific” clade of Eryngium (Apiaceae, Saniculoideae) comprises 39 species from the Pacific Ocean coasts of Chile, Australia, and western USA, and two species from east-central South America. Previous studies on Eryngium suggested reticulated events and trans-Pacific dispersals involved in the diversification of the clade. However, these hypotheses need to be tested with more thorough sampling and further analyses. In this study, we use chloroplast and nuclear DNA sequences and an exhaustive sampling of the “Pacific” clade to identify factors that potentially drove its diversification. In particular, we want to find out if hybridizations occurred within this clade, and also if expansion to different areas correspond to single trans-Pacific dispersals. Morphological shifts within the clade are also analyzed as potential drivers for diversification/dispersification. To recognize these events, we inferred a dated phylogeny of the “Pacific” clade that was used to: identify morphological shifts, analyze whether lineages within the clade are geographically structured, and detect incongruence between plastid and nuclear-derived trees. The study corroborates that the clade is geographically structured across distant Pacific coasts, suggesting that unique trans-Pacific dispersals resulted in the diversification of each sublineage. Besides, a reticulation event was estimated at the base of a sublineage that colonized and diversified in an extreme arid environment as the Atacama region. This reticulation event is also associated with morphological shifts to tap-rooted, monocarpic plants at the beginning of the Pliocene (ca. 5 Ma) that are related to arid environments. Therefore, a combination of events such as the emergence of morphological novelties, the colonization of distant geographical areas, and hybridizations are estimated as likely factors involved in the diversification of the "Pacific" clade.

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Biogeography

Topic: Contributed Papers Systematics

Title: Exploring the Impact of Last Glacial Maximum on the Demographic History of Asarum caudigerum

Author: ***Lei Zuo @ The Ohio State University***

Keywords: Asarum caudigerum,East Asia,Last Glacial Maximum

Abstract:

The Last Glacial Maximum (LGM) greatly influenced plant distributions and mass migrations in Europe and North America. However, the effects of climate oscillations on plant distributions in subtropical areas of East Asia, particularly understory herbs, remain understudied. Fossil-pollen based palaeovegetation maps suggest a long-distance contraction-expansion pattern in East Asia between glacial and inter-glacial periods. While this pattern has been extensively studied in trees, the herb layer, characterized by its unique growth forms and reproductive mechanisms, requires further investigation. This study aims to address this gap by examining Asarum caudigerum, an ideal system to explore alternative patterns in subtropical China. Through extensive sampling across its entire distribution and the adoption of a new reduced representation sequencing technique – ISSRseq, we explore: 1) whether large scale southward contraction occurred in response to climate oscillations during the LGM, 2) the extent of LGM's influence on the species' distribution and the presence of multiple southern refugia, and 3) the potential general recolonization routes during post/interglacial periods. Answering these questions will contribute to the understanding of the connection between climate oscillation and varied floral responses, and further provide guidance for flora conservation in the face of global change.

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Systematics

Topic: Contributed Papers

Title: Disentangling the evolutionary history of the tumbleweed crabgrasses

Author: ***Jordan Nikkel @ Iowa State University***

Keywords: Collections,Grasses,molecular phylogenetics,phylogenetics,Poaceae,Poales,systematics,Taxonomy ,molecular systematics

Abstract:

Leptoloma Chase is a genus of grasses (Poaceae: Panicoideae) comprising five species, all of which are endemic to North America. The taxonomic placement of Leptoloma has changed over time, and it is often treated as an infrageneric taxon within the genus Digitaria Haller. Leptoloma is distinguished morphologically from other closely related clades by having an open paniculate type inflorescence, with spikelets usually being solitary on elongated pedicels. All species of Leptoloma and a few others in Digitaria are often referred to as the ‘tumbleweed crabgrasses’ because most species in this group have an inflorescence that dehisces and forms a tumbleweed at maturity. To date, no molecular phylogeny performed on Digitaria has included any Leptoloma species other than L. cognatum leaving the taxonomic status of these species unclear. Understanding the relationship of Leptoloma to Digitaria is of interest, given that many species in these genera are economically important. Digitaria is a diverse genus, potentially containing up to 280 species, many of which are listed as noxious weeds, serve as forage for livestock, or are utilized as grains for human consumption. Within Digitaria, species relationships have yet to be fully resolved and phylogenies of the tribe Paniceae (subfamily Panicoideae) show Digitaria as being paraphyletic. Unraveling the evolutionary history of Leptoloma can help resolve some of these problems by increasing sampling size and supplying molecular data for species that have not previously been sequenced. Considering these issues, the overarching goal of this study is to perform the first comprehensive molecular phylogeny of Leptoloma, test its monophyly, and determine its relationship to Digitaria. Sequence data for six plastid markers that have already proven useful in resolving relationships in closely related groups within the grass family will be used. Leaf tissue for DNA extraction from previously unsequenced species was acquired through fieldwork and from herbarium specimens. DNA sequences of species that have already been sequenced will be obtained from GenBank. Once the monophyly of this group has been established, future work will seek to disentangle species relationships in this group through population-level analyses, and the evolutionary history of the tumbleweed trait and the molecular mechanisms behind rhizome development will also be investigated.

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Systematics

Topic: Contributed Papers

Title: Digitaria grasses of Madagascar: taxonomy to support grass identification, weed control, and forage management in a biodiversity hotspot

Author: ***Nantenaina Rakotomalala @ Royal Botanic Gardens Kew Madagascar***

Keywords: agricultural weed,phylogenetic diversity,finger-grass, taxonomy, Madagascar

Abstract:

Grasses (Poaceae) are one of the most agriculturally important plant groups in Madagascar, used for animal grazing and acting as crop weeds. A reliable taxonomy and identification system is needed for these species to improve agricultural efficiency. Currently, they are still poorly understood and documented in Madagascar due to an outdated taxonomy and small reproductive structures. Most herbarium specimens are at the Paris herbarium (P), making it difficult for Malagasy botanists to access herbarium sheets from their own country. In this project, we aimed to update the taxonomy of Malagasy species of Digitaria, a taxonomically complex genus of weeds, and understand their relationship with Malagasy agriculture. We performed a herbarium study towards a taxonomic revision and conducted 111 interviews with local farmers in the highlands of Madagascar for an ethnobotanical study, alongside phylogenetic and bibliographic work. We carried out four collecting trips and analysed 436 specimens of Digitaria from K, P, and TAN herbaria. The total number of Digitaria species in Madagascar was reduced from 34 to 30 species: four do not occur in Madagascar, three were placed in synonymy under D. fulva and D. didactyla, and 3 additional species were recorded. A new provisionally endemic species was found, and two new records for Madagascar were made: D. zeyherii from an unidentified old collection, and D. ternata from recent collections. A total of eight endemic species of Digitaria are reported, with four of them (D. ankaratrensis, D. fulva, D. andringitrensis, and D. perrieri) restricted to Ankaratra and Andringitra massifs, two of the highest mountains of Madagascar. We provide morphological descriptions for these species. The identity of Digitaria accessions in the Weed Identification and Knowledge in the Tropical and Mediterranean Areas portal (WIKTROP) will be updated according to this taxonomic revision. During our interviews, farmers identified 11 species of Digitaria as weeds or forages that also show some medicinal properties. The endemic Digitaria humbertii is reported to be the weed most damaging to cropping systems. Forage species with softer leaves, such as D. debilis, are preferred by cattle. Farmers differentiate, describe, and name these species according to their morphology, uses, effects, or damage caused, with variation observed between the Madagascar highland sites. Phylogenetic work shows that Malagasy Digitaria weeds are more likely to be polyphyletic and are more geographically and phylogenetically dispersed than non-weedy Digitaria. We are combining these data with brief notes on morphology, habitats, common names, uses, effects, and benefits into a new identification guidebook to the grasses of Madagascar, designed together with the Madagasca Ministry of Agriculture (MINAE) and the National Center for Applied Research on Rural Development (FOFIFA). This book will make it easier for non-specialists to identify grasses and to distinguish introduced weeds from useful forages and endemics, further underpinning agricultural productivity.

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Systematics

Topic: Contributed Papers

Title: The character evolution of the genus Burmannia (Burmanniaceae)

Author: ***Supakan Simachai @ Mahidol University***

Keywords: molecular evolution,nuclear gene,phylogeny,Bluethreads,Mycotrophy

Abstract:

Burmannia is a genus of mostly mycoheterotrophic plants, with ca. 61 accepted species found throughout the world, including 14 species in Thailand. Obtained from previous studies, it can be categorized into main two groups: Chlorophyllous and Achlorophyllous groups with and without chloroplasts, respectively. In this study we constructed a phylogenetic tree of 29 species, which included 12 species from Thailand, based on 18S rDNA and the internal transcribed spacer (ITS) regions using Bayesian, Maximum Likelihood, and Maximum Parsimony analyzes. Additionally, we also reconstructed the ancestral state of some interesting morphological characters, ie. the presence of rosette leaves, the presence of chloroplast, flower shapes, outer and inner perianth shapes.

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Tropical Biology

Topic: Contributed Papers Tropical Biology

Title: A semi-detritivorous pitcher plant, Nepenthes ampullaria diverges in its regulation of pitcher fluid properties

Author: ***Kadeem Gilbert @ Michigan State University***

Keywords: carnivorous plant,Nepenthes,symbioses,pH

Abstract:

Tropical pitcher plants (Nepenthes) are carnivorous plants that trap and digest prey using highly modified fluid-filled leaves known as pitchers. Prey are digested by plant-secreted enzymes and pitcher symbionts. Pitchers exert control over abiotic properties of the digestive fluid such as pH levels that can influence its symbionts. Here we examine natural variation in pH and dissolved mineral concentrations in three sympatric Nepenthes species, assessing correlations between fluid properties and pitcher traits. We use addition experiments to investigate differences in protein digestion/absorption rates between species. Fluid pH and dissolved mineral levels both showed distinct patterns corresponding to pitcher developmental stages in N. gracilis and N. rafflesiana, whereas N. ampullaria differs from its congeners in exhibiting far less variation in fluid pH, as well as less clear evidence of protein depletion. This study further elucidates the properties of pitchers as habitats, revealing ways in which the host plant regulates that habitat.

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Tropical Biology

Topic: Contributed Papers

Title: Biogeography of the Caribbean endemic clade of Wittmackia (Bromeliaceae). Preliminary results

Author: ***Natalia Ruiz-Vargas @ University of Illinois at Chicago***

Keywords: West Indies,Bromelioideae

Abstract:

Wittmackia is a genus in the family Bromeliaceae (Bromelioideae) distributed in the Brazilian Atlantic Forest, the Caribbean islands, and with a few representatives in Northern South America and the Yucatán Peninsula. The Caribbean-endemic species form a clade and are restricted to the Greater Antilles with most of them occurring in Jamaica; the genus is notably absent from Ayiti (Hispaniola). Using Target Sequence Capture with the Bromeliad1776 bait kit, I infer the phylogeny of this group and analyze it in a biogeographical context.

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Tropical Biology

Topic: Contributed Papers

Title: Comparing phenological shifts in tropical wet and dry habitats using herbarium specimens

Author: ***Skylar Graves @ University of Colorado Boulder***

Keywords: Angiosperms,flowering phenology,Tropic

Abstract:

The tropics contain over three quarters of the world's biodiversity and shifts in tropical

ecosystems can have ripple effects that can be felt throughout the entire world. Both wet and dry tropical habitats are threatened by climate change, however dry climates are at greater risk in many cases. A global investigation of phenological shifts in tropical flowering plants has never before been conducted. The nuances and complexities of flowering timing in the tropics have stymied researchers in the past. This relative lack of study to have emphasized tropical biomes is not trivial. Studies that document shifts in life events provide crucial evidence towards understanding the effects of global climate change on ecosystems. Such effects are furthermore used in predictive models to prepare for the future of these communities. Without a more comprehensive understanding of the effects of human activities, there will remain a fatal gap in our understanding of climate change, especially as it pertains to some of the most vast, biodiverse forests remaining on Earth. 20 representative locations were chosen in a pairwise fashion, comparing a wet and dry habitat in each region of the tropics. I used data from 219,618 digitized herbarium specimens, containing flowering structures, representing over 50,000 taxa, spanning 270 years to discern mean flowering times. A linear regression analysis was used to analyze a shift in the timing and frequency of the flowering events. Preliminary analyses support the prediction that there is a more drastic shift in flowering time in dry habitats as compared to their wet counterparts for multiple regions. Future projects will work to expand the parameters defining wet and dry habitats, as opposed to the binary categorization currently being used.

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Tropical Biology

Topic: Contributed Papers Tropical Biology

Title: **Plants on the remote, oceanic island of Pohnpei have shifted to more autogamous breeding systems than their self-compatible mainland relatives**

Author: ***Viann Marie Yomai @ Virginia Tech***

Keywords:

Abstract:

Plant community composition on small and remote, oceanic islands is expected to be governed by extremely low immigration, and high extinction, rates. In such communities, resident species are more likely to display reproductive features that mediated their establishment and short-term survival than to have evolved alternatives that ensure long-term persistence. In this extreme version of Baker’s law, small, remote island communities are always young and are dominated by species that arrived with highly evolved selfing syndromes. Alternatively, biological changes that increase selfing success might have evolved from more outcrossing mainland progenitors after arrival. In this study, we sought to determine the degree to which island species have diverged from their mainland conspecific or nearest-relative counterparts in their breeding and sexual systems.

We performed hand-pollinations on 36 native flowering species on Pohnpei, Federated States of Micronesia to characterize sexual systems and to quanitify the degree of compatibility, autonomous self-fertilization, and pollen limitation. We used phylogenetic generalized least squares analyses to compare these data with studies of their nearest phylogenetic relatives from continental mainlands, all of whom are typically animal-pollinated.

All 36 Pohnpei island taxa were hermaphroditic and self-compatible with bisexual flowers and incomplete dichogamy. The mainland counterpart taxa had either bisexual or rarely some combination of bi- and/or uni-sexual flowers, on the same plant, and all but three were self-compatible. On Pohnpei, all but two species had high autofertility indices (AFI > 0.4), and in these, self-pollination (autonomously and/or by hand) produced higher seed sets than either outcross or open, emasculated pollinations. Among 32 mainland-island pairs, Pohnpei island taxa had a 27% higher mean self-compatibility index (SCI, based on fruit set; $P = 0.0015$) anc a 42% higher mean AFI (based on seed set; P

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Topic: Discussion Session

Title: **NSF Information Session and Q&A**

Author: ***Judy Stone @ National Science Foundation***

Keywords:

Abstract:

The National Science Foundation funds basic research in plant biology, training of the next generation of botanists, and broader societal impacts. In this session, NSF program officers will provide an overview of new and ongoing programs and the merit review process, followed by an open-ended question and answer session.

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Functional Genetics/Genomics

Topic: Lightning Talks

Title: **Genome-wide, Organ-delimited gene regulatory networks (OD-GRNs) provide high accuracy in candidate TF selection across diverse processes**

Author: ***Rajeev Ranjan @ Purdue University***

Keywords:

Abstract:

Construction of organ-specific gene expression datasets that include hundreds to thousands o experiments would greatly aid reconstruction of gene regulatory networks with organ-level spatial resolution. However, creating such datasets is greatly hampered by the requirements o extensive and tedious manual curation. Here we trained a supervised classification model that can accurately classify the organ-of-origin for a plant transcriptome. This K-Nearest Neighborbased multiclass classifier was used to create organ-specific gene expression datasets for the leaf, root, shoot, flower, seed, seedling, silique, and stem in the model plant Arabidopsis thaliana. In the leaf, root, flower, seed and, a gene regulatory network (GRN) inference approach was used to determine: i. influential transcription factors (TFs) in that organ and, ii. the most influential TFs for specific biological processes in the organ. These genome-wide, organdelimited GRNs (OD-GRNs), identified de novo many known regulators o organ development and processes operating in those organs. Moreover, many previously unknown TF regulators were highly ranked as potential master regulators of organ development or organ-specific processes. As a proof-of-concept, we focused on experimentally validating the predicted TF regulators of lipid biosynthesis in seeds, with relevance to food and biofuel production. Of the top twenty candidate TFs, eight (e.g., WRI1, LEC1, and FUS3) are known regulators of seed oil content. Importantly, we validated that seven more candidate TFs, whose role was previously unknown in seed lipid biosynthesis, indeed affect this process by genetics and physiological approaches, thus yielding a net accuracy rate of >75% for the de novo TF predictions. The general approach developed here could be extended to any species with sufficiently large gene expression datasets to speed up hypothesis generation and testing for constructing gene regulatory networks at a high spatial resolution

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Ecology

Topic: Lightning Talks

Title: **Exploring the role of plant-plant interactions for community stability**

Author: ***Simone Cappellari-Rabeling @ University of Hohenheim***

Keywords: community ecology,Plant-pollinator Interaction,Pollination

Abstract:

825

Ecology

Topic: Lightning Talks

Title: **Bulbs are larger the deeper they are**

Author: ***Cody Coyotee Howard @ Oklahoma State University***

Keywords: Geophyte,bulb,Zambia,Ledebouria,underground storage organ

Abstract:

828

Systematics

Topic: Lightning Talks

Title: Landscape Predictors of Introgression and Population Structure in the Eastern North American White Oak Syngameon

Author: ***Gabe Ribicoff @ University of Chicago***

Keywords: landscape genomics,Phylogeography,population genomics

Abstract:

831

Phytochemical

Topic: Lightning Talks

Title: A "Peak" into Manzanita Metabolites

Author: ***Avrie Martello @ UC Riverside***

Keywords: manzanita,metabolite profiling

Abstract:

834

Phytochemical

Topic: Lightning Talks

Title: Identification of novel transcription factor regulators of fatty acid biosynthesis in Arabidopsis seeds

Author: ***Rajeev Ranjan @ Purdue University***

Keywords: Fatty acid biosynthesis, Gene regulatory network, seed oil

Abstract:

Vegetable oils are an important natural resource consumed by human and also serves as feedstock for biofuel production. Plant oils which are derived from fatty acids are stored in the form of triacylglycerol (TAG) in the seeds of oil crops. Extensive research has been done to understand the process of lipid biosynthesis and modifications in the seed. However, its regulatory network driven by transcription factors (TFs) is largely unknown and needs further investigation. Arabidopsis serves as an excellent model to study the regulation of lipid biosynthesis due to the availability of curated genomic resources and the accumulation high amount of oil in its seed. By using over 1500 RNAseq gene expression an Organ-Delimited Gene Regulatory Network (OD-GRN) was built and by inferring this OD-GRN, potential candidate TF regulators of lipid biosynthesis was identified. We obtained 11 previously uncharacterized TF regulators of seed oil biosynthesis. The role of these TFs was experimentally validated by analyzing fatty acid content and composition in the knock-out mutant and overexpression lines. Results suggested a high accuracy of (75%) of this gene discovery pipeline as two-thirds (7/11) of the predicted TFs exhibited phenotypes affecting seed oil content or composition. Among the most promising TFs, we observed that CESTA and bHLH93 control the initial step of lipid biosynthesis as they affected total seed oil content while HB25 altered seed oil composition reflecting its action during the chain elongation process. However, SRM1 is possibly involved in multiple steps, as it influences both oil content and composition. These findings not only enhance our understanding of the intricate mechanisms of fatty acid biosynthesis but also provides valuable insights into the potential manipulation of lipid content and composition in oil crops through targeted TF regulation.

813

Symbioses: Plant, Animal, and Microbe Interactions

Topic: Lightning Talks

Title: Acacia koa, Acacia melanoxylon, and Acacia mangium endophytes interact with Fusarium oxysporum f. sp. koae in antagonistic assays.

Author: ***Signee Storrud @ Utah State University***

Keywords: Fusarium oxysporum ,seed endophyte,Koa,Acacia koa,Acacia melanoxylon,Acacia mangium,koa wilt,Microbial antagonism assay,In-vitro assay,Foliar Endophyte,Biocontrol,Bacillus

Abstract:

843

Symbioses: Plant, Animal, and Microbe Interactions

Topic: Lightning Talks

Title: Thermotolerance of bacterial seed and foliar endophytes from Callitropsis bakeri

Author: ***Avery Kuehfuss @ Gonzaga University***

Keywords: seed endophytes,Thermotolerance,Callitropsis bakeri,,Baker's cypress,bacteria endophytes,foliar endophytes,serotinous cones,heat treatment,in-vitro assays

Abstract:

844

Conservation Biology

Topic: Lightning Talks

Title: The Million Orchid Project: The future of how we teach science

Author: ***Nichole Tiernan @ Fairchild Tropical Botanic Garden***

Keywords: Education,Orchid,orchid conservation,stem

Abstract:

846

Conservation Biology

Topic: Lightning Talks

Title: Analyzing trichome density as a predictor of drought tolerance in Quercus agrifolia

Author: ***Tyana Ortiz @ San Diego State University***

Keywords: Trichome,drought,Oaks

Abstract:

847

Ethnobotany

Topic: Lightning Talks

Title: Phylogeography of Psychotria viridis: Foundational knowledge and research methods for reconstructing the evolutionary history of a primary component of ayahuasca

Author: ***Elanor Fuller @ Louisiana State University***

Keywords: domestication,ethnobotany,Phylogeography,Rubiaceae,Psychotria viridis

Abstract:

852

Phylogenomics

Topic: Lightning Talks

Title: From WGS to Gels: Testing of PCR primers targeting toxic Digitalis in support of food safety

Author: ***Sara Handy @ US Food and Drug Administration***

Keywords: genome skimming,species identification,Food safety,toxicity,PCR

Abstract:

n/a

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Phylogenomics

Topic: Lightning Talks

Title: Phylogenomics of Brachypodium: Use of genome skimming to build the largest phylogeny of the grass model genus.

Author: ***Maria Angeles Decena @ University of Zaragoza***

Keywords: allopolyploidy,hybridization,molecular phylogenetics,perennials,brachypodium,plastome

Abstract:

842

Development and Structure

Topic: Lightning Talks

Title: Merism of Begoniaceae: an issue of numbers

Author: ***Junru Wang @ Royal Botanic Garden Edinburgh***

Keywords: morphology,Floral anatomy,Floral Development,Begoniaceae

Abstract:

Merism represents the number of parts per whorl in the flower (usually based on petals or perianth parts). Although merism is a relatively conserved character in flowers, it can shift, linked to the loss of a sector, combination of two whorls, or size changes of the floral apex. Begoniaceae, a unisexual-flowered family with more than 2000 species, shows a higher diversity of merisms, especially in female flowers, varying from hexamery or higher, pentamery, tetramery, trimery, to dimery. This study investigates the formation of different merisms in Begoniaceae using scanning electron microscopy, and illustrates the evolution of the merism through ancestral character reconstruction. The occurrence of dimery and tetramery are similar in male and female flowers. Two different trimerous patterns may have evolved from tetramery and pentamery respectively. Merism of Asian and NW II clades are of higher diversity, and there may be a relationship between the merisms of male and female flowers. The different merisms among species may be caused by the different pressures at the early development stage. And weaker pressure, higher spatial constraint caused by the development of hypanthium, and odd and higher merisms which are less stable may caused a higher merism diversity in female flowers of Begoniaceae.

814

Biodiversity Informatics & Herbarium Digitization

Topic: Lightning Talks

Title: The dwctaxon R package for editing and validating taxonomic data

Author: ***Joel Nitta @ Chiba University***

Keywords: Biodiversity Database,GBIF,Taxonomy ,R

Abstract:

Darwin Core (DwC) is a data standard that has become widely adopted across biodiversity databases because it enables transfer of biological data in a unified format. The DwC standard for taxonomic data is especially important since taxonomic names are often used as unique identifiers to join data from disparate sources. Here, we introduce a new R package for editing and validating taxonomic data in compliance with DwC, dwctaxon. dwctaxon automates typical taxonomic database management tasks such as transfer of synonyms and filling columns with ID numbers, thereby making workflows both more efficient and less error-prone. It also conducts data validation for typical problems seen in taxonomic data, including checks for nine major error categories. It has been designed to be maximally compatible with DwC while allowing for flexibility in database design. dwctaxon has passed code review at rOpenSci (https://ropensci.org/) and is freely available from https://github.com/ropensci/dwctaxon and the Comprehensive R Archive.

816

Population Genetics/Genomics

Topic: Lightning Talks

Title: Adding error to simulated genetic data

Author: ***Ash Hamilton @ University of Chicago***

Keywords: DNA Sequencing,Genetic diversity,simulation,conservation genetics,sequencing error

Abstract:

In the last 20 years, genetic data has become more readily available, leading to more widespread use of genetic data across nearly all biological fields, and the growth of genetic specific subfields such as population and conservation genetics. It is well known that along with genetic data comes genotyping errors that can result from many different steps during the processing of genetic data and occur at a fairly consistent rate across technologies. Despite the knowledge that genotyping errors are universally present within genetic datasets, these errors are either ignored or modeled with some nuisance error parameter in a lot of population genetic and conservation genetic studies. Simulated genetic data are used in both evolutionary and conservation biology because these data enable the testing of hypotheses in otherwise analytically intractable genetic systems. However, these simulations use idealized genetic data that typically does not account for errors that are known to occur during the genetic sampling process. Such errors can be stochastic errors, random changes to sequences due to human o machine error, or systematic, due to a mechanistic issue usually in the DNA amplification process. Either error can occur regardless of marker type and could potentially cause deviations in metrics calculated from the errored genetic reads. Metrics that are used as proxies for genetic diversity are likely to be particularly sensitive to error in real genetic datasets because erroneous reads have the potential to make a population look more or less diverse than the population truly is. Two proxies for genetic diversity that are particularly important to conservation genetics and are frequently calculated from simulations are 1) allelic diversity and 2) allelic rarity. In this project, we repeatedly subsample a simulated population and quantify how adding different types of error at various rates influences various proxies for genetic diversity. To do this, we simulate genetic data from microsatellite markers and compare several proxies for genetic diversity (heterozygosity, total allele counts, rare allele detection). From this study, we hope to elucidate to what degree sequencing error might affect metrics that are frequently used in both conservation and population genetics.

826

Phylogenomics

Topic: Lightning Talks

Title: The elusive chloroplast puzzle of Brachypodium distachyon complex

Author: ***Miguel Campos Caceres @ Universidad de Zaragoza***

Keywords: allopolyploidy,differential gene expression,hybridization,molecular phylogenetics,plastome,brachypodium

Abstract:

841

Symbioses: Plant, Animal, and Microbe Interactions

Topic: Lightning Talks

Title: New holobiont detected! The polyploid complex of Festuca rothmaleri hosts a new variety of Epichloë festucae

Author: ***Alba Sotomayor Alge @ University of Zaragoza***

Keywords: coevolution,DNA barcoding,Fungal endophytes,polyploidy,Taxonomy ,Amplicon Sequencing,plant-fungal interactions,genomics,Festuca rothmaleri,holobiont,Epichloë

Abstract:

845

Education and Outreach

Topic: Poster

Title: Teaching bioinformatics in an introductory level Botany course

Author: ***FLONA REDWAY @ BARRY UNIVERSITY***

Keywords: bioinformatics,introductory course,upper-level

Abstract:

The ability to generate and hold primarily pre-med biology majors' interest in the only plant course taught in their degree curriculum, is an ongoing challenge for any instructor. In an effort to address this challenge, a hands-on laboratory exercise with real-world applications was incorporated into the introductory Botany course curriculum (BIO 112). DNA barcoding provided an avenue for engaging the students with molecular techniques and Bioinformatics tools (Basic Local Alignment Search Tool (BLAST) and DNA Subway platforms). Students used these tools to identify plant species on campus and to determine phylogenetic relationships between them. The addition of this exercise created an opportunity for a new and exciting formal laboratory report topic. Students became so enthusiastic, as indicated in their reflections, that they prepared and presented their findings as a group at Barry's annual STEM Symposium. The addition of this exercise increased students' interests, expanded the scope o the laboratory techniques to which they were exposed, and provided an opportunity for them t present their findings at the local symposium. Botany is now under consideration for an upgrade to an upper-level course offering.

3

Bryology and Lichenology

Topic: Poster

Title: A Bryoflora of the Gifford Pinchot National Forest with an Emphasis on the Indian Heaven Wilderness

Author: ***Aiko Yamada @ Washington State University***

Keywords: bryophytes,Floristics,liverworts,mosses,hornworts

Abstract:

Bryophytes are land plants without vascular tissue, and they form the sister lineage to all other land plants (flowering plants, gymnosperms, ferns, etc.). Bryophyte distributions and abundance data is grossly underrepresented in floristics studies throughout the United States. Plant conservation efforts fall short if they do not also include bryophyte population distributions and abundance data, and so efforts to understand non-vascular plant distributions in the state of Washington is underway. The increasing occurrence of wildfires in the Pacific Northwest reinforces the importance of knowing what bryophyte microhabitats are present so that management plans can be designed accordingly. The Gifford Pinchot National Forest covers 1.3 million acres and extends from Mt. Rainer National Park to the Columbia River. Because the Gifford Pinchot National Forest has such a wide range in the western region of Washington, there is a substantial amount of recorded flora present in the forest. However, there are many sites still lacking bryophyte collection data, particularly in the designated wilderness areas of the forest. This study will focus on the Indian Heaven Wilderness, located in the southern area of the Gifford Pinchot National Forest, which encompasses land that has been utilized by the area’s Native peoples for over 9,000 years. The Indian Heaven Wilderness features many meadows and plateaus of a consistent 4,500 ft in elevation. A survey of the bryophytes in the Indian Heaven Wilderness could add previously unrecorded species for the Gifford Pinchot National Forest, as well as for this part of Washington. This study aims to establish a preliminary checklist of the bryophytes in the Gifford Pinchot National Forest based on previous and new data. The checklist will also feature a dichotomous key for the taxa represented.

18

Ethnobotany

Topic: Poster

Title: Decolonizing Botanical Field and Lab Methodologies of the UVSC Herbarium

Author: ***Tyler Shaver @ Utah Valley University***

Keywords: Decolonization,decolonizing,Decolonizing Methodologies,Methodologies

Abstract:

As part of a robust anticolonial methodology the UVSC Herbarium housed at UVU is striving to utilize an indigenist ideology in our lab, field work, and personal lives. This is "when one actively strives to hold the rights of Indigenous people as their primary political goal, while incorporating their own traditions in their work." (Sinclair, 2003) With Decolonizing Methodologies by Linda Tuhiwai Smith and Research is Ceremony by Shawn Wilson as starting points, the words of many Indigenous researchers were studied to understand what makes up an anticolonial research methodology.

We found that anticolonial work looks differently for everyone and every situation, but a few things are always necessary. First one must work to recontextualize research through an Indigenous perspective as, “for those who have been oppressed by colonization, research is a dirty word” that “has allowed for predatory exploitative behavior toward Indigenous communities” (Sinclair, 2003). Through honest study and by taking responsibility for our biases we can have “a more critical understanding of the underlying assumptions, motivations and values which inform research practices” (Smith, 2012).

As we decolonize our own views and biases in this way, we must also create space for alternative knowledge and ways of knowing. Through “respect, responsibility, and humility” we can ensure “we do not minimize anyone’s struggle through inappropriate contextualization or comparison” (Thambinathan, 2021) and create spaces that are accessible to all.

Lastly, we must understand the “shared aspects of relationality and relational accountability” and put them into practice “through choice of research topic, methods of data collection, form of analysis and presentation of information.” (Wilson, 2009). Keeping these in mind as we progress in our research will ensure we are continually working to decolonize our methodologies.

Smith, L. T. (2012). Decolonizing methodologies: Research and indigenous peoples (Second edition). Zed Books.

Thambinathan, V., & Kinsella, E. A. (2021). Decolonizing Methodologies in Qualitative Research: Creating Spaces for Transformative Praxis. International Journal of Qualitative Methods, 20, 160940692110147. https://doi.org/10.1177/16094069211014766

Wilson, S. (2009). Research Is Ceremony: Indigenous Research Methods. Fernwood Publishing Co., Ltd.

21

Ecology

Topic: Poster

Title: Composition and spatial distribution of invasive aliens and indigenous species in various vegetation physiognomies in Akure Forest Reserve, south west, Nigeria.

Author: ***AYOMIPOSI Akinkuolie @ Adeyemi federal college of education***

Keywords: Plant invasion,Soil seed bank,Akure Forest Reseve,physiognomies

Abstract:

The study investigated the composition and spatial distribution of the invasive aliens and native species in the various vegetation physiognomies in Akure forest reserve, Ondo state, South west Nigeria. The forest reserve was demarcated into five study sites (A,B,C,D,E). Site A-Natural forest, B-Teak plantation, C-Taungya system, D- Taungya +Teak +Gmelina, E- Teak +Gmelina + Pinus plantation. In each of dry and rainy seasons, ten study plots each measuring 25m×25m indicating two plots from each of the five physiognomies were selected for sampling. Within each plot, for all woody species that were{1m} and above, complete enumeration, separation of enumerated stems into aliens and natives, measurements of density, basal area, height, girth at breast height were determined. Shanon weiner diversity index of similarity, Sorensen’s index of similarity were used to measure the degree of similarity among the sites in their species diversity and floristic composition Differences in species richness, Shannon weiner index and eveness between the most invaded and the least invaded physiognomies were used to measure the effects of invasion on the biodiversity. Student t -test was used to test for significant differences in basal area, stem density and size distribution between aliens and natives. Result showed that there were ninety three (93) woody species consisting of five (5) alien species and eighty eight(88) natives in all the study sites though the aliens had low densities. Alien species found in the study area were Tectona grandis, Gmelina arborea, Pinus caribae, Gliricidia sepium and Carica papaya. The most invaded site which is a disturbed site being a source of revenue to the government is the teak plantation while the natural forest which is relatively undisturbed is the least with no alien species. These was no significant differences in the stem densities of the alien and native species. Size distribution of all stems fall into the lower size classes. The least invaded sites had the highest basal area, species diversity, species eveness. Species richness while the most invaded site had the lowest in each case except the basal area. Other sites had intermediate values. The lowest similarities index of 5.55% was observed between the least and most invaded. It is concluded that invasive alien woody species are well distributed in Akure forest reserve though the natural forest is still intact and not vulnerable to invasion by alien species. Natural areas resist plant invasion while disturbed areas are prone to invasion by alien plants which have significant impacts and effects on the biodiversity of the forest reserve by reducing species richness, diversity and eveness.

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Phytochemical

Topic: Poster

Title: Certain phytochemical compunds available in Eucalyptus leaf show herbicidal activity: in search of bio-agrochemicals for organic rice cultivation

Author: ***Jayani Wathukarage @ Rice Research and Development Institute, Sri Lanka***

Keywords: Phytochemicals, herbicide, Eucalyptus, rice weeds, active chemicals

Abstract:

Organic agriculture is a major dialog resulted due to the negative environmental impacts of agrochemicals. Application of herbal extracts as herbicide have been studied by different scientists, however, the results are not very promising. The inter-reactions of various chemicals in crude plant extracts, relative concentrations and volatalities of active compounds, etc. could be reasons for such research outcomes. Similar studies were conducted using Eucalyptus leaf extracts which show effectiveness agaist some weeds, however, the active compounds were never identified. Eucalyptus is available in Sri Lanka as large introduced and naturalized populations and show negative impacts on the biodiversity due to its invasive nature. Therefore, studying its herbicidal activity would be beneficial and feasible. Crude aqueous extract (200 g of leaf powder extracted to 1 l of water at 70OC diluted to 8 l) was tested against the weeds in rice cultivation to re-evaluate its herbicidal activity and other benefits. The results show that the extracts are effective in management of weeds at 4 days after broadcasting seeds. Then the crude extract was analysed for its constituents using HPLC followed by LC/MS and GC/MS. Out of the total of 32 detectable constituents identified 17 were previously reported to have herbicide activity. Results of the current study will be used in isolation of identified active compounds with herbicide activity and conducting small scale evaluation trials for validation of results followed by large scale researcher managed field trials. The treatments will be consisted of single chemical trials and possible combinations of the chemials after careful understanding of their chemical interactions. Finally it is expected to develop a novel commercial biobased herbicide which is ecologically friendly and suitable for effective weed management in rice.

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Education and Outreach

Topic: Poster

Title: "IMPORTANT ROLE OF THE BOTANY FOR STEM INNOVATIVE CULTURE IN ENVIRONMENTAL EDUCATION"

Author: ***Marina B. A Minoli, FRSB CSciTeach @ Biologists Order Federation - Royal Society of Biology***

Keywords: STEM BOTANICS;,CONTAMINATION BETWEEN DISCIPLINES,PLANETARY BIOLOGY

Abstract:

This botanical contribution was created and realized in different contexts as IBSE methodology, starting from innovative botany didactic STEM experience (from macroscopic botanics to microscopic botanics) were involved different high school classes and universities, reflecting on the botany evolution and on the opportunities of this teaching methods can offer for the Botanical work innovatively, creatively, flexibly to educate and to achieve learning successes. In all realized activities was important keeping the relationality alive with all students realizing different steps of an integrated botany STEM didactic itinerary with numerous experimental activities conceived and implemented in digital blended science teaching with microscope and macroscope botanical images. The educational actors of these project were aware that all innovative actitivities have long needed a process of profound innovation of botany teaching-learning methodologies that identify a different role for the science teacher, protagonist with students in the transformation processes in contamination between disciplines, promoter of knowledge that integrates soft skills and cognitive skills, far from «transmissive» didactic actions for learning by doing botanics in an innovative environmental education path using also model plant organism.

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Reproductive Processes

Topic: Poster

Title: Evaluating Population-Specific Variability in Reproductive Investment in Fraxinus nigra Across its North American Range

Author: ***Melissa Lehrer @ Pennsylvania State University***

Keywords: Reproductive Success,seed dispersal,seed morphology,seed size,seeds,Trees,ash

Abstract:

The emerald ash borer (Agrilus planipennis, EAB), a beetle native to East Asia, has decimated populations of trees in the Fraxinus (ash) genus since its unintentional introduction into Southeastern Michigan, USA in the late 1990s. The larval stage of the EAB lifecycle devastates ash populations through the consumption of phloem tissue beneath the bark, impacting system-wide carbohydrate transport. In addition to the increased mortality of ash trees themselves, EAB-induced death can have significant influence on the surrounding ecosystem. This is a particular concern for Fraxinus nigra (black ash) due to the unique habitat and ecosystem services it provides, including the swamps, bogs, and other moisture-rich wetland landscapes it dominates. The potential large-scale death of black ash from EAB infestation threatens the foundational ecosystem function of these hydric systems, as black ash is one of very few deciduous trees present in these wetland environments. As such, it is imperative to evaluate within and among population variability, at both phenotypic and genomic levels, to uncover drivers of EAB resistance that can be leveraged to conserve this keystone species. In this work, seed and samara morphology will be evaluated in black ash trees across its North American range to identify shifts in seed-related phenotypes that may contribute to differential, reproductive-based responses to EAB within and among populations. Responses will be assessed through the measurement of samara and seed traits derived from x-ray images, as well as seed weight. These findings will offer insight into putative population-specific mechanisms linked with seed dispersal and/or seedling establishment in the face of EAB infestation. We hypothesize that: 1) populations closer to the outbreak origin will exhibit lower seed weights and smaller samaras, suggestive of a generalized stress response to EAB that impacts reproductive success; this will also correspond with an increase in the amount of unfilled seeds per mother tree, and 2) populations further from the epicenter will display higher seed weights, larger samaras, and fewer unfilled seeds, facilitating population expansion with competitive seedlings.

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Systematics

Topic: Poster

Title: Unraveling the Taxonomic Classification of the Tolowa wallflower (Brassicaceae: Erysimum), a dune endemic of the California North Coast

Author: ***Cameron Jones @ Cal Poly Humboldt***

Keywords: Classification ,endemic flora,rare species

Abstract:

Found in Del Norte County, California, in the Tolowa Dunes State Park, there is an Erysimum population that does not fit the species boundaries of E.concinnum Eastw., its current assigned name. A closely related species, E. menziesi (Hook.) Wettst arguably better fits the morphology of the Tolowa Wallflower, with the caveat that it does not adequately depict the population. Because of the endemicity of the two aforementioned species and the Tolowa wallflower, correct taxonomic assessment and a clear definition of species boundaries are warranted. To evaluate the species boundaries and circumscription of the Tolowa wallflower, we would collect DNA samples from Erysimum from Monterey to Crescent City, California. Once the DNA has been extracted, we will use Angiosperm 353 to perform a high resolution phylogenetic analysis. Through our data collection, observations, and genetic study, we will test three hypotheses: 1) the current species name is correct for the Tolowa population, 2) the Tolowa population needs to be circumscribed to E.menziesi and, 3) the Tolowa population is its own species. The last two outcomes would lead to a rare species classification, leading to increased funding for the conservation effort of the species and the Tolowa Dunes.

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Population Genetics/Genomics

Topic: Poster

Title: Population Genetic Consequences of Fragmentation Across Native Prairie Remnants: A Case Study Using Helianthus maximiliani

Author: ***Kyra LoPiccolo @ Pennsylvania State University***

Keywords: conservation,gene flow,habitat fragmentation,population genomics,Prairies,connectivity,Ne,EEMS

Abstract:

Native prairie grasslands across the Northern Great Plains are critically imperiled due to land conversion and fragmentation. This poses a significant risk for many prairie plants, where reduced gene flow, isolation, and small population size may lead to loss of genetic diversity, reducing populations' capacity to adapt to change. This is of particular concern for self-incompatible species, where reduced population size and isolation may increase the probability of mating between close relatives, thus increasing the potential for inbreeding depression. To evaluate the impact of fragmentation on the evolutionary potential of native prairie plant populations, we examined genetic diversity and connectivity across remnant prairie plant populations, using Helianthus maximiliani as a model species. We sampled 24 populations of this perennial, out-crossing, native prairie sunflower species from remnant prairie fragments across the Northern Great Plains. We used reduced-representation sequence data (RADseq) aligned to the Helianthus annuus reference genome to generate a SNP dataset of 6,206 genetic variants for a range of population genetics analyses. To assess population genomic structure, we looked at genetic clustering and pairwise genetic differences (FST) across populations and found evidence of genomic structure. We tested for the role of neutral and non-neutral processes in shaping the population's genomic structure by evaluating the impact of geographic distance (i.e., IBD-Isolation by distance) and environment (i.e., IBE-Isolation by environment) on the evolution of genetic differences. However, neither IBD nor IBE was sufficient to explain the genetic differences among populations. We further estimated the long-term evolutionary potential across populations by estimating the effective population size (Ne) as a metric valuable to applied conservation management. Our analysis indicated that all populations exhibited extremely low effective population size (Ne < 2 00), suggesting that remnant populations may be increasingly susceptible to the consequences of genetic drift. Finally, we assessed population genetic structure and the distribution of genetic variation within and among populations. Using estimated effective migration surfaces (EEMS), we are identifying corridors of gene flow and potential areas to target conservation efforts to maintain connectivity and limit the fitness consequences of genetic erosion. Our results underscore the significance of maintaining connectivity across native prairie fragments and highlight the impact of anthropogenic changes on the evolutionary potential of native prairie plant populations.

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Ecology

Topic: Poster

Title: Diversity and abundance of Orchids across various forest habitats in Chhotanagpur Plateau (Jharkhand, India)

Author: ***Pankaj Kumar @ Texas Tech University***

Keywords: Orchidaceae,plant ecology,species richness

Abstract:

Chhotanagpur Plateau is a distinct biogeographic zone between the Indo-Gangetic Plains and the Mahanadi River Basin in the eastern part of India, where no prior orchid studies have been conducted in past. Inventorisation and ecological studies were conducted to identify the species and understand their distribution pattern accross various forested habitats in the region. Modified adaptive cluster sampling technique (a technique which was earlier used for amphibian surveys) was used for the ecological study of rare orchids in this landscape. Sampling was carried out in 10 m radius plots that were laid on the first orchid encountered. Total count of orchid and tree species within the plot was recorded. Data on ecological parameters such as temperature, altitude, canopy cover, herbaceous ground cover and host species were recorded. Four random plots of same size were laid adjacent to the orchid plot and similar parameters were documented. Habitat types were categorised based on the Importance Value Index (IVI) of tree species. Abundance of orchids across these habitats was studied. Data were analyzed using statistical packages like Biodiversity Pro, EstimateS, PCord and SPSS.

Five major habitat types (Shorea, Shorea dominant, Shorea-Diospyros, Shorea-Terminalia and Shorea-Madhuca) were identified and distribution patterns of 70 orchid species were studied in these habitats. Observed and estimated orchid species richness and, α and β diversity were high in case of Shorea dominated forests whereas least diversity was seen in pure Shorea forests, based on Jackknife-I and k-dominance plots. Based on nine microhabitat variables, habitat-heterogeneity was observed using boxplots. Both species abundance and species richness were positively correlated with the altitude. Species abundance was found to be highest between 300–500 m asl whereas the species richness was found to be highest between 500–700 m asl. Canonical Correspondence Analysis was performed to understand the species-environment correlation which was found to be highly significant. It was also observed that Shorea dominant habitat has the most diverse environmental conditions and one of the main reasons attributed to this could be the fact that this habitat occurs at wide elevational range. Shorea-Madhuca habitat had restricted environmental condition and even this kind of habitat is very rare as per observations.

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Ecology

Topic: Poster

Title: Effects of leaf litter depth on seed germination of non-native bittersweet Celastrus orbiculatus in a Pennsylvania forest

Author: ***Amy Faivre @ Cedar Crest College***

Keywords: non-native species,Seed germination,bittersweet,Celastrus orbiculatus

Abstract:

Celastrus orbiculatus is a non-native, invasive bittersweet in many eastern forests in the United States. It displaces native plant species and changes natural forest habitats by climbing and sometimes girdling trees. Individual C. orbiculatus plants produce many seeds. Thus, one way to reduce the presence of this species in forests is to understand more about the germination of its seeds. Previous studies have shown that depth of leaf litter in forests affects seed germination and early seedling growth. For our study we collected seeds of C. orbiculatus in November 2021 in a forest at Wildlands Conservancy in Emmaus, PA, cold stored them and set up two replicate germination trials in the Cedar Crest College greenhouse The three conditions were no leaf litter, a low level of leaf litter (1 Mg/ha), and a high level of leaf litter (16 Mg/ha). The number of seedlings germinated was greatest at the early stages of the experiment in the no or low leaf litter treatments, but by the end of the experiment in one trial the differences disappeared and in a second trial, the no litter seeds germinated significantly less ($p < 0 .001$). In both trials, significantly more seedlings growing in leaf litter than in no leaf litter reached later developmental stages (marked by the presence of two cotyledons) by the end of the experiment. Data for both trials were combined to analyze the over-dried seedlings. In the high leaf litter treatment, the seedlings had significantly longer roots ($p < 0 .005$), longer hypocotyls ($p < 0 .001$), and mass of roots ($p < 0 .001$) than the no and low leaf litter treatments. The leaf litter levels in the forest where the C. orbiculatus seeds had been collected fell between the low and high leaf litter treatments used in this study. Understanding the effects of leaf litter on seed germination success may help in controlling seedling emergence and future spread of this invasive plant.

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Functional Genetics/Genomics

Topic: Poster

Title: Chromosome and Karyotype analysis of Menyanthes trifoliata by FISH

Author: ***Kweon Heo @ Kangwon National University***

Keywords: cytology,endangered species,Heterostyly,Fluorescence in situ hybridization,M. trifoliata

Abstract:

Menyanthaceae is a family of aquatic plants in the order Asterales. There are 76 species in six genera (Liparophyllum, Nymphoides, Menyanthes, Ornduffia, Nephrophyllidium, Villarsia), some species used for medicine or edible. Menyanthes trifoliata is a monotypic genus that belongs to Menyanthaceae. This species is distributed in Northern Hemisphere, such as Asia, and Europe. It is designated as a second class rare and endangered species in Korea. Cytogenetic investigations based on chromosomes provide insight into basic genetic and genomic characteristics in species. However, genomic information based on chromosome characterization and physical mapping of cytogenetic markers has been very limited. Dual-color FISH karyotype analysis of M. trifoliata was conducted using 5S and 45S rDNA probes. The number of chromosomes is $2n = 54$. The chromosome length was 1.52 to 3.37 μm, and the average chromosome length was 2.34 μm. In the FISH, M. trifoliata represents two pairs o 45S rDNA signals and one pair of 5S rDNA signals. Also, in the same condition, 5S rDNA probe was localized to chromosome #5, and 45S rDNA was located at the secondary constriction of the acrocentric satellite chromosomes #3 and #24. These results would be used as basic data for genetic diversity and the preservation and restoration of endangered species.

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Mycology & Phycology

Topic: Poster

Title: A new species of Inosperma, and first record of I. afromeliolens from West Africa

Author: ***Hyppolite Aignon @***

Keywords: phylogeny,molecular systematics,muscarine,Basidiomycota

Abstract:

Here we present Inosperma macrocarpa as new to science and the first record of I. afromelliolens from West Africa. Inosperma macrocarpa is nested in an Old World Tropical clade, based on a molecular phylogeny inferred from sequences of ITS, LSU, RPB2 and TEF1. Complete description and illustrations, including photographs and line drawings, are presented for the new species. Morphological and molecular analysis based on collections from Benin also confirm the presence of I. afromelliolens in West Africa. A toxicity analysis shows that neither species contain muscarine which lend further support to the hypothesis that the ability to produce muscarine is a derived trait in Inosperma.

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Ecophysiology

Topic: Poster

Title: Does CAM explain C4-like d13C values in Bulnesia retama (Zygophyllaceae), a non-Kranz, non-succulent desert shrub?

Author: ***Daniel Mok @ University of Toronto***

Keywords: ecophysiology,photosynthesis,stem,Zygophyllaceae,CAM,Bulnesia

Abstract:

Isotopic screens of herbarium material designed to detect C4 species in the family Zygophyllaceae identified three distinct clusters of plants having C4-like isotopic values, one in the Zygophyllum simplex group (now Tetreana simplex), one in the Tribuloideae subfamily (Tribulus, Kallstroemia, and Tribulopis), and one in the species Bulnesia retama (subfamily Larreoideae) a drought deciduous desert shrub from Argentina. Tetreana and the Tribuloids are confirmed as C4 plants with distinct Kranz anatomy and C4 gas exchange traits. Bulnesia retama, however, shows no evidence of C4 anatomy or gas exchange signatures in leaf or stem, including single cell C4 photosynthesis. We considered CAM photosynthesis as an explanation for the high isotopic values, which range between -16‰ and -20‰. Clear succulence is lacking in all tissues, including stems; however, stems show tight packing of the photosynthetic cortical cells in a CAM-like manner. Leaves show typical non-succulent C3 anatomy. We therefore tested the hypothesis that B. retama is facultative CAM, which if true could explain the high isotopic values. If so, Bulnesia retama would represent a new CAM family, genus and species. The results of these tests will be presented in this poster.

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Biogeography

Topic: Poster

Title: Biogeography of C3-C4 evolutionary intermediates: insight into the selection environment for C4 photosynthesis

Author: ***Brett Kreinsen @ University of Toronto***

Keywords: biogeography,C4 photosynthesis,climate,ecological niche,ecoregion,GBIF,GIS analyses,WorldClim

Abstract:

Over 65 lineages of flowering plants have independently evolved the C4 photosynthetic pathway as a CO2-concentrating mechanism. Among these clades, there exists a gradient of intermediate character states between the ancestral, C3, and the derived, C4, pathways. These 'C3-C4 intermediates' represent transitional species and offer unique insights into the evolution of C4 photosynthesis. Current understandings of the physiology of C3-C4 plants suggest that they are found in areas that promote high levels of photorespiration and stomatal closure. These environments have been broadly described as low-CO2/high-O2, hot, dry, bright and/or saline; however, other factors, such as seasonal variations in temperature and precipitation, must be considered to fully describe the geographic range of each species. Using occurrence records obtained from the Global Biodiversity Information Facility (GBIF), this study aims to better define the ecological niches of C3-C4 species. Centers of high C3-C4 intermediate diversity are delineated with Geographic Information Systems (GIS) using an ecoregions-based approach. The climates of these centers are summarized with an average monthly time series for several atmospheric variables using historical raster files sourced from WorldClim. Here we find support that hot climates with seasonal precipitation favor C3-C4 species, though other contributing factors are usually involved. The centers of diversity, and their climates, contribute to the knowledge of the environments that are associated with a complex, primary metabolic trait.

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Hybrids and Hybridization

Topic: Poster

Title: Investigating underlying discordance and hybridization among nuclear phylogenies of Packera (Senecioneae; Asteraceae)

Author: ***Erika Moore-Pollard @ University of Memphis***

Keywords: phylogenomics,Astral-Pro,TEO,PhyloNetworks

Abstract:

The field of phylogenetics is drastically changing with the increased use of multi-locus and genomic data. A major challenge with this expansion is that conflicting genealogical histories often exist in different genes, and the answer is not as simple as increasing the amount of data. These differing gene histories can cause gene tree discordance that occurs when phylogenies obtained from individual gene trees differ among themselves and from the species tree, potentially leading to incongruent tree topologies. Underlying discordance and uncertainty are constantly seen in phylogenomic studies and are repeatedly explained as results of biological processes including gene flow, incomplete lineage sorting (ILS), or paralogous sequence duplication and loss. The North American endemic genus Packera Á. Löve & D. Löve (Asteraceae) is estimated to have about 64 species and varieties and is known to be complicated by hybridization, polyploidy, and reticulation, making resolving evolutionary relationships in the group complex. Previous phylogenomic work on the group has shown that there are high levels of underlying discordance, with only 49% of the gene trees represented i the final species tree, and the remaining 51% of the gene trees show differing evolutionary relationships. Additionally, 51% of internal nodes were not highly supported. Thus, to obtain a better understanding of potential gene flow and its effect on Packera, we investigated the causes and consequences of nuclear discordance, including evolutionary processes of ILS and gene flow, to understand how they influence the phylogenetic patterns seen in Packera. To do this, we compared the topology and support values of Packera phylogenies resulting from the normal paralog selection processes defined by HybPiper, along with other paralog selection or pruning methods. We then investigated whether pruning the paralogs instead of performing a selection process affected the topology and support of our phylogeny. To investigate hybridization and its effect on the species relationships in our tree, we used likelihood methods to infer phylogenetic networks to find any evidence of gene flow among species lineages in this complicated genus. We anticipate this work will provide further insight into how underlying biological processes can influence species relationships and levels of discordance within phylogenomic studies.

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Ecology

Topic: Poster

Title: LOCAL VALUATION AND ECOLOGICAL EFFECTS ON THE HABITAT OF BAOBAB (ADANSONIA DIGITATA L.) IN BENIN

Author: ***Monique Assongba @ Laboratory of studies and forest research***

Keywords: Habitat loss,Multiple uses,Adansonia digitata,West Africa

Abstract:

Adansonia digitata L. is a multipurpose species in Africa and is used therapeutically, for food, economically and socioculturally. This study on the conservation status of Adansonia digitata L. is part of the development of strategies for the conservation and sustainable use of the species due to the importance of its socio-economic potential of the species. It aims to determine the different uses and their implication in the destruction of natural habitats of Baobab in Benin. The data were on the uses of fruits, peels and seeds carried out in the Guinean zone located between 6° 25"N and 7° 30" N and in the Sudanese zone located between 9° 45 "N and 12° 25" N. The results show that the fruits are rich in calcium (12.5-15%) and the populations consume the fruits directly or transformed into juice. The seeds are used in the preparation of broths and the bark is used in the production of strings. Crop losses ranged from 10-25%, 15-36% and 8-45% respectively for fruits, seeds and bark according to the climatic zones of the study. Ecologically, the species is found in dry forests, savannas and on agricultural land with a high capacity for resistance and adaptation to climatic variability. However, human threats reduce the range of the species and cause habitat loss. The uses of the different parts of the species must be regulated and rational.

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Floristics & Taxonomy

Topic: Poster

Title: CONTRIBUTIONS TOWARDS A TAXONOMIC REVISION OF LOASACEAE FOR "FLORA DE CHILE"

Author: ***Rafael Acuna @ Universidad de Costa Rica***

Keywords: Cornales,Floristics,new species,South America,taxonomic treatments,transcontinental collaboration

Abstract:

The family Loasaceae comprises ca. 350 species, with its highest diversity in the Andean and peri-Andean regions of South America. Although significant progress has been made in clarifying the phylogenetic relationships and taxonomy of the family, there are still many questions that await resolution, even in relatively well-known contries.

Chile, with ca. 50 species, represents has the third highest species number of Loasaceae after after Peru (ca. 100 spp.) and the United States (94 spp.). Chile has not only a high number of species, but also a high percentage of endemism with ca. 50% of the species not recorded outside the national territory. The most recent taxonomic treatment for whole Loasaceae at a national level dates to 1901.

The flurry of newly described species in the 19th century was followed by a long slump in progress of the understanding of Loasaceae in Chile. Only two species were described as new to science (Caiophora deserticola from Chile and Peru and Loasa mollensis endemic to Chile). We are aware of only one published new country record for the period 1901-2008 (Loasa nitida). However, studies in the last 6 years, often involving transcontinental collaboration, have recovered 2 new country records, ''resurrected'' 2 distinctive, previously ''forgotten'' species (1 of those endemic to Chile) and found 2 previously undescribed taxa (both endemic to Chile).

Despite this progress, several challenges remain: The considerable infraspecific variation in species of Loasa ser. Macrospermae is inadequately reflected by current taxonomy and the correct use of some of the names remains obscure. Also, the taxa currently accepted in Pinnasa/Loasa ser. Pinnatae do not adequately reflect what is known about the phylogeny of the group.

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Pteridology

Topic: Poster

Title: Does Mutation Pressure Predict Polyploid Speciation? Testing the Neutral Model in Ferns

Author: ***Thomas Buchloh @ Washington State University***

Keywords: fern diversity,population genetics,speciation,whole genome duplication

Abstract:

In plants, reproductive isolation is commonly achieved through the doubling of nuclear DNA content (genome-wide duplication). Such polyploidization events are hypothesized to occur when incomplete meiosis forms diploid (2n) gametes which unite to form polyploid (4n) progeny. These resulting polyploid progeny and diploid progenitors, are reproductively isolated and may be considered biological species. This model frames polyploid speciation as a frequency dependent process where production of 2n gametes is expected to determine the prevalence of polyploid species. Despite the near universal acceptance of this model in biology textbooks, the predicted relationship between 2n gamete production and polyploid diversification remains untested. Ferns, having a high rate of polyploidy, are an ideal system in which to evaluate this model. We propose to estimate the predicted correlation between diploic gamete production and polyploid diversity at both genus and population levels. Flow cytometry will be used to estimate the 2n gamete production, while phylogenetic and cytological databases will be used to estimate polyploid occurrence at the genus level. After sampling, phylogenetic contrast methods will be used to quantify correlated evolution of these parameters across the fern phylogeny. If unreduced gamete frequency determines polyploid speciation, a significant positive correlation will be observed in the sampled species. These tests will determine whether the rate of fern polyploid speciation is driven by ploidal mutation pressure, or if differential survival and reproduction between diploids and their polyploids is a more important determinant of polyploid occurrence and diversification.

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Ecophysiology

Topic: Poster

Title: Light and Moisture Content as Determinants of Photosynthetic Activity in Southern Appalachian Mosses from Open and Shaded Habitats

Author: ***Leigha Henson @ Appalachian State University***

Keywords: bryophytes,Bryophyte,ecophysiology,eco-physiology,moss,mosses,photosynthesis,Photosynthetic capacity,physiology,Southeast US,Southern Appalachians,bryology

Abstract:

Mosses function as keystone species and bioindicators of forest integrity. They are sensitive to changes in atmospheric conditions and may influence ecosystem functioning out of proportion to their biomass. Yet despite their importance, there have been no studies of their ecophysiology in the Southern Appalachian Mountains (SAM). We performed light response and drying curves to determine their influence on photosynthetic responses of four native mosses, using two species from open habitats and two from forest understories. We used a custom-built cuvette attached to a Li-6800 gas exchange system to allow for better control of relative humidity. We calculated the following parameters on an areal and dry weight basis: maximum photosynthetic rate (Amax) at light saturation (LSP), dark respiration rate (Rd), light compensation point (LCP), and apparent quantum efficiency (AQE), as well as chlorophyll contents for each species. We hypothesized the following:

Understory mosses would have higher chlorophyll contents and lower a:b ratios than open-habitat mosses.
Open-habitat mosses would maintain physiologically suitable water contents for a longer period of time than understory mosses, extending their time for photosynthesis.
Open-habitat mosses would exhibit higher LCP, LSP, Amax and Rd, but lower AQE compared to understory mosses.

Polytrichum juniperinum and Ceratodon purpureus, open-habitat mosses, had higher LSPs (631 and 1098 µmol m-2 s-1, respectively), than understory species (Hypnum imponens and Thuidium delicatulum at 454 and 340 µmol m-2 s-1, respectively). Understory mosses had lower Amax values between 1.1 and 1.90 µmol m-2 s-1, while open-habitat mosses were higher at 4.6 and 17.0 µmol m-2 s-1, respectively. Open-habitat species had higher Rd rates than understory species. Ceratodon purpureus had the lowest chlorophyll content and a:b ratio. Photosynthetic rates peaked at intermediate water contents (70-80 %) before declining as the mosses dried with Ceratodon purpureus maintaining carbon uptake for the longest amount of time.

Our first hypothesis was partially rejected: Open-habitat species did not have statistically higher chlorophyll content and P. juniperinum did not have a lower a:b ratio than understory species.
Our second hypothesis was partially accepted: C. purpureus dried the slowest and therefore remained photosynthetically active longer than the other mosses.
Our third hypothesis was mostly accepted except that open-habitat species did not exhibit lower AQE as we predicted. C. purpureus had a similar AQE to understory species, and P. juniperinum had the highest AQE. P. juniperinum also had a LCP similar to understory mosses

Open-habitat moss species may be more tolerant of warming and precipitation alterations due to climate change because they are subject to greater light and moisture stress than understory species, especially in summer months. The results of this research should provide a basis for understanding how SAM mosses are adapted to their habitats, and with additional modeling, it should be possible to calculate daily and annual carbon uptake by SAM mosses and predict impacts of future climate change on their productivity.

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Population Genetics/Genomics

Topic: Poster

Title: Limited gene flow and genetic drift effects over an endemic bromeliad from the Atlantic Forest altitudinal gradient

Author: ***Tami da Costa Cacossi @ UNICAMP***

Keywords: high-throughput sequencing ,population genomics,microevolution,tropical forest,altitudinal gradient

Abstract:

The Atlantic Forest is the second-largest rainforest in the Neotropical region, considered a hotspot for conservation due to its high rates of endemism. Because of its complex geological history, environmental heterogeneity, ecological gradients, and species diversity and turnover, the rocky mountains of the Atlantic Forest are excellent systems to study the evolutionary and ecological dynamics of the Atlantic Forest. Pitcairnia flammea Lindl. (Bromeliaceae) is endemic to the Atlantic Forest, and occurs at an elevation gradient from sea level to more than 2000 meters above sea level, presenting high morphological differences and low gene flow among populations. In this study, we aim to understand how genetic drift and natural selection affect the genetic diversity of P. flammea along the altitudinal and environmental gradients of the Atlantic Forest Mountains. We obtained SNP markers derived from RAD-seq of >160 individuals from eight populations of P. flammea distributed along the Atlantic Forest altitudinal gradient. The SNP calling was performed using the reference genome of the species. Using this data, we will 1) describe diversity, effective population sizes, genetic structure, and gene flow among populations; 2) identify genomic outlier regions possibly under positive selection; and 3) reconstruct demographic variations over time. Our preliminary results evidenced varying levels of diversity (percentage of polymorphic loci; nucleotide diversity (π); observed and expected heterozygosity). The populations from the highest altitudes showed the highest levels of genetic diversity and lower inbreeding coefficients. Population structure with pairwise FST varied from 0.081 to 0.35 and was also higher for high-elevation populations, ranging from 0.27 to 0.35. In agreement, the neighbor-joining analysis revealed that the eight populations are clustered into two major groups, indicating closer connectivity between lowland and intermediate altitude populations compared to the high-elevation populations. The maximum likelihood analysis in ADMIXTURE revealed eight genetic clusters (K=8), each population as a single unit, except by two geographically close populations clustered together, and the highest-elevated population divided into two clusters. Together these preliminary results indicated high genetic structure and weak gene flow among populations, which suggests a strong genetic drif over P. flammea populations along the Atlantic Forest altitudinal gradient. Future analyses of outlier loci will allow us to evaluate the relative effect of natural selection and genetic drift on molding these populations' diversity. Additionally, demographic reconstruction will help to uncover the evolutionary history of P. flammea populations along the altitudinal gradient. Our study will help to understand the processes responsible for the high diversity and endemism patterns observed in the Atlantic Forest Mountain populations, and how they interact in molding this remarkable complex tropical forest.

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Ecology

Topic: Poster

Title: Environmental niche and demographic modeling of American chestnut near its southwestern range limit

Author: ***Robert Laport @ The College of Idaho***

Keywords: ecological niche modelling,_{conservation biology},deciduous forest,demographic modeling

Abstract:

The unintentional introduction and rapid spread of chestnut blight (caused by Cryphonectria parasitica (Murr.) Barr) in the early 20th century resulted in the demise of American chestnut (Castanea dentata (Marsh.) Borkh.; Fagaceae) as a major component of forest canopies resulting in negative impacts on eastern forest communities. Research efforts over the last century have documented the persistence of occasional remnant individuals throughout much of the species' historic range, providing the basis for ongoing breeding of blight-resistant trees and restoration efforts. Here we use environmental niche modeling to evaluate the climatic suitability and reintroduction potential near the southwestern range limit. We also use stage-structured matrix projection models to investigate the potential demographic future of C. dentata in a relatively understudied portion of the historical range based on observations of American chestnut in these areas over the last several decades. We found climatically suitable upland forest habitat with high canopy cover occurs throughout much of the southwestern portion of the historical range, but populations of American chestnut in these areas are predicted to drastically decline over the coming decades. These results suggest the southwestern extent of American chestnut's historical distribution should be incorporated into evaluations for future reintroduction, and emphasize the need for efforts to locate, conserve, and introduce genetic material from individuals with locally adapted genotypes into active restoration programs.

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Ecology

Topic: Poster

Title: Chemical analysis of extrafloral nectar in western Australian Solanum tudununggae (Solanaceae) to explore possible ant-plant relationships

Author: ***Kaitlin Henry @ Bucknell University***

Keywords: Solanaceae,Solanum,Australia,Dioecy,extrafloral nectary,HPLC,nectar,Plant Defenses,plant-animal interaction,Pollination,Undergraduate Research,ants,amino acids

Abstract:

Solanum tudununggae Symon (Solanaceae) is a dioecious species of bush tomato native to northwestern Australia. This narrowly-endemic species has few known localities, all of them in the remote Kimberley Region of Western Australia. One uncommon trait that sets it apart from most other species of Solanum is its secretion of extrafloral nectar. In fact, structurally complex extrafloral nectaries (EFNs) are currently known to occur on the back of the corollas in only three species of Australian dioecious Solanum. Consequently, little is known about the characteristics of its nectar - although botanists have noted abundant ant (and bee) activity around these nectaries. However, the relative lack of research on Solanum EFNs leaves a gap in knowledge regarding the nature of the relationship between these plants and ants. Previous literature has shown that the composition of extrafloral nectar, specifically the presence of essential nutritional amino acids, can cause ant populations to prefer certain nectars to others in other species of plants. With plants grown in Bucknell's greenhouse, this research aims to use high-performance liquid chromatography (HPLC) to analyze the composition of extrafloral nectar, specifically the presence of amino acids and sugars. Through HPLC, we hope to infer a possible correspondence between ant behavior and nectar content. We hypothesize that the presence of essential amino acids could suggest a mutualistic relationship between S. tudununggae and local ants, with the plant providing essential nutrients to the ant population, and in return the ants offering protection against herbivores that pose a threat to the plants.

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Ecology

Topic: Poster

Title: Geographic analysis of sex chromosome polymorphism in the Virginia wild strawberry

Author: ***Trezalka Budinsky @ University of Pittsburgh***

Keywords: Dioecy,Evolution,Fragaria,Herbarium,herbarium genomics,herbarium specimens,Sex chromosome,sex determination,wild strawberry

Abstract:

The evolution of sex chromosomes is a ubiquitous and essential diversifying mechanism in eukaryotes. Yet early stages of sex-chromosome differentiation are poorly understood. The subdioecious octoploid, Fragaria virginiana, provides a rare opportunity to study the beginnings of sex chromosome evolution due to its young, polymorphic ZW sex system. Females are ZW and males/hermaphrodites are ZZ. F. virginiana has a small sex-determining region (SDR) located on the female W chromosome that has undergone three transposition events between the strawberry's four subgenomes, resulting in three SDR haplotypes: alpha (the result of a first transposition and closest to a pre-sex chromosome ancestral state), beta (the result of a second transposition), and gamma (the result of a third transposition and farthest from its ancestral state). We collected leaf tissue from 315 female F. virginiana plants preserved in herbaria and the National Clonal Germplasm Repository. These spanned their North American range. Using diagnostic PCR and gel electrophoresis, we are in the process of inferring each individual's SDR haplotype. Our study aims to advance our understanding of the evolutionary history of sex chromosomes in F. virginiana by examining the geographic distribution of its SDR polymorphism. Specifically, by analyzing the acquired SDR haplotype distribution alongside known environmental variables such as temperature, elevation, and soil type, we seek to elucidate the potential adaptive significance of maintaining all three haplotypes within F. virginiana populations.

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Reproductive Processes

Topic: Poster

Title: Cloudy with a chance of floral responses: Rainfall induced anther closure and color change in Ripariosida hermaphrodita (Malvaceae)

Author: ***Emily Humphreys @ Morris Arboretum of the University of Pennsylvania***

Keywords: Malvaceae,Pollination,Anther,anther closure,rainfall,floral color change

Abstract:

Abiotic environments are constantly changing and plants must respond to these shifts when needed. Anther closure after rain is one such response to environmental factors. Seen in at least 17 families, it may protect pollen from washing away, contributing to male fitness. Floral color change is likewise responsive and widespread, occurring in more than 75 plant families. Color change is most often catalyzed by pollination or floral aging and can serve as a negative signal to pollinators, guiding them towards younger flowers with more resources. While observing Ripariosida hermaphrodita (Malvaceae), a globally vulnerable species from eastern North America, we witnessed the androecium in flowers transform in response to rain. Open, bright purple anthers became closed, dull beige anthers after a rainfall event. We observed 364 flowers on seven R. hermaphrodita individuals across 8 weeks of their flowering season, then confirmed our field findings with a simulated rainfall exposure experiment and time-lapse photography. Our report represents the first observation in Malvaceae of anthers closing after rainfall and, to our knowledge, the first ever report of floral color change in response to rain.

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Ecology

Topic: Poster

Title: The effect of habitat fragmentation on reproductive isolation in a popuation of Asclepas tuberosa

Author: ***massie jones @ University of Illinois at Chicago***

Keywords: Asclepias,Asclepius tuberosa,Microsatellites,paternity,reproductive isolation

Abstract:

The tallgrass prairie once covered over 22,000,000 acres of Illinois. Degradation of prairie ecosystems began with the European settlement of North America and accelerated as agriculture and development increased, reducing the prairie to its current coverage of 2,000 acres. The remaining prairie consists of isolated and fragmented remnants. Such fragmentation limits gene flow into prairie remnants, which may lead to genetic drift and inbreeding, lower remnant population viability, and even local extinction. Genetic declines also limit a species ability to adapt to changing selection pressures. I will conduct a study of gene flow into and within a population of Asclepias tuberosa (butterfly weed), a native milkweed species that supports many pollinators and serves as a larval food plant of monarch butterflies. My study site is James Woodworth Prairie (JWP), a 5-acre remnant isolated within an urban matrix in the Chicago area. Its isolation from other plant communities makes it an ideal location to study pollen mediated gene flow into a remnant prairie. I will combine DNA microsatellite genotyping and paternity assignment of individual plants and their progeny to assess gene flow and pollen dispersal into the prairie to determine the extent of reproductive isolation. I will also characterize pollen movement within the prairie. The unique pollination system of milkweeds, where pollen is delivered in a packet (pollinium) that likely fertilizes all the seeds in a flower, is expected to facilitate paternity assignment. My results will have important implications for conservation and restoration efforts of native prairies. Data analysis and results are pending.

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Population Genetics/Genomics

Topic: Poster

Title: Central California’s Checker Lilies: Exploring the Diversity of Fritillaria Species through Population Genetics

Author: ***Andrew Cardenas @ California State University Fresno***

Keywords: Fritillaria,phylogenetics,population genetics,Taxonomy

Abstract:

This project aims to evaluate how many species/taxa are actually in the group of Fritillaria populations in Central California (currently classified as Fritillaria atropurpurea and Fritillaria pinetorum) through genetic data from a broad geographical survey of populations. Fritillaria is a plant genus in the Liliaceae (lily) family, and these two species are native California wildflowers. Fritillaria pinetorum is a rare plant that is endemic to mountain forests around 3,000 meters in the southern Sierra Nevada Mountains into southern California, while F. atropurpurea has a much larger geographical range, from the Sierras to the Dakotas. They are generally found in different but contiguous parts of California, overlapping in the central Sierra Nevada region. These two species are phenotypically very similar aside from slight and inconsistent morphological differences, but are currently listed as two different species. Due to the large size of the nuclear genome in this group (between 30 and 83 Gb for a haploid genome in Fritillaria), chloroplast DNA has been utilized to answer our question. The chloroplast region psbA-trnH has amplified well for all central California species of Fritillaria (including F. atropurpurea, F. pinetorum, F. agrestis, and F. micrantha) and has been sequenced and analyzed. Resulting data have revealed an indel from bp 359-364, characterizing all F. pinetorum and one population of F. atropurpurea. Further genotyping with published chloroplast microsatellites is underway to distinguish and determine the number of Fritillaria taxa in the central California region. Thus far, most microsatellite primer pairs have amplified in our species, with the exception of some populations of F. atropurpurea, and several have shown peaks in the published allele size range. Our taxonomic investigation of the Central California members of the genus Fritillaria may have conservation implications for putative rare and new taxa in this group.

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Population Genetics/Genomics

Topic: Poster

Title: Pigweeds on the Move: Tracing the Californian Invasion of Palmer amaranth (Amaranthus palmeri)

Author: ***Kristine Fajardo @ California State University, Fresno***

Keywords: Amaranthus palmeri,agricultural weed,Amaranthaceae,Palmer amaranth,population genetics

Abstract:

Palmer amaranth (Amaranthus palmeri) is a summer annual native to parts of the Southwestern United States and northern Mexico. Yet, over the past two decades, it has become one of the most extensive agricultural threats in the Southeast, parts of the Midwest, and more recently in Central California. Adaptive traits, such as herbicide resistance, have aided it in becoming an extremely opportunistic plant in various agronomic settings. Despite its recent emergence in Central California, no genome-wide evaluations have been done on its northern range expansion into agricultural areas in California's Central Valley. As part of a larger population genetic investigation, we are using genotyping-by-sequencing to elucidate the origin of A. palmeri populations found in the Central Valley and attempting to identify any genes linked to adaptation in recent emerging California populations. Neutral markers and adaptive herbicide resistance genes are being used to explore genetic clustering of Central California populations relative to native and nonnative populations in other parts of the U.S. Results from raw sequenced data from sequencing carried out at the DNA Technologies and Expression Analysis Core at the UC Davis Genome Center revealed roughly 840,983,496 total sequences and good quality scores for a total of 167 samples in 17 populations from Central California, Southeastern and Midwestern U.S. introduced ranges. Data were mapped to a draf genome with the Burrows-Wheeler Aligner (BWA). Ongoing genetic analysis of this data and previously collected data from the Southwestern native range, using clustering algorithms (ADMIXTURE, STRUCTURE, and adegenet's implementation of discriminant analysis of principal components, DAPC), may suggest possible invasion scenarios of California populations. Support for different invasion scenarios will be further evaluated via analysis of single nucleotide polymorphisms (SNPs) using approximate Bayesian computation (ABC). In addition, selection analysis of SNP data from California populations will be used to screen for overlap in outliers possibly linked to adaptation to the climatic conditions in the Central Valley. This study has the potential to facilitate future research into how weeds spread, suggest alternative strategies for more sustainable weed management practices, and help create models for evolutionary adaptation applicable to invasions and other agronomic weedy plants.

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Systematics

Topic: Poster

Title: Unlocking the evolution of different sexes in the Hawaiian endemic Schiedea

Author: ***Mike Moore @ Oberlin College***

Keywords: breeding system,Caryophyllaceae,Dioecy,Evolution,Hawaiian Islands,phylogenetics,Pollination

Abstract:

Dioecy in plants is relatively common (~6% of all plant species) but the evolutionary transition from hermaphroditism to separate sexes in plants is not always fully understood. One of the plant genera that offers an excellent opportunity to study this process is Schiedea (Caryophyllaceae), a Hawaiian endemic genus consisting of 34 species. Schiedea exhibits an extremely diverse range of breeding strategies, varying from insect to wind pollinated, hermaphroditic to dioecious, and out-crossing to self-pollinating. Understanding breeding system evolution in Schiedea is of great importance as it can help to illuminate the evolution of separate sexes in plants, especially on oceanic islands where pollinators are fewer than on the mainland.

Previous phylogenetic studies suggest that the ancestor of Schiedea was hermaphroditic, and separate sexes have likely evolved multiple times, coinciding with the evolution of wind pollination in drier Hawaiian habitats. However, because of poor resolution in some parts of Schiedea phylogeny in previous work, the evolutionary transition between sexes is not fully understood. To investigate this question in greater detail, we are using targeted sequence capture to sequence ~1000 nuclear genes to reconstruct a well-built phylogeny of all extant Schiedea species. So far, we have data from 234 accessions representing multiple populations of almost all taxa plus 10 outgroups. The much larger number of genes should aid in resolving the relationships among Schiedea, which will allow for reconstruction of breeding system evolution with much greater confidence.

Ultimately, this study will contribute to our understanding of plant evolution and diversity, providing critical insights into the fascinating and complex process of reproductive evolution. Furthermore, our results will also have great implications for the conservation and management of the genus Schiedea, which is threatened by habitat destruction and invasive species.

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Ecology

Topic: Poster

Title: Invasive plants in a changing climate. Do microbes aid success?

Author: ***Josh Leon @ Utah Valley Univeristy***

Keywords: Brassicaceae,climate change,invasive species,Microbiome

Abstract:

The climate of the American Southwest is rapidly changing relative to other areas in the United States. Within the next 80 years, temperatures are expected to rise substantially and will be coupled with longer and more profound drought. How non-native plants may respond to these climatic changes is an important area of interest for land managers.This research examines an invasive plant and its microbe interactions under modeled climate projections. Particularly we are interested in the microbiome's impacts on non-native plant fitness and survival under climatic stress..

The African mustard (Strigosella africana) is a recently spreading invasive that is of particular interest to regional land managers.. We first examined whether increased heat, drought conditions and/or fertilizer affected plant survivability. We found significant differences in plant survivability under differing heat and/or whether a drought was applied. Next, we collected full plant samples using sterile techniques and separated them by shoots and roots to have their DNA sequenced. Using this data, we were able to determine the natural microbiome of this plant. Our next steps will use the same climate models as before on plants grown from seeds collected in the field. Plants from these trials will have their DNA sequenced and their microbial community structure will then be compared to the natural microbiome structure.

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Biogeography

Topic: Poster

Title: Exploration of gypsum soils in the Mojave Desert, U.S. via remote sensing technology

Author: ***Katelyn Gobbie @ John Carroll University***

Keywords: remote sensing,gypsum soils,gypsophiles,field sampling planning,spatial mapping

Abstract:

Geologic parent materials of soils and their geographic distributions can have profound effects on plant ecology and evolution. The widespread yet disjunct distribution of soils derived from gypsum ($\mathrm{CaSO4{\bullet}2H2O}$) often leads to restricted regions of edaphic endemic floras. Most pre-diagnostic methods of determining the spatial extent and composition of gypsum soils for field sampling can be imprecise, laborious, and costly, involving the reliance on soil surveys, georeferenced gypsophilic specimens, and ground-truthing via reconnaissance visits for classification. Dependence on these tactics for research planning is especially risky for botanically unexplored gypsum outcrops. We employed remote sensing technology and extrapolated data from thoroughly examined gypsum outcrops of the Iberian Peninsula, Spain, to reveal the previously undefined gypsum outcrops of the Mojave Desert, U.S. The Mojave Desert is a region where we will be conducting exploratory bryological and floristic surveys in the summer of 2023, but for which there is no available comprehensive spatial assessment of the distribution and composition of gypsum soils. We ultimately aim to (1) produce a map identifying Mojave Desert gypsum outcrops and (2) use the satellite and edaphic data from Spain to test whether remotely sensed data can predict percent gypsum content in Spain and the Mojave Desert. In contrast to the band combination utilized by prior gypsum remote sensing studies, we found that compositing Landsat-8 bands 7, 6, and 2 is more discriminatory for detecting the presence of gypsum, which appeared turquoise in color in both Spain and the Mojave Desert. Our preliminary results suggest that remote sensing technology is an effective method for identifying gypsum soils from freely available satellite imagery and aids in determining potential study sites for botanical gypsum research. Future research will validate the predicted gypsum composition of the Mojave Desert gypsum outcrops via soil sampling and chemical analyses. Additionally, we seek to use this technique to map gypsum soil distributions worldwide and further advance this methodology to build a global gypsum distribution model.

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Floristics & Taxonomy

Topic: Poster

Title: Evaluating the taxonomic status of Bromus rigidus Roth

Author: ***Zachary Oliver @ Utah State University***

Keywords: morphology,Taxonomy ,Bromus,weed

Abstract:

Bromus rigidus appears on the list of plants found in the Grand Canyon, however, it was placed in synonymy with Bromus diandrus in the Flora of North America. Many studies agree that it should be treated as a synonym, but others have identified B. rigidus as a separate species. Consequently, we decided to conduct a formal reevaluation of its status. We examined herbarium specimens labeled as either Bromus rigidus or Bromus diandrus plus the four other species of Bromus sect. Genea found in North America (B. madritensis, B. rubens, B. sterilis, and B. tectorum). After the initial analyses, we attempted to reidentify our specimens based on our data and reran the analyses. We also compared our specimens to morphological data from Australia where B. rigidus is recognized. Our data and research do provide some support for its recognition as a variety of Bromus diandrus but ultimately are inconclusive based on morphology. We recognize that a major limitation of our study is that it is based solely on the examination of herbarium specimens which do not provide sufficient information to evaluate differences in chromosome number or ecology. We recommend further investigation to settle the case of its taxonomical status.

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Conservation Biology

Topic: Poster

Title: The Relevance of Pedigree and Genomic-based Conservation Management to Exceptional Plant Species: A Case Study Using Amorphophallus titanum

Author: ***Justin Tutt @ University of Illinois at Chicago***

Keywords: _{conservation biology},Amorphophallus titanum,ex situ living collections,metapopulation dynamics,next generation sequencing,population genomics

Abstract:

As many plant species around the world are threatened with extinction, botanic gardens play an increasingly important role in conservation efforts by managing species across ex situ collections. However, a lack of best practices outlining the collective management of living collections among continents, termed continental collections, jeopardizes the long term stability of ex situ conservation collections. No research to date has explored a botanic management plan using pedigree and empirical genetic data to minimize relatedness between individuals, maximize founder representation, and preserve genetic diversity. To address this gap, we will be comparing the effectiveness of pedigree and genomic data for the management of Amorphophallus titanum, an exceptional species commonly cultivated in the botanic community. Amorphophallus titanum is an ideal focal species to implement this protocol on given its lack of genetic exchange between continental collections. Anticipated results will compare breeding recommendations, for both within and between continental collections, and estimated metapopulation genetic parameters derived from the pedigree and genomic data using PMx, a zoo management software. This study will be an important first step in bettering collections management for this endangered plant species and in the design of more successful breeding programs for other exceptional species worldwide.

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Ecology

Topic: Poster

Title: Woody cover negatively affects diversity of the aboveground plant community and soil seedbank in central Texas.

Author: ***Peter Eludini @ Louisiana State University***

Keywords: shrub expansion,shrubs,Soil,Soil seed bank,Texas,juniperus

Abstract:

The rangelands of central Texas have experienced striking shifts in vegetation dominance over the past century. Open savannas and grasslands are increasingly threatened by the encroachment of woody plants, as a consequence largely of past grazing and reductions in fire frequency. Restoration of such rangelands is a major focus of management in the region. Following clearing of shrubs by fire or mechanical thinning, restoration depends upon seed dispersal from existing stands of vegetation, sowing of seed purchased from seed companies, or seed germination from soil stored seedbanks. Soil seed banks, however, represent cryptic diversity and are difficult to study. The focus of our research was to determine how woody invasive species alter the soil stored seedbanks in Texas. We showed that the understory plant population reduces drastically with an increase in Juniperus cover and mean annual precipitation. Generally, we found that there are few seeds stored in the soil seedbanks of central Texas. The soil stored seeds under Juniperus reduces with increasing cover. This work provides important predictions of restoration potential and vegetation resilience through the quantification of seed stored in the soil seed bank.

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Floristics & Taxonomy

Topic: Poster

Title: Phylogenetic analysis of Sceptridium (Ophioglossaceae) in Japan: dismantling the three subgenomes in hexaploids

Author: ***Sosuke Ishii @ Chiba University***

Keywords: Asia,BEAST,Botrychium,Ferns,phylogeny

Abstract:

Gametophytic selfing is a unique reproductive system found in homosporous ferns, wherein a zygote is formed by the fusion of genetically identical egg and sperm produced by a single bisexual gametophyte. The mechanism of gametophytic selfing influences the promotion of allopolyploid speciation. Polyploidization is a significant evolutionary process in plants, and many fern species have arisen through reticulate evolution (i.e., evolution by hybridization, including allopolyploid speciation). In lineages that exhibit consecutive gametophytic selfing, manifestation of intraspecific variation and taxonomic problems are likely to occur, as phenotypic discontinuities become more pronounced and easier to recognize. The Ophioglossaceae taxon, which is the focus of this study, is known to have a selfing rate of over 80%. Sceptridium (Ophioglossaceae) in Japan includes a diploid group and a polyploid group, and diversification is expected by reticulate evolution, as the polyploid group is included. Moreover, some taxonomic problems, such as undescribed and unidentifiable phenotypes in polyploid species, exist. The narrow-leafed type, which is the subject of this study and known as "Motomachi-hanawarabi" in Japan, is one such example. The goal of this study is to investigate the origin of the polyploid species of Sceptridium, to reconstruct the reticulate evolutionary process, and to identify the taxonomic substance of the narrow-leafed type. To achieve this objective, we performed a phylogenetic analysis using three chloroplast regions (about 2800bp) and several nuclear markers (13 types). The phylogenetic tree using nuclear DNA suggested that hexaploid (S. japonicum, S. atrovirens, and the narrow-leafed type) was an allohexaploid that originated from an interspecific hybridization event between the related species or ancestor of S. formosanum (tetraploid) and unspecified diploid species. In addition, the phylogenetic tree using cpDNA suggested that tetraploid is maternal ancestral species and diploid is paternal ancestral species. We then constructed a species tree using the multispecies coalescent model to identify the paternal species. The dataset used included the sequences of the extant diploid and hexaploid subgenome of the ancestral diploid. As a result, the hexaploid group was shown to be monophyletic, and their sister group comprised S. nipponicum, S. triangularifolium, and S. microphyllum. Therefore, it was suggested that the related species or common ancestor of these diploids were the paternal parental species. To investigate relationships of hexaploid, we conducted Bayesian clustering. The results supported genetic differentiation between S. japonicum and S. atrovirens, but not between S. atrovirens and the narrow-leafed type. To further support these results, we performed the analysis using genome-wide SNPs by MIG-seq. Neighbor-Net analysis for 3,610 SNPs also showed no genetic differentiation between S. atrovirens and the narrow-leafed type. From these results, we concluded that the narrow-leafed type is a manifestation of intraspecific variation in S. atrovirens and that its appearance is due to a high selfing rate. In addition, the cpDNA tree and Bayesian clustering suggested introgression between S. japonicum and S. atrovirens.

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Pteridology

Topic: Poster

Title: A Western viewpoint on the extreme Palearctic separation of Woodwardioideae ferns.

Author: ***Sonia Molino @ Universidad Complutense de Madrid***

Keywords: biogeography,Disjunction,GBS,Phylogeography,pteridophyte,Blechnaceae

Abstract:

The Paleotropical floristic element of the Western Palearctic has been greatly diminished due to geological and climatic fluctuations during the Cenozoic. Among the representatives of this element stand out ferns, particularly the subfamily Woodwardioideae. This subfamily shows a great disjunction on both sides of the Palearctic, with Woodwardia unigemmata Makino (Nakai) in East Asia and Woodwardia radicans (L.) Sm. (Blechnaceae) surviving in climate refugees in Western Europe and the Macaronesian archipelagos. This distribution makes Woodwardioideae an ideal candidate for testing the evolution of the Paleotropical Geoflora in the Palearctic.

To investigate the origin of this disjunction, we reconstructed the phylogenetic relationships and divergence times of the subfamily Woodwardioideae using four plastid DNA regions. Additionally, we sampled W. radicans throughout its distribution range and performed phylogenomic analyses based on genotyping by sequencing (GBS).

Our results show a divergence between W. radicans and W. unigemmata in the Pliocene, 3.7 (1.35-7.18) Mya. Subsequently, in the western part of the distribution, W. radicans took refuge in Macaronesian archipelagos, from where it appears to have recolonized the continental enclaves in the last 0.8 Mya.

The study provides new insights into the evolutionary history of Woodwardioid ferns, challenging the traditional view that certain Paleotropical elements are relicts from the Miocene. Furthermore, our findings highlight the pivotal role played by archipelagos as biodiversity refuges at the extremes of disjunct ranges, and as sources of diversity for recolonization of continents. This holds significant implications for conservation endeavors, particularly for populations of island species threatened by climate change and habitat loss.

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Ecology

Topic: Poster

Title: Local Adaptation of the Dominant Prairie Grass across the Midwest Rainfall Gradient:

Decadal Patterns of Adaptation and Trait Variation in Response to Drought

Author: ***Jack Sytsma @ Kansas State University***

Keywords: adaptation,Climate Gradients ,community ecology,tallgrass prairie

Abstract:

Drought is one of the most severe abiotic stresses resulting in the greatest losses in plant productivity. Many studies have addressed community and ecosystem responses to drought. However, little is known about intraspecific variation in plants responding to drought. We used wet, mesic, and dry grass ecotypes to test the role of intraspecific variation on plant function across the natural rainfall gradient of the Great Plains. Our focal species is big bluestem (Andropogon gerardii), is the dominant grass that is important for cattle forage, conservation, and restoration. It has a wide distribution across the Midwest rainfall gradient (500-1200 mm rain/yr) giving rise to ecotypes adapted to regional rainfall. Reciprocal gardens were established in 2009 in an ecological community and measured for over a decade. Canopy cover and aboveground biomass were monitored over time in four sites (driest to wettest: Colby, Hays and Manhattan, KS to Carbondale IL). To examine drought, rainfall was reduced by up to 50% using rainout shelters in three sites. For individual plants, height, blade width, SPAD, photosynthetic rate, biomass, and reproductive phenology were measured. At the plot-level, we measured cover and biomass. The objectives were to 1) characterize functional traits of A. gerardii ecotypes across the natural gradient, 2) measure functional trait response to experimental drought using rainouts and 3) determine the impact of local adaptation on the surrounding plant community. First, we expected local adaptation, or home-site advantage, of A. gerardii ecotypes in response to rainfall across the natural gradient. Second, we hypothesized that traits aiding in drought tolerance would be observed in the dry ecotype and in dry sites. Third, we expected that experimental drought would delay reproductive phenology Finally, we hypothesized that strong local adaptation of the A. gerardii ecotype would result in competitive dominance over the surrounding plant community. At the plant-level, the dry ecotype had higher photosynthetic rates and SPAD, narrower blade width, and shorter height compared to the wet ecotype across sites. Experimental drought delayed and reduced flowering of all ecotypes and decreased biomass. At the plot-level, wet and dry ecotypes had highest cover and biomass in their home site, demonstrating local adaptation to rainfall. Rainouts increased cover and biomass of the dry ecotype in the wet site, demonstrating its adaptation to low rainfall. Lastly, the local ecotype became dominant over the surrounding plant community whereas low cover of the non-local ecotype resulted in competitive release of the other forbs and grasses. These results indicate the deterministic role of ecotypes across a rainfall gradient on community assembly and informs the use of climate-adapted ecotypes in anticipation of future droughts.

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Floristics & Taxonomy

Topic: Poster

Title: The Flora of Cape Bathurst and Baillie Island, Northwest Territories, Canada

Author: ***Paul Sokoloff @ Canadian Museum of Nature***

Keywords: arctic,Biodiversity,Floristics,Northwest Territories

Abstract:

Situated at the northernmost point of the continental Northwest Territories, Cape Bathurst and neighbouring Baillie Island are prominent coastal landmarks within the Inuvialuit Settlement Region. From the Smoking Hills on the south of the peninsula to the rapidly-eroding tip of the Cape, this area includes a wide range of plant habitats on both glaciated and unglaciated lands. As the only known locality for the rare hairy braya (Braya pilosa), Cape Bathurst and Baillie Island have long been focal points for botanical collecting – the first herbarium specimens from this areas date back to 1826, when Dr. John Richardson collected sheets of the Hairy Braya on the second Franklin Expedition.

Since then, major vascular plant collections have been made here by Frits Johansen (on the Canadian Arctic Expedition in 1916), Reider Elven (1999), Jim Harris (2004), Bruce Bennett (2011, 2015), and Paul Sokoloff, Jim Harris, and Joanna Wilson (2017, 2022). Here we present a preliminary checklist of the vascular plant biodiversity of Cape Bathurst and Baillie Island, based on these herbarium-vouchered collections. This flora includes 181 taxa from 26 families, including many common amphi-Beriginian and circumpolar Arctic species. Four taxa: the Jakutsk snow parsley (Cnidium cnidiifolium), the Yukon saxifrage (Micranthes reflexa), the northern primrose (Primula borealis) and the sand bluegrass (Poa ammophila) reach the northeastern extent of their Canadian Arctic Range on Cape Bathurst. In addition to the hairy braya, another species of conservation concern in the Northwest Territories, the Drummond bluebell (Mertensia drummondii) may also occur on Cape Bathurst based on new georeferencing of another Richardson specimen (1826) deposited at the New York Botanical Garden.

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Systematics

Topic: Poster

Title: Unraveling the Allopolyploid Origins of Eutrema edwardsii

Author: ***Tiffany Gentry @ University of Colorado Denver***

Keywords: allopolyploidy,Brassicaceae,Disjunct Species,polyploidy,systematics,Eutrema

Abstract:

Polyploidization has been a critical force in the diversification of flowering plants. Allopolyploidy, involving hybridization coupled with whole genome duplication, results in offspring having the complete diploid chromosome complements of each parent. As such, it effects reproductive isolation and facilitates speciation; allopolyploidy has also been shown to lead to adaptation to new landscapes and range expansion. Genus Eutrema (Brassicaceae) is an excellent study system to better understand allopolyploid origins. Eutrema has received a great deal of attention in the systematics literature, includes well-studied model species, and exhibits cytotype variation both within and among lineages. The near circumarctic Eutrema edwardsii, which comprises tetra-, hexa-, and octoploids of allopolyploid origin, is particularly well-documented across its range. A progenitor-derivative relationship for E. edwardsii has recently been documented with the federally listed Colorado endemic E. penlandii, a diploid species from which E. edwardsii is highly disjunct. However, it is suspected that an additional 1-2 diploid progenitors exist for tetraploid and hexaploid populations of E. edwardsii. Although no other diploid species have been described from the E. edwardsii complex, recent evidence from flow cytometry provides evidence for a cryptic taxon from Nunavut, Canada. The goal of our research is to further document phylogenetic relationships among the diploid species of Eutrema, while providing additional insight into the allopolyploid origin of E. edwardsii.

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Phylogenomics

Topic: Poster

Title: Characterizing conflict and congruence of molecular evolution across organellar genome sequences for phylogenetics in land plants

Author: ***eric bretz @ University of Illinois Chicago***

Keywords: Chloroplast genome,phylogenetics,phylogenomics,plastome,mitochondrial genome,combinability,phylogenetic conflict

Abstract:

SourceURL:file://Document1

Chloroplasts and mitochondria each contain their own genomes, which have historically been and continue to be important sources of information for inferring the phylogenetic relationships among land plants. The organelles are predominantly inherited from the same parent, and therefore should exhibit phylogenetic concordance. In this study, we examine the mitochondrion and chloroplast genomes of 226 land plants to infer the degree of similarity between the organelles' evolutionary histories. Our results show largely concordant topologies are inferred between the organelles, aside from four well-supported conflicting relationships that warrant further investigation. Despite broad patterns of topological concordance, our findings suggest that the chloroplast and mitochondrial genomes evolved with significant differences in molecular evolution. The differences result in the genes from the chloroplast and the mitochondrion preferentially clustering with other genes from their respective organelles by a program that automates selection of evolutionary model partitions for sequence alignments. Further investigation showed that changes in compositional heterogeneity are not always uniform across divergences in the land plant tree of life. These results indicate that although the chloroplast and mitochondrial genomes have coexisted for over 1 billion years, phylogenetically, they are still evolving sufficiently independently to warrant separate models of evolution. As genome sequencing becomes more accessible, research into these organelles' evolution will continue revealing insight into the ancient cellular events that shaped not only their history, but the history of plants as a whole.

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Biodiversity Informatics & Herbarium Digitization

Topic: Poster

Title: Come make your labels! Downloadable resources for botanical collectors and collections

Author: ***Paul Sokoloff @ Canadian Museum of Nature***

Keywords: Collections,Collections management,herbaria

Abstract:

Far from the old ways of scrawled annotations and typewritten collection data, herbaria and collectors now almost exclusively create specimen data and annotation labels with the aid of spreadsheets or computerized databases. Despite this, many collectors and collections lack a straightforward tool to generate herbarium labels, especially those at the start of their botany journey or working outside botanical institutions. Creating and formatting herbarium labels from scratch can present a daunting challenge to such collectors or impose unnecessary time costs on them or on herbarium teams that receive unlabeled specimens. In the herbarium, of course, costs of illegible or under-informative labels are borne by collection staff and users repeatedly, over time!

Here we present downloadable utilities based on the free Microsoft Access Runtime that empower users to create quality collection data labels and annotation labels for botanical specimens.

Herbarium label generator: Informative, complete labels make specimens much more valuable. For donating specimens to a herbarium or building a collection at home, this tool guides users in capturing collection data and publishing formatted labels that can be forwarded to herbarium staff, or printed, trimmed and added to specimens.

Annotation label generator: This utility helps botanists and herbarium staff to create any quantity of clearly legible annotations to confirm or update identifications, or to document taxonomic changes. References and synonyms can be captured, along with the standard identification, identifier, affiliation, and date.

These free utilities are available in both English and French from the Canadian Museum of Nature at https://nature.ca/en/our-science/collections/botany-collections/

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Comparative Genomics/Transcriptomics

Topic: Poster

Title: Prospects for obtaining RNA broadly across the plant tree of life

Author: ***Alexa Tyszka @ University of Illinois at Chicago***

Keywords: herbariomics,phylogenomics,phylotranscriptomics,RNAseq,RNA-Seq,Transriptome

Abstract:

Typically, the gold standard of tissue collection for DNA or RNA sequencing is fresh tissue, but immediate tissue processing is not always feasible, especially when sampling non-model plants under field conditions. The Smithsonian Institution recommends that botanical genetic samples be preserved in silica gel for DNA analysis and in liquid nitrogen for RNA analysis. In both cases storing at -80 °C is recommended for long term storage. Liquid nitrogen and their transportation Dewars can be difficult to obtain in remote locations and even harder to transport and use in the field, and -80 °C storage will not be available in all circumstances. Areas with high plant diversity are often remote or extreme locations where liquid nitrogen may not be available. Alternate methods for RNA preservation, such as RNAlater(R) and freeze-drying have been proposed to combat such logistical issues. However, both alternate methods eventually require some level of cold storage. Given the fragility of non-prepared RNA under room temperature conditions, the investigation of ancient RNA may seem futile, yet dozens of examples exist of ancient RNA recovery. Especially promising are studies investigating the germination of ancient seeds – the germination process necessitates functional RNA . Recent sampling has also recovered RNA viruses in herbarium-dried plant tissues up to 90 years between initial collection and sequencing. Thus far, one study has harnessed the potential of silica-dried RNA samples for phylotranscriptomics, and many others are sure to come. There is great potential for expanding such techniques due to the ample herbarium resources available. A thorough investigation of sampling and sequencing techniques will guide the field towards expanded sampling of underserved and remote areas for the benefit of marginalized communities and undersampled plant communities.

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Phylogenomics

Topic: Poster

Title: Defining the morphological differences of ecotypes of Sida fallax

Author: ***Josephine Collier @ San Francsicso State University***

Keywords: morphology,Hawaii,Ecotype,Sida fallax

Abstract:

Sida fallax is a native Hawaiian species of plant that grows on many of the Hawaiian islands in both coastal and inland ecosystems. Since this plant grows in two very different ecosystems, the characteristics of the plant differ greatly. Coastally, Sida fallax grows prostrate, or flat and spread out, and has small and dense (succulent-like) leaves with rounded teeth. Inland, Sida fallax grows more erect and has large thin leaves with serrate, or sharp, teeth. The two ecotypes of this plant are very different morphologically, and yet are classified as the same species. We are also aware that hybrids of these two ecotypes are possible but do not tend to appear naturally in the field. It is important to distinguish how morphologically different these two ecotypes are, establish the morphology of a hybrid, and establish species/ecotype identifying methods. This work establishes the morphological differences in the leaves of the two ecotypes, how their reproductive morphology differs, and what method of identifying morphological differences is most comprehensive and descriptive in this species of plant. This work is helpful in order to determine conservation methods and gather a greater understanding of evolution with a unique lens, since Hawaii is a relatively young archipelago.

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Comparative Genomics/Transcriptomics

Topic: Poster

Title: Paando - A de novo transcriptome assembly tool for non-programmers

Author: ***Miles Woodcock-Girard @ University of Illinois at Chicago***

Keywords:

Abstract:

Transcriptome data is a cost-effective approach to obtaining the coding regions of the genome Recent advances in sequencing technologies have led to a rapid expansion in newly acquired and publicly available transcriptome data. At the same time, advances in bioinformatics have led to computationally efficient approaches to cleaning and assembling transcriptome data. However, de novo assembly methods often require some fluency in programming if labs wish to perform them in-house. Here we present PAAnDO (Pipeline for the Assembly and Analysis of De Novo Transcriptomes), a user-friendly package enabling the streamlined assembly and differential gene expression analysis of de novo transcriptomes from short-read RNA sequence data for non-model organisms. Requiring no programming knowledge, PAAnDO utilizes the newest bioinformatic approaches to maximize the efficiency and accessibility of de novo transcriptome assembly for non-programmers.

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Systematics

Topic: Poster

Title: Re-examining the classification of the Pitcairnia (Bromeliaceae) species complex from the Dominican Republic

Author: ***Natalia Ruiz-Vargas @ University of Illinois at Chicago***

Keywords:

Abstract:

There are six potential species, five of them formally recognized, for Pitcairnia in Ayiti (Hispaniola). With transcriptome data obtained from silica dried samples we analyzed their relationships, which don't support the current classification. PCA, Construct, and FEEMS analysis all support the treatment of this group as one species. However, increased sampling which includes individuals from Haiti is needed to corroborate the results.

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Ecology

Topic: Poster

Title: Ecological Separation in an Ongoing Speciation Event

Author: ***Sam Ingram @ Utah Valley University***

Keywords: morphology,Asteraceae,Evolution,flowering phenology,gene flow,Phenotypic variation,Pollinators,speciation

Abstract:

Sympatric speciation is not commonly recognized as one of the more important modes of speciation. This may be due to the slow rate of evolution in this mode as well as its often cryptic nature. Pollinators and small micro-ecological differences are likely important drivers of sympatric evolution. Importantly in plants, pollinators can have a significant impact on breeding between different individuals even when they are growing close together. This discrimination o pollinators is driven by a variety of morphological traits in a plant, thereby possibly leading specific pollinators to have a strong plant preference. In addition small ecological differences related to phenological cycles may create a feedback loop further altering pollinator preference.

In Western North America, Ericameria nauseosa (Asteraceae) is a common shrub with over 20 named varieties that co-exist and may exchange genes. Despite their interbreeding, these varieties often appear as, seemingly, stable evolutionary units. In this study we ask: 1) Do pollinators discriminate between varieties of E. nauseosa? 2) What maintains the differences between E. nauseosa varieties when growing in sympatry?

We completed a series of experiments comparing different varieties for; viability of seeds, morphological floral measurements, identification of insect communities, and observational field trials with fluorescent pigment as a proxy for gene flow.

Green varieties had a 36% germination rate compared with the gray varieties that had a 12% germination rate. The gray varieties g erminated 1.7 times faster than the green. There were differences in floral morphological measurements of the corolla and anther lengths with the gray variety having 1.3 times the length of the green. Pollinator communities also differed with the green varieties having more species in the Hymenoptera and Diptera orders with species in the Lepidoptera and Hemiptera orders dominating the gray varieties. Lastly, pollen flow among all sites typically were between green varieties to gray as well as green varieties to green and gray varieties to gray, but not from gray varieties to green.

Preliminary data suggests that due to floral morphological differences, these varieties of E. nauseosa have different pollinator communities. These pollination traits are likely further enhanced by variation in seed germination that contribute to different phenology. Thereby, providing evidence of pollinator impact on speciation events through gene flow. This study provides an understanding of the ongoing diversification events in E. nauseosa.

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Symbioses: Plant, Animal, and Microbe Interactions

Topic: Poster

Title: The Role of Plant-Soil Feedbacks in Structuring the Microbiome of Native Legumes

Author: ***Cian Dotson @ Loyola University Chicago***

Keywords: Fabaceae,legume-rhizobia symbiosis,Microbiome,plant-microbe interactions,plant-soil interactions

Abstract:

Legumes are heavily dependent upon the activities of microorganisms such as bacteria, archaea, and fungi to overcome ecological stressors. Immediate soil environments hold a cornucopia of microorganisms for legumes to select for plant microbiome colonization (Brown, Grillo et al. 2020). The composition of the soil microbiome is dependent upon a series of plant-soil feedbacks between legumes and soil microbial in which specific microbial taxa within the soil are enhanced through excretion of a series of photosynthetically-derived exudates through legume roots. From these enriched communities, plants can select and acquire microbes that mediate plant functional traits such as nutrient acquisition, abiotic stress tolerance, and pathogen and parasite resistance (reviewed in Friesen et al. 2012; Gutierrez & Grillo 2022). The enrichment of rhizobial bacteria has consistently been a taxa of interest within legume-soil feedback systems due to their ability to infect nodules, a distinct plant compartment in which rhizobia can fixate nitrogen into usable forms for legume growth and development. However, the impact of plant-soil feedback on the structure of larger soil microbiomes is largely unknown. To elucidate further the relationship of rhizodeposition and the structure of soil microbial communities seven different legume species will be grown in rhizosphere soils collected from the Chicago region, soils collected ~100 yards from rhizosphere soil collections, and a common garden soil to represent soil communities at vary levels of enrichment prior to planting. 16S amplicon sequencing will be used to characterize the soil communities at varying stages before and after enrichment.

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Population Genetics/Genomics

Topic: Poster

Title: Simulating Impacts of Novel Transcription Factor Recruitment on Enzymatic Diversification

Author: ***Gabriel Jones @ University of California, Davis***

Keywords: biosynthesis,fitness,population genetics,simulation,specialized metabolism,transcription factor binding motif,mutation,enzyme

Abstract:

Mutations in coding regions of enzymes necessary for organismal functioning generally have negative impacts. However, little is known about how mutations in transcription factor binding motifs (TFBMs) can modify the impact of mutations in coding regions of enzymes. This study uses population genetic simulation to assess the correlative fitness impacts between accruing mutations within TFBMs and coding regions of an enzyme. We find that, generally, increases in expression through the recruitment of novel TFs can compensate for accruing mutations that confer negative impacts on fitness within an enzyme's coding regions. Further, we find the optimal quantity of fixed mutations within TFBMs fluctuates in response to the quantity and types of mutations within coding regions. This optimum has a direct relationship with the number of mutations that confer negative fitness impacts in coding regions and an indirect relationship with the number of mutations that confer positive fitness. Our study provides a novel and translatable method of simulating the effects of TFBMs on potential enzyme diversification.

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Floristics & Taxonomy

Topic: Poster

Title: Translating herbarium labels

Author: ***Mary Barkworth @ Utah State University***

Keywords: digitization,herbarium specimens

Abstract:

In many parts of the world, the default language for herbarium labels is not English and the alphabet used in not the Latin alphabet. Interpreting such labels is difficult, if not impossible, for many English speakers. The problem is not confined to English speakers. Many taxonomists have difficulty interpreting labels written in a language other than their own and the one they use in their professional activities. Today's technology makes the task simple. One does not even have to know the original language. The procedure is as follows.

Copy high resolution JPG images to Google Docs. The text captured will appear below the screen. Copy it.
Open ChatGPT. Type "Translate." into the box followed by the copied text and then press "Enter". The translation will appear soon appear.

For translations into other than your default language, state "Translate to language." Rather than just "Translate."

We have found the process effective in producing translating typewritten labels from Russian, Chinese, Korean, and Persian into English and vice versa. The quality of the translation is, of course, dependent on the clarity of the text. Handwriting is a challenge to ChatGPT, just as it is to humans but irregularities in the background seem to be more of a challenge to ChatGPT than humans, at least at present. With practice, one can complete data capture for about 20 labels per hour. Integrating the process into herbarium data management software will probably increase this rate. For unidentified duplicates from China, the translation may enable location of identified specimens in the Chinese Virtual Herbarium.

We shall demonstrate the process at the meeting. The poster will also provide a link to a YouTube video about it.

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Systematics

Topic: Poster

Title: Exploring the secondary head trait in Asteraceae

Author: ***Serena Blais @ The University of Memphis***

Keywords: Asteraceae,secondary head,dyssodia

Abstract:

Since Darwin's "On the Origin of Species", evolutionary biologists have continued to marvel at the "endless forms most beautiful and most wonderful" that organisms express, yet we are only beginning to understand how this enormous diversity arises at the mechanistic level. Angiosperms are the most diverse group within the plant kingdom, representing nearly 300,000 species worldwide and thriving in most environments, forming complex relationships with many biotic (e.g., pollinator syndromes, mycorrhizal symbiosis) and abiotic factors (e.g., soil specializations, adaptability to different precipitation levels), which leads to great variety in both form and function. The Asteraceae family is the most speciose of all angiosperms and exemplifies diversity of form and function, adapting to almost every biome on the planet, comprised of over 30,000 species and 1,900 genera, or roughly 10% of all species of angiosperms. The Asteraceae inflorescence, a capitulum, is thought to be a major driver of diversification in the family. The capitulum is a composite structure which comprises multiple flowers often mimicking the structure and shape of a single flower. Some members of the family arrange multiple heads together into a higher order functional unit, a secondary head, also known as capitulescence or syncephalium, that in many cases also resembles a single flower. In this presentation I will give an overview of the prevalence of secondary heads across the Asteraceae family and will also review the leading hypothesis on how secondary heads have arisen. The two hypotheses outlining the genetic underpinnings of the evolution of the secondary head are 1) secondary heads arose from a single determinate meristem which subdivided into a multiflowered head, or alternatively, 2) secondary heads arose from cymose units which normal capitula have lost over their evolutionary history. Whichever may be the case, secondary heads have been hypothesized to affect pollinator preference and play a role in species and habitat diversification. Secondary heads occur within 70 genera of Asteraceae, most of which are of the New World. One such genus, Dyssodia, is a small clade of only four species possessing both normal capitula, as well as one species that produces secondary heads and for these reasons I will use this system as a model to investigate the genetic underpinnings of secondary head evolution.

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Ethnobotany

Topic: Poster

Title: Ethnobotany and tropane alkaloid variation: A meta-analysis of chemical variation in the genus Datura.

Author: ***Lia Rabellino @ Utah Valley University***

Keywords: ethnobotany,Medicinal Plants,Datura,Atropine,Scopolamine,entheogenic

Abstract:

Datura (Solanaceae) is an iconic genus of plants found throughout the world. It is primarily known for its beautiful flowers, but is also well documented as an entheogenic plant across numerous cultures, historically and contemporarily. Within many of these cultures, use of Datura is reportedly taboo, restricted to specific occasions, and handling/preparation is typically limited to certain adept individuals. Customary applications associated with Datura include rites of passage, recreation, and herbal remedies resulting from the psychotropic and medicinal properties of the plant. Datura's entheogenic properties can be attributed to biologically active tropane alkaloids, likely anti-herbivore compounds, that can be dangerous or deadly to humans in large doses. In this study, we hypothesize that the observed restricted use is the result of a genetically based unpredictability of two tropane alkaloids: atropine and scopolamine (hyoscine). We completed a comprehensive meta-analysis of reported concentrations of atropine and scopolamine across the genus Datura. Our primary search utilized the Web of Science database and produced 89 papers, 18 of which we were able to extract data from. Our secondary search involved pulling sources from the original literature and completing detailed web searches for reported chemical concentrations of specific species. The combined searches resulted in a total database of 24 studies covering concentrations of tropane alkaloids from 13 Datura species. In addition to recording the variation of alkaloid concentrations, we searched ethnobotanical records and documented if a species of Datura was used widely or if use was restricted to a certain group of individuals within a culture. We observed that many cultures with restricted societal uses of Datura appeared to use species that have a higher variability of alkaloid concentrations. These cultural limitations may be an important measure that developed as a way to communicate the safe and responsible use of these entheogenic compounds.

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Population Genetics/Genomics

Topic: Poster

Title: Between Two Dunes: Investigating the demographic history of Penstemon haydenii

Author: ***Erin Bentley @ University of Wyoming***

Keywords: GBS,Phylogeography,Plantaginaceae,delimtR

Abstract:

Penstemon haydenii (blowout penstemon) is a federally listed endangered species, endemic to sand dune blowouts of the Ferris Dunes of Wyoming and the Sandhills region of Nebraska. These two populations are separated by 175 miles. Given the disjunct nature, the recent discovery of the Wyoming populations of this narrow endemic, and reported morphological differences between Nebraska and Wyoming populations, we investigated the phylogeographic history of the species using demographic modeling, species delimitation, and species distribution modelling approaches.

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Conservation Biology

Topic: Poster

Title: “Micropropagation of Lepidium papilliferum (slickspot peppergrass).”

Author: ***Anne (Jenny) Knerr @ University of Idaho***

Keywords: _{conservation biology},Micropropagation,Slickspot peppergrass,Lepidium papilliferum

Abstract:

Lepidium papilliferum (slickspot peppergrass) is one of Idaho’s federally threatened plant species. Slickspot peppergrass is believed to grow only in southwest Idaho, often in distinct microsites characterized by high sodium soils referred to as “slick spots”. Mechanical damage, invasive weeds, wildfire, and seed herbivory are the primary threats to this species. Creating additional populations in uncolonized slick spots maybe key to this species’ recovery. Slickspot peppergrass reproduces by seed but only a small portion of the persistent seed bank will germinate each year and insect seed predation can be prevalent. Micropropagation and subsequent out-planting may be an alternative method to seed introduction for establishing new populations. This study evaluated the feasibility of axillary shoot production of slickspot peppergrass. Seeds were surface sterilized and transferred to germination media. Stabilization in culture was completed on Murashige and Skoog (MS) medium with 0.5 µM indole-3-butyric acid and 1.1 µM 6-benzyaminopurine. Axillary shoot proliferation, in vitro rooting, and greenhouse acclimatization were completed. Interestingly, both annual and biennial growth forms arose in tissue culture. Micropropagation has been shown to be a feasible and potentially superior method to broadcast seeding for the conservation and restoration of slickspot peppergrass.

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Bryology and Lichenology

Topic: Poster

Title: One probe to unmask them all

Author: ***Raul Diaz San Roman @ Universidad Autónoma de Madrid***

Keywords: Hyb-Seq,Orthotrichaceae,Lewinskyinae,specific probe

Abstract:

Orthotrichaceae Arn. is the second most speciose family among mosses, with an estimated of ca. 900 described taxa. This family is further divided into two subfamilies, Orthotrichoideae Broth. and Macromitrioideae Broth., which exhibit distinct morphological, biogeographic and ecological traits. Orthotrichoideae is better known from both phylogenetic and species diversity points of view. During the last two decades, the taxonomic complexity of the traditional major genera has been unraveled, although the diversity could still be gratly underestimated.

The use of genomics data has proven to be a powerful tool in the field of systematics and evolutionary biology. Next Generation Sequencing (NGS) can generate vast amount of data, resulting in increased genealogical resolution compared to the traditional Sanger approach. Among the newest and most promising NGS methodologies is Hyb-Seq, a mixed method that combines aleatory sequencing through genome skimming, with target capture sequencing. This approach has been succesfully enployed to efficiently produce genome-sclae data sets for plants phylogenomics that can help to resolve the relationships among closely related species and to determine species boundaries. This is especially valuable for studying groups with few, and often homoplasious, morphological characters, such is the case of Orthotrichaceae, in which systematic and taxonomic delimitations, have been traditionally difficult and contentious.

Recently, a target enrichment probe specific to flagellate land plants was developed in the GoFlag project frame. The GoFlag408 enrichment kit, designed to capture up to 408 exons from 229 nuclear genes, has proved to be useful in resolving the phylogeny of Orthotrichoideae, since the resolution obtained is increased when compared to previous phylogenetic reconstructions, based on Sanger sequencing. However, incongruent signals anc resolution problems were detected within the tribe Lewinskyinae that make difficult the resolution of its infrageneric systematic. To solve this problem, we intend to develop a specific probe for the family Orthotrichaceae.

With the use of a new specific kit, we aim to achieve a complete and robust phylogenetic reconstruction of Orthotrichoideae and to establish solid bases and conclusions related with its taxonomic, evolution and biogeography. In addition, it is expected to unravel cryptic species and contribute to the resolution of species complexes, and thus, unmasking the possibly hidden diversity of this group of mosses.

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Ecophysiology

Topic: Poster

Title: A new high-throughput relative electrolyte leakage (HTREL) system for assessing plant cold tolerance

Author: ***John Butnor @ USDA Forest Service, Northern Research Station***

Keywords: freezing tolerance,Phenotyping,relative electrolyte leakage,cold tolerance

Abstract:

Plants differ in their ability to withstand freezing temperatures, even within a given species. Knowledge of cold tolerance allows for deployment of planting stock in appropriate climates. This is especially important for breeding programs for disease resistance and crop improvement where progenitors may be adapted to different climates, as well as selecting populations for assisted migration. Relative electrolyte leakage (REL) has been used for decades to provide a laboratory assessment of the degree of injury caused by exposure to freezing temperatures. Replicates of tissue are exposed to increasingly cold temperatures in a test chamber and sequentially removed at specific minimum temperatures. When cells freeze and rupture, electrolytes are released and are detectable in solution with a conductivity meter. Electrolyte leakage at specific minimum temperatures is relativized to maximum leakage from total cell lyses caused by freezing in liquid nitrogen, boiling, autoclaving or heating to dryness. The temperature where 50% leakage has occurred (Tm50) and cellular repair is unlikely is frequently used to quantify REL results and compare cold tolerance between groups. Currently here are few commercially available options for rapid measures of electrical conductivity in liquid samples.

I developed a high throughput relative electrolyte (HTREL) system to multiplex sequential measurements of electrical conductivity of plant tissue samples in solution via a bridge circuit. The conductivity bridge measures 96 electrode pairs in a few seconds compared to over an hour for manual measurements with handheld conductivity meter. The high throughput nature of this equipment is essential to making the thousands of observations necessary to build robust relative electrolyte leakage curves. The conductivity bridge was designed to be used with large volume, disposable well plates (3.5 ml per well) and constructed at the University of Vermont Instrument Manufacturing Facility in Burlington Vermont. A Campbell Scientific Inc. (Logan, Utah) data logger connected to several multiplexers sequentially moves through the 96 electrode pairs and measures electrical conductivity in a few seconds and records the results. Complementary to the hardware developments are R based programs to calibrate the electrodes to standard solutions and create the temperature response curves . The hardware design and R code will be published with an open source license and made freely available to enable wider adoption of the REL technique and advance research into climate suitability of plant populations.

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Functional Genetics/Genomics

Topic: Poster

Title: Evaluating Regulatory Module Function within the Mitochondrial Pyruvate Dehydrogenase Complex

Author: ***Caroline Keller @ UC Davis***

Keywords: CRISPR/Cas9,Gene editing,gene expression,Gene regulatory network,genetic mechanisms

Abstract:

Regulatory networks coordinating changes in metabolism are central to how a plant adapts to biotic and abiotic stress. Critical to these coordinated changes are transcriptional shifts programmed by cis-regulatory elements bound by transcription factors. I am testing the role shared cis-regulatory elements play in controlling the co-regulation of all the genes for a single enzyme complex. These cis-regulatory elements control gene expression when they are bound by transcription factors. Because the cis-regulatory elements are shared across the genes in the complex, their coordinated regulation by a transcription factor creates a regulatory module, but it is unclear if all the genes need to be coordinated for maximal module function. For example, if one gene in the complex loses a cis-regulatory element, it may not alter complex function as residual expression from other modules and protein stoichiometry can be sufficient to compensate.To understand how modular membership shapes enzymatic function, I am using CRISPR/Cas9 to abolish mutual cis-regulatory elements within the promoters of genes required for the Pyruvate Dehydrogenase enzyme complex. This complex is composed of three apoenzymes and is an important intermediary between glycolysis and the TCA cycle. This will be tested by transforming Arabidopsis thaliana with different combinations of these cis-element mutations. Plants will be phenotyped with detached leaf assays, metabolomics, and transcriptomics. This study of modular organization will provide data to predict genotype-to-phenotype relationships for regulatory interactions, biotechnology, and crop improvement in California.

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Systematics

Topic: Poster

Title: Morphological Variation and Dioecy in Mesoamerican Solanum sect. Anarrhichomenum

Author: ***Jacob Bryant @ University of Cincinnati***

Keywords: morphology,Solanum,Dioecy,Solanaceae,systematics

Abstract:

Solanum sect. Anarrhichomenum is a subclade of viny, non-tuber bearing, node-rooting plants of the potato clade, consisting of both South and Central American species groups. Within the potato clade, most systematic attention has been focused on relatives of the cultivated potato and tomato, while other more inconspicuous groups, like Solanum sect. Anarrhichomenum, remain particularly understudied. This study presents part of an ongoing effort to revise the Mesoamerican species of Solanum sect. Anarrhichomenum by determining species-limits from morphometric, palynologyical, and molecular data. Morphometric analyses were conducted on a sample of 73 variables measured from 175 herbarium specimens representing all known species of Mesoamerican Solanum sect. Anarrhichomenum (S. appendiculatum, S. skutchii, S. subvelutinum, S. tacanense, S. ionidium and the new species currently in manuscript, S. tavinuuyuku). These data were then explored using FAMD and multivariate statistical analyses, which revealed a series of taxonomically informative morphological characters separating species and aided in the initial discovery of S. tavinuuyuku, the first new species to be added to Mesoamerican Solanum sect. Anarrhichomenum in over 70 years. To better understand the reproductive biology of the members of this group, morphological investigations were followed up by examination of pollen grains. Flowers of S. appendiculatum the only known dioecious species in the potato clade, are hermaphroditic but distylous, as are all members of the S. appendiculatum species group. Previous work found that pollen produced by anthers of long-styled plants of S. appendiculatum were inaperturate and non-functional. Similarly, we looked at pollen grains from long and short-styled flowers in other members of the S. appendiculatum species group, using phase contrast microscopy, to determine whether dioecy exists throughout the group. Inaperturate and tricolporate pollen were discovered in long-styled and short-styled flowers, respectively, of all species in this study and suggests that all Mesoamerican members of Solanum sect. Anarrhichomenum are dioecious.

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Paleobotany

Topic: Poster

Title: A Fossil Perspective on Cenozoic Genome Size Evolution in Ginkgo

Author: ***Bryton Smith @ Wesleyan University***

Keywords: Cenozoic,genome size,Gymnosperms,molecular evolution,transposable elements,Leaf cuticle,Ginkgo,cell size

Abstract:

The fossil record complements molecular data and provides invaluable opportunities to calibrate molecular methods. The Ginkgo fossil record with its cuticles preserving cellular features provides an excellent chance to test the botany community’s understanding of neutral molecular evolution in gymnosperms. Liu et al. (2021) found that Long Terminal Repeat retrotransposons (LTR-RTs) are prevalent in Ginkgo’s repetitive DNA sequences. To estimate insertion times, they utilized the intergenic nucleotide substitution rate for Picea abies published in Nystedt et al. (2013). Liu et al. (2021) arrived at an estimate of 12-8 Ma for a time of LTR-RT proliferation in the Ginkgo genome. The fossil record is relevant to investigating such genomic topics in virtue of the strong genome size (GS)-cell size positive correlation. To investigate GS evolution in Ginkgo, we are measuring epidermal cell areas and stomatal pore lengths on cuticles spanning from the Latest Cretaceous to the present day. Our first goal is to determine whether cell size in Ginkgo has increased over the course of the Cenozoic. If cell size did increase, our next objective is to assess how the timing of the cell enlargement relates to the timeline of GS evolution and the rate of neutral molecular evolution in Ginkgo. We will also use the past cell sizes to make estimates of GS in gigabase pairs in deep time. Ultimately, we hope to evaluate whether botanists can confidently apply the substitution rate in neutral P. abies genome regions to understand the evolutionary history of other gymnosperms such as Ginkgo or whether more work is needed to refine substitution rates for specific gymnosperm taxa.

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Paleobotany

Topic: Poster

Title: Insights into Climate Reconstruction From Palm Leaf Traits

Author: ***Michael Machesky @ University of Michigan***

Keywords: paleobotany,Paleoclimate,stable isotopes,Stomata,VLA,carbon isotope,Arecaceae

Abstract:

In order to mitigate the impacts of anthropogenic climate change on extant organisms and modern ecosystems, it is important to understand how life responded to past changes in climate. Plants are of specific interest to global change scientists, as their leaves interact directly with the atmosphere via photosynthesis and transpiration. Certain traits of plants are sensitive to environmental, climatic, and ecological factors and thus create a record of the plant's local environment through its leaf morphology and chemistry. Presently, the majority of paleoclimate reconstruction using plant fossils has been applied at mid to high-latitudes, leaving a gap in the tropics and sub-tropics for paleoclimate reconstruction analyses. Arecaceae (palms) are particularly promising for low-latitude paleoclimate study because of their worldwide low-latitude distribution and persistence in extreme climatic conditions, their commercial and agricultural importance, and their extensive fossil record dating from the Late Cretaceous through the entirety of the Cenozoic. This study investigates how palm leaf traits record climate changes both geographically (across ~7.5° latitude gradient and ~12° longitude gradient) and temporally (1864-present) with implications for tracing (sub)tropical paleoclimatic conditions. Models combining leaf traits such as stomatal density and size with leaf carbon isotope discrimination (Δleaf) yield reliable pCO2 estimates, but could potentially be further constrained with vein density, measured as vein length per area (VLA), by refining mesophyll conductance estimates. We measured each of these traits on leaves from the palm species Sabal palmetto (n=184), Caryota urens (n=32), and Phoenix dactylifera (n=25) collected both from living plants across the Southeastern United States (n=149) and from worldwide historical collections housed in herbaria dating back as far as 1864 (n=92). Climate data were compiled for each collection location and analyzed for their relationship to individual leaf traits from PRISM Climate Group and WorldClim2; these climate variables included mean annual temperature (MAT), mean annual precipitation (MAP), and vapor pressure deficit. While the average Δleaf of each species fell within the expected range of C3 plants (~18.00–22.00‰), S palmetto and C. urens showed much greater ranges in Δleaf values with maxima above the expected range (17.49–25.98‰ and 18.02–28.07‰, respectively) and showed higher discrimination overall than P. dactylifera (17.44–21.95‰). This difference suggests that P. dactylifera and its fossil relative Phoenicites is the best candidate for paleoclimatic reconstruction, as its isotopic behavior is most similar to that of plants currently applied to existing models.

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Paleobotany

Topic: Poster

Title: Leaf shape as a climate proxy: do incomplete leaves retain a strong signal?

Author: ***Dana Royer @ Wesleyan University***

Keywords: morphology,climate,paleobotany,leaf physiognomy,taphonomy

Abstract:

For over a century, leaf shape in woody non-monocotyledonous species has been used to reconstruct aspects of climate related to temperature and precipitation. These methods are typically calibrated with complete leaves from living forests. An understudied issue is how appropriate these calibrations are to incomplete leaf compression fossils that dominate most fossil leaf assemblages. We sought to test the fidelity of the leaf-climate signal with analogous modern leaves, excavated from within the sediment layer at two temperate research forests, Harvard Forest and the Smithsonian Environmental Research Center. At both locations, we targeted leaves that underwent transport and deposition in environments that commonly contain fossil leaves in the geologic record: swamp and river margins. In this regard, these incomplete leaves represent a natural experiment of leaf taphonomy that is a good partial analog for leaf fossilization. We are measuring a suite of size and shape variables that are used in the multivariate leaf-climate method called digital leaf physiognomy. These variables are mostly related to tooth size, tooth abundance, and leaf dissection. We will then compare the distributions of these shape variables to complete fresh leaves of the same species sampled from the same sites. We anticipate that our results will provide a more robust framework for interpreting paleoclimate from leaf shape.

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Bryology and Lichenology

Topic: Poster

Title: Geography, climate and habitat shape the microbiome of the endangered rock gnome lichen (Cetradonia linearis)

Author: ***Julianna Paulsen @ Eastern Washington University***

Keywords:

Abstract:

Bacterial symbionts are essential components of healthy biological systems and are increasingly identified as essential factors in the study and management of threatened species and ecosystems. Despite management shifts at the ecosystem level, microbial communities are often excluded from discussions of holobiont conservation in favor of the primary members of a symbiosis. In this study we sought to fill the bacterial community knowledge gap for one of two federally endangered lichen species in the United States, Cetradonia linearis. We collected 28 samples of the endangered rock gnome lichen (Cetradonia linearis) from 15 sites to investigate the factors influencing microbiome composition and diversity within the thallus. DNA was extracted using a Powersoil Extraction kit and sequenced using 16S rRNA barcoding. Sequence processing and analyses of diversity were conducted in QIIME2. Core bacterial constituents of the microbiome were determined and visualized using the R package microbiomeutilities. Proteobacteria (37.8 % ± 10.3) and Acidobacteria (25.9% ± 6.0) were the most abundant phyla recovered. Habitat, climate and geography were all found to have significant influences on the bacterial community. A BLAST search of the nucleotide sequences of core members at a 90% threshold revealed shared amplicon sequence variants in the microbiomes of other lichens in the family Cladoniaceae. We concluded that the bacterial microbiome of Cetradonia linearis is influenced by environmental factors and that some bacterial taxa may be core to this group. Further exploration into the microbiomes of rare lichen species are needed to understand the importance of bacterial symbionts to lichen diversity and distribution.

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Phylogenomics

Topic: Poster

Title: Phylogenetic reconstruction of Genisteae (Fabaceae): a look at quinolizidine alkaloid distribution

Author: ***Sarah Hunter @ The University of Texas at Austin***

Keywords: chemical defense,Fabaceae,phylogenetics,Phylogenetic Distribution,Genisteae,Quinolizidine Alkaloids

Abstract:

Phylogenetic reconstruction of Genisteae (Fabaceae): a look at quinolizidine alkaloid distribution

Authors: Sarah Hunter, Brian Sedio, Domingos Cardoso, Tracey A. Ruhlman and Robert K. Jansen

Abstract:

Quinolizidine alkaloids, or QAs, are naturally occurring chemical compounds unique to certain groups of plants, including the legume tribe Genisteae. This tribe contains several kinds of Lupinus grains, which grow readily in nutrient poor soils in a diverse range of climates, serving as an interesting potential economic crop. The QAs in many plants in Genisteae can act as a double-edged sword, with one edge providing a natural defense mechanism against pests, like aphids, which can hurt grain yield and spread plant diseases. On the other edge, QA concentration in grain tissue must be kept below the regulated industry threshold, which can be a challenge. Since there have been surprisingly few attempts at constructing a complete phylogeny for Genisteae, many relationships among genera remain unresolved. This study aims to build a phylogeny on which to assess the distribution of QAs. Currently, 45 species representing 26 genera have been obtained. So far, tissue has been sampled and genomic data has been collected from 17 taxa representing 10 genera, with plastid, mitochondrial, nuclear, and chemical data for each. The plastomes have been assembled, and mitogenome assembly and low-copy nuclear gene retrieval is underway. The assembled plastomes have been found to be colinear with an average size of 125,738 base pairs. The smaller plastome size reflects that fact that Genisteae is a member of the inverted repeat lacking clade. Phylogenies will be constructed using markers from all three genomes (plastid, mitochondrial, and nuclear) and QAs will be plotted on the tree in order to examine their phylogenetic distribution. So far, a maximum likelihood tree of the plastomes has found Lupinus forming a clade, while Genista appears sister to Gonocytisus in a separate clade. Meanwhile, Dichilus and Melolobium have diverged at the base of Genisteae, and are sister to each other. These results agree with previous phylogenetic studies, and support the Lupinus clade and the Cytisus-Genista complex. Additionally, the Argyrolobium group, traditionally including Argyrolobium, Melolobium, and Dichilus, is at the base of Genisteae, in its predicted position. When the QAs are plotted, the Lupinus clade shows a pattern of sparteine and lupanine production, while the taxa from the Cytisus-Genista complex tends toward cytisine. These results represent a progress report and the data included are part of a larger project tha will include representative species from all genera of Genisteae and outgroups from other tribes in the genistoid clade.

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Ethnobotany

Topic: Poster

Title: Socio-Economic impacts of Threaten Rattan species (Arecaceae) and Conservation Approaches

Author: ***RONI SAHA @ Vidyasagar University, India***

Keywords: Diversity loss,IUCN conservation status,Rattan,Natural fiber,Chemical analysis,Chemical modifications,Optic fibers,SEM,XRD,XPS,NMR,TGA

Abstract:

Novel natural fibers in polymer-based composites will help to promote the invention of novel reinforcement and their possible applications. Rattan (Arecaceae) is an important forest product of India and South-East Asia because of the contribution of structural complexity, food, shelter, and medicine. Most species of rattans are IUCN-threatened species some are endangered and red-listed. The current research explores the durability, thermal, mechanical, and morphological properties of untreated and various chemically modified rattan fibers. The rattan fibers were extracted from the rattan stem in two different ways by natural way decay and by chemical extraction. The extracted fibers were then characterized by Fourier transform infrared (FTIR) spectroscopy, X-ray diffraction (XRD), Scanning electron microscopy (SEM), X-ray photoelectron spectroscopy(XPS), Tensile strength property, NMR, Water absorption property, Thermogravimetric analysis(TGA) and Chemical analysis (Cellulose, hemicellulose, lignin, and wax). The extracted rattan fibers by two different methods were gone through various chemical treatments like alkali (NaOH, KOH), Potassium permanganate treatment, Silane treatment, Sodium chloride treatment, benzoyl treatment, and acrylic acid. Then the treated fibers were examined through SEM, XRD, XPS, NMR, TGA, Tensile, water absorption, and Chemical analysis. After treatment with different modificant chemicals the fiber strength and durability were increased which will be used on an industrial basis. Mainly optic fibers are found in their bark and this fiber is used as a reinforcement of electrical wars. Destruction of their natural green forests and habitat has affected effect broad genetic base of rattan. This has a high economic value at the industrial level and due to extensive uses, it needed to be conserved. In this situation, various rattans are not available in the forests to meet the demands of the rattan industry. So it can be grown as a cultivated plant. In my research, I conserved the threatened rattan species by a new approach titled “Cultivation Cum Conservation of Palms”.

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Phycology

Topic: Poster

Title: Ecosystem disrupting harmful algal blooms of Prymnesium parvum consist of multiple cryptic species

Author: ***Nathan Watervoort @ Purdue University***

Keywords: Algae,comparative genomics,Cryptic Species,phylogenetics,phylogenomics

Abstract:

Prymnesium parvum is a unicellular, biflagellated alga in the lineage Haptophyta. P. parvum forms toxic blooms around the world, which are very disruptive to local ecosystems. In the United States, the first documented bloom of P. parvum occurred in the Pecos River of Texas in 1985. Since then, the frequency and intensity of P. parvum seasonal blooms have increase and spread from the American Southwest to freshwater systems as far north as Ohio River tributaries. Recently, P. parvum has been characterized as a cryptic species complex consisting of at least three member species. These member species are referred to as A-, B-, and C-types based on their unique chemotypes. Previously, all known strains of P. parvum from Texas were characterized as A-types. However, the genetic diversity of Texas P. parvum is not well understood outside of a handful of isolated strains. From Winter 2018 to Sumer 2020, we isolated an additional 35 P. parvum strains from eight separate bloom events in Central and Western Texas. The genomes of these newly isolated strains were sequenced using Illumina, and all strains were characterized in terms of their genome size, heterozygosity, and ploidy. We performed a comparative phylogenomic analysis that included a total of 56 P.parvum genomes from Texas and around the world. Our analysis uncovered the first known occurrence of B-type P.parvum in Texas. Moreover, we found that A-type and B-type species of P. parvum co-occur in Texas blooms. Texas A-type strains showed significant intraspecific genetic variation, with haploids, diploids, and hybrids strains identified. In contrast, all B-type strains were diploids and showed limited sequence level divergence. Overall, this analysis reveals significant genetic diversity within Texas blooms of P. parvum. Future work is needed to integrate these results with behavioral and metabolic differences between the two cryptic species and to determine the relative impact of both species to ongoing blooms in Texas.

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Population Genetics/Genomics

Topic: Poster

Title: **Whole Genome Sequencing and Inferred Roles of MADS-Box Genes in Sex Determination in Red Mulberry (Morus rubra)**

Author: ***Madhav Nepal @ South Dakota State University***

Keywords: endangered species,whole genome sequencing,Morus rubra,MADS-box gene family,Sex determination in mulberries,Subdioecious breeding system

Abstract:

Native Red Mulberry (Morus rubra) is found in riparian habitats in eastern North America stretching from the east coast to the eastern boundary of the Great Plains. Its range extends as far south as Florida and as far north as southern Ontario, Canada. Previous studies reported that M. rubra exhibits a subdioecious breeding system, with over 90% of trees being unisexual. While the flowers of M. rubra are consistently unisexual, some trees can have either unisexual or hermaphrodite catkins. Additionally, the monoecious plants of this species produce either staminate and pistillate catkins or mixed catkins on the same tree. The main objective of this research was to identify and characterize M. rubra genes involved in sex determination. Currently, whole genome sequencing and gene annotation works are in progress. In addition, for the RNA-seq analysis, sampling of tissues from the developing male and female flowers is underway. This poster presentation will showcase the findings of the whole genome sequencing, and identification of MADS-Box genes believed to play important role in sex expression and breeding system of M. rubra.

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Ecophysiology

Topic: Poster

Title: **How do the form and function of flowers and leaves differ among tropical Mountain ecosystem species?**

Author: ***Dario Paiva @ Florida International University***

Keywords: adaptive traits,Biodiversity,Campo rupestre,drought tolerance

Abstract:

Flowers are essential for reproduction for most flowering plants (angiosperms). By ensuring pollen production and ovule fertilization, flowers maximize outcrossing and enable fruit and seed production, thus directly impacting plant fitness. Despite the importance of flowers to plant function and evolution, remarkably little is known about how and when they become vulnerable to water stress in natural environments. This knowledge is especially urgent because increasingly frequent extreme drought events could threaten flower function and, by extension, reproduction. Remarkably few studies have measured the physiological tolerances of flowers, and their sample designs have almost completely ignored the ecological and environmental contexts in which flowers live. Here, I aimed to characterize morphological and physiological traits linked to flower and leaf water balance and construction costs. I measured flower and leaf mass per area (FMA and LMA, in g m-2), flower and leaf water content (%), petal and leaf thickness (mm), flower and leaf area (cm2), and residual transpiration (gmin, mmol m-2 s-1) for 34 species belonging to 16 plant families. The ranges of trait variability were in the same order of magnitude for both flowers and leaves, with flowers and leaves being of similar size (7.67 ± 7.02 cm2 and 8.05 ± 9.82 cm2, respectively). Flowers have greater water costs but lower dry mass costs than their conspecific leaves despite being thinner than leaves. This is shown by the higher proportion of water content in flowers and the lower values of flower mass per area compared to the leaf mass per area. The mean water content in flowers was 81.82% (SD = 5.01) while in leaves, it was 61.22% (SD = 5.01), and the mean thickness of flowers was 0.14 mm (SD = 0.19) while in leaves, it was 0.55 mm (SD = 0.40). As expected, the biomass per unit area was greater in leaves than in flowers, 170.48 (SD = 51.34) and 55.44 g m-2 (SD = 68.49), respectively. Thus, contrary to leaves that have multiple strategies to store water (e.g., low values of LMA and thickness or high values of LMA and thickness), flowers tend to exhibit just high values of water content that trades-off for low tissue quality (i.e., low biomass per area, FMA). This structural pattern should reduce the production costs of flowers and is predicted from their relatively short lifespan. Lastly, the gmin values were slightly greater in leaves (18.30 mmol m-2 s-1, SD = 13.68) than in flowers (14.51 mmol m-2 s-1, SD = 10.67), suggesting that flowers are better able to restrict water loss during droughts. This work reveals previously overlooked factors affecting plant distributions and their sensitivity to climate.

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Physiology

Topic: Poster

Title: **Growth of Platanthera dilatata Orchid Seeds with Different Nitrogen Sources**

Author: ***Sofia Baez @ Old Dominion University***

Keywords: in-vitro germination,Mycorrhizae,Orchids

Abstract:

Orchids use their relationships with mycorrhizae in the soil around them to facilitate germination in the wild. In the lab, the seeds can be germinated in petri plates using an agar-based medium supplemented with elements like carbohydrates, nitrogen, potassium, and phosphorus to replicate the nutrients they receive in the wild. In this experiment, the germination of seeds of a temperate terrestrial orchid, Platanthera dilatata was measured over time to evaluate the effect of different nitrogen sources on their growth. Varying nitrogen sources were tested because although most orchid species respond to environmental factors at the germination stage, few of these species have been studied in-depth to identify their specific responses to these factors. Two sources of nitrogen, sodium nitrate and ammonium nitrate, in two concentrations were added to BM-1 medium, and seeds were plated. Additionally, seeds sampled from four populations were tested to look for intraspecific variation in germination response. Early germination results throughout all populations indicate contamination from seed or airborne sources is a persistent problem with asymbiotic germination, but the plates with ammonium nitrate seem to have far less contamination than that of the plates with sodium nitrate. This work is important because it adds to our understanding of orchid seed germination and how species respond at different life stages to a constantly changing environment.

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Mycology & Phycology

Topic: Poster

Title: **Genome-wide association of growth in Botrytis cinerea**

Author: ***jaisy huang @ University of California, Davis***

Keywords:

Abstract:

During plant-pathogen interactions, pathogens can leverage a variety of virulence mechanisms to infect their host. However, energetic investment in these mechanisms may come at the expense of growth and proliferation. Furthermore, the impact of host immunity on a pathogen is influenced by the ability of the pathogen to detoxify defenses which scale with size. Two strategies of growth and virulence investment , may be inherently linked traits. Thus we leveraged an association mapping population of Botrytis Cinerea, a host-generalist necrotrophic pathogen that leverages a wide range of virulence mechanisms, to identify genomic regions associated with growth rate under high resources conditions using genome-wide association. This work establishes links between virulence mechanisms aimed at attacking the host with basic investment growth to potentially dilute the impacts of host immunity.

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Biodiversity Informatics & Herbarium Digitization

Topic: Poster

Title: Toward a 3D Printed Laboratory: Innovating the Future of Plant Science

Author: ***Mason McNair @ Michigan State University***

Keywords: 3d printed,Accessibility,Citizen Science,DNA extraction,open source,Phenotyping,wet lab

Abstract:

Low-cost, repairable lab equipment is rare within the biological sciences. By lowering the costs of entry using 3D printing and open-source hardware, our goal is to empower both amateur and professional scientists to conduct research. We have developed and remixed 3D printable lab equipment that can be inexpensively printed, assembled, and repaired for a fraction of the cost of retail equivalents. Here we present novel tools that utilize 3D printing to enable a wide range of scientific experiments. We include additional resources for scientists and labs that are interested in utilizing 3D printing for their research. By describing the broad potential that 3D printed designs can have in biological sciences, we hope to inspire others to implement and improve upon these designs, improving accessibility and enabling science for all.

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Ecology

Topic: Poster

Title: Investigating the Result of Fungal Pathogen Competition on Host-outcomes in Complex Disease Ecological Networks

Author: ***MINH TRAN @ UNIVERSITY OF CALIFORNIA, DAVIS***

Keywords:

Abstract:

Pests and pathogen threaten crop yield worldwide, leading to products and financial losses. While pesticides may mitigate yield loss, farmers and consumers are wary due to potential health hazards and negative environmental impact. Biological controls are an alternative to common pesticides using organisms to control negative plant-biotic interactions. The fungi Beauveria bassiana is common insect biological control agent, popularized due to insect host-generality. In addition, B. bassiana is observed to promote growth in their vector-plant. In contrast, Botrytis cinerea, another host-generalist fungi, is a plant-pathogen capable of infecting various crops and wild plants. While evidence supports B. bassiana inhibition of B. cinerea grown in planta, impacts of this relationship on entomopathogenic outcomes have not been assessed. Our works seeks to (1) identify potential changes of B. bassiana entomopathogenicity due to competition with B. cinerea in-planta, and (2) determine if fungal growth rate explains observed pathogenicity differences.

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Floristics & Taxonomy

Topic: Poster

Title: Is the widely-cultivated katsura-tree (Cercidiphyllum japonicum, Cercidiphyllaceae) an invasion threat in Pennsylvania?

Author: ***Kayleigh Long @ Bucknell University***

Keywords: Pennsylvania,Undergraduate Research,Cercidiphyllum,Invasive Potential

Abstract:

This project explores the invasive potential of Cercidiphyllum japonicum (katsura-tree, Cercidiphyllaceae), a dioecious tree species native to temperate regions of China and Japan. Due to its characteristic heart-shaped leaves and attractive fall color, C. japonicum is commonly used as an ornamental and shade tree in temperate regions of North America. While the species has been identified as capable of escaping cultivation and/or becoming naturalized, little research on this has been published so far. A unique opportunity on the campus of Bucknell University occurred as regular landscaping/weeding that normally minimizes the possibility of establishment of unwanted plant species was reduced due to the onset of the COVID-19 pandemic until fall of 2022, allowing early stages of germination of C. japonicum to be observed in various locations in the area. For this reason, two surveys were conducted on campus in order to assess the invasive potential of C. japonicum when left undisturbed in ideal conditions. Seedling recruitment data was collected utilizing a 1 x 1 m quadrat method alongside buildings with well-draining gravel. Additionally, an incursion of young C. japonicum trees discovered in a campus woodland was surveyed for size and potential age-class. These surveys of recruited and established individuals allow us to predict what conditions are most conducive to the escape and possible naturalization of C. japonicum in the Mid-Atlantic region of the United States. We suggest that the species be considered “potentially invasive” in this region.

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Symbioses: Plant, Animal, and Microbe Interactions

Topic: Poster

Title: Relationship of Virulence and Diet Complexity of Botrytis cinerea Over Generational Time

Author: ***Angela Gao @ University of California, Davis***

Keywords: Fungus,In Vitro,Pathogen,Plant Defenses,botrytis

Abstract:

Virulence is the extent of damage a pathogen can do to its host. In vitro, some pathogens lose virulence over time. Observing loss of virulence in vitro poses questions about pathogenicity and mechanisms of fungal traits, one being the role of diet complexity. Observed loss of virulence in Botrytis cinerea may be a trade off for energy efficiency, leading to the pathogen to saprophytism. One way pathogenicity is restored is to rear the pathogen on its preferred host. Thus we hypothesize that one reason for the maintenance of pathogenicity is access to complex nutritional sources. Using different in vitro diet sources, we assess changes in a virulence and growth rate in a common host-generalist necrotrophic fungal pathogen, B. cinerea.

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Mycology & Phycology

Topic: Poster

Title: Picky Eaters: Metabolic Diversity Across the Botrytis Genus

Author: ***Lori Pradhan @ University of California, Davis***

Keywords: Metabolism,Pathogen,botrytis,Pangenome

Abstract:

The genus Botrytis consists of several fungal pathogens known to be highly destructive to agriculture worldwide. Common species of Botrytis can infect a variety of hosts, and while some species are more host-specific, their potential host ranges are not well studied. As one of many mechanisms underlying host-pathogen ranges, we use a comparative genomics approach centering on primary metabolism to describe variation amongst Botrytis species with variable host ranges. We constructed individual de novo metabolic models to assess growth-rate variation under controlled resource-rich conditions and constructed a pangenome of 16 fungal species to assess the presence or absence of orthologous primary metabolic genes. We concluded that Botrytis cinerea had the fastest growth rate of our metabolic models and found about 30,000 orthologous genes across the genus with the pangenome. Our results serve to suggest possible new host ranges for host-specific species.

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Systematics

Topic: Poster

Title: The floral diversity of Symbolanthus (Gentianaceae) – adaptations and variations in neotropical ring-gentians

Author: ***Lena Struwe @ Rutgers University***

Keywords: floral evolution,flower,Gentianaceae,Hummingbird Pollination,Neotropics,systematics,bat pollination,Anatomy,Pollinators

Abstract:

The first revision of ring-gentians (Symbolanthus, Gentianaceae) highlights the broad floral morphological diversity that can be present in neotropical asterid genera. Our research during the last 20 years has revealed that the number of Symbolanthus species is at least 38 (including 9 species soon to be described) and is present from Bolivia in the south to Costa Rica in the north, with outliers on the tepuis in Venezuela and Guyana (on the Guiana Shield) and in the lesser Antilles in the Caribbean. The highest species diversity is known from Peru and Colombia. Many species are local endemics, and one species is only known from lowland white-sand areas in the Amazon. Their funnel- to salvershaped corollas, up to 12 cm long, present a multitude of sizes, shapes, and coloring patterns, with basic colors from green, white, and yellow to pink and deep magenta, depending on species. Pollinator information is remarkably poor for such a large-flowered taxon, but herbarium records and new investigations have revealed visits by bats and hummingbirds. The Symbolanthus flowers are unique in the presence of a circular corona and/or staminal pockets where the stamens are inserted in the corolla tube. Corona morphology is highly variable and appears to be possibly linked to size of flowers, with larger more fleshy corollas having thicker more ring-shaped coronas with a potentially stabilizing function in the corolla tube (e.g., S. vasculosus). The diversity in floral characteristics may be adaptations to optimize pollination by specific animal groups. Such potential adaptations are observed in the diversity of basic corolla color and corolla tube size and shape, the shape of the corona, as well as in the symmetry of the whole corolla. The symmetry of Symbolanthus corollas varies between mostly radial (e.g., S. pulcherrimus) to strongly bilateral (e.g., S. solaris, to be described.). The distinct disposition of the petals may force the contact between a pollinator's body and the reproductive organs in a specific way that affects the efficiency of the deposition and removal of pollen. Additionally, Symbolanthus' strongly zygomorphic reproductive organs (i.e., the long stamens and style) and long reinforced pedicels suggest primary pollination by vertebrates (i.e., birds and bats). Many species present distinct darker or lighter lines in the mouth and throat of the corolla that may function as nectar guides for insect pollination or for regulating corolla temperature and/or absorption of UV light to prevent degradation of the anthers pollen. The coronas are hypothesized to provide a secondary barrier to the nectar produced at the base of the ovary, with only animals with narrow, long tongues (i.e., the effective pollinators) getting easy access to nectar. Small arthropods may also get nectar access but do not appear to be efficient pollinators (anthers are generally on long filaments and either exserted or inserted), in fact, they might get trapped at the bottom of the flower. We present here an overview of the floral morphology of Symbolanthus as related to potential pollinators, species diversity, and geographic distribution.

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Pteridology

Topic: Poster

Title: A preliminary report of the genome of the invasive climbing fern, Lygodium microphyllum

Author: ***Jessie Pelosi @ University of Florida***

Keywords: fern,gametophyte,genome,invasive species

Abstract:

The Old World Climbing fern, Lygodium microphyllum, is a highly successful invasive species in the southeastern United States. Native to much of eastern Asia, the Pacific Islands, and Africa, introduction of the species to Florida in the late 1800s through the cultivated plant trade has led to rapid population establishment, growth, and spread in the state over the past four decades. Lygodium microphyllum forms thick mats that smother and shade native plants and vulnerable ecosystems with fronds that can reach up to 30m in length by indeterminant growth Herbicide and biological control measures have been largely unsuccessful at mitigating the spread of this fern. Here, we report on a preliminary assembly of the genome of L. microphyllum using a combination of long- and short-read sequencing technologies. Using this new genomic resource, we aim to explore functional differences between the gametophyte anc sporophyte life stages through multiple facets including physiological, transcriptomic, and epigenomic avenues. We hope the integration of these genomic tools with applied sciences will yield downstream applications to aid in the prevention of further spread and containment of Lygodium microphyllum.

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Ecophysiology

Topic: Poster

Title: Morphological and physiological adaptation in an ancient plant lineage

Author: ***Zachary Smith @ University of Wisconsin - Madison***

Keywords: morphology,Stomata,conservation,Cycads,ecophysiology,gas exchange,physiology

Abstract:

Cycads are an ancient lineage that originated more than 200 million years ago. During their long evolutionary history, cycads have survived tremendous changes in Earth's climate and landscape, yet little is known about how cycads cope with environmental stress. Here, we examine the anatomical, morphological, and physiological determinants of plant function in the ecologically diverse cycad genus, Ceratozamia. Specifically, this study aims to link how anatomical features promote or constrain plant function and how function and stress responses drive ecological patterns of 18 species of Ceratozamia. In a common garden, we measured stomatal and hydraulic anatomy, and gas-exchange response curves, and performed linear regressions in relation to native environmental factors. Linear regressions have shown no correlation between stomatal size (SS) and density (DS), in contrast to most other plant groups. We found that variation in maximum stomatal conductance was driven by stomatal density, not stomatal size. We also found vein density and leaf hydraulic conductance to be strongly correlated with native environmental conditions related to water-availability and drought. These relationships point to underlying traits that have shaped the stomatal function and the regulation of plant water-status in this plant group. Additional analyses will shed light on the mechanisms that drive stomatal responses to rapid changes in environment and the potential adaptive value of variation in stomatal regulation in this group. Stress response data in cycads provide a deeper understanding of the connection between environmental stressors and trait adaptation which could aid in the conservation of this genus.

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Symbioses: Plant, Animal, and Microbe Interactions

Topic: Poster

Title: Soil bacteria affect male induction, rhizoid development, and male to hermaphrodite conversion in gametophytes of the fern Ceratopteris richardii

Author: ***Mike Ganger @ Gannon University***

Keywords: fern,gametophyte,sex determination,Ceratopteris,male to hermaphrodite conversion,soil bacteria

Abstract:

Gametophytes of the fern Ceratopteris richardii may be either hermaphrodites or males. Hermaphrodites contain both archegonia and antheridia as well as rhizoids, while the male contains antheridia and rhizoids. The presence of a hermaphrodite-secreted hormone called antheridiogen (ACE) influences individuals to develop as males (male induction), while its absence leads to hermaphrodite development. The continued presence of ACE is required to maintain the male program. Removal of the male from ACE leads to conversion of the male to a hermaphrodite. A soil bacterium, Pseudomonas nitroreducens, has been shown to increase the proportion of gametophytes that are hermaphroditic in culture and to increase the length of rhizoids in both hermaphrodites and males. Here we investigate the effects of other soil bacteria on rhizoid development, male induction, and conversion. Thirteen soil bacteria (8 gram negative and 5 gram positive), isolated from fern roots, were tested for their effect on rhizoid growth. Preliminary experiments for six of these soil bacteria (4 gram negative and 2 gram positive) were also performed to determine potential effects on fern sex determination. One gram-negative soil bacterium, P. nitroreducens, was tested for its effect on time to conversion. In general, gram-negative bacteria were more likely to increase rhizoid length and increase the proportion of hermaphrodites in culture. P. nitroreducens shortened the time to conversion. Overall, bacteria that resulted in longer rhizoids also concurrently increased the percentage of hermaphrodites in culture.

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Biogeography

Topic: Poster

Title: A trait-based approach to determining principles of plant biogeography

Author: ***Thais Vasconcelos @ University of Michigan***

Keywords: correlated trait evolution,Tropical Botany,Phylogenetic comparative methods,functional biogeography,environmental variables

Abstract:

Lineage-specific traits determine how plants interact with their surrounding environment. Unrelated species may evolve similar phenotypic characteristics to tolerate, persist in, and invade environments with certain characteristics, resulting in some traits becoming relatively more common in certain types of habitats. Analyses of these general patterns of geographical trait distribution have led to the proposal of general principles to explain how plants diversify in space over time. Trait–environment correlation analyses quantify to what extent unrelated lineages have similar evolutionary responses to a given type of habitat. In this poster, I give a short historical overview on trait–environment correlation analyses, from some key observations from classic naturalists to modern approaches using trait evolution models, large phylogenies, and massive data sets of traits and distributions. I discuss some limitations of modern approaches, including the need for more realistic models, the lack of data from tropical areas, and the necessary focus on trait scoring that goes beyond macromorphology. Overcoming these limitations will allow the field to explore new questions related to trait lability and niche evolution and to better identify generalities and exceptions in how plants diversify in space over time.

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Comparative Genomics/Transcriptomics

Topic: Poster

Title: A high-quality nuclear genome of the carnivorous plant Triantha occidentalis (Tofieldiaceae)

Author: ***Philippa Stone @ University of British Columbia***

Keywords: carnivorous,carnivorous plant,carnivory,genome,genome assembly,Nuclear genome

Abstract:

Triantha occidentalis (Tofieldiaceae, Alismatales) is a semi-aquatic, perennial, rhizomatous herb found along the west coast of North America from Alaska to California. Triantha occidentalis was recently discovered to be carnivorous, catching insects using a sticky trap directly below its inflorescence. Triantha occidentalis is of particular interest as it is one of only five species of carnivorous monocot, representing four independent evolutions of carnivory within the clade. We confirmed the karyotype of T. occidentalis to be 2n = 15 using chromosome squashes, and estimated its genome size to be 1C = 2.3Gb using flow cytometry. We sequenced the nuclear genome of T. occidentalis using PacBio HiFi technology and assembled it using Hifiasm. Our combined-haplotype assembly for the nuclear genome of T. occidentalis is over 2.1 Gb long, has a contig N50 of over 42 Mb, and a GC content of 43.2%. The current assembly has a complete BUSCO score of 98.2% and only 0.8% of BUSCOs are missing. We are currently sequencing a chromosomal confirmation capture (Hi-C) library to improve our assembly, and are annotating the genome using the BRAKER pipeline supported by RNA-seq data from the leaves, sticky trap, and inflorescence of the plant. We will use this later to explore gene expression differences that may have consequences for our understanding of the plant's ecology, evolution and function.

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Development and Structure

Topic: Poster

Title: Assessing the role of the NAM/CUC3 gene families in floral fusion

Author: ***Nola Rettenmaier @ Cornell University***

Keywords: NAM/CUC3,organ fusion,evo devo

Abstract:

The developmental mechanism responsible for floral organ fusion has been posited as a key innovation in the evolution of angiosperms, enabling the diversification of angiosperm lineages and the emergence of novel and adaptive floral morphologies. Previous research has pointed to the role of the NAM and CUC3 genes in the fusion pathway, suggesting that the transcription factors encoded by these genes promote organ separation and boundary formation. NAM and CUC3 are members of the NAC family of plant transcription factor genes, and may be characterized as paralogous genes with many sequence similarities. This research builds upon previous research into the behaviors of these genes in regulating floral organ fusion, investigating the evolution and expression patterns of NAM and CUC3 in the monocot order Zingiberales, with an emphasis on the whorl-specific expression of these genes in Costus spicatus or spiral ginger. The aim of this research is to contribute new insights to our understanding of the underlying genetic and developmental mechanism of floral fusion, in a monocot order distinguished by unique fused floral morphologies.

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Systematics

Topic: Poster

Title: Untangling the Genus Haploësthes (Asteraceae): A Story of Gypsophile Speciation

Author: ***Konrad Oman @ Oberlin College***

Keywords: Asteraceae,Chihuahuan Desert,genome sequencing,gypsum,speciation

Abstract:

The Earth is composed of multiple chemical compositions of soil, some of which are more hospitable to plant life than others. The less hospitable of these soils can prevent the growth of most plant species, although some species have evolved to withstand and even thrive in such conditions. This evolutionary response to difficult soil conditions can be seen in plants that strictly grow in gypsum. Gypsum ($CaSO4·2H2O$) is typically a very harsh environment for plants to grow in, due to its characteristic hard crust and lack of many essential nutrients necessary for the growth of most plants. Nevertheless, a subset of plants known as gypsophiles are only known from gypsum soils.

Within North America, gypsum is most commonly found in island-like outcrops within the Chihuahuan Desert of northern Mexico and the southwestern US. This non-continuous distribution of gypsum soil may promote speciation in gypsophile plant groups, as gene flow is generally limited among gypsum outcrops. Haploësthes (Asteraceae) is a small genus of five species and three varieties, all of which grow only in gypsum soils in the Chihuahuan Desert region. The taxonomy of Haploësthes has mainly been based on the morphology and chromosome counts, and species boundaries are not entirely clear. To define the species boundaries and build a clearer picture of the evolutionary relationships present within Haploësthes, we are sequencing 300 genes from multiple individuals from multiple populations of all taxa in Haploësthes. We will also be able to investigate patterns of possible gene flow among and within species in the genus.

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Systematics

Topic: Poster

Title: Painting a picture of paintbrush evolution: Species delimitation in Castilleja cusickii Greenm. (Orobanchaceae)

Author: ***Caroline Brose @ University of Wyoming***

Keywords: GBS,Pacific Northwest,Phylogeography,Cusick's paintbrush

Abstract:

Castilleja cusickii Greenm. (Orobanchaceae) is a widespread and highly polymorphic species found growing in wet meadows throughout the northern portion of the Intermountain West and interior Pacific Northwest. Multiple populations throughout its range have been identified and long known to vary both morphologically and ecologically from its typical populations and may constitute distinct taxa. The aim of this study is to revisit the species limits of C. cusickii using a combination of phylogenetic and population genomic approaches. In addition, we have collected an extensive morphological dataset that will be used in combination with molecular data to support our efforts in understanding the diversity of this species complex.

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Symbioses: Plant, Animal, and Microbe Interactions

Topic: Poster

Title: Assessing Pollinator Assembly and Efficacy Across Species Ranges in the Genus Triodanis (Camplanulaceae)

Author: ***Kate Tillotson @ Southern Illinois University***

Keywords: breeding system,generalist pollinator,native plants,Plant-pollinator Interaction,Texas

Abstract:

Plant-insect interactions are a key topic in evolutionary ecology, especially in the face of anthropogenic changes which threaten to disrupt these mutualisms. An in-depth pollinator survey for species in the genus Triodanis is performed here for the first time, with sampling covering four species or subspecies and spanning a large portion of their geographic ranges (i.e., spanning four US states). All species in the genus exhibit dimorphic cleistogamy with variability in allocation to open (chasmogamous) flowers among populations and taxa. The genus Triodanis, therefore, provides an opportunity for understanding possible associations between pollinator assemblies and variation in species, breeding system, and geography. To assess these relationships, I sampled four species of Triodanis at field sites (n=11) in four states. Sampling encompassed a broad area across the midwestern U.S. and Texas, and across a gradient of anthropogenically disturbed habitats. When population sizes were sufficient, I also quantified allocation to open flowers for multiple populations (mean proportion of open, chasmogamous flowers). To increase knowledge of general plant-animal interactions for this group, I also collected general arthropod associates for these species, and briefly documented those results. We found that for species of Triodanis: 1) small bee and fly generalist pollinators showed some floral constancy during feeding bouts but did not differentiate between species, 2) pollinator community for Triodanis was less diverse and abundant in highly degraded habitats, 3) while allocation to open flowers varied among specie and populations, we found no association between breeding system (or species) on pollinator identify or abundance. This study represents the first in-depth survey of both pollinator and general arthropod visitors of Triodanis and serves as foundational knowledge about the natura history of this group, provides resolution for members of Campanulaceae exhibiting floral traits of generalist hosts, and important documentation of plant-insect interactions in an era of ongoing anthropogenic changes.

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Physiology

Topic: Poster

Title: Botrytis cinerea energy investment in Secondary Metabolites

Author: ***Julia Cook @ University of California, Davis***

Keywords:

Abstract:

Botrytis Cinerea is a fungal pathogen capable of infecting most plants, leading to negative impacts on agricultural production across the globe. Among B. Cinerea's repertoire of virulence factors, specialized metabolites can induce cell-death across a variety of plant species. The investment of energetic resources into the production of specialized metabolites in host plants comes at a cost, however in a pathogen system these metabolites lead to the acquisition of more nutrient resources reducing the energetic cost over the lifetime of the organism. To assess energetic investment by B. Cinerea into specialized metabolism we created a genome-scale metabolic model to simulate the growth of B. Cinerea under various nutrient conditions. We find large differences in the growth rate of B. Cinerea on a non-limited media compared to a carbon limited media. We further describe the impacts of nutrient limitation on the simulated investment of B. Cinerea into specialized metabolites associated with pathogenicity. On a broader scale, our research furthers our understanding of the intersection of specialized metabolism and nutrient limitations in the context of host-pathogen interactions.

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Ecology

Topic: Poster

Title: Roles of resource co-limitation and genome size during seedling establishment in big sagebrush (Artemisia tridentata)

Author: ***Treyton Harris @ Idaho State University***

Keywords: genome size,co-limitation

Abstract:

Genome size is a trait that can greatly influence phenotypic performance in ecological communities. Theory predicts that organismal demands for nutrients such as nitrogen (N) and phosphorus (P) increase with genome size because genetic material requires more of these resources than many other biomolecules. Thus, this demand may translate into stronger limitations in performance for individuals with larger genomes, as N and P availability are limiting in many natural systems. In plants, the impact of increased genome size may be particularly severe, as the availability of N and P often affect access to one another in many species, known as co-limitation. Additionally, water availability is known to impact plant access to N and P, which may suggest a possible three-way co-limitation. Though resource co-limitation is common for plants, it is unclear how genome size affects the strength of this co-limitation, and therefore competitive ability and success. These effects may be particularly important to understand during the establishment life-history phase, including seed germination and seedling growth, which is a demographic bottleneck for many plant species. Here, we studied big sagebrush (Artemisia tridentata, Asteraceae) as a model system to investigate the relationships between genome size, resource co-limitation (N, P, and water) and competitive ability during the establishment-life history phase. Using a greenhouse common garden experiment with a response surface design, we grew sagebrush seedlings paired in competition pots according to parental genome size variation under 8 factorial treatments of high or low N, P, and water supply. Analysis of height data across treatments found a significant interaction effect of competitor seedling parental genome size, P and water on focal plant height, where focal plant height decreased with greater parental genome size of the competitor only when there was low P and water availability. This suggests that competition was strongest under low P and water conditions and with competitor plants with larger parental genome sizes. Also, we found significant main effects for N and water supply, with seedling height increasing additively with both of these resources. These results suggest that big sagebrush is co-limited by N availability and water supply. We are currently collecting data for seedling biomass and foliar chemistry responses to the experimental factors, as well as direct measurements of seedling genome size to better understand the role of this factor. Our future analyses will consider the effects of genome size and resource availability on plant resource allocation and biomass.

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Systematics

Topic: Poster

Title: Verifying the Taxonomic Validity and Resolving the Subspecific Boundaries of the Lomatium foeniculaceum Complex

Author: ***Daniel Botello @ Boise State University***

Keywords: Angiosperm353,Apiaceae,Lomatium,phylogenetics

Abstract:

The Lomatium foeniculaceum complex of the Perennial North American Clade (PENA) in Apiaceae is present across much of the Great Plains and Intermountain Region, and as far north as northeast British Columbia. It is comprised of five subspecies and is the most widely distributed complex in the PENA clade. As delineated by previous taxonomic treatments, these infrataxa, which were once recognized at the specific rank, are separated by the presence or absence of variable characters such as petal ciliation, petal color, and involucel geometry. Recent phylogenetic research has found that morphology alone in the PENA clade does not always reflect evolutionary history and is often misleading when used for species delimitation. Fifty populations of L. foeniculaceum were selected based on general distribution, and to include all named subspecies and areas where sympatry or peripatry of subspecies occurs. The Angiosperm353 bait kit is being employed in conjunction with next generation sequencing for this project. Phylogenetic analyses will be used to test congruence with associated historic climate data and soil sample data from representative sites. Results from this project will enhance the current understanding of species relations within the PENA clade and will help verify the taxonomic validity and subspecific boundaries within the complex.

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Systematics

Topic: Poster

Title: Systematics of the eastern Asian-North American disjunct genus Physocarpus (Rosaceae)

Author: ***Audrey Spencer @ Denver Botanic Gardens, University of Colorado Denver***

Keywords: biogeographic patterns,Rosaceae,systematics,phylogenetic

Abstract:

The eastern Asian-North American disjunction has drawn the attention of botanists and biogeographers since the mid-19th century and laid the groundwork for early biogeographic theory. Since then, the floristic affinities between eastern Asia and North America have been extensively studied. Physocarpus (Rosaceae) provides an under-studied example of this intercontinental distribution pattern. As currently circumscribed, the genus comprises seven species of temperate deciduous shrubs, with one species in eastern Asia and six in North America. Physocarpus has received relatively little systematic attention to date. A previous phylogenetic study found complex intrageneric relationships, including polyphyletic as well as unresolved taxa. Additionally, the study was not able to resolve the earliest-diverging lineage. However, advances in phylogenomics have the potential to resolve these complex relationships as well as determine the earliest-diverging lineage, which has biogeographic implications. While Physocarpus exhibits an intercontinental disjunction at the genus level, P. intermedius occupies an intracontinental disjunction between eastern and western North America. Its range is further characterized by apparent sympatry with P. opulifolius in the Great Lakes Regions. Although the Flora of North America North of Mexico treats P. intermedius at the species level, this taxon is often treated as P. opulifolius var. intermedius in regional or state floras. Previous work on the geographic distribution of follicle morphology, an important diagnostic trait, supports the recognition of two taxa, but the appropriate rank remains unresolved. The present study has two primary objectives: 1) to infer the earliest-diverging Physocarpus lineage, and 2) to clarify the evolutionary relationship between P. opulifolius and P. intermedius. These are addressed by inferring a coalescent species tree in a Maximum Likelihood framework, as well as phylogenetic inference in a Bayesian framework. The results from this project will inform the systematics and biogeographic history of this disjunct genus.

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Physiology

Topic: Poster

Title: Intraspecific variation in hydraulic traits of cycads: environmental correlation and conservation implications

Author: ***Nicolas Zepeda @ Stanford Online High School***

Keywords: conservation,Cycads,ecophysiology,intraspecific variation,South Africa

Abstract:

Cycads (Cycadales) are among the world's oldest and most threatened seed plant lineages. Protecting species in this group from extinction threats such as poaching, habitat destruction, and climate change will require a holistic approach that incorporates many elements of organismal biology. However, several fundamental aspects of cycad biology remain

unknown, and data on the ecophysiology of these unique plants is particularly scarce. The extant members of the cycad genus Encephalartos, which inhabit southern Africa, are particularly vulnerable, and urgent conservation interventions are needed to preserve these organisms. Here, we present the first data from wild populations on intraspecific variation in hydraulic anatomy and investigate the role of physiology as a potential factor in determining climate vulnerability of 3 species of Encephalartos. Leaf samples were collected from 12 wild populations and 3 ex situ collections and analyzed for a variety of leaf hydraulic trait anatomica determinants paired with environmental data. We found a high degree of intraspecific trait variation in the three species we examined. We also found that most hydraulic traits can be predicted by native environments, but that trait by environment relationships differed between species. Overall, our results show that threatened Encephalartos spp. are able to adjust key functions across spatial environmental gradients. Thus, conservation efforts should consider these biodiversity patterns when prioritizing species and sites of high conservation value, selecting in situ approaches, and planning ex situ interventions. Ongoing work will shed light o possible hydraulic trait differences between ex situ collections and wild populations and on the implications of those findings for conservation ecology research.

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Symbioses: Plant, Animal, and Microbe Interactions

Topic: Poster

Title: Investigating the differences of Cirsium pitcheri's floral scent according to the predation of novel weevil, Larinus planus

Author: ***Rina Talaba @ Chicago Botanic Gardens***

Keywords:

Abstract:

Cirsium pitcheri–a rare dune plant species endemic to the Great Lakes–is under threat by the invasive predator weevil, Larinus planus. Though it is known that L. planus predation on the flowering head bract of C. pitcheri causes a decline in seedling production, little is known about other floral traits that are affected. Floral scent, in particular, can be analyzed through its volatile organic compounds (VOCs) and these VOCs can change when a plant is put under stress. Larinus planus predation on flowering heads should be investigated further to understand whether their infestation can cause a change in floral scent–which is an important trait that attracts pollinators. Cirsium pitcheri populations within White Fish Dunes in Sturgeon Bay, Wisconsin are an ideal study site as they contain both L. planus infested and non-infested populations. By collecting floral scent from the flowering heads, we are then able to compare VOCs between individuals with L. planus predation and no predation. Considering C. pitcheri is recorded to be one of the most important floral resources to the Great Lakes pollinator network, understanding how L. planus may affect VOCs is vital to uncovering the best way to conserve and restore the sensitive dune plant.

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Ecology

Topic: Poster

Title: Host preference in hemiparasitic plants: a case study in Pedicularis (Orobanchaceae)

Author: ***Samantha Kish-Levine @ University of Chicago***

Keywords: Pedicularis,biogeography,California,hemiparasite,Host-parasite,Orobanchaceae

Abstract:

Hemiparasitic plants are broadly classified as generalists with respect to their host specificity. However, a generalist species may be associated with different host communities throughout its geographic range, possibly leading to locally adapted host preferences that may ultimately drive speciation through ecological isolation. Because haustorial connections to hosts can be difficult to identify in natural populations, little is known about the evolution of host range in hemiparasitic plants and the role that host-switching plays in their diversification. Pedicularis (Orobanchaceae) is a genus of facultative root hemiparasites that parasitizes a taxonomically diverse array of hosts. Here I examine the variation in potential host communities of Pedicularis densiflora and Pedicularis aurantiaca, a pair of putative sister species distributed around the Central Valley of California. Potential host use was determined by compiling mentions of co-occurring plant species from herbarium labels. Preliminary results indicate that P. densiflora and P. aurantiaca pararisitize different hosts, and that host preference within each species varies by location. Genetic analysis of P. densiflora and P. aurantiaca populations across their geographic range will be conducted in order to investigate how host preference has affected genetic variation between and within each species. This research will shed light on the evolution of host specificity and the role it plays in the diversification of parasitic plants.

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Education and Outreach

Topic: Poster

Title: Research experiences for pre-service teachers in biodiversity studies

Author: ***Michael Grillo @ Loyola University of Chicago***

Keywords: Biodiversity,Education,urban biodiversity,teacher,reu,ret

Abstract:

There is a long history of professional scientists providing summer research experiences for practicing teachers (RETs). Yet, rarely do preservice teachers have opportunities to immerse themselves in authentic research experiences. With funding from NSF this project provides summer research experiences for pre-service teachers (i.e., undergraduates pursuing a degree in STEM education) at Loyola University Chicago with a research focus on biodiversity in an urban setting. Program activities are informed by prior research and best practices that show the benefits of: 1) involvement in all stages of scientific inquiry from asking research questions to communicating and defending findings; 2) exposing participants to diverse research areas and applications through seminars and reading primary literature; 3) systematic reflection on the inquiry experience; 4) "hands-on" mentoring by research faculty; and 5) opportunities to demonstrate competence in tangible ways. While there is a body of research that supports these types of research experiences for teachers, there is less known about how immersive research experiences influence pre-service teachers' knowledge and understandings of the ideas, concepts, practices, norms and discourses of science. In turn, there is also limited literature on how these types of research experiences, early in teachers' preparation, can contribute to their capability to support their students' science learning and engagement. Thus, this project will contribute to broader understandings about how pre-service teachers research experiences can best be incorporated into the preparation of secondary science teachers.

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Systematics

Topic: Poster

Title: Reproductive Phenology of Species of Hackelia from Western North America

Author: ***James Cohen @ Weber State University***

Keywords: phenology,Boraginaceae,Hackelia

Abstract:

Phenology, the study of reoccurring, natural events in biological lifecycles and the impact of these events by external stimuli, is becoming an increasingly important field of research as Earth's climate progressively changes. Plants' ability to respond and adapt to their changing environment has significant implications for future ecological challenges, particularly for species with small geographic ranges. While many studies on plant phenology explore species in similar types of ecosystems, studies that focus on the phenology of multiple, related species are less common. To examine multiple congeners from western North America, phenological data was compiled from over 200 herbarium specimens encompassing 10 species of Hackelia Opiz. (Boraginaceae). Along with date, location, elevation, and reproductive phenological stage, historical temperature and precipitation data were gathered. For each species, linear regression models were employed to examine the patterns of phenology as they relate to temperature, precipitation, and elevation. Several trends were observed, including a positive correlation between temperature and later flowering in multiple species, suggesting that increased temperatures do not result in earlier flowering. The inclusion of levels of precipitation produced varied results, which may relate to distinct biomes or microclimates, for each studied species. Overall, these data support the idea that the phenological stages of several Hackelia species in western North America may not be impacted as much by the changing climate as other species investigate in other geographic regions and ecosystems.

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Education and Outreach

Topic: Poster

Title: Do microbes help or hinder germination? A learning game designed by USDA-REEU undergraduate students to explore seed-endophyte interactions

Author: ***Julie Beckstead @ Gonzaga University***

Keywords: plant-microbe interactions,stress experiment,Education,seed endophytes

Abstract:

Today, plants are facing many challenges in both agricultural and natural habitats. Disease and environmental stressors (e.g., drought, heat, abrupt freeze, and high soil salinity) can reduce germination and seedling development. Climate change poses a further threat by enhancing environmental stress factors and potentially increasing the spread of disease. Microbes (e.g., bacteria and fungi) are known to provide plants various benefits against both abiotic and biotic stress through symbiotic interactions. However, the beneficial aspects of microbes have largely been unexplored, and they are an untapped resource that has the potential to solve important problems in plant communities around the world. Undergraduate students participating in a USDA-REEU summer research program designed a card game to disseminate concepts that were part of their research program. The REEU student research projects focused on microbial seed endophytes and stressors that cause cell damage in seeds. Students surface sterilized seeds of several species and plated them on four types of agar media to isolate endophytic microbes. Plates were examined for germination status, presence of bacteria and fungi, along with morphological microbial traits. Our results found that there were more bacteria endophytes isolated from flax seeds than fungi. Other students in the group explored different types of stress on seeds by examining cell damage following the stress events during the germination life stage. Stressors included drought stress, freeze stress, and heat stress. Cell damage was measured by electrolyte leakage. We found that stressful events resulted in higher electrolyte leakage of germinating forb yarrow (Achillea millefolium, family Asteraceae). Seeds experiencing multiple stress events sustained 3x higher cell damage than controls and nearly 2x higher than seeds experiencing only one stressful event compared to controls. In addition, grass seeds of Bromus tectorum (family Poaceae) experienced 25% higher cell damage than a forb species (A. millefolium) when warm conditions were followed by an abrupt freeze. These experiments inspired the design of a card game exploring seed-microbe interactions with a focus on seed endophytes and germination. The goal of the game is to germinate your seed before the other players by adding endophytes to reduce your days for germination. The game consists of Seed Plant Cards that show plant traits, maximum number of endophytes that the plant can host, and the number of days for germination. Players choose one Seed Plant Card for the game. Another deck of cards contains fungal endophytes, bacterial endophytes, and pathogens. Although pathogens negatively impact germination, the fungal and bacterial endophytes can reduce days for germination and benefit the seed. However, these endophytes may interact with each other and may only help some plants and not others. While playing this game, students learn about endophytes, microbial interactions, and impacts of microbes on seeds. This fun learning experience provides students with an opportunity to discover a world they have never considered before. Plant restoration and agriculture tomorrow will depend on future biologists that can tap into unexplored tools to help plants establish under stressful conditions.

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Phylogenomics

Topic: Poster

Title: Environmental, Phylogenetic, and Morphological Investigations of Tropical to Temperate Transitions in Prunus

Author: ***Sundre Winslow @ Smithsonian Institute***

Keywords: morphology,environmental variation,Machine Learning,phylogenetics

Abstract:

The genus Prunus (Rosaceae) includes economically important species such as peaches, plums, almonds, and cherries. Past phylogenetic studies identified three major clades within the genus corresponding to inflorescence types: corymbose, solitary, and racemose. The corymbose and solitary groups are found in temperate regions, whereas the racemose group occurs in temperate, neotropical, and paleotropical regions. These previous phylogenetic studies reported discordance between nuclear and chloroplast phylogenies. In chloroplast phylogenies, the racemose group was invariably monophyletic, whereas the relationships among the major lineages in nuclear phylogenies were unclear. Phylogenetic uncertainty has clouded biogeographic reconstructions, although the origin of Prunus is hypothesized to be in eastern Asia, with several tropical to temperate transitions allowing it to spread to its current range.

In this study, morphological, environmental, and genetic data were used to examine how these transitions occurred. Environmental conditions were examined using principal component analyses of bioclimatic variables, morphology was analyzed using machine learning algorithms applied to digitized herbarium sheet image data, and phylogenetic analyses were conducted based on 610 nuclear loci and complete chloroplast genomes generated via HybSeq.

Our nuclear phylogeny supports that the temperate racemose species form a clade with the solitary and corymbose lineages, which are then sister to the tropical racemose group. Machine learning classification of herbarium images inferred that most of the temperate species were more similar morphologically to paleotropical species as opposed to neotropical species. This result, in combination with the environmental space occupied by each major lineage within the genus, suggests that the temperate species' morphological similarity to neotropical species did not arise due to shared environmental conditions. Further investigation of individual species such as Prunus serotina, reveals the morphological, genetic, and environmental variation found throughout their large North American range, informing our understanding of the temperate to tropical transitions. This work improves our understanding of the biogeographic transitions from

tropical to temperate regions throughout the evolutionary history of the genus Prunus, and illustrates how morphological and environmental data can be used to supplement our phylogenetic research.

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Bryology and Lichenology

Topic: Poster

Title: Novel Research into Bacterial Nitrogen Fixation in Vegetative Cells of Mosses and Liverworts

Author: ***Nicole Vaccaro @ Rutgers***

Keywords: bacteria,liverworts,Microbiome,microscopy,mosses,Symbiosis,cell biology,microbiology,STRUCTURE,Nitrogen,Bryology,,rhizoid,filaments

Abstract:

A lot of research has been done showing that biological nitrogen fixation occurs inside the roots of vascular plants via the rhizophagy cycle. Although such research in higher plants has been instrumental to understanding the function of biological nitrogen fixation, similar research in bryophyte symbiosis remains inconclusive. The bryophyte clade is older than seed plants and might reflect more ancestral associations and symbiotic relationships between plants and bacteria. Bryophytes have been associated with nitrogen-fixing bacteria in nitrogen-cycling studies, but the specific mechanism of how bacteria are providing nitrogen to the bryophyte cells is unknown. We utilized new staining methods and freshly collected materials of several mosses and liverworts to get a better understanding of the cellular activities of bryophytes and the bacteria incorporated in some of their cells. Different chemical stains were used on specimens under microscopic magnification and often showed bacterial endosymbionts moving inside the bryophyte's rhizoids in the apices of immature filaments, as well as in other non-photosynthetic structures. The goal of this project is to get a better understanding of the mechanisms through which these bacteria obtain nitrogen from the air, their function and development, and the patterns associated with how nitrogen is acquired and moves inside the bryophyte cells. A close association between bryophytes and nitrogen-fixing bacteria is hypothesized to be beneficial to bryophyte growth and survival. Such mutualism, or potential 'plant farming', where the moss uses bacteria to produce nitrogen inside its cell, could indicate early species-interactive relationships in land plant lineages from over 400 million years ago.

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Paleobotany

Topic: Poster

Title: Ecological Strategy of Pacific Northwest Forests During the Miocene Climatic Optimum

Author: ***Melanie Cham @ Wesleyan University***

Keywords: deciduous forest,ecosystem function,gas exchange,Miocene,paleobotany,Clarkia

Abstract:

The U.S. Pacific Northwest (PNW) hosts an extensive suite of Miocene-aged fossil plants sites, with the potential to document changes in plant community ecology in response to regional climatic change during the Miocene Climatic Optimum (MCO; 17-14 Ma) and the ensuing Middle Miocene Climatic Transition (MMCT; ~14 Ma). The MCO was the most recent period of sustained global warming and thus provides some analogy to anthropogenic climate change. An important component of characterizing plant community ecology is the diversity and prevalence of ecological strategies present within a community. Many previous paleoecology studies rely on a nearest living relative approach to infer components of ecological strategy (e.g., plant functional types) from fossil plant assemblages. In contrast, much work in neo-ecology stresses the importance of functional traits in elucidating prevalent ecological strategies and functional diversity within plant communities. Here we take advantage of exquisitely preserved leaf compression fossils from Clarkia, northern Idaho (~16.9 Ma), representing the height of the MCO, to measure leaf functional traits and elucidate ecological strategies of dominant species in this ancient temperate mixed conifer-deciduous-evergreen forest. We focus on 13 species, representing the most abundant angiosperm taxa in the assemblage, including Betula, Castanea, and Quercus. We reconstruct assimilation rates using gas exchange modeling, address leaf hydraulic efficiency by measuring leaf vein density, and reconstruct water use efficiency by accounting for the ratio of carbon assimilation to transpirational water loss. As these species are prevalent in many other Miocene floras of the PNW, this study provides a benchmark by which to interpret changes in the dominance or presence of these species through time and, by inference, how Miocene climatic changes impact the functional composition and diversity of this forest type. We are also providing an example of how present-day mixed deciduous forests may respond to current anthropogenic changes in CO2.

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Biogeography

Topic: Poster

Title: Improving MaxEnt ecological niche models: assessment of some limitations and assumptions using virtual and real species.

Author: ***Gerry Allen @ University of Victoria***

Keywords: ecological niche modelling,Quercus garryana,virtual species

Abstract:

Ecological niche models are widely used to identify ecological niches and project these in geographic space, but understanding their limitations and underlying assumptions is essential. The ENM method MaxEnt contrasts species occurrence points with sampled background points to estimate ecological niches. We generated virtual species with the R package virtualspecies using climate data from a region of western North America, and analyzed these with MaxEnt to explore the effects of various model parameters and assumptions. We considered the effects of different background areas (defined by radii of 10 to 500 km drawn around occurrence points), and found that larger backgrounds gave better fit of model predictions to species occurrences. Including ecologically divergent outliers led to overestimates of niche breadth, especially for species with narrower niches. Two assumptions implicit in MaxEnt and other methods are that a species is in equilibrium with its environment (it occurs in all suitable habitats) and that it has niche homogeneity (its ecological requirements are similar throughout its geographic range). We used virtual species with some occurrence points removed to simulate disequilibrium along a known directional gradient, and found that model predictions were sensitive to the background selected. We created composite species by combining pairs of virtual species, and showed that model predictions for these were similar to the combined predictions for the individual species pairs. These results can be used to investigate spatial ecological patterns in real species. We tested our conclusions using Quercus garryana, a western white oak with a well-documented geographic range.

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Bryology and Lichenology

Topic: Poster

Title: Ultramafic lichens: an ecological investigation of an understudied organism in a well-studied system.

Author: ***Michael Mulroy @ Althouse and Meade, Inc.***

Keywords: community ecology,Lichenology,ultramafic geoecology

Abstract:

Saxicolous lichens are a major, ecologically significant component of the biodiversity present in rocky outcrop habitats, including ultramafic outcrops. While multiple studies have investigated the biotas of ultramafic outcrops, few have directly compared ultramafic and non-ultramafic lichen communities. As a result, the importance of substrate factors (elemental composition, surface pH, microtopography) in relation to other abiotic factors is poorly understood for saxicolous lichen communities. In a regional community ecology study, we sampled lichen biotas of eight ultramafic and eight sandstone outcrops along a 70 km maritime influence gradient in order to test three hypotheses: 1) a substrate effect hypothesis that saxicolous lichen communities of ultramafic and sandstone outcrops are compositionally distinct; 2) a maritime gradient hypothesis that coastal and inland communities are compositionally distinct; and 3) a maritime moderation hypothesis that coastal ultramafic and sandstone communities are more similar than those of inland ultramafic and sandstone.

Our results provide support for the substrate effect hypothesis and the maritime gradient hypothesis. Lichen communities of 1) ultramafic and sandstone outcrops and 2) coastal and inland outcrops were compositionally distinct. The maritime moderation hypothesis was not supported; lichen communities of ultramafic and sandstone outcrops were significantly differentiated across the maritime gradient. A total of 134 taxa were recorded - 81 taxa from ultramafic outcrops and 100 taxa from sandstone, with 47 taxa found on both rock types. Ultramafic outcrops were characterized by greater similarity between samples, lower lichen cover, larger differences in cover between north and south aspects, and higher abundance and diversity of cyanolichen taxa compared to sandstone. This study is one of few to quantitatively examine lichen communities of two rock types and is unique in that it does so at a regional scale. These results add to our understanding of the interactive roles of substrate and maritime influence in lichen community assembly.

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Mycology & Phycology

Topic: Poster

Title:

Impacts on Growth of Linalool on B.Cinera Isolates

Author: ***Melanie Madrigal @ University of California, Davis***

Keywords:

Abstract:

Fungal pathogens like Botrytis Cinerea pose a constant threat to agricultural production. Botrytis cinerea can infect a wide variety of crop plants, reducing quality and harvestability at multiple stages of production. Due to B. cinerea's wide host range, developing pesticide applications is a more feasible opportunity for pathogen control than the genetic engineering o resistant crops. Plant-derived terpenes, like linalool, have demonstrated inhibitive effects on single isolates of B. cinerea. However, few studies have examined the variation in inhibitive properties of terpenes on populations of genetically distinct isolates of B. cinerea. In-vitro cultures of different isolates and growth assays can be used to describe the variation in the inhibition of growth and germination of a selection of genetically distinct botrytis cinerea isolate under varying concentrations of select terpenes. Our results serve to develop plant-derived pesticides as an alternative to other longer-lived pesticides which biomagnify within the environment and hinder ecosystem processes.

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Ecophysiology

Topic: Poster

Title:

Effects of stomatal size, spacing, and shape on water vapor diffusion through the leaf epidermis

Author: ***Paul Schulte @ University of Nevada, Las Vegas***

Keywords: computational,Stomata,diffusion

Abstract:

Stomata play a key role in regulating the exchange of water vapor and CO2 between the leaf and the atmosphere. Computational models were developed to solve Fick's Law and investigate the roles of the size, spacing, and shape of stomata on the rate of water loss through the stomatal pores. Simple models of stomata as round were considered with various sizes and spacing of the pores. Increasing the pore size from 5 to 25 µm led to a 16-fold increase in flux through a group of 5 pores. Increasing the spacing between stomatal pores from 20 to 90 µm for a 7 x 7 array of pores led to a 27% increase in flux. When water flux through the pores was calculated per unit pore area the wider 25 µm pores had 36% lower flux than the narrow pores. These reductions in flux for wide and closely spaced pores are likely due to interactions between the flux fields of pores when in close proximity. Models were also developed based on shapes of actual stomata from Populus trichocarpa leaves. Flux through an actual pore was closely similar to a round pore of equal area. However deviation from round to more elliptical pores of equal area led to an increased flux per pore area.

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Population Genetics/Genomics

Topic: Poster

Title:

The role of immune system incompatibilities in the evolution of isolating barriers within an ongoing adaptive radiation

Author: ***Hossein Madhani @ University of Nevada, Las Vegas***

Keywords: adaptive radiation,disease resistance genes,Hawaiian Metrosideros,hybrid incompatibility,hybrid necrosis

Abstract:

Hybrid necrosis (HN) is a common type of hybrid incompatibility in plants that results from negative epistasis between alleles at resistance genes (R genes), leading to hyperactivation of the plant immune system (autoimmunity) in hybrids. Recent studies demonstrate the importance of selection on R genes in the evolution of HN and their role as barriers to gene flow during speciation. However, such studies are largely restricted to model species. Adaptive radiations that capture different stages of speciation are among the best candidates to test the role of selection on R genes in the evolution of gene flow barriers during speciation. Hawaiian Metrosideros is an ongoing adaptive radiation in trees that captures a wide range of isolating barriers between populations, including HN in multiple F1 hybrid genotypes. To explore the possible role of R gene incompatibilities in HN in Metrosideros, we identified putative R genes in the five reference genomes available for Hawaiian Metrosideros using the NLR-Annotator pipeline and HMM search implemented in HMMER. We verified the presence of canonical domains of R proteins in the identified R proteins using PfamScan. We searched for known motifs and domains of plant R genes using MEME-suite and CD-Search, respectively. Firstly, we identified a set of more than 200 pseudogenes in the reference genomes, suggesting a dynamic and complex evolutionary history of R genes in the Hawaiian Metrosideros radiation. We also identified 180 putatively functional R genes and used variant-calling and population genetic analyses to investigate evidence of selection in these R genes across the radiation. Specifically, we calculated π and pairwise FST and Dxy values using SNP data from 131 individuals in 12 populations. While overall π, pairwise FST and Dxy values for all R genes between populations were similar to the genome-wide values, a subset of R genes on chromosomes 3, 7, and 10 showed high nucleotide diversity and were highly differentiated between most taxa examined in pairwise comparisons. These results suggest that a subset of R genes are under selection across the radiation and are possibly involved in necrosis observed in F1 hybrids. To measure introgression between taxa and further investigate the possible role of R genes in reproductive isolation between taxa that produce necrotic F1 hybrids, we calculated D statistics in sliding windows. The D statistics revealed genomic regions that are less introgressed between taxa that produce necrotic hybrids; however, these regions were not limited to the genomic regions containing the identified R genes. Overall, our results suggest a role for R genes in the HN observed in the Hawaiian Metrosideros radiation and point to a subset of candidate R genes underlying reproductive isolation in these trees. This work sets the stage for the precise identification of the locus (loci) putatively causing HN, and exploring the genetic and physiological mechanisms of HN in Hawaiian Metrosideros using RNA sequencing and metabolite profiling. By illuminating the role of immune system incompatibilities in the evolution of reproductive isolation in adaptive radiations, this study advances our understanding of the mechanisms underlying speciation in plants.

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Ecophysiology

Topic: Poster

Title: Seasonal Reproductive Rates of Dasysiphonia japonica: Implications for its Invasive Success

Author: ***Bryce Hegstrom @ University of New Hampshire***

Keywords: phycology

Abstract:

Dasysiphonia japonica is a red algae species that has recently invaded the northeastern coast of North America, spreading over 435 miles from Rhode Island to Maine in just 15 years. The invasion has resulted in a significant reduction in native algal and sessile species richness, and it now constitutes 14% of subtidal benthic communities. To investigate the factors promoting the rapid invasion of D. japonica, we conducted a study on its reproductive rate under summer and winter environmental conditions. We collected samples weekly from the field, weighed them, and allowed them to grow and reproduce asexually in growth chambers under summer (16-hour days at 14°C) and winter conditions (10-hour days at 4°C). After a week, we weighed the samples and counted the clonal fragments. The experiment was duplicated four times. ANOVA analysis confirmed that seasonal conditions significantly influence the number of clones produced per unit mass, with D. japonica producing significantly more clones per unit mass under summer conditions. These findings suggest that further research is necessary to explain how D. japonica has proliferated so quickly on the northeastern coast of North America. Additionally, our observations indicate that D. japonica has increased survivability in winter conditions, which may contribute to its success as an invasive species.

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Floristics & Taxonomy

Topic: Poster

Title: Updates in Neotropical Ericaceae: a preliminary overview in Agarista (Lyonieae)

Author: ***Claudenice Dalastra @ UFRGS***

Keywords: campos rupestres,endemism,Ericales,grasslands,phylogenomics,typification,tro
pical mountains

Abstract:

Agarista is a little-known and understudied genus of subshrubs to trees in the blueberry family (Ericaceae). The genus includes about 33 species, with one variable and widely distributed species occurring along the mountains of tropical Africa and the islands of the western Indian ocean, and the other around 32 species endemics to tropical mountains and temperate lowlands of the Americas. Despite the monographic and cladistic previous works providing an excellent opportunity to test the monophyly of Agarista and species circumscriptions through a phyletic approach, sampling for phylogenetic assessment has been sparse. Only 6% of the Agarista species are represented in phylogenetic, biogeographic and evolutionary studies based on molecular data. Thus, my research is in view of provide a systematic study of Agarista focusing on the Neotropical species, especially in the Brazilian diverse center. My study comprises morphological data, taxonomic revision, molecular phylogenetic analysis, evolutionary character reconstruction, and biogeographic analysis. I am testing the monophyly of Agarista and reconstructing a phylogenetic hypothesis for its evolution. We know that the American species are distributed among five main geographic areas previously defined. Except for Agarista duckei with a disjunct distribution, each of these areas comprises an endemic set of species. On this hand, I am also looking for to understand how morphological characters evolved within the group and, based on biogeographic analysis, test hypotheses of past connections among these currently isolated set of species in South America. In view to accomplish it, besides the literature review and analysis of the protologues and types, 22 Brazilian and six North American herbaria were revised in person, plus the herbaria revised through their specific websites. Besides that, 15 taxonomic entities, including species, varieties and hybrid morphotypes were collected in three fieldwork expeditions. Until now, 17 typifications were proposed for the names in Agarista, being one neotypification, 16 lectotypifications and five epitypes designations. Currently, we confirm the occurrence of 33 species in the Neotropics, 22 of them Brazilian, being 20 endemics to this country. The next steps comprise the molecular analysis that are in progress in the Botanical Research Institute of Texas in view to clarify the evolutive and biogeographical history of the genus.

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Molecular Ecology

Topic: Poster

Title: Whole-genome sequencing of an herbicide selection experiment identifies a chromosomal region associated with herbicide resistance in Eurasian watermilfoil (Myriophyllum spicatum L)

Author: ***Ryan Thum @ Montana State University***

Keywords: adaptation,gene expression,Herbicide,QTL mapping

Abstract:

The evolution of herbicide resistance is a fascinating example of contemporary evolution, and provides opportunities to study the genetics and genomics of adaptation. In addition, identifying the genetic architecture of resistance has practical value for developing tools for nuisance plant management (e.g., genetic tests for herbicide susceptibility versus resistance). Although much attention has been paid to the genetics and genomics of herbicide resistance in terrestrial weeds of agricultural significance, comparatively little attention has been paid to invasive aquatic plants, which are also frequently managed with herbicides. Here, we focus on the genetic architecture of herbicide resistance in the invasive aquatic plant, Eurasian watermilfoil (Myriophyllum spicatum L). We developed a genetic mapping population for fluridone resistance by crossing a known resistant strain to a known susceptible strain. We identified resistant versus susceptible progeny from this cross by exposing them to 6 ppb fluridone for several weeks. Then, we performed whole-genome sequencing on the most resistant (‘resistant bulk’) and most susceptible (‘susceptible bulk’) progeny to compare DNA sequence variant frequencies across the genome between the two bulks. We identified a large effect quantitative trait locus (QTL). Interestingly, the gene for the phytoene desaturase enzyme (PDS) – the molecular target for fluridone – is not located on this chromosomal region. This indicates that structural mutation in the phytoene desaturase enzyme is not the mechanism of resistance for this strain. Further, comparison of PDS expression in susceptible versus resistant strains suggests that resistance is not related to increased PDS expression. Taken together, these results suggest that fluridone resistance in this strain is non-target site resistance (e.g., metabolism, reduced uptake or translocation). Current research focuses on 1) identifying the causal variant(s) for fluridone resistance in this population, 2) developing a molecular test for resistance in this population, and 3) comparing QTL from a second fluridone resistance mapping population to study repeatability of herbicide resistance mechanisms.

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Physiology

Topic: Poster

Title: CAM (Crassulacean Acid Metabolism) photosynthesis in Native Hawaiian Peperomia

Author: ***G Young Kim @ University of Connecticut***

Keywords: CAM,Peperomia

Abstract:

CAM (Crassulacean Acid Metabolism) photosynthesis in vascular plants has evolved independently numerous times from the ancestral C3 pathway to minimize water loss in response to drought stress. To minimize evapotranspiration, CAM plants close their stomata during the daytime. At night, when temperatures are lower and transpiration is relatively less, CAM plants open their stomata and fix CO2 via an enzyme called PEPC (Phosphoenolpyruvate carboxylase). The fixed carbon is stored as an organic acid in the vacuole. Stored malic acid becomes available in the daytime via decarboxylation and provides a high concentration of CO2 to the Calvin cycle. The CAM pathway largely occurs in desert plants, however, it also is found in epiphytic plants which reside in non-soil environments. Some epiphytes employ a stress-induced CAM called facultative CAM, which uses both the standard C3 pathway under normal conditions and the CAM pathway under stressed conditions. Peperomia (family Piperaceae) is an epiphytic taxon that is widespread throughout tropical regions. Pacific lineages of Peperomia have diversified into native and endemic species to the islands of Hawaii. Likely due to its epiphytic habitat, Peperomia species use CAM photosynthesis, though data is limited and only a small fraction of species have a photosynthetic pathway known. Here we aim to determine the photosynthetic pathway in native Hawaiian Peperomia. Five epiphytic, native Hawaiian Peperomia were used in this project: P. blanda, P. cookiana, P. hypoleuca, P. mauiensis, and P. sandwicensis. Plants were grown in common conditions and measured for photosynthetic traits, including gas exchange and titratable acidity, under both well-watered and drought-stressed conditions. Leaf anatomical sections were measured for cell size, air space, and overall thickness. We find a spectrum of CAM phenotypes in the species measured, from strong CAM to weak CAM and C3. One species, P. sandwicensis, had induced CAM under drought. Further work will examine gene expression differences across a gradient of C3, weak CAM, and facultative CAM species in Peperomia.

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Phytochemical

Topic: Poster

Title: Leveraging comparative phylogenetics to explore the evolution of cuticular waxes in the succulent genus Kalanchoe

Author: ***Nicole Groth @ University of Minnesota Duluth***

Keywords:

Abstract:

Kalanchoe is a valuable study system that utilizes CAM photosynthesis and demonstrates high water-use efficiency, as well as extreme drought-tolerance qualities. Many Kalanchoe species produce wax blooms, which are accumulations of hydrophobic surface chemicals that aid in water retention and buffer against temperature fluctuations. The purpose of this study is to evaluate the chemical composition of wax blooms among Kalanchoe and to examine the tempo and mode of evolution of wax bloom traits across the Kalanchoe phylogeny. We presen a newly-generated phylogeny, based on sequences of the internal transcribed spacer (ITS) region of 18–26S nuclear ribosomal DNA, in an effort to establish a comparative phylogenetic framework. Our initial maximum likelihood and Bayesian reconstructions reveal uncertain relationships among the species of Kalanchoe sampled, suggesting that additional loci might be needed to improve overall confidence across the evolutionary tree. We are currently in the process of collecting wax bloom chemistry data for the species sampled in our phylogeny using gas chromatography-mass spectrometry. Progress-to-date regarding the observed patterns of wax bloom abundance and composition across Kalanchoe, and related phylogenetic comparative analyses will be discussed.

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Symbioses: Plant, Animal, and Microbe Interactions

Topic: Poster

Title: Non-Native Plants and Caterpillar Immune Systems

Author: ***Mason Hoffman @ Utah Valley University***

Keywords: Competition,ecology,Herbivore,monkeyflower,caterpillar

Abstract:

The ability of non-native plants to successfully invade and dominate ecological communities is a central area of ecological study. Many important hypotheses such as the evolution of increased competitive ability and the novel weapons hypothesis suggest that the reason for non-native success is the ability of non-native plants to have reduced herbivore attack, allowing them a competitive advantage over native plants that are attacked by insect herbivores. The insects that “choose” the “winners and losers” of plant-plant interactions are also dealing with their own antagonistic relationships, particularly parasitoid predators. Many herbivores have been found to deal with these parasitoids by medicating themselves through their diets. We tested to see if this self-medication may help explain herbivore preference for native or non-native plant species by testing the immune responses and survivability of Trichoplusia ni fed on the native Mimulus guttatus and the non-native Nasturtium officinale. We also tested the plant consumption rates for caterpillars with and without a parasitoid proxy when presented with N. officinale and M. guttatus together. Immune responses of 5th star T. ni were elevated while feeding on N. officionale compared to those feeding on M. guttatus. Further, we found that T. ni neonates were not able to survive on N. officionale while neonates survived on M. guttatus. During immune response trials, we found that T. ni percent consumption based on injection type had a statistically significant difference. However, plant type and plant type with an interaction term were not significantly different in percent of leaf consumed, indicating no diet preference. During behavior trials, we found no statistically significant preference change after injection for the T. ni when given both N. officinale and M. guttatus together. Our results suggest that herbivores may alter plant-plant competition when they are faced with their own top-down pressures, while still having significant restraints on their ability to consume.

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Education and Outreach

Topic: Poster

Title: METHODS ON INCLUSION OF BIPOC AND LGBTQ+ STUDENTS IN AN ONLINE BOTANY COLLEGE COURSE

Author: ***Keri Maricle @ Barton Community College***

Keywords: situational cues,inclusive teaching,BIPOC students,LGBTQ+ students,higher education

Abstract:

Social identity threat is a psychological concept that states some people can feel they may be treated differently because of their identity in certain environments. Some of this can be explained by situational cues that can indicate to individuals of a particular race, ethnicity, socioeconomic status, sexual identity, or sexual orientation that they may or may not be subject to prejudice. In some cases, long term health is influenced by repeated social situations that cause stress (i.e., minority stress theory), which has been indicated to be a major cause of mental health issues in the United States. Among groups most susceptible to these risks are BIPOC and LGBTQ+ individuals. Educational institutions can serve as a tool to combat these issues through innovative and inclusive curriculum modifications. The methods presented here are centered around psychological approaches to fostering inclusion of BIPOC and LGBTQ+ students through application of situational cues in an online classroom that facilitate a sense of belonging. This involves updates to curriculum and presentation to indicate to students they are welcomed and can see themselves adequately represented in instructional materials. Specific methods used in this study include a preliminary student survey to inquire about student goals and identity, course instructor information including preferred name and pronouns, highlighting scientists from historically marginalized groups, and updating visual aids to include inclusive imagery. An online classroom setting was used to facilitate these updates to curriculum with student feedback being used to gauge response. Having an online classroom allowed for a more diverse sample size including students with disabilities and representation of students living in different areas across the United States. Overall, student feedback was positive with comments made specifically about having a sense of belonging even in an online setting. This preliminary work has facilitated the advancement of more psychological research with emphasis shifting toward campus climate and differences in inclusive practices between courses in the sciences and humanities.

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Macroevolution

Topic: Poster

Title: Systematics of the Genus Silphium (Family Asteraceae)

Author: ***Connor Root @ Missouri Western State University***

Keywords: Evolution,phylogenetics

Abstract:

The genus Silphium, better known as the "Rosin-weeds", belongs to the sunflower family Asteraceae. Silphium is native to North America and has species that stretch across the eastern United States, parts of Canada, and the midwest. Missouri is home to 4 native species of Silphium. Silphium has been identified as a potential source of biofuels. Silphium was last studied in 2000 and therefore requires reevaluation with modern DNA analyses methods. We utilized the bioinformatics programs MrBayes on XSEDE and BioEdit to help us understand whether signatures of evolution would vary among different species, taxonomical sections, and subsections within the group based on the data we derived from nucleic and chloroplast markers. Combining data from a variety of loci has allowed us to develop a better understanding of the relationships present between members of the Silphium genus.

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Ecology

Topic: Poster

Title: Understory Shrub Community Composition of Mesic Hardwood Forests Influenced by Local Heterogeneity in Light and Soil Environments

Author: ***Samuel Anderson @ University of Wisconsin Madison***

Keywords: Community composition,community ecology,shrubs,temperate forest

Abstract:

Despite great contributions to the diversity of temperate deciduous forests, shrubs tend to be underrepresented in both ground layer herbaceous studies and overstory assessments. Likewise, intermediate-stature shrubs persist in an understory forest layer of notable environmental heterogeneity. Treefalls and edge effects produce a mosaic of light availability, while substrate characteristics vary dramatically based on underlying geology, microtopography, and uprooting disturbance. When considered with the paucity of community data, there is a considerable gap in our understanding of temperate shrub microsite specificity within temperate forest understories. Given the prevalence of gap-phase disturbance in temperate deciduous forests and the influence of soil texture on mesic forest establishment, we hypothesized that understory shrub community composition and diversity are shaped by microsite heterogeneity in light availability, soil texture, and topography. Throughout Wisconsin, 50m2 quadrats were surveyed for shrub abundance, light environment, microtopography, and soil texture analysis at sixteen mature hardwood forest sites throughout northern and southern Wisconsin. Soil cores were taken to record the depth of the A1 soil horizon as well as ratios of sand, silt, and clay. Light environment was characterized using hemispheric photography, while site-level climatic data was derived from 20-year averages from Wisconsin weather stations

Species richness and Shannon Diversity varied fivefold between sites, though generalized linear models revealed no significant impacts across variables assessed. Composition and species cooccurrence differed greatly between northern and southern forest sites. Multiple regression analyses of NMDS axes with a Bonferroni adjustment determined that percent clay and climatic variables significantly shape understory community composition at the site level, while quadrat level analyses show soil texture and canopy openness to significantly impact community composition. These results reveal that though climatic factors and underlying geology shape shrub community composition, the microsite composition of shrub communities is impacted by both soil texture and light availability. Such findings highlight the importance of considering microenvironment when managing and restoring temperate understory shrub communities.

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Symbioses: Plant, Animal, and Microbe Interactions

Topic: Poster

Title: Resilience Through Complementarity: Assessing the Compatibility of Corn, Bean, and Squash Root Architecture, Exudates, and Soil Associated Microbes in the Three Sisters Polyculture

Author: ***Bailey Kretzler @ University of Vermont***

Keywords: Common Bean,Maize,root exudates,soil microbes,root system architecture,Squash,polyculture

Abstract:

Resilient agroecosystems used in smallholder production support global food security and producer livelihoods. Many of these systems, including the three sisters polyculture, display remarkable resilience to abiotic and biotic stressors. The three sisters is a polyculture of corn, bean, and squash used by indigenous people in North America that offers a lower input alternative to high input conventional agriculture. Previous studies show that corn, bean, and squash adopt complimentary root architectures when grown in polycultures. Such changes in root architecture are shown to impact root exudate profiles and soil microbial identity and function. Thus, differences in plant root traits and soil microbial characteristics may support the three sisters' resilience. However, the plant-soil-microbe interactions driving the three sisters ability to maintain stable yields under stress remain understudied. It is important to identify the plant root traits and soil microbial characteristics enabling the polyculture's ability to endure and rebound from stress in order to design more resilient agroecosystems. We use a combination of growth chamber experiments and common gardens to understand how crop root architecture, exudates profiles, and soil microbial communities differ between polycultures and monocultures of corn, bean, and squash. In growth chamber experiments, corn and beans were grown in Hoagland's media solidified with gellan gum to determine the impact of growth in co-culture on root exudates and architecture. Plants were grown for 10 days alone, with each other, and with themselves. 3-D root architecture was determined by taking picture of plant root systems on days 3, 5, 7, and 10 using the Topp lab gel imaging platform. At the end of the growth period, media was collected from interacting and isolated root tips to assess root exudate profiles. In complement to this work, common gardens will be established in Maine and Vermont to assess the additive impact of corn, bean, and squash on soil microbial characteristics. Crops will be grown in monoculture, biculture, and triculture. We will collect rhizosphere and bulk soil samples and root and shoot material to determine each crops impact on soil microbial communities and crop above and below ground complementarity. Our research highlights how the three sisters polyculture can support healthy agroecosystem function. Plant traits identified in our research as supporting resilience can be used in indigenous breeding efforts to promote food security while preserving cultural relevance. Unpacking the complex plant-soil-microbe dynamics of the three sisters ultimately enables us to design and execute more resilient agroecosystems and sustainable food production.

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Phytochemical

Topic: Poster

Title: ## Re-examining the functional significance of betalains

Author: ***George Garnett @ University of Cambridge***

Keywords: Anthocyanins,Caryophyllales,convergent evolution,pigments,specialized metabolism,betalains

Abstract:

Specialised metabolites are common in plants, with many of these compounds conferring some fitness benefit to the individuals that produce them. My work focusses on two plant specialised metabolites: anthocyanins and betalains. Together, these pigments are responsible for much of the red colouration visible in plants. Despite their similar appearance, there are important differences between these two pigments. Anthocyanins are ubiquitous in plants; contrastingly, betalains are rare, being found only in the order Caryophyllales where they have evolved convergently up to four times. Curiously, betalains and anthocyanins are mutually exclusive, having never been found to co-occur. Some have attributed this to functional redundancy; however, the role of betalains in plants is poorly understood. The replacement of anthocyanins with betalains in some members of the Caryophyllales could suggest that betalains possess novel adaptive advantages over anthocyanins that favoured their repeated recruitment. My research seeks to better understand the functional significance of betalains, using several interdisciplinary approaches. This knowledge should reveal the extent to which natural selection played a role in the convergent evolution of betalains. It is hoped this will improve our understanding of the evolutionary forces that drive convergence more generally; in turn helping to answer a fundamental biological question – how repeatable is evolution?

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Ecophysiology

Topic: Poster

Title: ## Effects of watering treatments on growth and development of important crop species

Author: ***Tori Ott @ Saginaw Valley State University***

Keywords: Aerenchyma,Trifolium,Zea,Triticum,Hordeum,Guillenia,SPAD,chlorophyll

Abstract:

Environmental conditions, particularly water stress, impact crop growth and development, and therefore influence crop productivity and yield. The purpose of our research was to examine how five important crop species were affected by flood, drought, and well-watered conditions. Corn, wheat, barley, mustard, and clover were exposed to flood, drought, and well-watered treatments in greenhouse conditions. Plant morphology, photosynthetic ability, leaf chlorophyll content, biomass, and root anatomy were measured and were affected by drought and flooding treatments in all species. Plants responded differently to watering treatments based on species. Growth, in terms of biomass and plant height, was affected by drought and flooding, with flooding having a greater impact. Both flooding and drought reduced biomass by more than half. Flowering was reduced by drought or flooding to different degrees across species, which would reduce grain production in crop plants. Leaf chlorophyll content was reduced most notably by flooding, reducing photosynthetic ability. Root aerenchyma was increased by flooding, which supplies oxygen internally to support respiration in submerged tissues. Flooding had a greater effect on the overall growth and development of plants than did drought. Taken together, these impacts of water stress can profoundly affect the growth of crop species and reduce agricultural productivity. The negative impacts of water stress should be mitigated for ideal crop growth and agricultural output.

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Systematics

Topic: Poster

Title: ## A Hyb-Seq approach to species delimitation and hybridization in Andinocleome

Author: ***Henry Landis @ Washington State University***

Keywords:

Abstract:

Hyb-Seq approaches have been broadly successful at illuminating relationships at the species level. An appealing extension of these methods is the application of Hyb-Seq data to patterns of species delimitation and hybridization. The genus Andinocleome (Cleomaceae), native to the Andes, has recently undergone a taxonomic revision and currently comprises nine species. Of these, hybridization has been suspected between A. anomala and A. glandulosa, as well as A. moritzana and A. longifolia, based on morphological similarity. To date, no genetic investigation into species boundaries among Andinocleome has been performed. We conducted a Hyb-Seq protocol using the Angiosperm353 probe set to 69 individuals of Andinocleome covering all nine species. We utilize both novel field specimens and herbarium vouchers to account for the full geographical and morphological distribution of the genus. To search for signals of hybridization, we plan coalescent modeling to construct population-level relationships, and subsequently apply the Species Networks applying Quartets (SNaQ) function in the phylogenetics software PhyloNetworks to evaluate the likelihood of competing hypotheses for the timing and directionality of hybridization events. The results of this approach are expected to clarify species boundaries among Andinocleome that have long been considered cryptic, as well as identify where these boundaries are permeable and permit reticulating evolution within the genus.

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Population Genetics/Genomics

Topic: Poster

Title: ## Triploids, Tetraploids, and Hexaploids, Oh My! Cogongrass Ploidy Distribution Throughout the Invaded Range

Author: ***Elizabeth Esser @ Mississippi State University***

Keywords: Diploid and polyploid ,Genetic diversity,Microsatellites,Plant invasion

Abstract:

Cogongrass (Imperata cylindrica) is one of the worst invasive plants impacting the southeastern United States, where it threatens native biodiversity and economic productivity by forming dense monocultures, altering fire behavior and regimes, and is a major obstacle to restoration and afforestation efforts. Unlike many invasive plants that only have one ploidy level in the invaded range, cogongrass has been shown to have high levels of genetic diversity and has been found to be variable in ploidy, including diploid, triploid, tetraploid, or hexaploid in the invaded range of the southeastern United States. The effectiveness of cogongrass management could be variable due to cogongrass ploidy level; however, only preliminary research has been conducted to assess ploidy levels. The potential impact regarding the spatial distribution or ecological implications of variable ploidy on its spread and management has yet to be studied. Microsatellites have been successfully used to identify ploidy in other plants, but microsatellites have not yet been tested for ploidy identification in cogongrass. This study investigates potential use of microsatellite markers to map the spatial distribution of cogongrass's variable ploidy in the invaded ranges. Preliminary results from this study will be presented and discussed. We predict that microsatellite markers will be capable of detecting ploidy in cogongrass, and we will use accessions with known ploidy levels previously determined by flow cytometry and squashes of meristematic tissues to test accuracy of these microsatellite markers. Understanding ploidy distribution may help target and refine control efforts by identifying populations that have higher or a diversity of ploidy levels and thus may possess higher genetic diversity, and therefore, adaptive capacity, which could increase the likelihood of invasion success or resistance to management.

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Tropical Biology

Topic: Poster

Title: Quantifying and Testing for Leaf Venation Patterns Within Araceae.

Author: ***Malinda Barberio @ University of Michigan***

Keywords: fossil leaves,leaf traits,vein density,VLA,Anthurium,Philodendron,leaf architecture

Abstract:

Leaf venation patterns have been used as an important resource for reading the leaf fossil record of angiosperms. Leaf trait evolution, climate reconstruction, and community construction have been derived from dicot venation patterns. However, monocots exhibit very different venation patterns and whose diversity is largely understudied, which obscures our understanding of their evolutionary history. Araceae, a very diverse family of monocots in the order Alismatales, diverged in the early Cretaceous. Their diverse leaf shapes, vein architectures, and growth habits may help provide more information on monocot venation that can be used to read the fossil record. Araceae leaves include both reticulate patterns with higher-order venation similar to dicots, as well as monocot typical parallel (costadromous, pinnacostadromous) patterns. Previous research hypothesized that there are significant differences between venation patterns in Araceae at the subfamily level that can be used for leaf material identification, however, no standardized vein classification or statistical models have been applied. This study used cleared leaves to analyze the vein density (vein length per area; VLA) of the total, parallel, cross, and higher-order veins and morphological traits (e.g., leaf perimeter, area, and shape) among Araceae to determine if there are morphological or phylogenetic patterns that can be applied to material identification and explain the evolutionary history of Araceae venation. The species-rich and morphologically diverse genera Anthurium (with dicot-like reticulate venation) and Philodendron (with parallel venation) were used to specifically test if there is a relationship between leaf shape and size with venation. Linear regression and MANOVA tests between all vein types determined significant differences between subfamilies, and between Anthurium and Philodendron. Ternary plots demonstrated clear separation of each subfamily based on the parallel, cross, and higher-order VLA. Although vein patterns are significantly different among Anthurium and Philodendron, they are not correlated with leaf shape, size, or perimeter. These patterns are likely a result of transport and mechanical support due to different Anthurium and Philodendron growth habits. The results support previous hypotheses that fossilized and extant Araceae exhibit clear venation patterns among subfamilies and can be used for sample identification. Further studies can incorporate additional genera to expand on these relationships and consider Araceae diversity growth habits, and geographic range.

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Ecophysiology

Topic: Poster

Title: The effects of drought and intraspecific competition on the development and growth of corn

Author: ***Brian Maricle @ Saginaw Valley State University***

Keywords: Zea,SPAD

Abstract:

Corn is an important agricultural plant. Production of corn is influenced by environmental factors such as drought and crowding of plants. In this experiment, the effects of intraspecific competition and drought were measured to evaluate the growth and development of corn. Height, chlorophyll content, anthesis, flowering, and biomass were measured in pots with varying densities of corn. Densities of five, four, three, two, and one corn plant(s) were sown in control or drought treatments in greenhouse conditions. Drought and crowding conditions both reduced growth of plants, with each causing a decrease in biomass by 25 to 50 percent. Similarly, flowering and anthesis were both reduced by drought and crowding, with drought having a particularly strong effect. In droughted plants, most plants did not reach anthesis. Drought and crowding conditions caused a decrease in anthesis, height, biomass, and flowering. Crowding causes plants to compete for resources such as water, nutrients, and sunlight. Drought limits a plant’s intake of water, which also manifests in reductions of photosynthesis, growth, and development. Drought and crowding conditions should be considered when grown for agricultural purposes, especially with corn being such a vital crop.

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Population Genetics/Genomics

Topic: Poster

Title: Population structure in invasive Blue Mustard (Chorispora tenella)

Author: ***Kathryn Turner @ Idaho State University***

Keywords: biological invasions,invasion,Invasive,invasive species,Plant invasion,population genomics,STRUCTURE,PCA

Abstract:

Invasive weeds can spread rapidly, compete for limited resources, and cause harm to the novel habitats they invade. Understanding how and the degree to which these invasive species adapt to novel environments is key to managing their expansion and reducing negative impacts. Blue mustard (Chorispora tenella, Brassicaceae) is native to southern Russia and southwestern Asia and invasive in North America, spreading predominantly in disturbed habitats such as along roadsides and in agricultural settings. This has created competition with crops like winter wheat, which can result in loss of grain yield. Examining genetic variation in these invasive populations could uncover traits contributing to invasiveness. Using genomic data gathered across five Rocky Mountain and Cascade states from 83 individuals spanning 32 populations, we investigate population structure and genetic variation in invasive C. tenella. We use reduced-representation genomic data to gain insight into the current underlying genetic structure among populations of this invasive weed.

One key question regarding invasive species is the degree of the genetic bottleneck caused by the introduction. Preliminary principal components analysis indicates 2 to 4 genetic clusters in this data set. One of these clusters comprised populations from all five states, while one only includes two Wyoming and one Colorado population. Interestingly, two of the other potential clusters consisted of only Wyoming. Within one of the Wyoming exclusive clusters contained five different populations from the state. This could be indicative of multiple separate introductions or genetic variation that has evolved post-introduction. An estimated Fst provides a certain amount of support for divergences between these populations of C. tenella. Further analyses are ongoing.

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Ecology

Topic: Poster

Title: Effects of genome size variation on germination success in big sagebrush (Artemisia tridentata)

Author: ***Elizabeth Mandala @ Idaho State University***

Keywords: ecology,genome,genome size variation,Germination,Seed germination

Abstract:

The establishment-life history phase of many plants, including seed germination, is crucial to plant success. This is particularly important in the case of threatened foundational species, whose success is linked with ecosystem health. Understanding traits that impact germination success is necessary, as this is not well understood in many systems. Genome size is a trait that is known to affect phenotypic expression of plants in an ecosystem. However, the extent to which genome size affects germination success is unclear. Understanding these influences are of great importance to threatened ecosystems, including the threatened sagebrush steppe. Artemesia tridentata (Asteraceae), big sagebrush, is a vital shrub to ecosystems of western North America and occurs across a large range of environmental variation. Multiple species rely upon this shrub, some exclusively, for habitat and food throughout the seasons including the greater sage grouse, pronghorn antelope, and the pygmy rabbit. The sagebrush steppe ecosystem has been threatened by expanding rangeland, encroachment of competing vegetation, and most significantly, by fire incidence. Successful restoration of big sagebrush is of great importance to reestablishing sagebrush steppe ecosystems and protecting the wildlife of the region. Big sagebrush also includes individuals representing a large range in genome size and multiple ploidy levels. Our aim was to assess the influence of genome size on germination success of A. tridentata. We conducted a growth chamber experiment in which sagebrush seeds with varying parental genome sizes from 26 individuals from each of three locations across Idaho were germinated under identical conditions and the proportion of seeds germinated from each parent was assessed. Preliminary statistical analysis of these data show a significant interaction effect of genome size and site on germination proportion. This result suggests that the proportion of germination increases with genome size at different rates dependent on site, thus illustrating the importance of genome size on germination success.

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Paleobotany

Topic: Poster

Title: Macro- and microfossil analysis of the P-40 locality of the Lake Clarkia Fossil Beds.

Author: ***Ian Spendlove @ University of Idaho***

Keywords: paleobotany,Palynology,Clarkia,middle Miocene

Abstract:

Ancient Lake Clarkia was formed 15.78 million years ago when a Priest Rapids flow of the Wanapum Formation of the Columbia River Flood Basalts dammed the ancient St. Maries River near Clarkia, Idaho. The Clarkia Fossil Beds contain exceptionally preserved fish, plants, and palynomorph fossils that record high temperatures of the Mid-Miocene Climatic Optimum. While there has been extensive macrofossil and palynomorph work done on the P-33 and P-37 localities over the last 60 years, neither has been performed on the P-40 locality due to poor access to the site.

Here, we have performed palynomorph and macrofossil analysis of a 10 cm x 30 cm x 30 cm section of the P-40 site. This is the first study to be done comparing the differences between the plant macro- and microfossil assemblages of the P-40 locality. Preliminary results show that the macrofossils represent the near-shore plant assemblages of the mixed mesophytic forest, with the microfossils representing the regional flora around the lake.

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Education and Outreach

Topic: Poster

Title: The Next Generation: Receiving Mentorship in Herbarium Practices as an Undergraduate

Author: ***Izzy Hudson @ University of Connecticut***

Keywords: Course-based undergraduate research experience ,Herbarium curation,Herbarium Digitization,herbarium specimens,student mentoring

Abstract:

The 1984 -1985 Louise Young herbarium collection box has sat untouched for 40 years in the dry collection storage section of UConn's George Safford Torrey Herbarium. Like much backlog material, it had been lost in the endless stream of projects that continuously cycle through the herbarium. I received this box to process independently after over a year of receiving training and mentorship as an undergraduate curatorial assistant. Louise Young had some of the best quality specimens that I have seen collected during this time. Each of the 175 specimens perfectly fits the standard herbarium sheet size, displays useful plant traits, and comes with complete label data. However, her specimens presented a new challenge: associating 12 zip lock bags of underground root structures with their aboveground shoots. Additionally, most mounted specimens were on non-archival acidic paper, so I determined whether they fit criteria for remounting onto archival-grade sheets. I practiced sewing bulkier specimens to sheets, assessed both paper and specimen quality, transferred specimens onto archival sheets, created high-resolution images, and entered label data into a relational database (BG-BASE). Louise Young's collection now has potential to aid the scientific community by being accessible to anyone online and providing valuable spatial, temporal, and phenotypic data on a wide range of plants.

This poster provides a student perspective on the importance of involving undergraduate students at an advanced level within this crucial backbone of botanical science. Students, mentors, and collections benefit greatly from the development of strong student-mentor connections. Using the Louise Young box as an exemplar, this project explores student achievements from acquiring skills such as data management, careful handling of specimens, and confidence in making independent choices on the best route for specimen curation. In addition, it showcases the advantages for mentors and collections of training self-sufficient student assistants, particularly at the undergraduate level or younger, who may pursue careers as the next generation of herbarium curators.

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Ecology

Topic: Poster

Title: Floral and pollinator trait variation in high-elevation meadows of the Madrean Sky Islands

Author: ***Liliana Benitez @ University of Texas, Austin***

Keywords: Pollination,sky islands,functional floral traits

Abstract:

In the face of shifting global biodiversity patterns, it has become increasingly critical to recognize that ecosystem function is not only mediated by species-level diversity, but also by interactions between species. Mutualistic interactions, such as those between plants and their pollinators, seed-dispersers, and mycorrhizal associates, play a critical role in ecosystem function. Previous research has shown that greater species-level diversity in partner trophic levels enhances plant reproductive success, gene flow, and nutrient cycling. This is believed to be driven by species' functional trait diversity, however, it is understudied in the context of mutualistic interactions. Furthermore, complementary traits between interacting partners, known as trait matching, have been proposed as an additional mechanism governing ecosystem function, particularly for functions that rely on interspecific partnerships.

Over the period of 3 years, we collected floral and bee trait data at 25 independent and approximately 3 ha-sized meadows across the Madrean Sky Islands system, an iconic region consisting of over 30 isolated mountain tops with high-elevation meadows. We additionally obtained climate and soil data for the region from the PRISM climate group database and the U.S. Forest Service Terrestrial Ecological Unit Inventory geodatabase. We aim to evaluate whether ecologically similar patches contain plant and pollinator communities with similar trait spaces.

Preliminary results also show that our sites exhibit substantial variation in trait diversity (e.g. mean tongue lengths range from 1.06mm - 4.27mm, mean corolla tube lengths range from 3.6mm - 13.2mm), and trait matching (e.g., site regression coefficients for tongue and corolla lengths range from 0.03-0.98, with a value of 1 representing full trait matching). Climate conditions also varied considerably across sites and years. For instance, total July precipitation during the start of the monsoon season ranged from 83 mm to 249 mm in 2017, 79mm to 183 mm in 2018, and 66 mm to 236 mm in 2021.

Our ongoing work will assess the impact of trait composition on pollination network metrics within the same study sites.

391

Macroevolution

Topic: Poster

Title: Dynamics of evolution in Irano-Anatolian and Caucasus biodiversity hotspots: Evolutionary radiation and its drivers in Gypsophila (Caryophyllaceae)

Author: ***Hossein Madhani @ University of Nevada, Las Vegas***

Keywords: evolutionary radiation,Fossil Calibration,nrDNA ITS,cpDNA matK,cpDNA rps16,diversification rate

Abstract:

Irano-Anatolian and Caucasus biodiversity hotspots, which are characterized by a high degree of alpine endemism and extremely dynamic geographical history, are among the 35 globally defined biodiversity hotspots. However, the dynamics of evolution and the contributors to diversity have not been studied in these areas. To assess the evolutionary dynamics and its cofactors within this area, we used Gypsophila L. (tribe Caryophylleae: Caryophyllaceae) as a model, which is a large and diverse genus of flowering plants with a high degree of endemism in Irano-Anatolian and Caucasus biodiversity hotspots. We used the sequences of nuclear ribosomal internal transcribed spacer (ITS), the chloroplast gene rps16, and the Maturase K gene (matK) for 228 species across the family, including about half of the species diversity inside Gypsophila. To infer the phylogenetic relationship within the Caryophylleae we used Bayesian inference (BI) and maximum parsimony (MP) analyses. We calibrated the phylogenies using the only studied fossil of the family, Caryophylloflora paleogenica G.J.Jord. & Macphail, using BEAST v.1.10.4 and estimated net diversification rates in stem and crown groups using the Magallón & Sanderson method implemented in the R package GEIGER. Then the change in diversification rate and its biotic and abiotic cofactors were tested using a series of time-dependent, trait-dependent, and paleoenvironmental-dependent models implemented in BAMM, R package diversitree, and RPANDA, respectively. The ancestral distribution ranges were also reconstructed using the Bayesian Binary Method (BBM), and Dispersal-Extinction-Cladogenesis model (DEC). We identified a shift in the diversification rate of Gypsophila that started about 3 million years ago and was influenced by both biotic and abiotic forces. Our results suggest that the diversity inside Gypsophila evolved due to evolutionary radiation that was triggered by both paleoenvironmental factors and new morphological novelties. The study demonstrates a highly dynamic evolutionary history across the Caryophylleae clade and Gypsophila, which is consistent with the extensive fluctuation in the geological and climatological history of Irano-Anatolian and Caucasus biodiversity hotspots. This study significantly improves our understanding of the dynamics of evolution in Irano-Anatolian and Caucasus biodiversity hotspots and the impact of environmental changes on the rate of diversification in this area.

397

Population Genetics/Genomics

Topic: Poster

Title: Conservation genetics in the endangered whorled sunflower Helianthus verticillatus (Asteraceae)

Author: ***Samantha Drewry @ University of Memphis***

Keywords: Helianthus,conservation,Genetic diversity,genetics,Microsatellites,SNPs

Abstract:

Genetic diversity among and within populations of species is critical for survival in a changing world. Conservation genetics links studies of population genetic variation with conservation managers to provide scientific data for species management strategies. We study the conservation genetics of whorled sunflower, Helianthus verticillatus (Asteraceae), an endangered sunflower species endemic to the southeastern United States. Until about five years ago, only five populations were known to exist in Alabama, Georgia, and Tennessee, but additional populations of the species have been discovered in Mississippi and Virginia. Population genetic work using microsatellites revealed that the newly discovered Mississippi plants were genetically distinct from all other populations. To further investigate these new Mississippi individuals and compare them with the rest of the species, we used a combination of genome-wide SNPs and sequencing of phylogenetically informative loci to assess genetic diversity and relatedness on a small subset of individuals. We also included the closely related species, H. grosseserratus, using a collection from Shelby County, Tennessee from the University of Memphis Herbarium. This specimen was collected with only the top portion of the plant. Interestingly this sample fell within the H. verticillatus clade in some analyses. We report the comparative genetic analysis from this subset of samples and note that additional work will be required to further define the extent of genetic diversity in the whorled sunflower.

401

Population Genetics/Genomics

Topic: Poster

Title: Using methylation-dependent restriction digests to reduce repetitive element representation in whole genome sequencing

Author: ***Fae Bramblepelt @ University of Alabama***

Keywords: DNA methylation,genome resequencing,population genomics,Shotgun Sequencing

Abstract:

Angiosperm genomes are often large, complex, and composed of highly repetitive segments, such as transposable elements (TEs). Gene space is relatively small compared to overall genome content, so studies addressing questions of genetic variation either generate large amounts of non-genic sequencing data or employ reduced representation sequencing to focus on regions of interest. Resequencing large genomes can be expensive reducing the overall diversity of sampling due to budget limitations. Though more cost-effective per sample, reduced representation sequencing limits the number of loci sampled in a genome. In this study, we wanted to determine if we can use the methylation landscape of a genome to enrich low-cost, low-coverage whole genome shotgun data for gene space. Repetitive elements are often methylated to control their expression, although not all methylation occurs in repetitive regions, and not all repetitive regions are methylated. Using Sorghum halepense as an experimental system, we treated DNA with two methylation-dependent restriction digest enzymes, FspEI and LpnPI, separately and together, to selectively digest and filter out methylated regions. We then followed standard Illumina library protocols to make libraries, sequenced using paired-end reads, and analyzed the data against a non-digested control to determine if we could achieve selectively-biased higher coverage of non-repetitive regions. Preliminary results suggest a marked increase in gene space coverage along with a decrease in the proportion of reads mapping to repetitive elements. They also indicate more plastome read coverage, suggesting this technique may have applications in large-scale population genomics practices. By achieving higher coverage of non-repetitive elements in whole genome sequencing, we can more cost-effectively investigate genome diversity and evolution.

406

Functional Genetics/Genomics

Topic: Poster

Title: Developing Stable Plant Transformations in the Zingiberales: Pitfalls and Progress

Author: ***Heather Phillips @ Cornell University***

Keywords:

Abstract:

Developing stable plant transformations is a costly and time intensive endeavor, however it is an essential tool for developing novel new model organisms in plant research. For this poster, will present my progress in developing stable tissue culture lines in several representative species of the Zingiberales, including establishment, regeneration, and transformation protocols. I will then show how these systems can be utilized to develop knockout and overexpression lines of floral developmental genes, allowing for the development of comparative developmental studies across a model lineage.

409

Biodiversity Informatics & Herbarium Digitization

Topic: Poster

Title: Modernizing Washburn's Herbarium Collection: Designing a Workflow to Grow Digital Shoots from Analog Roots

Author: ***Jason Emry @ Washburn University***

Keywords: Herbarium curation,Herbarium Digitization,PUI,Workflow

Abstract:

Natural history collections are a vital resource for studying biodiversity and documenting historical changes in species' populations. High-quality herbarium specimens provide a wealth of information on plant morphology, geographic distribution, ecology, and evolution. However, organizing and maintaining such collections can be an onerous task.

Washburn University's herbarium houses approximately 15,000 specimens with more than 75% of the specimens collected within 100 miles of the Topeka, Kansas campus. The collection provides a hyperlocal record of measurable data at fine spatial and temporal scales. However, only half the specimens have been digitally documented and recent renovations uncovered nearly 2,000 additional specimens with neither recorded data nor assigned collection numbers. These facts have prompted us to reassess the state of our collection, determine specific challenges, and define measurable goals.

Specific challenges to Washburn's herbarium collection include an incomplete catalogue, specimens in need of repair, and ineffective databasing and organization methods. To address these challenges, research students at Washburn University designed a workflow that incorporates a stepwise protocol for assessing, repairing, and digitally cataloguing specimens, with a focus on maintaining the quality of each specimen and ensuring accurate identification.

The team's workflow has proved to be effective in cataloguing the Washburn University herbarium collection. It has allowed for improved organization and increased efficiency in recording new data. It has also helped prioritize the repair and annotation of existing specimens. This workflow can serve as a model for other institutions with small herbaria facing similar challenges. These efforts will also ensure that institutions and individuals outside of the area can more easily access the valuable data found in our unique collection.

410

Symbioses: Plant, Animal, and Microbe Interactions

Topic: Poster

Title: Effects of colonization by arbuscular mycorrhizal fungi on Artemisia tridentata seedlings responses to drought under field and greenhouse conditions

Author: ***Marcelo Serpe @ Boise State Universi***

Keywords: arbuscular mycorrhizal fungi,drought,sagebrush

Abstract:

Interactions with other organisms can affect a plant's ability to cope with drought. The re-establishment of Artemisia tridentata, a keystone species of the sagebrush steppe, is often limited by summer drought. This study investigated the effect of the symbiosis with native arbuscular mycorrhizal fungi (AMF) on the drought tolerance of Artemisia tridentata ssp. wyomingensis (Wyoming big sagebrush) seedlings. For this purpose, we compared the responses of non-inoculated and AMF-inoculated seedlings to drought in field and greenhouse experiments. In the field, we evaluated the effect of AMF colonization on leaf water potential, survival, and inflorescence development. The addition of trap culture inoculum increased AMF colonization by 23%, representing a more than 100% rise over the levels measured in non-inoculated seedlings. The seedlings experienced water stress during the summer, as evidenced by water potentials ranging from -2 to -4 MPa and a decrease in stomatal conductance. However, despite the continued drought, the water potentials did not reach letha levels and remained relatively constant after midsummer. There were no differences in water potential or survival between non-inoculated and inoculated seedlings, with both treatments showing survival rates above 90%. The only response variable affected by inoculation was the percentage of plants developing inflorescence. These percentages were 45.4 and 59.0% for non-inoculated and inoculated seedlings, respectively ($p = 0.028$). The greenhouse experiments investigated whether AMF colonization affected the decline in stomatal conductance and photosynthesis induced by drought. AMF colonization did not affect photosynthesis under well-watered conditions. In contrast, AMF colonization delayed the drought-induced decrease in stomatal conductance and photosynthesis, or this decrease occurred at a lower soil water content. These effects were not related to a lower water potentia threshold for stomatal closure but to an increased ability to extract water from the potting substrate. Overall, the greenhouse results are consistent with the notion that AMF colonization enhances drought tolerance of A. tridentata seedlings. However, the significance of the observed effect on increasing survival in natural habitats remains to be tested under more extreme water stress conditions than those experienced by the plants in our field experiment.

413

Population Genetics/Genomics

Topic: Poster

Title: Population genetics and breeding system estimation of four mixed breeding and one exclusively chasmogamous species of Viola

Author: ***Samuel Lockhart @ Ohio University***

Keywords: Cleistogamy,GBS,population genetics,reproductive biology,Viola

Abstract:

Plant sexual reproduction strategies can be represented by a continuum from outcrossing, where two genetically distinct plants contribute hereditary material to offspring, and selfing, where the entirerity of the offspring's genetic information comes from a single parent. Plant species can be placed on this spectrum according to the degree to which they employ either strategy for sexual reproduction. In mixed-breeding species, those that utilize both outcrossing and selfing, the genetic diversity of populations will differ based on the degree to which either strategy is used for seed production. Therefore, by examining the genetic structure of mixed-breeding populations, plant breeding systems can be estimated and placed on this continuum.

The genus Viola is well known for its exhibition of cleistogamy, an extreme form of selfing characterized by the formation of closed, budlike flowers. In addition, violets also produce chasmogamous flowers, most of which can outcross and self. However, the extent to which these floral form contribute to the establishment and growth of populations is understudied and unknown in the taxonomically complex high polyploid stemless blue violet lineage.

The present study seeks to address these questions by examining the population genetics of four species of stemless blue violets and comparing them to the exclusively chasmogamous and self-incompatible V. pedatae. Five individuals from a total of 15 populations were sampled and submitted for genotyping-by-sequencing. SNPs were called with iPyRad, as this method incorporates ploidy information. Population genetic parameters were estimated with GenoDrive and patterns of population structure were analyzed with STRCUTURE and DAPC. From the results of this study, we aim to evaluate how chasmogamous and cleistogamous flowers contribute to seedling recruitment and differ among species and populations.

416

Ecophysiology

Topic: Poster

Title: Responses of Leaf Stomata to 50 Years of CO2 Increase Using Herbarium Specimens

Author: ***Jazlyn Salazar @ Texas Tech University***

Keywords: Guadalupe Mountains,stomatal conductance,stomatal density

Abstract:

Herbarium specimens provide a glimpse into various past characteristics of plants, which includes the ways that they interacted and responded to the environment. Plant gas exchange is a key process shaping global hydrological and carbon cycles and is often able to be characterized by plant water use efficiency. Plants are able to balance CO2 intake with water loss by regulating the stomatal pore aperture and guard cell signaling is regulated by both environmental factors and plant hormones from plant fossil records, it is suggested that plant adaptation to changing atmospheric CO2 has a correlated evolution in stomatal density and size. Together, stomatal density and size contribute to determining the maximum leaf conductance of CO2, and in this study we used herbarium specimens to track stomata over time. A collection of over 1500 plant specimens housed in the E.L. Reed Herbarium at Texas Tech is from a survey of Guadalupe National Park in the 1970s. From this collection to modern specimens of the same species, we identify how plants responded to over 50 years of CO2 addition. Our results can use a look into the past in the floristic biological diversity to predict how plant communities will respond to future climate changes.

423

Tropical Biology

Topic: Poster

Title: Heterospecific pollen transfer effect on pollination success in a tropical biodiverse community

Author: ***Nathalia Susin Streher @ University of Pittsburgh***

Keywords: community ecology,high altitude plant,plant-pollinator interactions,heterospecific interactions,campos de altitude

Abstract:

Most plants depend on adequate quantity and quality of pollen delivery by pollinators for successful reproduction. Suboptimal reproductive output can be attributed to pre-pollination processes (e.g. few coflowering mates and low floral visitation) and post-pollination processes that occur from interacting communities of conspecific pollen (CP) and heterospecific pollen (HP) grains on stigmas. Even though HP deposition is widespread in nature we still have sparse evidence of its effects on community reproduction limiting our understanding of how pollinator-mediated interactions influence community assembly. Moreover, HP effects can vary widely in sign and strength calling for approaches involving multiple species interactions. We investigated the pollen load composition naturally deposited on stigmas of 30 plant species in a biodiverse tropical community with high levels of pollinator sharing. We tested whether HP affects recipient pollination success (i.e. CP tubes/pollen grain) and whether this effect increases with HP diversity. We identified that even in the absence of HP, conspecific pollination success is halved indicating pollen tube germination limitation by CP quality. The presence of a single heterospecific donor species in the stigma pollen load diminished even more recipient pollination success and this effect was accentuated when two or more HP donor species were involved. Therefore, heterospecific pollen transfer limits the studied plant community reproduction contributing to the understanding of pollen transfer consequences in biodiverse ecosystems.

425

Development and Structure

Topic: Poster

Title: Shedding light on architectural development: The effects of light intensity on plant architecture and reproductive potential in Mimulus gemmiparus

Author: ***Deannah Neupert @ Miami University***

Keywords: Mimulus,comparative methods

Abstract:

The size of a population and its diversity are important aspects of a healthy population. The critically imperiled species Mimulus gemmiparus reproduces asexually by mode of the bulbil, a novel structure that is a combination of an axillary meristem and leaf not found in its sister species, Mimulus guttatus. Asexual reproduction may lead to decreased genetic diversity, increasing the endangerment of the plant. We have an interest in how light conditions affect the structure of the plant, specifically its branching and bulbil and flower production. The focal point of this study is to detect differences in architecture and reproductive potential in Mimulus gemmiparus under varying light intensity. This is relevant for conservation studies as reproduction is a direct result of the architectural complexity of the plant. I devised two treatments for each species, one with shade cloth and one without. Hankin's Gulch was the initial population chosen because it has not been found to produce flowers in nature, but produces flowers in a growth chamber or greenhouse setting. After experiencing some complications with germination, a different population was chosen and the experiment was begun again with the population, Peaceful Valley. So far in the study, we have observed some pigmentation from anthocyanin in the full light treatment and far fewer in the shade treatment. We have also observed some elongation between nodes in some plants within the shade treatment. We will continue to monitor the plants until the end of their life cycle and will perform a final measurement of numbers of flowers and nodes, height, internode length, and branching. We will finish with logistic growth models and significance testing between treatments and species. What we find from this study could contribute to conservation efforts and a greater understanding of the species.

427

Conservation Biology

Topic: Poster

Title:

Paxistima canbyi A. Gray (Celestraceae), a rare plant species of the Central Appalachian region of the United States: Preliminary assessment of threats using population genomics

Author: ***Isaac Buabeng @ Bucknell University***

Keywords:

Abstract:

Understanding the migratory patterns of genes in the clustered metapopulations of Paxistima canbyi across its entire range is important for conserving this species. This project, which is born out of a collaboration between scientists and experts from the Pennsylvania Natural Heritage Program and Bucknell University will assess the genetic diversity and phylogeography of two major disjunct Paxistima canbyi (Canby's mountain lover or Cliff green, Celastraceae) populations - occupying the limestone-rich interior low plateaus of central Kentucky, Northern Tennessee, and southern Ohio, and the similarly limestone-rich central Appalachian mountains of southern Pennsylvania, West Virginia, Maryland, and Virginia - using a reduced-representation sequencing method i.e. Genotype-By-Sequencing (GBS). Data acquired through the Genotype-By-Sequencing (GBS) approach will be used to generate genomic libraries for assessing gene flow, genetic diversity, and migration patterns between other subpopulations and the phylogenetic relationships and historical introgression of populations within and between the two major disjunct Paxistima canbyi metapopulations.

428

Bryology and Lichenology

Topic: Poster

Title:

Testing for evidence of cryptic species in the widespread moss Physcomitrium pyriforme

Author: ***Anij Mackey @ Texas Tech University***

Keywords: bryophytes,cross-compatibility,geographical distribution,hybridization,morphometrics,spores

Abstract:

According to the biological species concept, species in the same genus should be more genetically distinct than individuals within a species due to reproductive isolation. However, in the widespread moss Physcomitrium pyriforme, we have evidence of three distinct genetic clusters unrelated to geographic isolation. We hypothesize that P. pyriforme contains cryptic species - taxa- morphologically indistinguishable but genetically different. We aim to confirm whether the three clades are morphologically distinct in microscopic characteristics including spore and stomatal size. Using a controlled cross-experiment, we also aim to test for reproductive isolation across clades. We crossbred three clades from eastern North America in a growth chamber to test for the production of hybrid offspring. The lack of offspring would suggest that P. pyriforme has cryptic species under its genus. An alternative explanation is that species are not cryptic but are instead defined by microscopic characters including size differences in spores and stomata. Each genetic cluster having different stomatal characteristics of size, density, and count would support the description of new species of the common bladder moss.

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Population Genetics/Genomics

Topic: Poster

Title:

Complex and Cryptic: Giant Rat’s Tail Grass (Sporobolus pyramidalis) in the Southeastern United States

Author: ***Emma Edmondson @ University of South Alabama***

Keywords:

Abstract:

Invasive species are usually managed after their introduction and spread, which is often expensive and ineffective. If potentially invasive, non-native species are identified and tracked closer to introduction, management could become more proactive and cost-effective. However early identification of invasives is often challenging, as non-native species can be similar both genetically and morphologically to closely-related, native species. Misidentification is a common occurrence that can result in a potential invasive going unnoticed. Called cryptic invasion, this results in the spread of a non-native species going undetected because it is morphologically similar to a native species or scientific names are unresolved or misapplied. Unclear species boundaries are at the root of cryptic invasion, and fine-scale genetic and morphological data are needed to help define and identify all species present. Rat’s tail grasses (Sporobolus indicus complex) have been inconsistently classified in literature as containing anywhere between one to twelve species. The Sporobolus indicus complex exhibits variation in plant size, flowering structures, and fruit morphology, but these characters form a gradient of morphology between described species. Additionally, the complex is globally-distributed, and many species are invasive or naturalized outside of their native ranges. Abnormally tall Rat’s Tail grasses were observed and recorded in Alabama. The native species (S. indicus and S. jacquemontii) overlap morphologically with non-native species (S. fertilis and S. pyramidalis, respectively), leading to questions of whether the tall individuals belonged to the native species or were unnoticed invaders. Preliminary results from chloroplast data (rpl32) show that although S. indicus is morphologically distinct, S. indicus and S. jacquemontii are genetically indistinguishable. Samples belonging to the S. jacquemontii-S. pyramidalis morphological cluster were identified genetically as S. pyramidalis, supporting cryptic invasion. A reduced representation genomic dataset will be generated by sequencing inter-simple sequence repeat regions (ISSRseq) to determine (1) if S. indicus and S. jacquemontii are distinct evolutionary units and (2) population structure and gene flow between species.

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Symbioses: Plant, Animal, and Microbe Interactions

Topic: Poster

Title: Antagonistic activity is observed from seed endophytes: A potential tool to aid seeds in establishment during restoration

Author: ***ALEXANDRITE GREENHOUSE @ Gonzaga University***

Keywords: Anti-fungal,plant-microbe interactions,Symbiosis,anti-bacterial

Abstract:

Ecological restoration of damaged habitats is of major concern for many ecosystems today. In the arid Inland Northwest, harsh conditions and microbial diseases can reduce the rate of establishment of seedlings used in restoration. Seed endophytes are potential tools that have yet to be explored in restoration. The goal of our research was to isolate and identify seed endophytes from plant species often used in restoration in the Inland Northwest and to test the antagonistic interactions between endophytic bacteria and fungi. To isolate seed endophytes, we surface-sterilized seeds from two species commonly used in field restoration in the Inland Northwest, the common burnet (Sanguisorba minor, abbreviated as Sami) and a species of needle and thread grass (Hesperostipa comata, abbreviated as Heco). We plated these sterilized seeds on four different agar media (PDA, TSA, R2A, and LB) in order to isolate a more diverse set of endophytes, both bacteria and fungi. Once we isolated the endophytes, we then chose four bacteria and four fungi from each seed species and set them up on agar plates to test the degree of their antagonism. We set up our antagonism plates by taking 4mm plugs of the fungi from a pure culture as well as a swab of bacteria and placing them on PDA plates approximately 2 cm apart. We then compared the degree of inhibition of the bacteria and the fungi to our controls. From our census of endophytes on our seed plates, we discovered that there was a higher frequency and greater richness of fungal morphotypes than bacterial morphotypes (72% more fungal morphotypes than bacterial for S. minor and 28% more fungal morphotypes than bacterial for H. comata). We also found that there was a greater total richness of endophytes for H. comata seeds than for S. minor seeds (58% more morphotypes for H. comata than for S. minor). From our antagonism data, we found that three out of four of the bacteria isolated from H. comata seeds and one out of four from the S. minor seeds were at least somewhat antagonistic to the fungi. Meanwhile, one of four H. comata bacteria and two of four bacteria for S. minor were completely overtaken by all fungi. These results imply that the antagonistic interactions were driven by the antifungal properties of the different bacterial morphotypes rather than by the fungal morphotypes. This is relevant to our research goal in that it could mean endophytic bacteria could be more effective at promoting early seedling establishment in the face of fungal pathogens.

440

Ecology

Topic: Poster

Title: The effect of polyploidy and mating system on floral size and pollination niche in Brassicaceae

Author: ***Nathalia Susin Streher @ University of Pittsburgh***

Keywords: Floral traits,herbarium specimens,whole genome duplication,heterospecific pollen,pollination generalization,self-incompatibility

Abstract:

Polyploidy is a major evolutionary process in flowering plants yet its effects on biotic interactions are still unclear. Whole genome duplication is expected to have impacts on floral traits and selfing propensity which can have cascading effects on pollination interactions. Since the vast majority of flowering plants rely on animal-mediated pollination, the degree of pollination generalization is also expected to play an important role in polyploid population establishment as well on the structure of their communities. Here we used herbarium specimens to assess the effects of polyploidy and mating system on floral traits and pollination niche of 40 Brassicaceae species. For each species, we obtained mating system (self-compatible=SC or self-incompatible=SI) and chromosome counts from the literature and inferred ploidy level (polyploid or diploid). Specifically, we investigated the influence of polyploidy and mating system on 1) flower size and 2) shape (evaluated using PCA analysis of flower tube, length, and width of the attractive portion of petals), 3) the frequency of stigmas with heterospecific pollen, and 4) the richness of heterospecific pollen morphotypes. Based on phylogenetically controlled models, we found an interaction effect of the polyploidy and mating system on flower size, with SI polyploid species having larger flowers than SC polyploids. Floral shape also changed with mating and ploidy but not significantly. With respect to the pollination niche, we only detected an effect of mating system. That is, SI species had more stigmas with heterospecific pollen and more heterospecific pollen morphs on average than SC species, regardless of their ploidy. Our results suggest that mating system moderated the influence of ploidy on morphological features of pollination generalization but that of ecological generalization is more variable.

441

Physiology

Topic: Poster

Title: Uptake of microcystin-LR in tomato occurs via diffusional pathways and is not mediated by specific nitrogen transporters

Author: ***Clare Muller @ University of Toledo***

Keywords: Algae,hydroponics,tomato,microcystin

Abstract:

Harmful algal blooms (HABs) can contain toxins, like microcystins (MC) produced by Microcystis aeruginosa and other species, that have serious implications for human health. Plants can take up many algal toxins, which can accumulate in their tissues (e.g., when irrigated with HAB water). Since the mechanism of uptake and transport of algal toxins in plants is not understood, we investigated the uptake of MC in tomato. Soil-grown tomatoes (4 adult leaves) irrigated with M. aeruginosa-contaminated nutrient solution had lower biomass compared to plants receiving only nutrient solution, indicating uptake of toxin by roots. Then, we treated similar-sized tomatoes for five days in hydroponic nutrient solutions each lacking one of five forms of N (1 mM urea, glycine, NO3, NH4, and a peptide mix) in solution with 200 µg/L MC-LR. We found no significant differences in MC-LR uptake among N treatments, indicating that the major N-uptake proteins were not responsible for MC-LR uptake into roots. Next, we grew tomatoes hydroponically over a range of MC-LR concentrations (0, 10, 100, 250, 500, and 1000 µg/L), and found that MC-LR uptake rate per g root scaled with toxin concentration, indicating that uptake is via diffusion. These results suggest that strategies to improve plant tolerance to algal toxins might focus on traits that limit general root diffusion-uptake pathways, rather than specific uptake proteins.

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Symbioses: Plant, Animal, and Microbe Interactions

Topic: Poster

Title: Characterizing Temporal Changes in Microbial Diversity in Herbarium Specimens from Guadalupe Mountains National Park

Author: ***Mara Hosaka @ Texas Tech University***

Keywords: 18S rRNA,AMF,Fungal endophytes,Metabarcoding,Microbiome,mycology,phylogenetic diversity,leaf endophyte,arbuscular mycorrhizal fungi

Abstract:

Microbial endophytes (fungi and bacteria that live within plant cells) are understood to play a significant role in the ecology of their plant hosts, but little is known of their response to climate change. Now, the diversity of microbes can be easily quantified with DNA sequencing, but there is little historical data with which to compare modern findings. Herbarium specimens may provide an historical record of bacterial and fungal endophyte communities, allowing for study of how endophytic communities may have changed over time. In this study we analyzed changes in endophyte biodiversity over the past 50 years in the Guadalupe Mountains, a biodiversity hotspot in Texas spanning seven ecoregions. We sample roots and leaves of herbarium specimens from several species collected from Guadalupe Mountains National Park. For each species we take samples from both an older specimen collected from 1973-1977 and from a recent specimen collected in 2022. We extract and sequence DNA from herbarium specimens and analyze data using standard microbiome data processing pipeline. We characterize endophyte species richness and phylogenetic relatedness across time points and plant host species and contribute to building a better understanding of the change in composition of plant microbiomes over fifty years.

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Biodiversity Informatics & Herbarium Digitization

Topic: Poster

Title: Best Practices and Minimum Guidelines for Imaging Lichen Herbarium Specimens

Author: ***Eli Denzer @ New York Botanical Garden***

Keywords: digitization,Herbarium Digitization,Imaging,Lichenology,Professional Standards,lichens

Abstract:

Digitization is an increasingly important part of collection management and collections-based research. Imaging and digitizing specimens allows access to collections without in-person visitation, limits risk of loss or damage caused in shipping and transport, and increases efficiency by allowing the collections user community to better focus inquiries or loan requests. Having publicly accessible digital records, that are populated with high quality, standardized data and images, opens up a collection for new and innovative uses. In lichen collections, where specimens can be small, cryptic, and/or piecemeal, there is an urgent need for imaging best practices and standards to maximize the usability of images both now and in the future. Establishing and implementing these practices is particularly urgent given that the resources (time, effort, support and expertise) required to image lichen specimens mean there is a low likelihood of reimaging the majority of collections in the future. Moreover imaging can cause wear and tear to fragile specimens. Images must be high resolution, with specimens accurately placed to display the key characteristics required for identification and ideally be aesthetically pleasing. This poster will present guidelines aimed at maximizing the usefulness of images captured during lichen digitization based on experience gained from a large-scale project on Appalachian lichens.

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Systematics

Topic: Poster

Title: Patterns in northward movements of southern plant species in New Jersey

Author: ***Fitz Dettmer @ Rutgers University***

Keywords: climate change,Coastal Plain,flora,North America,Range expansion,Vascular Plants,spatial mapping,Floristics,New Jersey,range shift,distribution

Abstract:

New Jersey (USA) on the northeastern coast of North America is a notably ecologically and species diverse state, containing four different physiographic provinces, five level III ecoregions, and the only occurrence of one level IV ecoregion—84b, the Pine Barrens—in the United States. The southern half of New Jersey consists of the Coastal Plain physiographic province and is remarkably different from the northern half, which also was glaciated during the last glacial maximum (LGM) while the Coastal Plain was not. Despite constituting only 0.26% of the land area of the U.S., New Jersey contains 13% of the floral species found in the country. Of New Jersey's more than 2100 native vascular plant species, 356 (17%) are considered endangered by the state. New Jersey is also the fastest-warming US state, having had the largest increase in its average annual temperature over the last century. Species distributions are expected to shift towards higher latitudes as the climate warms, but there have been no studies conducted on New Jersey flora to ascertain whether species ranges are shifting as expected. This study is a first investigation into whether flowering plant species that have historically occurred exclusively in the southern half of New Jersey have moved north within the last 40 years. We develop a simple, non-projecting technique for determining patterns of movement utilizing existing occurrence data from herbarium collections and iNaturalist. Of the species that were only occurring in the Coastal Plain physiographic province as of 1983 (as per Mary Y. Hough's New Jersey Wild Plants), we selected the 20 species with the most herbarium and iNaturalist occurrence data. Each species was categorized as either being restricted to the Pine Barrens area or to occur throughout the Coastal Plain. We geolocated and mapped to municipality level all specimens and observations with locality information and a year of observation/collection, and rasterized and sorted by the earliest year each species was observed across the state and by 10-year periods after 1983. For each species and both range categories, the ratios of cells where the first occurrence was before versus after 1983 above and below the northern boundary of the Coastal Plain were compared using the Fisher exact probability test in R. Our results found that no southern species that were noted to be present primarily within the Pine Barrens has been found north of the Coasta Plain after 1983. In contrast, just under half of the southern species noted to occur outside of the Pine Barrens or throughout the Coastal Plain were found to occur north of the Coastal Plain after 1983 at rates that were significantly greater than their occurrence after 1983 in the Coastal Plain (p-values < 0.05). In conclusion, certain species are moving north, but not those restricted to the Pine Barrens habitat. We include a discussion of potential data bias caused by lack of or uneven collections efforts, not reporting obscure plants in iNaturalist, and other human behavioral effects.

449

Symbioses: Plant, Animal, and Microbe Interactions

Topic: Poster

Title: ELUCIDATING HOST-MICROBE SYMBIOSIS IMPACTS ON HOST GENETIC DIVERSITY THROUGH A LONG-TERM STUDY

Author: ***Maya Shamsid-Deen @ University of New Mexico***

Keywords: Fungal endophytes,GBS,Genetic diversity,long term,plant-microbe interactions,Poaceae

Abstract:

Plant-microbe interactions have shaped the evolutionary pathways of both taxa, and hold promise for allowing these lineages to persist in the future. Microbes may function as a benefit to plants during harsh climatic years, which may allow more individuals to persist and reproduce under climate change. Through this buffering effect, we hypothesize that symbiosis may lead to more genetic diversity in plant populations. Currently, there are no studies assessing how microbial symbiosis impacts host genetic diversity. Using genotype-by-sequencing (GBS) data we quantified genetic diversity in paired endophyte-present and -absent plots of six native North American grasses from a ten-year long-term study. We calculated the average allelic diversity present in each plot. A type II ANOVA (Response variable ~ Endophyte Status * Species) was used to test if endophyte status was a significant predictor of allelic diversity. Endophyte status was a significant predictor of allelic diversity. All taxa when endophytes were present had higher averages of allelic diversity than when endophyte were absent. Further, our demographic data indicate demographic performance is more consistent in taxa with fungal endophytes. Through broadening our understanding of the impact host-microbe context-dependent interactions have on genetic diversity, we are better equipped to make predictions about maintenance of biodiversity under anthropogenic climate change.

454

Conservation Biology

Topic: Poster

Title: The Impact of Burn Management on Biodiversity and Bloom Time in Urban Prairie Systems

Author: ***Jose Soto @ Maryville University***

Keywords:

Abstract:

Controlled or prescribed burns are common practice within nature reserves, mainly those with tallgrass prairies for the promotion of healthy plant growth. The goals of controlled burns are to increase the richness and diversity of plant species while impacting bloom times. At Litzsinger Road Ecology Center, burns are rotated yearly, and the close positioning of a north and south prairie allows for observation of these effects in a controlled, compact urban prairie.

When a controlled burn occurs within a prairie system, it is typical to see changes in soil pH, increases in plant diversity, and longer bloom periods post-burn. Soil pH was different between the north and south prairie with the south prairie (post-burn) having a significantly higher pH. There was no significant difference of plant biodiversity pre and post controlled burn between the prairies. The north prairie had a statistically consistent higher number of blooming species over a 7-year period. Plant diversity measured within prairies also showed no evidence of change as a result of controlled burns. Within a group of focal species that span across both the north and south prairie, there was not a statistical difference in the bloom time lengths that presented themselves within each individual prairie or across all prairies. Further research is needed to understand the potential effect on microhabitats within each prairie. The controlled burns provide an opportunity for both research and in furthering the community education goals at Litzsinger Road Ecology Center.

456

Systematics

Topic: Poster

Title: A molecular phylogeny of the genus Melica (Poaceae: Pooideae)

Author: ***Mark Mullinger @ University of Vermont***

Keywords: Angiosperms353,phylogeny,Poaceae,systematics,Melica,Pooideae

Abstract:

The temperate grass clade Pooideae includes some of the world's most important cereal crops like wheat, barley, rye, and oat. The widespread genus Melica (~90 species) is situated phylogenetically between these crops and rice. Melica species exhibit notable variation in both flowering and belowground traits. This makes the group well-suited for comparative and evolutionary studies of grasses. However, the genus is missing a well-supported phylogenetic framework to contextualize those studies. We aim to use the universally applied Angiosperms353 target probe to develop a rigorous phylogeny of Melica. Results of this work will be an invaluable resource in developing the genus as a model group for trait evolution in grasses.

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Systematics

Topic: Poster

Title: Phylogenomics of the genus Asparagus reveals many instances of paraphyly with narrowly distributed taxa nested within locally widespread species complexes

Author: ***Philip Bentz @ University of Georgia***

Keywords: asparagaceae,asparagus,Monocots,phylogenomics,phylogenetic

Abstract:

Paraphyletic species relationships are problematic for taxonomic purposes but may represent true evolutionary phenomena in which new species form from within a larger species complex. Across the Asparagus phylogeny, there are multiple instances of new species forming via divergent population(s) from within a larger species complex. In many cases branching patterns within such complexes are polytomous. Here, we explore the implications of these results from a recent phylogenomic analysis of the genus Asparagus, focusing on a clade containing Asparagus exuvialis Burch. - a species widespread across southern Africa. Using over 1,700 nuclear loci in phylogenomic analyses, A. exuvialis is paraphyletic with two other distinctive species that are more narrowly distributed.

462

Phylogenomics

Topic: Poster

Title: Plastome phylogeny for the native Hawaiian lobeliads (Campanulaceae: Lobelioideae): implications for interisland dispersal events within the Hawaiian archipelago and origin of the lobeliads of the South Pacific via long-distance dispersal

Author: ***Bing Li @***

Keywords: adaptive radiation,long distance dispersal,molecular phylogenetics,Campanulaceae

Abstract:

The native Hawaiian lobeliads include six genera and 141 described species, are the largest group of native plants endemic to the Hawaiian archipelago, and form one of the most striking examples of adaptive radiation and geographic speciation among plants on oceanic islands. The great majority of species are restricted to individual islands, each of known age; roughly one-fifth of all described species are thought to be extinct. Earlier analyses — based on seven plastid loci sequenced for 23 species across all six genera – indicated that this group was derived from a single colonist that arrived in the archipelago roughly 13 Mya, long before any of the current tall islands had emerged, and then radiated into a broad spectrum of growth forms, floral morphologies, and leaf shapes as the group dispersed southeastward toward younger islands, mostly from one island to the next younger in the chain in line with the so-called progression rule. To extend our analyses to a much larger share of the lobeliad radiation, supported by a much larger data set, we sequenced, assembled, and aligned the entire plastomes for nearly every extant Hawaiian taxon. We reconstructed lobeliad phylogeny using maximum likelihood applied to two data sets, involving exon-only sequences and full plastome assemblies. Only the exon-only phylogeny resolved a trichotomy of Brighamia-Delissea, Lobelia §Revolutella, and Trematolobelia-Lobelia §Galeatella. The last two clades are well supported as being sister to each other, forming a clade marked by terminal inflorescences and capsular fruits, in contrast to the axillary inflorescences and fleshy fruits seen in Brighamia-Delissea (fleshy only early in development in Brighamia) and Cyanea-Clermontia. Clermontia is strongly supported as being monophyletic, except for Cl. pyrularia embedded in Cyanea; the remainder of Clermontia is sister to the orange-fruited clade of Cyanea, with both jointly sister to the purple-fruited clade of Cyanea. This larger clade is itself sister to Apetahia/Sclerotheca from the Marquesas, Society Islands, and Cook Islands, pointing to an origin of this group of South Pacific lobeliads via long-distance dispersal from Hawaii. Analyses of historical biogeography point to several inter-island dispersal events within the Hawaiian archipelago, with almost all conforming to the progression rule within each genus and subgenus. We have also sequenced several hundred single-copy nuclear genes based on hybrid DNA capture; we will present analyses of these data soon to test for discordance and evidence for hybridization, introgression, and/or incomplete lineage sorting.

464

Ecophysiology

Topic: Poster

Title: An Investigation of Morphological and Physiological Differences Between Two Closely Related Species of Southeastern Azaleas, Rhododendron prunifolium and R. cumberlandense (Ericaceae)

Author: ***HeavenLee Pagan @ Auburn University at Montgomery***

Keywords: morphology,Rhododendron,ecophysiology

Abstract:

Determining the degree of differentiation among individuals and populations is the foundation of species delineation. Morphological traits can provide good indication as to the variation that exists within and among species, but these traits can be flexible across growth environments, reflecting acclimation, rather than genetic differentiation. The southeastern azaleas present a complex problem in this respect because populations can show highly variable morphology (e.g., leaf shape), while at the same time, different species can have strongly similar traits. The geographic distributions of the southeastern azaleas show separation of species along temperature gradients, indicating a role for physiological temperature tolerance in speciation of this group. Here we report an analysis of morphological and physiological climate tolerance traits of specimens of R. prunifolium and R. cumberlandense grown in a common garden at the Auburn University Donald E. Davis Arboretum. We predict that R. cumberlandense and R. prunifolium will show significant differences in their physiological climate tolerance traits, with R. cumberlandense being adapted to colder, high-elevation environments compared to R. prunifolium.

467

Development and Structure

Topic: Poster

Title: Patterns in monocot leaf architecture: a preliminary synthesis and proposal for standardized terminology

Author: ***Selena Smith @ University of Michigan***

Keywords: Monocots,venation

Abstract:

Leaf venation patterns (leaf architecture) are integrally linked to ecology, function, and phylogeny. Within angiosperms, research has largely focused on understanding leaf architecture in dicotyledonous taxa, while monocots have been relatively neglected. However, monocots are a diverse group of ecologically and economically important plants, and standardizing their leaf venation pattern terminology is critical for synthesizing patterns in evolution, morphological disparity, and analyzing the fossil record. Monocot leaves are characterized by a closed venation system with all parallel veins converging at the apex and the presence of entire margins. Additionally, the majority (independently of their gross morphology) of monocot species have veins running parallel to the primary direction of lamina extension, with transversely-oriented veins (cross veins) connecting adjacent parallel veins. These parallel veins vary in thickness in repeated patterns, which we propose referring to as A veins, B-veins, etc.; they are potentially homologous to primary, secondary, and tertiary veins in other angiosperms. Reticulate venation patterns occur in four separate orders of monocots: Alismatales, Dioscoreales, Liliales, and Asparagales. While some monocots (e.g. Dioscorea) possess a dicot-type pattern of reticulation, with a main branching vein and free-ending veins in aereoles, other 'reticulate' monocots have a distinctly different pattern where the reticulation is formed by anastomosing and irregular veins within the parallel and cross-vein network. In both cases we refer to these non-parallel and non-cross veins as "higher order." We will present a standardized terminology and traits to describe and characterize monocot leaves. This new terminology will contribute in understanding the functional, ecological, and evolutionary significance of monocot venation features.

475

Education and Outreach

Topic: Poster

Title: Maximizing the impacts of inclusive CUREs from hypothesis to undergraduate conference participation

Author: ***Matt Johnson @ Texas Tech University***

Keywords: Course-based undergraduate research experience ,herbarium specimen,education research,museum specimen

Abstract:

Course-based undergraduate research experiences (CUREs) increase student learning and self-efficacy but are often difficult to implement across a variety of class types and institutions. CUREs built using digital Natural History Collection (dNHC) data are more accessible as they do not require expensive equipment or wet lab resources. Four CUREs recently developed by the Biological Collections for Ecology and Evolution Network (BCEENET) provide students with research experience employing digitized natural history collection data and have been implemented at over 20 institutions serving over 3000 students. Although students gain experience with data management, georeferencing, GIS, and data analysis it is unknown whether these digital data CUREs provide the same gains in student self-efficacy and content knowledge as more expensive laboratory CUREs. We describe a new CURE assessment project that aims to assess dNHC CUREs through the development of new survey instruments and cognitive interviews. We also aim to assess the impact of participation in scientific conferences on outcomes for CURE students. To assist instructors in implementing its dNHC CUREs, BCEENET provides resources for implementation of its CUREs and also offers opportunities to participate in assessment activities.

476

Conservation Biology

Topic: Poster

Title: Evidence of interspecific hybridization and high genetic diversity in the federally endangered Deeringothamnus rugelii (Annonaceae)

Author: ***Christine Edwards @ Missouri Botanical Garden***

Keywords: conservation,endangered species,hybridization,reintroduction

Abstract:

Deeringothamnus rugelii (Annonaceae) is a federally threatened shrub endemic to Volusia County, Florida. The species is historically known from 29 populations, which are threatened by development and habitat degradation. Only a few sites are protected, and the proportion of the total genetic diversity protected in these sites is unknown. D. rugelli may also be threatened by the loss of genetic integrity through hybridization with the more widespread, co-occurring close relative, Asimina pygmaea, and another rare congener, Deeringothamnus pulchellus. In this study, we asked the following questions: 1) Are D. rugelii, A. pygmea, and D. pulchellus genetically distinct? 2) Is there genetic evidence for interspecific hybridization between these species? And 3) What are patterns of genetic diversity and structure within D.rugelii and what are implications for conservation? Analyses of genetic structure indicated that most individuals of D. rugelii, A. pygmea, and D. pulchellus formed cohesive genetic groups, but some individuals were assigned to more than one genetic cluster, indicating that they are likely the products of hybridization. Most putative hybrids were crosses between D. rugelii and D. puchellus, with evidence of backcrossing with the parental species. We observed F1 hybrids between A. pygmaea and D. rugelii in sites where they co-occurred, with no sign of backcrossing, suggesting that hybrids may be sterile. D. rugelii shows high levels of genetic diversity, with most variation partitioned within populations, indicating high levels of intraspecific gene flow among populations. Because most variation of D. rugelii is partitioned within populations, only a subset of populations across the range of the species needs to be protected to conserve most of the genetic variation in the species. Given the populations that are already publicly protected, results indicate that the majority of the genetic diversity in the species is already protected. Thus, current conservation efforts are sufficient to protect the extant genetic diversity in D. rugelii, and future efforts should instead focus on maintaining good quality habitat to help support large populations of D. rugelli. Resutls were also used to select genetically appropriate germplasm for population introductions and to help determine whather to mix population sources into introduced populations.

479

Population Genetics/Genomics

Topic: Poster

Title: Spatiotemporal variation in transposable element content across the invasive and native ranges of Microstegium vimineum

Author: ***Dhanushya Ramachandran @ USDA-ARS***

Keywords: Genetic diversity,rapid adaptation,invasion genomics,abiotic environmental variables,mobile elements

Abstract:

Invasive species are pervasive drivers of global change, and are considered as the second greatest threat to native biodiversity after habitat loss. Yet, the mechanisms underlying rapid adaptation of invasive species despite reduced genetic variation in novel environments has been a paradox for decades. Although sudden change in the environment is considered as an intense stress to the organism, these perturbations may facilitate rapid adaptation by affecting the genome structure and function via activating transposable elements (TEs). TEs are mobile genetic sequences that constitute a large portion of plant genomes, and are known to experience increased transposition events in response to environmental stress. Therefore, being the most variable component of the genome, active TEs have the potential to rapidly introduce genetic diversity by inserting themselves near or within exons, introns, or other regions. Through their mobility, TEs alter gene expression, promote gene shuffling, trigger chromosomal rearrangements via ectopic recombination, thereby contributing to the rapid adaptation for species with low genetic variation. Here, we explore the adaptive potential of transposable elements (TEs) in one of the notorious invasive grass species in North America, stiltgrass (Microstegium vimineum). As a shade-tolerant, polyploid, C4 grass, it invades a range of habitats in the USA, displays a high degree of phenotypic plasticity, has a mixed mating system, and exhibits prolific reproductive output with seeds being viable in the soil up to five years. With the reference genome sequenced for M. vimineum, it is known that the TEs comprise >60% of the genome and majority of the LTR-retrotransposons were derived from a significant expansion in the past 1-2 million years (relatively young lineages). To test whether TEs could drive rapid adaptation in invasive species, we sequenced more than 250 stiltgrass samples (contemporary and historical) from the native and invasive ranges. The software Transposome was used to estimate the relative genomic proportions of TE in 102 contemporary and 108 historical stiltgrass samples. A preponderance of Copia retrotransposons was found in southeastern US (SE-US) samples compared to samples collected from northeastern US (NE-US) and native Asia. Following TE abundance estimation, we used a multivariate landscape genomic method, redundancy analysis (RDA), to identify relationships between seven TE superfamilies and abiotic climatic variables (19 BIOCLIM variables). To avoid issues with multicollinearity, we selected five uncorrelated BIOCLIM variables. Preliminary findings from RDA and multivariate regression analysis show at least two low-abundance TE superfamilies that have significant relationships with mean temperature of wettest quarter (BIO 8) and annual precipitation (BIO 12). In addition, we found TE variation between SE-US and NE-US, whereas not much variation is observed in Eastern Asia, corroborating our earlier hypothesis of two separate invasions in the USA for stiltgrass. Future investigations will involve identification of active transposition activity in contemporary and historical samples to track the dynamics of specific TE families over time. Linking TE activity to nearby genomic regions will provide critical information on the role of TEs in the evolution of invasiveness.

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Paleobotany

Topic: Poster

Title: First evidence of anisotomous dichotomy in Stigmaria ficoides

Author: ***Michael D'Antonio @ Field Museum of Natural History***

Keywords: Paleozoic,Root,lycopsid

Abstract:

Stigmaria ficoides is the late Paleozoic form species of rooting organ for the members of the core of the arborescent lycopsid phylogeny (families Diaphorodendraceae and Lepidodendraceae). This organ has been traditionally described as four primary axes each dividing dichotomously twice to yield sixteen terminal axes, all bearing lateral appendages or "rootlets." Until now, the dichotomies constituting the organ system architecture have only been known to be isotomous (i.e., the two daughter branches are roughly the same dimension), unlike the architecture of some sigillarian Stigmaria morphospecies such as S. asiatica, which bore minor geotropic axes on the underside of the stigmarian arms. Here we describe two S. ficoides specimens that branch by anisotomous dichotomies (i.e., the two daughter branches are of unequal dimension). The assignment is made to S. ficoides based on rootlet scar morphology and insertion pattern. Each specimen exhibits minor axes branching off a larger parent axis. This finding demonstrates a greater degree of developmental plasticity than had previously been known for the rooting system form species and suggests that there is still much to be learned about arborescent lycopsid developmental biology.

485

Ecology

Topic: Poster

Title: Historical climate change shifts flower shape and production of a common annual plant, Orange Jewelweed (Impatiens capensis)

Author: ***Amber Stanley @ University of Pittsburgh***

Keywords: climate change,ecology,Herbarium,Plant-pollinator

Abstract:

Climate change is a major-human mediated stressor that alters temperature and precipitation patterns across the globe. In the Eastern United States, projections show that annual temperatures will increase 3-5oC and precipitation will increase 20% by 2100. Such changes in the environment have the potential to disrupt key species interactions. For example, nearly 90% of all flowering plants rely on insect pollinators to transfer pollen between individuals. Higher temperatures cause many plant species to flower up to 3-4 weeks earlier in the year, but pollinator activity has not shifted with the same magnitude, meaning that flowers are produced when fewer pollinators are active. Flower size can be limited by increasing temperatures, which makes it harder for larger pollinators to transfer pollen. Some plant species can produce self-pollinating flowers to mitigate disruptions in pollination, however this can decrease genetic diversity. Here, I ask How have temperature and precipitation increases due to climate change influenced floral traits of a common focal species? To investigate this question, I used a focal plant species, Orange Jewelweed (Impatiens capensis). This well-characterized annual plant is common in wetlands and floodplain forests of the Eastern United States. It primarily relies on bumblebees to transfer pollen between individuals, but can also produce selfing flowers. Using digitized herbarium collections, I measured the timing of flowering, flower size and production on herbarium specimens of 650+ collected in Pennsylvania between 1900-2020. I used CRU-TS climate projections to extract temperature and precipitation for each specimen. I hypothesize increasing temperatures are highly correlated with H1) earlier flowering time and H2) increased production of flowers, and increasing precipitation is correlated with H3) increasing flower size. Such changes in floral traits due to increasing temperatures may alter the pollination interaction and could increase extinction risk.

491

Education and Outreach

Topic: Poster

Title: Student Exploration of the Plastid Genome

Author: ***Sue Harley @ Weber State University***

Keywords: chloroplast DNA,chromoplast DNA,plastid genome

Abstract:

One of the fascinating aspects of plant biology that students are often unfamiliar with is their three genomes: nuclear, mitochondrial, and plastid. We put together a laboratory experience with a follow up phylogenetics exercise to provide students the opportunity to explore the plastid genome, using either chloroplasts or the usually less familiar chromoplasts. After an overview of the structure of the plastid genome, types of plastids, and plastid heredity, students isolate chloroplasts or chromoplasts from leaves, flowers, or fruits using a high salt method (Shi et al., 2012). We have found that this method works well for both chloroplasts and chromoplasts from a variety of flowering plants. With the high salt method, highly pure plastids suitable for subsequent DNA extraction can be obtained using benchtop centrifuges without the need of sucrose, Percoll, or Ficoll gradients. Students use one lab period to isolate plastids and a second period to extract DNA using a plant-specific DNA prep kit. They then check the quality of their DNA preps by A260/A280 ratio and electrophoresis. As a follow up exploration, students are introduced to using the plastid genome in phylogenetics. They can look up the plastid DNA sequence for their plant or a related one and select restriction enzymes for further study of their chosen plastid's DNA.

497

Ecophysiology

Topic: Poster

Title: An encroaching woody species (Cornus racemosa) does not alter gas exchange in response to drought as much as the dominant herbaceous species in a managed temperate grassland

Author: ***Katherine Charton @ University of Wisconsin-Madison***

Keywords: drought,management,photosynthesis,stomatal conductance,tallgrass prairie,water potential,woody enroachment

Abstract:

Woody encroachment, or the spread of woody species into previously herbaceous-dominated ecosystems, is often attributed to the loss of historic disturbance regimes, such as frequent, low-intensity fire. Once established, woody species can withstand the reintroduction of fire, continue to spread via clonal reproduction, and ultimately lead to the decline of historically dominant herbaceous species. Thus, controlling woody species often requires mechanical and/or chemical management practices in addition to the reintroduction of fire. Management outcomes, however, are inconsistent. One potential reason that is difficult to predict the outcomes of woody management is the concurrent influence of climate change. In many temperate regions, the intensity of summer precipitation events is projected to increase but the frequency decrease, increasing drought-like conditions between events. We designed a full-factorial field experiment to test how different woody management practices and drought impact management outcomes, using physiological variation among plant functional groups to inform the mechanisms underpinning these outcomes. We established eight 32-m2 plots randomly placed within patches of gray dogwood (Cornus racemosa) – a prevalent encroaching species of high management concern – at two unplowed remnant tallgrass prairies in southern Wisconsin, one dry and one mesic. We treated each plot with one of four woody management types (mechanical, chemical, mechanical and chemical, or unmanaged) and either ambient or reduced precipitation (i.e., drought) using rainout shelters. We collected data on management outcomes in nested 10-m2 subplots by estimating the percent cover of gray dogwood. We also collected physiology data – including pre-dawn (ΨPD) and mid-day (ΨMD) leaf water potential and mid-day photosynthetic rate (Anet) and stomatal conductance (gs) – on gray dogwood and the most dominant graminoids (Sorghastrum nutans, Carex stipata) and forbs (Helianthus pauciflorus, H. grosseserratus) at each site. We found a clear impact of management on gray dogwood, as percent cover significantly declined in both chemical treatment types (chemical and mechanical and chemical). However, management outcomes were much more variable under drought conditions, and mechanical and unmanaged treatments trended toward greater gray dogwood cover under drought. We also found significantly lower ΨPD and ΨMD across species under drought than ambient conditions, with greater differences between drought and ambient conditions in ΨPD than ΨMD. However, the drought effects were greater for the dominant herbs than for gray dogwood. Graminoids and forbs showed large fluctuations in water potential, whereas gray dogwood showed less response to daily and especially treatment-caused water fluctuations. With this, gas exchange did not vary under drought conditions in gray dogwood, while graminoids and forbs neared zero Anet. These findings provide important insights into the differences in drought stress response among an encroaching woody species and dominant herbaceous species, suggesting that encroachment may continue to worsen under drought conditions where woody species are already well established, even with management.

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Comparative Genomics/Transcriptomics

Topic: Poster

Title: Comparative genomic analysis of two Boechera species highlights adaptation to the desert habitat

Author: ***Talieh Ostovar @ SDSU/UCR***

Keywords: Abiotic stress,Boechera,comparative genomics,desert adaptation

Abstract:

As global temperatures increase, understanding the genomic basis of plant adaptability to extreme environments and tolerance to abiotic stresses, especially heat and drought, has a major role to optimize productivity and survival of crops and other important plant species. Prior studies have shown that several species in a group of native California plants in the genus Boechera can survive longer than their closely related model species, Arabidopsis thaliana, under environmental extremes. The two species of interest in this study include Boechera arcuata, found in low-elevation coastal areas, and Boechera perennans, found in desert and inland chaparral regions. To elucidate the molecular level of their adaptations to diverse environments and more specifically to desert conditions, we first generate chromosome-level genome assemblies and annotations of the two Boechera species and then integrate comparative and functional genomics approaches. Based on our results, a total of 42.73% and 40.24% of the assemblies contain repeat elements in B. arcuata and B. perennans, respectively with recent TE amplifications and mostly LTR elements expansions. The results also identify 1505 specific genes in B. arcuata and 1531 specific genes in B. perennans and reveal relatively conservation of synteny. Functional analysis of the species-specific genes provides substantial evidence of specific over-enriched GO terms related to photosynthesis in B. perennans. Collectively, these results will be used to find the evidence of transposon-mediated evolution, especially for recent LTR insertions into gene regions contributing the adaption of B. perennans to the desert habitat. Moreover, identification of candidate gene families associated with survival under environmental extremes will provide the basis for analyzing the evolutionary history of each family. The integration of omic-scale information will ultimately help us in predicting evolutionary responses of various species to desertification and effective utilization of available knowledge for the management of stress tolerance in plants.

503

Ethnobotany

Topic: Poster

Title: DNA Barcoding of Hmong Postpartum Herbs

Author: ***Alex Crum @ University of Minnesota - Twin Cities***

Keywords: DNA barcoding,ITS,traditional knowledge,taxonomic identification

Abstract:

In Hmong culture it is tradition to purify the body for 30 days with a chicken soup diet after giving birth. Recent work to provide culturally equitable healthcare has led hospitals in the Twin Cities, MN, where there is a large Hmong community, to offer the postpartum chicken soup to new mothers. We worked with local Hmong farmers and stewards of their family chicken soup recipe, Zongxee and Mayyia Lee, to identify the medicinal herbs used in postpartum chicken soup using the internal transcribed spacer (ITS) region and sequencing the DNA after PCR. PCR results were analyzed using Geneious. The resulting sequences were compared against sequences in GenBank using BLAST and phylogenetic reconstruction The experiment was designed to improve medicinal herb research and knowledge for the benefit of postpartum recovery patients. The results will provide a foundation for evidence based research on medicinal herbs and be returned back to the Hmong community to help preserve cultural knowledge.

504

Conservation Biology

Topic: Poster

Title: Evaluation of Alnus maritima germination and viability for seed banking and conservation

Author: **Cathy Borer @ Berry College**

Keywords: conservation,rare species,seed banking,Alnus maritima

Abstract:

Alnus maritima is a very rare alder species that is only known to grow at three geographically disjunct sites in the United States: Bartow County, Georgia, central Oklahoma, and the Delmarva Peninsula. In this project we are evaluating the viability and germination rate of seeds from the GA population and conditions in which they can be stored, to focus on long-term conservation of germplasm. In November 2021, we collected seeds from 15 trees in the GA population of A. maritima. We are using these seeds to evaluate germination rate, as well as embryo viability via a chemical analysis to determine the proportion of seeds that contain metabolically active embryos. We are also evaluating the cold tolerance of the seeds to determine the most appropriate temperature for long-term seed storage. We placed seeds in treatments of 20℃, 4℃, -30℃, and -80℃ for 5 months and then reevaluated seed germination and viability to evaluate sensitivity of seeds to these storage temperatures. Preliminary data demonstrate that of the seeds with living embryos, the majority germinate, however a low proportion of seeds contain live embryos. This low percentage of viable seeds may help to explain one reason that this species is so rare. Preliminary cold tolerance data show no significant differences in the proportion of viable embryos in the different storage temperatures. A long-term seed repository can help to ensure the conservation of this rare species to avoid a total loss if there were a catastrophic event at the only site where they grow.

505

Hybrids and Hybridization

Topic: Poster

Title: Chloroplast capture in a natural hybrid zone between Populus trichocarpa and P. balsamifera

Author: **Brianna Sutara @ Penn State University**

Keywords: chloroplast,hybrid zone,hybridization,Poplar Trees

Abstract:

Hybridization is an important evolutionary process that contributes to the creation of novel genetic recombinants where species interbreed. Following recombination, differential introgression of bi-parentally and uni-parentally inherited genomes can provide signatures of the extent and direction of gene flow. Assessment of biparental and uniparental genome introgression is key to understanding cytonuclear interactions following secondary contact. Indeed, comparison of nuclear and chloroplast introgression can provide a test for incongruencies that may arise during hybridization. In this study, we leverage whole genome resequencing data from 576 Populus trees across seven latitudinally distributed transects spanning the natural contact zone between Populus trichocarpa and P. balsamifera. We used replicated hybrid zones to test for differential introgression between nuclear and chloroplast genomes across environments. Populus provides an excellent model to evaluate differential patterns of introgression due to its weak barriers to reproduction that lead to extensive hybridization in nature. Furthermore, small genome size, ease of clonal propagation, and importance as a source of lignocellulose, make Populus an important economic model to evaluate the fitness consequences of cytonuclear interactions. We assembled the chloroplast genome for 576 Poplar genomes using NOVOPlasty. Following this, we identified the probability of chloroplast genome ancestry using maximum likelihood phylogenetic trees. We then compared nuclear genomic ancestry with chloroplast genome ancestry to test for potential cytonuclear discrepancies across replicate hybrid zones. Finally, Ka/Ks ratios were used to test for signatures of selection in the chloroplast genome across the replicated hybrid zones. Overall, the chloroplast genome of both species is highly conserved with genome sizes varying from 156,235 to 157,980 bp, includes 77 coding regions, and the typical quadripartite structure (LSC, SSC, IRA, and IRB) of angiosperms. Across the southern transects, we observed a transition from the P. trichocarpa chlorotype to the P. balsamifera chlorotype suggesting the maintenance of both haplotypes across the hybrid zone. However, in the northern transects, the P. balsamifera chlorotype was the sole chlorotype present. Comparisons between nuclear and chloroplast introgression suggest that unidirectional gene flow of P. balsamifera chlorotypes into a P. trichocarpa nuclear genomic background may persist across the hybrid zone. Tests for selection indicate that some chloroplast genes exhibit more than one non-synonymous substitution, but the distributions of non-synonymous substitutions vary geographically across latitudinal transects. Future work will evaluate how cytonuclear interactions influence phenotypic variation using common garden experiments.

506

Ethnobotany

Topic: Poster

Title: A map of perennial flowering plants and demographic analysis of the Zuber Cemetery in Rome, GA, USA

Author: ***Cathy Borer @ Berry College***

Keywords: ethnobotany,History,perennials,cemetery

Abstract:

The Zuber Cemetery, located in Rome, Georgia, USA is the final resting place of many Black Americans who lived during the nineteenth and twentieth centuries. Many of those buried at the Zuber Cemetery were slaves or former slaves with limited financial means, so families typically could not afford expensive gravestones. Instead, many of the graves at the cemetery were marked by perennial plants placed by loved ones; plants include Narcissus pseudonarcissus, Yucca filamentosa, and Iris sp. In this project, we are creating a map of the cemetery to further understand how flowering perennial plants were used as ornamental grave markers and to provide a historical record for families whose ancestors are buried at the site. We are mapping the cemetery by surveying known graves and groups of flowering plants, which may represent the locations of graves. In addition, we are collecting demographic information from the existing headstones at the site, such as names and dates of life, to analyze the average age at time of death and to identify family clusters in the cemetery. This project is allowing us to further understand historical uses for perennial plants and document the underrepresented history of Rome, GA. We are providing a valuable resource for site management and for descendants of those buried there. The Zuber Cemetery is not the only historical cemetery in northwest Georgia, and there is potential for future projects to bring more awareness to the community about historical uses for plants and otherwise unprotected family histories.

513

Floristics & Taxonomy

Topic: Poster

Title: Vascular plant, bryophyte, and lichen biodiversity of Agguttinni Territorial Park, Baffin Island, Nunavut, Canada, a new Arctic protected area

Author: ***Lynn Gillespie @ Canadian Museum of Nature***

Keywords: arctic,Biodiversity,bryophytes,Canada,Floristics,lichens,Vascular Plants

Abstract:

In 2021 we conducted a botanical inventory of Agguttinni Territorial Park, a large (16,465 km2) new protected area on the east-central coast of Baffin Island in Nunavut, Canada. The park stretches from the Barnes Ice Cap to Baffin Bay and encompasses ice-capped mountains and deep fiords up to 120 km long. Previous knowledge of the plant and lichen biodiversity was very limited and based mostly on collections made during the 1950 Baffin Island Expedition. Based on our 2021 collections and those by other botanists, we documented a comprehensive park vascular plant flora of 141 species (3 with 2 subspp. each) of vascular plants belonging to 25 families. Although not the focus of our 2021 inventory, our preliminary list of bryophytes includes 69 species belonging to 27 families, and of lichens includes 95 species (1 with 2 subspp.). All species are native; no introduced species were recorded. The majority of vascular plant and bryophyte species are newly reported for the park area. The largest vascular plant families are Poaceae (22 spp., 1 with 2 subsp.), Cyperaceae (22 spp.), and Caryophyllaceae (15 spp.), and the largest genus is Carex (16 spp.). Noteworthy records include the northernmost records of Diapensia lapponica in Canada and the first record of Puccinellia bruggemannii from Baffin Island. Our bryophyte list for the park includes 7 taxa newly reported for Nunavut. One rare lichen was documented: Parmelia skultii, which appears to be new to Baffin Island. Vascular plant species diversity varied greatly among localities within the park, with inland valleys at the heads of fiords the most diverse (up to 107 spp.) and interior rocky barrens the least diverse (< 1 0 spp).

514

Comparative Genomics/Transcriptomics

Topic: Poster

Title: New reduced chloroplast genome structure in Mammillaria (Cactaceae)

Author: ***Juan Pablo Ortiz-Brunel @ Universidad de Guadalajara***

Keywords: Inverted repeats (IR),plastome,cacti

Abstract:

Among angiosperms, Cactaceae chloroplast genomes are one of the most variable in structure and gene content. Many groups have lost the inverted repeat regions (IR) and show gene inversions and deletions. The genus Mammillaria has a very variable plastome structure. So far, three different chloroplast genome structures have been identified in seven species. This variation could be useful in determining infrageneric relationships within Mammillaria. To test this, we assembled and analyzed four new chloroplast genomes of Mammillaria series Stylothelae. This series has been proposed based on the combination of morphological characters and by the lack of the rpl16 gene intron, which is present in all other Mammillaria species. It is unknown if the loss of rpl16 is from a single or recurring events, and further study of Mammillaria series Stylothelae may present novel instances of chloroplast genome structure variation. Here, we isolated chloroplasts, extracted DNA, and then sequenced it using Ion Torrrent sequencing with 200 base pair reads. Chloroplast genome contigs were de novo assembled using SPAdes. Then, we aligned them using the BWA program and evaluated the percentage of coverage versus the seven previously known plastomes to identify the most similar structure. The chloroplast genome of sampled species from Mammillaria series Stylothelae ranged from 100 to 103 kb. The number of genes varied from 97 to 99 with four to six pseudogenes. All plastomes exhibited a similar structure and gene content compared with Mammillaria pectinifera, but they were 6 to 8 kb shorter and lacked the IR regions. Furthermore, we detected the loss of some ndh genes in all the species. Using these new chloroplast genomes, we explore the extent of structural variation across Mammillaria. Our results support a high variation in the chloroplast genome of Mammillaria, which could be useful for phylogenetic inferences and to determine group boundaries.

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Education and Outreach

Topic: Poster

Title: Somaliland Biodiversity Foundation - progress and plans

Author: ***Mary Barkworth @ Utah State University***

Keywords: Education,Floristics,Outreach

Abstract:

Somaliland is an unrecognized country on the south side of the Gulf of Aden that has held five democratic elections since declaring its independence from Somalia in 1991. Despite its lack of recognition, it is a peaceful, democratic country that is increasing the opportunities open to its people. The Somaliland Biodiversity Foundation's mission is to assist in these efforts by help in developing, within Somaliland, resources for contributing to knowledge and management of the country's biodiversity. The herbarium it established at the University of Hargeisa now houses over 700 specimens. Its records are available via OpenHerbarium and GBIF and their data have been used in more than 160 publications. For the last three years, the herbarium manager, Faisal Game Jelle has been teaching a plant taxonomy course at the University of Hargeisa for which the Foundation has provided had lenses and some teaching materials. In 2022, after discovering that that the university had no introductory teaching laboratory, it purchased locally made laboratory tables that were delivered in 2023. These have made adopting a hands-on approach to teaching much more feasible. Our plans for 2023 include publishing a bilingual version of Introduction to the Plants of Central Somaliland; engaging more individuals in documenting Somaliland's flora by partnering with other institutions and organizations; developing a vouchered seed bank of native species for use in restoration work in conjunction with Somaliland's National Garden; and enhancing the teaching laboratory by equipping the tables with electrical outlets and providing more appropriate chairs

519

Population Genetics/Genomics

Topic: Poster

Title: Identification of novel genetic markers for the southeastern azalea, Rhododendron prunifolium (Ericaceae)

Author: ***Isabella Soto @ Auburn University at Montgomery***

Keywords: Rhododendron,phylogenetics,population genetics,speciation,SNPs

Abstract:

The southeastern azaleas (genus Rhododendron, section Pentanthera) are a complex group of species that show evidence of rapid diversification and widespread hybridization. Species within the clade often have substantial morphological overlap but also show evidence of morphological differentiation and geographic separation along temperature gradients. To understand speciation in the southeastern azaleas, more genetic resources must be developed for phylogenetic and population genetic analyses. The objective of this study was to identify single nucleotide polymorphisms (SNPs) in R. prunifolium from sequence data. We isolated DNA from thirteen R. prunifolium individuals using a modified CTAB protocol followed by bead clean-up. We then prepared sequencing libraries for paired-end read sequencing using the Illumina method. Here we report the results of the sequence analysis and genetic marker identification.

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Biogeography

Topic: Poster

Title: Literature Review of the Patterns and Evolutionary Drivers of Island Plant-Pollinator Systems

Author: ***Giulia de Gennaro @ University of Missouri - St. Louis***

Keywords: Island Ecology,Literature Review,Plant-pollinator Interaction,evolutionary ecology

Abstract:

Studies of island biogeography and ecology have shown how island-specific features like area and degree of isolation can strongly influence island communities and species. Island plants, their pollinators, and interactions between them have been specifically influenced by both barriers faced when colonizing islands and evolutionary forces post-establishment. These forces encompass both stochastic and selective processes that drive differences between island plant-pollinator communities and species compared to their mainland counterparts. As anthropogenic change leaves island communities especially vulnerable to disruption, understanding the forces shaping these systems may help us predict how species will react and aid in building community resilience. Determining how evolution has acted in these isolated systems will also provide insight into broader evolutionary trends in pollination. This research encompasses an extensive review of current literature on island plant-pollinator networks and their included species that reveals ecological patterns specific to island plant-pollinator systems, and explores how island geography and ecosystems have driven the evolution of island plants and their pollinators. Observational studies show an increased reliance on opportunistic and vertebrate pollinators by plants, and increased generalism throughout plant-pollinator networks as some of the characteristics that separate island systems from their mainland counterparts. While some of these differences may be the result of filters associated with colonization, phylogenetic analyses suggest many are the result of evolution post-establishment. Phylogenetic studies also suggest islands may be the origin for nectarivory specialization in several vertebrate clades. Further research will be required to fully understand how plants and pollinators have adapted to island conditions. Specifically, in situ or greenhouse experimental approaches, and studies focusing on insect pollinators are largely absent from the current literature. Future work should aim to address these gaps as well as expand on community-wide analyses and direct comparisons between mainland and island counterparts.

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Ecology

Topic: Poster

Title: Ecological Selection for ‘Alternative Designs’ and its Contribution to Phenotypic Integration

Author: ***Kristen Nolting @ University of Georgia***

Keywords: functional trait,phenotypic integration,Phenotypic variation,species co-existence,trait-performance relationships

Abstract:

Trait variation observed across the Kingdom Plantae is the outcome of dynamic evolutionary histories and present-day ecological and evolutionary processes that act to generate and maintain trait diversity across biological scales. Traits that consistently relate to performance across taxa and environments – often referred to as ‘functional traits’ – provide a functional link between plants and their environments giving context for how these traits reflect adaptation to aspects of the environment. Within a given community, we often observe substantial variation in functional traits among co-occurring species and this variation is assumed to reflect some aspect of niche partitioning that promotes species co-existence. If these functional traits are related to performance, and there is large among species variation in these traits, we might then also expect large differences in performance among species that could lead to competitive asymmetries and potentially competitive exclusion.

Marks and Lechowicz (2006) presented a possible explanation for this paradox. Using a simulation approach, they demonstrated that selection on phenotypes in a single environment can lead to ‘alternative designs,’ such that different combinations of traits (with high variation in traits underlying performance) can achieve relatively similar performance (i.e., little variation in performance itself). Here we expand upon this observation by demonstrating that the presence of ‘alternative designs’ can occur under a unique scenario: specifically, plants that differ in traits affecting performance can have similar performance, if the major axes of trait variation are not aligned with the functional axis representing the link between the functional traits and performance.

While our model is perhaps one of several explanations to help explain the presence of ‘alternative designs,’ it has important implications for community ecology and for phenotypic integration. First, our solution is consistent with the expectation that co-existing species differ in traits that relate to differential niche usage, while also consistent with the expectation that in order to co-exist, species differ minimally in performance thus preventing competitive exclusion. This model also suggests that ecological selection operating to maintain ‘alternative designs’ among species within communities might in part contribute to the stability of phenotypic integration of populations (i.e., an emergent property that reflects the presence and strength of multivariate trait correlations). The degree to which phenotypes are integrated can both facilitate and hinder plant ecological and evolutionary responses to environmental changes.

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Hybrids and Hybridization

Topic: Poster

Title: **Hybridization and coexistence in the wild mustard Boechera**

Author: ***Kallol Mozumdar @ Utah State University***

Keywords: Competition,extinction,hybrid zone,hybridization,modelling,theoretical modelling

Abstract:

The genus Boechera in the mustard family (Brassicaceae) is widely distributed across diverse habitats, ranging from arid deserts to alpine and montane regions. Hybridization and its correlated transition to apomixis are thought to play a crucial role in the morphological diversification of this genus. The process of hybridization, defined as mating between closely related species producing viable offspring, can lead to different evolutionary outcomes, giving rise to stable hybrid zones, speciation, or even the extinction of one or both parental species. Despite the risk of extinction through hybridization, we see rampant hybridization among the roughly 80 species in the genus found in North America. Coexistence between these hybrid populations and their parental taxa is common in the natural environment. How have these wild plants maintained a balance between rapid hybridization events, adaptation, and coexistence? To gain a preliminary understanding of the mechanism behind coexistence in hybridizing species, we designed a 3-species competition model based on the Lotka-Volterra competition equations. The predictions from our model suggest extinction through hybridization is heavily influenced by the demography, growth rate, and rate of hybridization, regardless of the inter- and intra-species competitive abilities of both parental taxa and the hybrid. Even a hybrid with reduced fitness can cause complete parental extinction through demographic swamping (the rapid decline in parent taxa growth rate due to outbreeding depression). Our study shows that taking a population-level theoretical approach to studying hybridization events can provide significant information about the consequences of gene flow between species and its impacts on species and hybrid coexistence.

545

Paleobotany

Topic: Poster

Title: **The long and the short of it: exploring the functional role of spore and pollen ornamentation**

Author: ***Marco D'Ario @ Stanford***

Keywords: Devonian,Dispersal,Spore sizes

Abstract:

Wind dispersal of spores and pollen grains is crucial for many living plants and is likely to have been a dominant mode of reproduction for much of land plant history. Many spore and pollen grains display conspicuous ornaments, including various types of spines, ridges, flanges, and bladders, that may aid in wind dispersal by increasing drag and thus increasing potential dispersal distance. But determining the aerodynamic effects of spore or pollen ornamentation is difficult, because such small particles are inherently hard to work with and additional factors such as grain shape and density will also affect aerodynamic properties. Here we use cutting-edge computational fluid dynamics (CFD) software to analyze drag for pollen grains that have spines and ridges. We focus on intermediate fluid flow regimes, at the transition between laminar and turbulence, a change likely experienced by those particles due to their size. Preliminary results suggest that ornaments do increase drag coefficients in proportion to propagule size; spores or pollen grains above 100 microns in particular may see substantial increases in drag relative to comparable spheres. We contextualize these results with a quantitative morphospace spanning from the late Silurian through the Middle Devonian, when spore size and ornament size increase dramatically. Both simulations and morphospace analysis suggest that the effects of ornaments on smaller particles may be less important, consistent with the well-known lack of ornaments on most wind-pollinated extant angiosperm pollen.

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Systematics

Topic: Poster

Title: **Fruits of Burseraceae—diagnostic traits and their recognition in the fossil record**

Author: ***Steven Manchester @ Florida Museum of Natural History***

Keywords: fossil fruits,Fruits,micro-CT scanning

Abstract:

Although the drupe-like fruits of Burseraceae are not particularly distinctive when observed with their mesocarp and exocarp intact, the woody pyrenes within them display distinctive morphology that can allow for recognizing the family and for the distinction of putative clades at generic and/or intrageneric levels. We surveyed pyrene morphology and locule configuration for species representing most extant genera of the family using micro-CT scanning to provide a framework for interpreting fossil pyrenes and locule casts. Typically the fruits develop from an ovary of three to five carpels (ten in Beiselia), but in some genera only one carpel develops fully resulting in a single unilocular fertile pyrene (e.g., Bursera, Commiphora), while in others all carpels may form pyrenes at maturity (e.g. five in Aucoumea). In several genera the pyrenes are readily separable from one another, but in Canarium and Trattinnickia the pyrenes are mutually fused. Abortive pyrenes are obvious in Bursera, Commiphora, Dacryodes and Santiria, remaining attached in the apical half to the ventral surface of the larger, developed carpel. Bursera and Commiphora pyrenes are typically thick-walled, whereas Dacryodes, and most Protium species (including Crepidospermum and Tetragastris) have relatively thin-walled pyrenes. The presence and configuration of germination valves in the pyrenes differs among the genera as well. Similar observations of fossil specimens allow us to trace the Burseraceae back to the latest Cretaceous and early Paleocene of India. The pentacarpellate fruit of Sahniocarpon from the late Maastrichtian Deccan Intertrappean beds of central India shows five pyrenes which are triangular in cross section, hypogynous perianth, and axial placentation, with mesocarp and exocarp opening septicidally as valves exposing the pyrenes. Burseraceous pyrenes and locule casts are well represented in the Eocene of North America and Europe indicating that the family was more widely distributed at middle northern latitudes during warmer times.

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Ecology

Topic: Poster

Title: **Great Basin Native Forb Reciprocal Transplant Experiments with Rocky Mountain Research Station, Boise**

Author: ***Nyika Campbell @ U.S. Forest Service***

Keywords: adaptive plasticity,common garden,Great Basin,Local adaptation,native plants,native seed,native species,phenology,transplant study,fruiting phenology,leafing phenology,flower morphology,forb

Abstract:

Beginning in 2017, the Rocky Mountain Research Station (RMRS) in Boise has initiated reciprocal transplant experiments with the goal of understanding local adaptation in native forbs and developing genetic seed transfer zones. With a focus on sage grouse habitat and shrubland ecosystems, RMRS has developed multiple partnerships within federal land agencies and state universities across the Intermountain Region.

In contrast to previous seed transfer studies focused on wind pollinated species, research on forbs across a large geographic area presents several unique challenges. Local adaptation and plasticity may be expressed through widely varying traits among taxonomic groups. Furthermore, spatial patterns and phenological timing in populations may vary across both an ecoregional scale and microclimate scale. Selection of target species and field-collection across multiple states using limited personnel pose continuing difficulty. Through an iterative process starting with species selection and ending with common garden data collection, a complex work-flow has been developed. As part of this work-flow, novel protocols have been established in order to balance research needs with practical application. Ongoing work has resulted in numerous secondary products, including the improvement of seedling grow-outs, techniques for dryland garden installation, field identification guides, and germination trials.

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Phytochemical

Topic: Poster

Title: Relaxed purifying selection is observed in genes at the branches of the flavonoid biosynthetic pathway in Nicotiana species that do not produce anthocyanins compared to those that do

Author: ***Abigail McCoy @ SUNY Cortland***

Keywords: Nicotiana,Anthocyanins,d_N/d_S analysis,Evolution,Flower color

Abstract:

The evolution of flower color in the genus Nicotiana has been dependent on the presence of various pollinators. Different colored flowers are created by pigments of different hues, which are produced by the branched pattern of the flavonoid biosynthetic pathway. The objective of this study is to identify the genetic basis of flower color shifts in Nicotiana by determining which evolutionary pressures are present on flavonoid biosynthetic pathway genes. We obtained available transcriptome data and extracted the sequences of the flavonoid biosynthetic pathway genes. Sequences of each gene were then used to infer phylogeny and analyses were run to determine the ratio of the rate of nonsynonymous mutations to the rate of synonymous mutations (dN/dS). This ratio will indicate which evolutionary pressure is acting on the flavonoid biosynthetic pathway genes including: purifying selection (dN/dS 1). Overall, we observed that the flavonoid biosynthetic pathway genes tended to be under purifying selection. We hypothesized that species that do not produce anthocyanins will be under more relaxed purifying selection in comparison to those that do, suggesting that there is less pressure to maintain the original sequence as the genes encoding for anthocyanins are not being used by these species. In flower color comparisons between species without anthocyanins versus those with anthocyanins, we saw significantly different dN/dS ratios for the genes DIHYDROFLAVONOL 4-REDUCTASE (DFR), FLAVONOID 3'-HYDROXYLASE (F3'H), and FLAVONOID 3',5'-HYDROXYLASE (F3'5'H). For the genes F3'H and F3'5'H, we observed relaxed purifying selection acting on the species without anthocyanins, supporting our original hypothesis. However, for the gene DFR, we observed relaxed purifying selection acting on the species with anthocyanins, contradictory to our original hypothesis. We found a frameshift mutation resulting from a one base pair deletion in the N. sylvestris homeolog of DFR in some N. tabacum accessions, which likely contributes to the relaxed purifying selection seen in species producing anthocyanins. Based on their placement at branching points in the pathway, it is unsurprising that DFR, F3'H, and F3'5'H have significantly different dN/dS ratios in species with and without anthocyanins since mutations in these genes may alter the flux of the pathway to produce different pigments. When simulating the evolution of the pathway using computational models, the mutations that accumulated to produce flower color shifts were concentrated in the genes at the branches of the pathway, suggesting the corroboration of simulated and empirical data.

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Development and Structure

Topic: Poster

Title: Expression of the YUCCA family of auxin biosynthetic genes in leaves of hybrid poplar

Author: ***Rachel Spicer @ Connecticut College***

Keywords: Leaves,poplar,cambium,auxin

Abstract:

Members of the YUCCA gene family encode a flavin monooxygenase-like enzyme that catalyzes the final step in auxin biosynthesis, the conversion of indole-3-pyruvic acid (IPyA) to indole-3-acetic acid (IAA). As this is generally considered the rate limiting step in IAA biosynthesis, the YUCCA genes are thought to be central to this process. In order to better understand the sites of IAA biosynthesis in shoot systems of hybrid poplar, we measured the expression levels of multiple YUCCA genes in the leaves of young, greenhouse-grown Populus tremula x alba clone INRA 717-1BA using qRT-PCR, normalizing expression against three reference genes. Previous work had shown that shoot apices (defined as tight clusters of young leaves at the apex with indistinguishable internodes) contained the highest concentrations of IAA, and that IAA dropped down to low and stable levels by L16, the 16th leaf beneath the apex. Both YUC1 and YUC12 followed a pattern similar to IAA concentrations, with peak expression in apices, but YUC12 showed more than 10x the expression of YUC1 and was consistently the dominant YUCCA expressed in whole leaves that were still undergoing expansion. In order to determine relative expression levels within leaves, L8 – which is about one-half fully expanded in poplars of this size and age – was further dissected into margin, blade, midvein and petiole. YUC2 and YUC12 were both highly expressed in the blade and leaf margin, but YUC2 dropped down to near-negligible levels in the midvein and petiole while YUC12 expression remained high. A neighbor-joining phylogenetic tree supports multiple pairs of YUCCA homologs in Populus, and suggests differential expression in leaf development within at least some of these pairs. These results provide important insight into the source(s) of leaf-derived IAA during both leaf expansion and cambial development in the stem.

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Ecology

Topic: Poster

Title: A Citizen-Science Approach: Testing the Effect of Native and Non-Native Milkweed Species on Monarch Butterfly (Danaus plexippus) Development in the Midwestern United States

Author: ***Theresa Culley @ University of Cincinnati***

Keywords: Citizen Science,migration,milkweed,monarch butterfly

Abstract:

In recent decades, the monarch butterfly (Danaus plexippus) has faced a major decline, leading to its listing as an endangered species on the IUCN Red List. As monarchs depend upon milkweed species for their larval food source, the restoration of local milkweed plants is vital for the survival of monarch populations. Many conservation groups now propose that milkweed species to planted throughout the North American landscape to the aid this iconic butterfly species. Citizen scientists have been leading the fight to preserve monarch populations in the Midwest, through both the restoration of the native milkweed populations, planting of milkweed in residential gardens, and the indoor raising and eventual release of adult monarch butterflies. This study aimed to mimic the conditions used by citizen scientists to rear monarchs and compare the effects of different milkweed species on butterfly growth and survival. The host plant species examined were swamp milkweed (Asclepias incarnata L.), common milkweed (A. syriaca L.), butterfly weed (A. tuberosa L.), honeyvine (Cynanchum laeve [Michx.] Pers.), and non-native tropical milkweed (A. curassavica L.). Monarchs raised on swamp and tropical milkweed exhibited the best growth and survival rates during each life stage (larvae, pupae, and adult), compared to the other host plant species. However, tropical milkweed is not native to the Midwestern United States and may create an ecological trap for monarch butterflies, preventing their southward migration in late fall. Therefore, we recommend that Asclepias incarnata is best used for monarch rearing and release in the Midwest, at least based on captive rearing conditions.

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Ecophysiology

Topic: Poster

Title: Genetic variation in drought response across vegetative development

Author: ***Erica Lawrence-Paul @ Pennsylvania State University***

Keywords: Arabidopsis thaliana,Development,drought tolerance,Vegetative phase change

Abstract:

Developmental transitions impact ecology and evolution by altering the way plants interact with their environment. Studies of germination and flowering show that developmental timing has significant impacts on plant fitness and performance, but very little attention has been given to the juvenile-to-adult transition: vegetative phase change (VPC). In this study we used 160 diverse genotypes of Arabidopsis thaliana and mutant lines with altered developmental timing to investigate how plants differentially respond to drought across vegetative development. Specifically, we used measures of growth, fitness, and drought physiology to understand how the timing of vegetative phase change, and the phase a plant is in when exposed to drought, impact the plant's ability to respond to these stressors. Further, we looked for associations between natural variation in the timing of vegetative phase change and climate-of-origin to understand whether this developmental transition contributes to environmental adaptation. Finally, we conducted a genome-wide association study to identify the genetic loci associated with differential response to drought stress, and natural variation in the timing of VPC.

Overall, we found that the timing of vegetative phase change has significant impacts on plant performance in response to drought stress and that the developmental phase of a plant (i.e., juvenile or adult) alters the impacts of drought on plant growth and fitness. We also found significant variation in response to drought among the 160 different genotypes tested. Further, we found significant relationships between the timing of vegetative phase change and climate-of-origin indicating that the timing of this transition may contribute to both adaptation and acclimation in plants. Our study provides further evidence that vegetative phase change results in important physiological shifts in plants that contribute to their success and should not be overlooked.

569

Crops and Wild Relatives

Topic: Poster

Title: Analysis of Rare Vigna Species: Vigna Kirkii and Vigna Stenophylla

Author: ***Kaycie Melville @ Utah Valley University***

Keywords: Abiotic stress,Biodiversity,genome size,phylogenetics,rare species,Vigna

Abstract:

Vigna Savi consists of more than 40 wild species and several domesticated plants of high nutritional value. With resilience to a variety of abiotic stressors (i.e., flooding, drought, infection, etc.), wild species represent a reservoir of potentially useful traits that could be used to improve crops. Recent phylogenetic analyses of cpDNA and ribosomal DNA (matK and ITS, respectively) suggest a unique lineage comprising V. kirkii and V. stenophylla, two relatively unknown wild species that may represent a possible new subgenus. Interestingly, chloroplast and nuclear phylogenies provide differing hypotheses of Vigna stenophylla and Vigna kirkii relations. However, due to these species' rarity, little to no information is known about these species. Through this research, we seek to analyze their genomes via flow cytometry to estimate genome size and ploidy to see if they are possibly polyploids or hybrids with other species. To begin this analysis, we grew plants from seed for each species. Through the growth period alone, we have discovered more information about V. stenophylla and V. kirkii life history. These species differ from most other Vigna s.s. species in aspects of structure and growth patterns: V. stenophylla grows in a bushy manner with long, thin leaves and a smooth stem and is far slower growing than V. kirkii, which vines and has wide leaves, a thick layer of hairs on the stem, and a quick germination period. From our observations, there are a myriad of possibly favorable traits that could be used in currently domesticated crops. Of these are V. stenophylla's bushy growth pattern and both V. stenophylla and V. kirkii's quick recovery from viral infections—a period as short as a couple of days with a quick reaction to shedding leaves and producing shoots and branching. In addition to growth observations, we explore propagation via tissue culture in the hopes of establishing a protocol for production to increase in plant yield for further analysis of species growth patterns and tendencies, and plant reproduction, and to gain more information of flower characteristics and seed production.

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Systematics

Topic: Poster

Title: Optimizing the lysis step in CTAB DNA extractions of silica-dried and herbarium leaf tissues

Author: ***Jamie Carey @ Ohio University***

Keywords: DNA extraction,cell lysis,cetyltrimethylammonium bromide,CTAB,molecular biology,plant genetics

Abstract:

Cetyltrimethylammonium bromide (CTAB) DNA extraction in plants is an effective and cost-efficient method, and therefore widely used across genetic studies. The versatility of CTAB has led to specialization and variation in DNA extraction methods; however, protocols often do not detail the modifications that are applied to optimize the extraction of DNA. To determine the effects of modifying extraction protocols on DNA output, experimental studies of each step of the extraction process are required. Our study tested alterations to the lysis step of CTAB extractions of silica-dried and herbarium specimens to systematically determine the effects of incubation temperature and duration across four representative angiosperm groups. Due to high levels of secondary metabolites in extractants of one species, we performed additional tests with chemical additives (sodium dodecyl sulfate [SDS], polyvinylpyrrolidone [PVP], and sorbitol) added during the lysis step. We evaluated the effects on extractant purity, DNA concentration, and fragment length, and found the changes in extractant purity were significant. Preservation method (silica or dried herbarium specimens) also significantly impacted DNA fragment length, purity, and yield, with silica-preserved tissue resulting in higher yields of unfragmented and clean DNA. Results from the additive experiment showed only PVP as significantly effective when measuring DNA yield compared to the other additives, and slightly more effective when compared to extractions using only CTAB. We recommend shorter and cooler lysis periods in CTAB plus PVP DNA extractions and using silica-preserved tissues due to the lower fragmentation, higher purity, and time effectiveness when compared to the hotter and longer lysis periods.

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Ecology

Topic: Poster

Title: Terrestrial orchid Platanthera cooperi (Orchidaceae) utilizes different OMF partners at different development stages in response to temperature, and the origin of seeds

Author: ***SHAN WONG @ Texas Tech University***

Keywords: Mycorrhizae,Seed germination,Ceratobasideace,Tulasnellaceae,Protocorm formation

Abstract:

The influence of abiotic factors, such as temperature and edaphic factors, on seed germination and development, is well-known for plants. However, orchid seeds also require biotic components such as the orchid mycorrhizal fungi (OMF) which are often the determining factor for seed germination and protocorm development. Previous studies have shown that the OMF communities associated with Platanthera cooperi, native to the California Floristic Province, varied across populations and ontogeny. In roots of plants from the larger populations, the OMF Operational Taxonomic Units (OTUs) belonging to the family Tulasnellaceae (LT) were dominant while Ceratobasidiaceae (LC) OTUs were rare. Conversely, smaller populations showed the opposite pattern [OTUs from the smaller populations: Ceratobasidiaceae (SC) and Tulasnellaceae (ST)]. We hypothesize that native fungi and native temperature will enhance seed germination and protocorm development. We isolated and used the fungi representing the dominant and rare OTUs from large and small populations to test whether the fungi dominating the roots of plants in large and small populations, combined with the native soil temperature, providing a competitive advantage to the seeds belonging to the respective populations. Seeds from the large and small populations were exposed to the four fungal isolates (LC, LT, SC, ST) in combination with two temperature treatments (22C, 15.5C). Un-inoculated controls were also used as a fungal treatment. Consequently, the experiments included 20 treatment combinations, each of which was replicated 10 times. After 124 days of incubation, seed germination and protocorm development were recorded.

We detected a three-way interaction among the seed provenance, OMF, and incubation temperature whereby the seeds from the small or large population inoculated with LT and incubated at 22C showed the highest germination. Furthermore, the highest protocorm formation was observed when seeds from the large population were inoculated with LC and ST and incubated at 15.5C, or when the seeds from either population were inoculated with SC at both temperature conditions, or when seeds from the small populations were inoculated with all fungi and incubated at 15.5C, indicating that the conditions required for germination and protocorm development are distinct. We showed that seed germination favored the warmer temperature, while protocorm development was enhanced at the cooler temperature.

577

Phylogenomics

Topic: Poster

Title: Advances in the systematics of Melocactus Link & Otto genus (Cactaceae) using a genomic approach.

Author: ***Milena Telhe @ UFSCAR***

Keywords: Cactaceae,phylogenomics,target-capture

Abstract:

Phylogenetic reconstructions can be difficult in recently diverged lineages, such as those found in the family Cactaceae, due to a lack of phylogenetic signal and an excess of incomplete lineage sorting in genetic data. Large polytomies may result from the absence of phylogenetic signal, while incomplete lineage sorting can produce incongruent phylogenetic relationships with with morphology and the group's evolutionary history. To overcome these obstacles, multiple independent loci from different genomes should be combined with phylogenetic approaches that consider the heterogeneity of gene trees. Melocactus Link & Otto (Cactaceae), a widely distributed genus in South America and Caribbean, has not been comprehensively studied using genetic data. We have generated a multi-locus dataset using high-throughput sequencing of target nuclear loci, which allowed a robust phylogenetic inference. Our results partially support the taxonomic groups proposed for Brazilian species based on morphological variation and ecological characteristics, with a divergence time estimated in the Pliocene. These findings provide insight into the evolutionary history of this genus and will be useful in future studies, such as biogeographical and comparative phylogenetic approaches.

581

Systematics

Topic: Poster

Title: Molecular Systematics and Biogeography of Dieteria (Asteraceae: Astereae)

Author: ***David Morgan @ University of West Georgia***

Keywords: Asteraceae,biogeography,phylogenetics,Taxonomy,molecular systematics

Abstract:

Dieteria occupies most of the western half of the United States, and extends short distances into Canada and Mexico. The genus is marked by substantial variation in morphological characters, notably leaf morphology, leaf and stem vestiture, and a number of phyllary characteristics such as size, shape, vestiture, and orientation of the herbaceous apices. This morphological variation has led to more than 50 species names having been proposed. The most recent complete treatment of Dieteria by B. L. Turner divided it into three species and 16 varieties: D. asteroides (3 varieties), D. bigelovii (3 varieties), and D. canescens (10 varieties). The objectives of this research were to assess variation in nrDNA ITS and ETS sequences, to see if phylogenetic analysis of this variation could help identify well-supported groups of taxa within the genus, and to determine how well these results corresponded with morphological variation, taxonomy, and geographic distribution. We started with ITS and ETS sequence data from 35 samples representing a large part of the distribution of Dieteria, and also representing 13 of Turner's 16 varieties. Phylogenetic analyses produced phylogenies containing three relatively well supported major clades. Comparison of these results with morphological characteristics and with Turner's taxonomy showed little correspondence between the molecular results and either morphology or taxonomy. On the other hand, there was substantial correspondence with geographic distribution. One of the three major clades consisted entirely of samples from Washington, Oregon, and northern California. The second one included samples from southern California and western Arizona, plus additional ones from northern California, northern Nevada, and southeastern Idaho. The third clade was the largest, and consisted of samples from the remaining part of the distribution of Dieteria. Except for the second and third clades' distributions overlapping in Nevada and eastern California, the distributions of the three were mostly distinct from one another. A number of samples were not included in the initial analyses because their sequences contained polymorphic nucleotide positions. Several of these had been collected in areas where two of the three major clades neared one another or overlapped, suggesting that these samples may represent intergradation between the major clades. They are being investigated further by cloning and sequencing their ITS and ETS.

584

Biodiversity Informatics & Herbarium Digitization

Topic: Poster

Title: Digital information from herbaria for forest restoration in eastern Amazonia

Author: ***Fernando Matos @ CRIA (Centro de Referência em Informação Ambiental)***

Keywords: ecological niche modeling,Recovery of degraded areas,Reference forests,Altered forests recovery,Open data sharing,Collaborative networks

Abstract:

The intensive process of degradation and deforestation of tropical forests is a reality in the Brazilian Amazon, whose intensive and unsustainable use of its natural resources not only leads to the loss of forest cover, but also to the degradation of forests and large areas. The National Policy for the Recovery of Native Vegetation sets forest recovery goals, confirming the reality that ecosystem restoration has become a challenge and a priority in Brazil. The more the chosen species correspond to the regional flora, the greater the success chances of the restoration project. However, if this information is not available in the literature, it is necessary to carry out floristic surveys to guide the choice of priority species for the work of vegetation recovery or search for information on occurrences in the herbaria databases. There is little botanical and ecological information about plant species suitable for initial restoration. In this way, the IAN Herbarium aims to establish a partnership with the speciesLink network, which is a consolidated e-infrastructure, developed to provide free and open access to primary data on Brazilian biodiversity. Thus, the installation and monitoring of experiments to restore forests degraded by agriculture, livestock and mining, in addition to carrying out floristic inventories and installing a seed bank in reference preserved areas, as proposed in this work, will directly contribute to expanding the search bases on species used for re-vegetation, especially on native ones. Therefore, to expand the data infrastructure and developing computational tools that support the development of field activities and research in forest restoration will enable improvements in sustainable forest management and the reversal of land degradation and loss of biodiversity.

585

Population Genetics/Genomics

Topic: Poster

Title: Microsatellite Variation and Local Adaptation in Common Milkweed

Author: ***Soren Brauner @ Ashland University***

Keywords: Asclepias,Local adaptation,milkweed,population genetics,Microsatellites

Abstract:

Common milkweed (Asclepias syriaca), the host plant of the Monarch butterfly, occurs across a wide geographic range in eastern North America. Restoration efforts to support the declining Monarch populations involve planting milkweed to provide host plants for the caterpillars. Informed choices of plant materials for restoration efforts require an understanding of the patterns and degree of divergence for traits that may be locally adapted. The microsatellite study is part of a larger project testing for local adaption that is composed of two parts, 1) three large replicated common gardens in Minnesota, Ohio, and Virginia with seeds collected from throughout the native range that will provide data on growth, phenology and defenses that will be used to test hypotheses of local adaptation for biotic and abiotic factors over three seasons of growth, and 2) microsatellite analysis of the same populations grown in the common gardens to estimate the patterns of genetic structure and differentiation based on neutral markers.

DNA was extracted from 260 greenhouse grown plants representing 30 populations including those grown in the three common gardens. Twelve microsatellite markers were used to estimate genetic variability and population structure. Initial analysis using AMOVA indicates that 8% of variation is between populations, 26% among individuals, and 66% within individuals. STRUCTURE and PCA analyses have not revealed significant structuring among the populations, and our results parallel a recent study using SNPs from genotype by sequencing that concluded that common milkweed populations across its native range are roughly panmictic (J.F Boyle et al., 2023, BioRvix preprint). The common garden study is entering the third year of growth, and the results will be compared with microsatellites as neutral markers in Fst vs. Qst types of analyses to test hypotheses about local adaptation.

586

Ethnobotany

Topic: Poster

Title: A Poet and her Plants: An ethnobotanical and biochemical study of Monotropa uniflora from Emily Dickinson's Herbarium.

Author: ***Senaa Mirza @ Maryville University in St. Louis***

Keywords: Medicinal Plants,anti-inflammation,anti-microbial,monotropa uniflora,Native American

Abstract:

This study explores the ethnobotany of the plants in the Herbarium of Emily Dickinson, a 19th-century poet, who was well-known for her gardening and botanical knowledge. In the early 1860s, Dickinson developed inflammation in her eyes possibly due to infection. Due to her sensitivity to light, she had to tend her plants very early in the morning or at night. Her photophobic and phantom-like behavior resembled that of Monotropa uniflora, or the ghost pipe, which she referred to as her “preferred flower of life.” Historically, the sap of this plant was used in Native American medicine as a topical ointment to treat ophthalmic infections or inflammation. In this study, the main objective was to determine if this plant contains the necessary bioactive components to potentially treat Emily Dickinson's eye condition. Using an ethanol extraction and rotary evaporation, the M. uniflora extracts were collected. These extracts were tested for antimicrobial activity using the Kirby Bauer Method and Staphylococcus pneumoniae. M. uniflora does not display antimicrobial activity in the presence of S. pneumoniae. It may be that the antimicrobial properties of M. uniflora are present with higher concentrations of plant extract.

594

Ecophysiology

Topic: Poster

Title: Physiological response of selected common bean genotypes under low phosphorus condition

Author: ***Manuel Guzman @ AGROSAVIA***

Keywords: photosynthesis,stress,Tropical biodiversity,Phaseolus,landraces

Abstract:

The Common bean (Phaseolus vulgaris L.) is an economically important crop cultivated worldwide, with a high digestible plant protein content of up to 27%. In Colombia is cultivated ir soils with low Phosphorus (P) availability or with adverse soil chemical conditions. A field experiment was conducted at Rionegro, Colombia, to quantify the contribution of each physiological process to yield and to identify traits that improve common bean productivity. Eight common bean genotypes, climbing type, were evaluated at three P-restriction levels (25, 50, and 75% of P-relative to the control), according to the recommended dose. The P-restrictions were imposed 30 days after sowing. Treatments were laid out in a randomized complete block design with a split-plot arrangement and three replications, where P-doses were the main plots. Physiological data were recorded at five growth stages using the GreenSeeker® and MultiSpeQ® devices for the normalized difference vegetation index (NDVI), photosynthetically active radiation (PAR), quantum yield of photosystem II (Phi2), non-photochemical quenching (NPQt), ratio of incoming light that is lost via a non-regulated process (PhiNO), and relative chlorophyll (SPAD). Statistical differences ($P < 0 .05$) were found among treatments (P-restrictions) and genotypes for all variables studied. Results showed that the 50 and 75% P-reduction treatments had the largest reduction effect on the bean genotypes. Three genotypes showed higher Phi2 and SPAD values at 50% of P-reduction. NDVI values during flowering ranged from 0.72 to 0.80, suggesting this phenologica stage as a marker to identify P-stress. SPAD values among treatments indicated high genotype susceptibility to P-deficit at 75% restriction. The genotype “G51018” showed high performance under severe and moderate P-restriction. This kind of physiological data was useful to identify superior or candidate genotypes, and will be used for procedures for genome-environment associations, including physiological data to dissect complex quantitative traits such as yield.

608

Floristics & Taxonomy

Topic: Poster

Title: A review of the woody bamboos (Poaceae: Bambusoideae: Bambuseae) of Trinidad and Tobago

Author: ***Christopher Tyrrell @ Milwaukee Public Museum***

Keywords: bamboo,Bambusa vulgaris,Floristics,Arthrostylidium

Abstract:

The dual island nation of Trinidad and Tobago is an important keystone for neotropical woody bamboo taxonomy. Trinidad is a type locality for two widely applied but poorly defined species: Arthrostylidium pubescens Rupr. and A. excelsum Griseb. and two potentially endemic species: Chusquea cylindrica L.G. Clark and Rhipidocladum prestoei (Munro) McClure. Few resources exist for the islands to adequately identify all the woody bamboo species that putatively grow there. The serialized vascular flora of Trinidad and Tobago, for instance, lacks a treatment for Poaceae. Moreover, the most speciose native genus, Arthrostylidium, is only partially revised, with the emphasis on the South American species and not those of the West Indies. Our objective is to critically review the woody bamboos of Trinidad and Tobago, clarify which species are or have been known from the islands, and provide an identification key, species accounts and distribution maps for the revised list of taxa. We conducted fieldwork campaigns in 2022 and 2023, and reviewed herbarium specimens and human observation records of woody bamboos from the islands. Newly collected specimens were vouchered and all woody bamboo records were georeferenced and plotted using QGIS v.3.24. Estimates of species distribution models (SDM) were generated for several species growing on the islands. We confirmed three species of native woody bamboo and three species of introduced woody bamboo were extant on Trinidad. An additional three western hemisphere species may have dynamic occurrence on the island(s). Native species diversity correlated well with previously identified floristic hotspots. One introduced species, B. vulgaris, is common on Tobago. To the best of our knowledge, there are currently no native woody bamboo species present on Tobago, however, A. pubescens appears to have been growing along the Main Ridge in the past. The historic presence of some species not currently found may indicate an instance of source-sink populations dynamics between the islands and mainland South America.

613

Biogeography

Topic: Poster

Title: Wringing out species boundaries in ringstems (Anulocaulis, Nyctaginaceae)

Author: ***Jake Balmuth @ Oberlin College***

Keywords: Chihuahuan Desert,Edaphic Endemism,Nyctaginaceae,Phylogeography,gypsophiles,Species boundaries

Abstract:

Gypsum exposures occur in an island-like distribution throughout the Chihuahuan Desert region of southwestern North America. For gypsophiles, migration between gypsum exposures can be very rare because of this island-like distribution. This lack of gene flow results in isolation and therefore genetic differentiation among gypsophile populations. Anulocaulis (Nyctaginaceae) is a genus of five species, all native to northern Mexico and the western USA and commonly referred to as “ringstems.” Anulocaulis includes a clade of two gypsophile species (A. leiosolenus and A. reflexus) that have long floral tubes and are hawkmoth-pollinated, but whose fruits are likely gravity-dispersed. Because of the island-like distribution of gypsum, gypsophilic Anulocaulis populations are isolated from each other, which promotes divergence. However, hawkmoths can carry pollen long distances, and thus, hawkmoth pollination may help to maintain genetic connectivity between these disparate populations. This push-pull between divergence and genetic connectivity may be responsible for the confusing patterns of morphological variation that exist in gypsophilic Anulocaulis, with some groups of populations having been called different species while others having been called different varieties within the same species. The taxonomy of this group has been established through morphological study; however, the taxonomy has only been studied using DNA sequence data from a few genes, giving inconclusive results. We are sequencing DNA of hundreds of genes from populations throughout the range of gypsophile Anulocaulis to test the traditional species and variety boundaries. We hypothesize that although they look similar, A. leiosolenus var. leiosolenus populations in Nevada and Arizona are genetically quite different than other populations of this variety because they are so geographically separated and may represent a cryptic species. We also hypothesize that given the strong morphologica differences between A. leiosolenus var. gypsogenus and other A. leiosolenus varieties, our molecular data will show that it should be recognized as a separate species.

627

Ecology

Topic: Poster

Title: Long-term seed viability in the emerging invasive species wavyleaf basketgrass (Oplismenus undulatifolius) in USA mid-Atlantic forests

Author: ***Carrie Wu @ University of Richmond***

Keywords: invasive species,Plant invasion,Seed germination

Abstract:

Invasive non-indigenous species pose a serious threat to native biodiversity and ecosystem functioning. Understanding how species performance varies under conditions in the current and potential invaded range can help to predict dynamics of the invading species in its new environment. Plants with the ability to alter growth or vegetative architecture in response to variation in light regimen may be favored in landscapes that experience frequent disturbance, which is known to be a key mechanism promoting plant invasion, as they may be able to exploit novel niches. Seed bank persistence may also play a critical role in successful plant invasion, as seed viability for an extended time increases species survivability in unfavorable conditions, maintains population genetic diversity, and may allow re-invasions. This study investigated seed bank longevity and the effect of light intensity on germination of wavyleaf basketgrass (Oplismenus undulatifolius), a newly established invasive species in US mid-Atlantic forest understories. We germinated wavyleaf basketgrass seeds collected across five years from the original site of introduction at Patapsco Valley State Park, MD under four light conditions in a controlled growth room. Seeds remained viable for at least 9 years, with a dramatic drop after 7 years, while light intensity did not significantly impact seed germination. Our study shows the importance of evaluating environmental and temporal effects on germination traits, since the scope of surveillance may need to be expanded based on new information about environmental tolerance. Long-term monitoring may be necessary to effectively control invasive plant populations capable of forming a persistent seed bank.

631

Conservation Biology

Topic: Poster

Title:

Can Lake Superior Arctic Relicts Survive the Anthropocene? Population Viability Analysis for Three Species Across Three Years

Author: ***Ryan Carlson @ University of Minnesota Duluth***

Keywords: arctic,Disjunct Species,Great Lakes region,disjunct distribution,population viability

Abstract:

In North America, relict arctic plant populations from the last glacial maximum persist in disjunct locations south of their normal range. These fringe populations may be particularly threatened by stressors associated with climate change like increased temperature and decreased water availability. In Minnesota, USA, several arctic relicts of conservation concern are confined to the rocky coast immediately adjacent Lake Superior, where they comprise an ‘arctic-alpine’ community in restricted microclimates that provide suitable habitats for their survival. We monitored populations of the arctic relicts Primula mistassinica, Pinguicula vulgaris, and Euphrasia hudsoniana along the shoreline for three growing seasons between 2020 and 2022 to track growth, reproduction, and survival of individuals. Using these factors, Population Viability Analysis models were created for each species to project population growth or decline at each site. Well below average spring and summer precipitation in 2021 provided an opportunity to study how arctic relict populations react to and recover from droughts, and how they may fare under future climate with increasing intensity of weather events. Declines in reproduction and survival during and following the drought were site specific for each species and not latitude dependent. Variability of these factors between sites, species, and years reinforces the important role that microclimates play in the health and future viability of these plant populations.

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Crops and Wild Relatives

Topic: Poster

Title:

Pears (Pyrus, Rosaceae) as a Nutritional Source of Food

Author: ***Nina Baghai-Riding @ Delta State University***

Keywords: Pyrus communis

Abstract:

There are over three thousand pear varieties worldwide, and ten commonly grow in the United States. Pears are classified as a pome fruit. Trees of Pyrus grow best in cold and wet climates, with rich loamy soil. It can take three to seven years for a pear tree to bear fruit. In the Fall 2022 Economic Botany course at Delta State University, one group studied six different pears species/varieties: the common/European pear (Pyrus communis L.), Bartlett (Pyrus communis ‘Williams' Bon Chrétien’), green and red D’Anjou (Pyrus communis 'Anjou'), Bosc (Pyrus communis ‘Bosc’), and Asian pears (Pyrus pyrifolia). Similarities and differences for each pear type were noted. Unique characteristics include the time of harvest, color, overall shape, and nutrients. Pears are harvested throughout the year. The Asian pear had the shortest harvest period (August through September). In comparison, the red and green D’Anjou had the longes harvest season (October to July). The red D’Anjou and common pear shapes are typically longer while the green D’Anjou and Asian pear tend to be rounder. The Bosc and Bartlett pears typically are a golden color and have a pyriform shape. Nutritional websites regarding these six pear species/varieties indicate the green D’Anjou pears have the highest daily nutritional quantities of vitamins (1% vitamin E, 7% vitamin C, and 5% vitamin K) and the Asian pear had the lowest value. All six pear species/varieties associated with this study possessed Vitamin K and Vitamin C. The Asian pear was the only one that did not contain Vitamin E. Besides vitamins, pears contain copper, magnesium, and potassium. Copper and magnesium are important for maintaining the nervous system. Future research can incorporate the analysis of other nutritional components of different pear varieties by using the Energy Dispersive X-Ray Fluorescence Spectroscopy associated with the JSM-6010LA scanning electron microscope at Delta State University. New varieties may then become more available for the general consumer.

635

Paleobotany

Topic: Poster

Title:

Floral Shifts in Relative Dominance, not Species Turnover, in the Pre-Angiosperm World: Palynological Evidence from the Yellow Cat Member, Cedar Mountain Formation, East Central Utah, USA

Author: ***Nina Baghai-Riding @ Delta State University***

Keywords:

Abstract:

The ?Berriasian-Cenomanian Cedar Mountain Formation (CMF) in Utah is a significant unit as it preserves the transition from Jurassic to Cretaceous ecosystems. It preserves distinctive faunal, especially dinosaur, assemblages, and encompasses an interval of fluctuating climate and dramatic biotic changes (in the terrestrial realm, origin and spread of angiosperms). Recent stable C isotope and zircon analyses have revealed that the basal Yellow Cat Member of the CMF may at some localities be as old as Berriasian, with zircons from two localities providing well-constrained maximal depositional ages of approximately 135 mya (early Valanginian). The Yellow Cat Member is a laterally constrained unit deposited by a northward-trending, low sinuosity river system, and comprises fluvial, lacustrine and paleosol sediments. We present here palynological data from two measured sections of the Yellow Cat Member that are approximately 11 km apart, Jim’s Pond and Lake Madsen. Samples from the lower Yellow Cat, represented by seven samples at Jim’s Pond, are overwhelmingly dominated by the xerophytic conifer Classopollis (Cheirolepidiaceae) and its frequent co-dominant, Exesipollenites, an unknown seed plant likely representing a wind-pollinated canopy tree (?Cupressaceae). Other conifers (Pinaceae, Araucariaceae, unquestioned Cupressaceae, ?Podocarpaceae, ?Voltziales) are distinctly subordinate. Other seed plants are rare and include Caytoniaceae, Gnetales and Ginkgoales or Bennettitales. Spores are rare, and include bryophytes, smooth triletes of uncertain affinity and members of the Osmundaceae, Lycopodiales, and Schizaeales. Species of Schizaeales are particularly important for palynostratigraphy, and support correlation of the lower Yellow Cat Member with basal Cretaceous assemblages from England, Germany, France and the Netherlands. The upper Yellow Cat, represented by only one sample, shows a drop in the xerophyte Classopollis and concomitant increase in other conifers and Exesipollenites. Spores remain low in overall abundance, but display a distinct increase in diversity. Both observations may suggest cooling and/or increased precipitation in the upper Yellow Cat, although local facies effects may have greater impact on floral composition. Yellow Cat palynofloral assemblages resemble underlying Jurassic Morrison Formation assemblages in that many of the same morphotaxa are recognized in both formations, but relative abundance of certain taxa shifts. Notably, Classopollis is present but quite rare in the upper Morrison Formation but becomes much more abundant in the Yellow Cat Member, and many of the same conifer morphospecies extend through both formations. However, the Yellow Cat Member is marked by first appearance of numerous taxa, including species of the Schizaeales, as well as Foraminsporis, Densoisporites, Couperisporites, Interulobites and others, rather than by extinctions. It is not until the spread of angiosperms in the Albian-Cenomanian that terrestrial macrofloras undergo dramatic biotic turnover.

636

Pteridology

Topic: Poster

Title: Towards understanding the evolution of gene expression in gametophytes of mycoheterotrophic ferns and lycophytes

Author: ***Marielle (Mari) Wilson @ University of British Columbia***

Keywords: comparative transcriptomics,Mycoheterotrophy,pteridophyte

Abstract:

Several plant lineages have wholly or partly lost their photosynthetic ability and instead rely on carbon acquired from soil fungal associations, to varying degrees. One manifestation of this mycoheterotrophic lifestyle is in the gametophytes of several fern and lycophyte groups. In contrast to their photosynthetic sporophyte generation, these gametophytes rely solely on fungal carbon for nutrition throughout their life. Thus, their independently living haploid and diploid generations effectively switch trophically, a form of initial mycoheterotrophy in which only the haploid stage is fully mycoheterotrophic. Initial mycoheterotrophy has arisen independently multiple times across ferns and lycophytes and critical genetic changes accompanying this shift have yet to be explored. We are generating transcriptomes from photosynthetic sporophytes and mycoheterotrophic gametophytes of ferns (Psilotaceae, Ophioglossaceae, Gleicheniaceae, Schizaeaceae) and lycophytes (Lycopodiaceae). We will then contrast gene expression between generations of the same species and between mycoheterotrophic gametophytes and those of completely photosynthetic taxa. We will use these datasets to better understand: (1) the genetic and molecular changes that accompany trophic switching between generations within species, and (2) the evolution of mycoheterotrophy in fern and lycophyte lineages, by comparing changes in gene expression among sporophytes and gametophytes with different or similar trophic status. Our study will provide insights into the evolution of mycoheterotrophy, the genetic basis of trophic switching across generations, and nuclear genome evolution in relation to plant-fungi interactions.

638

Pteridology

Topic: Poster

Title: Coexistence of two species of bracken (Pteridium) in a narrow but expanding zone of range overlap

Author: ***Jeffrey Dosdall @ Archbold Biological Station***

Keywords: distributions,Florida,microhabitat,congeneric species,Archbold Biological Station,Pteridium caudatum,Pteridium aquilinum ssp. pseudocaudatum

Abstract:

Congeneric species that occupy similar niches in distinct geographical ranges but whose natural ranges narrowly overlap present an eco-evolutionary conundrum: How can species evolved to occupy the same niche in distinct ranges coexist? Research suggests that for a stable coexistence the species should differ at least subtly in their ecological niches, otherwise their coexistence would be unstable. Peninsular Florida represents such a range overlap between two closely related bracken (Pteridium) species, P. caudatum and P. aquilinum ssp. pseudocaudatum. We investigated whether these species share a habitat and coexist locally, and whether that coexistence is predicted to be stable. We surveyed bracken populations from seven sites at Archbold Biological Station (Venus, Florida, USA) and characterized elements of their biotic and abiotic microhabitat. We also evaluated reports of P. caudatum north of its known range from vouchered specimens to verify if the zone of overlap is expanding. Both bracken species cooccurred at three sites and shared a preference for high litter cover. Importantly, P. caudatum favored lower canopy cover than control plots, while P. a. pseudocaudatum favored lower fire frequency. Pteridium caudatum also grew at higher densities and biomass than P. a. pseudocaudatum. We confirmed that the range of P. caudatum has expanded along the Gulf Coast to Texas and along the Atlantic Coast to Virginia. These results suggest both bracken species occupy similar yet distinct microhabitats suggestive of a stable coexistence, which may help to explain their expanding zone of range overlap.

639

Ecology

Topic: Poster

Title: A Plant Anatomical Investigation of Hydrocotyle bonariensis Comm. ex Lam. (Araliaceae)

Author: ***Nina Baghai-Riding @ Delta State University***

Keywords:

Abstract:

Hydrocotyle bonariensis Comm. ex Lam. (largeleaf pennywort, Araliaceae) is native to the Mississippi Gulf Coast. Its native range is from Argentina to North Carolina, and it is an ecological indicator in coastal areas including estuaries, sand dunes brackish wetlands, riparian habitats, and more. However, a population consisting of over two hundred individuals exist in Bolivar County, MS by a clay-rich ditch bordering the Bear Pen Park softball field. Hydrocotyle bonariensis has an underground rhizome; round, orbicular leaves with rounded scalloped serrations, and an umbel inflorescence, which may possess several levels of pedicels. Leaf petioles are slender and attached in the center of the leaf lamina. The flowers are greenish-white and are approximately 2-3 mm in size. Anatomical observations for this plant species have not been described previously. Using fresh samples, anatomical observations and cell measurements on stems, roots, leaves, and inflorescence components were completed. Single-edged razor blades and hand-held microtomes were used in preparing thin-sections. Prepared slides were stained with neutral red, safranin, or toluene blue. Digital photographs were taken using an Olympus BX43 microscope with an attached Q-color 3 camera. A JEOL scanning electron microscope was used to analyze petiole and leaf epidermal sections as well. Thirty-five measurements were taken on major cell components: parenchyma in petiole, pedicel, rhizome and peduncle; collenchyma in petiole and peduncle; guard cells on the abaxial and adaxial leaf surfaces; and more. Several cell types had a significant size range: cortex parenchyma (length 29 - 70 µm and width 20 - 81 µm), pedicel epidermal cells (length 8 - 20 µm and width 8 -22 µm) and subsidiary cells on the leaf adaxial surface (length 8 - 45 µm, width 16 - 46 µm). Significant anatomical features include amphistomatic stomata, arrangement of vascular bundles in the petiole (seven in a ring and one in the center), prolate pollen, absence of collenchyma in upper areas of the peduncle and pedicels. Future research includes making cross-sections of roots and leaves using a microtome to discern how it differs from other species in the Araliaceae.

640

Population Genetics/Genomics

Topic: Poster

Title: Uncovering the Population Structure of Florida's Threatened

Pine-Pink (Bletia purpurea) Orchid

Author: ***Bethany Simpson @ Florida Atlantic University***

Keywords: Florida,molecular ecology,Orchidaceae,population genetics,threatened species

Abstract:

Orchids are facing global threats and extinctions at an alarming rate. Florida is a hotspot for native orchid biodiversity; making up at least half of the species diversity found in continental United States and are mainly distributed in the Everglades and Fakahatchee Strand. Anthropogenic activity has had significant negative impacts on orchid biodiversity in the state such as; habitat loss, climate change, and illegal collection. It is estimated that roughly 50% of Florida natives are listed as threatened, endangered, or critically imperiled. The Pine-Pink orchid, Bletia purpurea is a state-threatened terrestrial species that was historically abundant throughout South Florida. Urbanization and development of the Greater Everglades ecosystem over the last 200 years have left populations of B. purpurea reduced and fragmented overtime. As a space-dependent species, they can be locally abundant but only occur in a limited number of sites. Dispersal may be restricted due to natural factors or anthropogenic activities, and may be reproductively isolated. Local adaptations have been observed between the east and west coasts of South Florida; such as differences in habitat preference and blooming periods. Bletia purpurea in Florida has developed self-fertilization, a form of autogamy, which is not commonly reported in their Caribbean and Latin counterparts. It is becoming increasingly clear that genetic information is critical for forming conservation strategies to help mitigate the disappearance of threatened species from the wild. Conservation research scientists from the Atlanta Botanical Garden designed and developed a lineage-specific target sequence capture bait set for the Orchidaceae family to reliably sequence orthologous loci across many orchid lineages. This bait set has not yet been tested on any species from the genus Bletia, but shows great promise for estimating population genetic diversity and structure, especially within the Epidendroideae subfamily. To date, there is nothing known about the historic or current population structures of Bletia purpurea or its intraspecific genetic diversity among the known distribution areas in Florida. This study aims to focus on their distribution throughout Palm Beach, Miami-Dade, and Collier County. Due to the cleistogamous nature of this species in Florida and the large physical distances from each area (>100km), it is hypothesized that each region will be genetically distinct with high variation between populations.

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Functional Genetics/Genomics

Topic: Poster

Title: Breeding Switchgrass: The genetics of mycorrhizal community assembly in an ecologically and economically important plant species

Author: ***Katie Stahlhut @ Miami University***

Keywords: arbuscular mycorrhizal fungi,community assembly,Community composition,genetic architecture,GWAS,plant-microbe interactions,switchgrass

Abstract:

Plant genetic variation plays an important role in structuring root-associated mycorrhizal communities, but how this variation is partitioned within plant species is currently unknown. This research utilizes switchgrass genetic resources to identify the drivers of mycorrhizal community assembly within a plant species and to elucidate the plant genetic architecture of mycorrhizal community traits. We use fifteen replicated genotypes to identify variation in community assembly within and among switchgrass genotypes and to test whether mycorrhizal community assembly is phylogenetically conserved or associated with physiological trait adaptations. We use a larger, unreplicated selection of more than 600 tetraploid switchgrass genotypes to identify genes and gene regions that are associated with mycorrhizal community composition. We also use this large dataset to assess differences between subpopulations and ecotypes, to determine whether community composition is associated with other plant physiological traits that have also been measured in the switchgrass, to identify colocalized genes across the switchgrass species, and to assess the heritability of mycorrhizal community assembly. Finally, we compare the mycorrhizal community assembly of roots from tetraploid switchgrass individuals to octoploid switchgrass individuals grown in the same common garden to characterize the effect of genome duplication on mycorrhizal community composition. This data provides some insight into how mycorrhizal community assembly is affected by plant genotype and may potentially be a trait under selection. The results of this study provide valuable insights into the genetic architecture of plant-mycorrhizal interactions in switchgrass.

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Population Genetics/Genomics

Topic: Poster

Title: Association of selective sweeps and multi-trait associated genomic regions in cultivated Helianthus annuus

Author: ***Samantha Leano @ University of California, Davis***

Keywords: bioinformatics,population genomics,sunflower,Biotechnology

Abstract:

The domestication of many crops resulted in reduced genetic diversity. One of the most extreme examples is in cultivated sunflowers, Helianthus annuus, for their oils and confectionery cultivars. Due to these breeding practices, only a certain number of sunflower species were selected to emphasize these favorable traits. Doing so creates a selective sweep, where a mutation fixes in a population and then reduces the genetic variation that are similar to the mutation. This signifies extremely low genetic diversity compared to the wildtype and causes a population bottleneck effect. Understanding whether a specific trait or a variety of similar traits are more popular among an entire population is still a current topic being studied. Using machine learning and simulation tools, we investigate selective sweeps using a deep learning approach to identify hard and soft sweeps related to the population bottleneck effect. Hard sweeps indicate that there is a single variant that will arise in frequency over time, while soft sweeps indicate multiple alleles that will arise over time. The main difference between hard sweep and soft sweep is that the soft sweep can identify other variants that are not strong of a match within that population. These sweeps were created through a highly computerized cluster by a training dataset program called diploSHIC. In our findings, we conclude that there are multiple variants of confectionary cultivars that are found among different species of sunflowers in both hard sweeps and soft sweeps. With our findings, we detail the relationship between the genetic architecture of phenotypic traits in cultivated sunflowers in the context of potential selective sweeps.

645

Education and Outreach

Topic: Poster

Title: Community-Engaged Learning in a Plant Taxonomy Class

Author: ***James Cohen @ Weber State University***

Keywords: community-engaged learning,plant taxonomy

Abstract:

Community-engaged learning is a pedagogical approach that brings together students and community organizations to work toward a shared, cooperative goal. This activity allows students to bring their subject-matter knowledge and skills to bear on a project that is of interest to and in collaboration with the community partner. At Weber State University, the Taxonomy of Vascular Plants class has been taught, for the past two years, as a community-engaged learning course. Students have actively engaged in different ways of working with community partners to focus 1) on developing accurate botanical resources on the local flora that would be used for producing interpretive hikes for the public, and 2) on creating and presenting activities for a Plant Party at the Treehouse Museum, the community's children's museum. As part of the community-engaged component of the class, students spend time meeting with the community partner to understand the organization and its goals, which helps inform the students' approach to the project. Additionally, students write reflections on their experiences with community-engaged learning and discuss these in class. While the results are only qualitative presently, students have enjoyed this type of class project as they are able to be out in the community and use their botanical knowledge in a novel manner. This experience can help students understand the types of jobs they can pursue with their degree. Students also gain a different perspective on a class project because a community partner relies on their work, rather than only an instructor seeing the final result.

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Development and Structure

Topic: Poster

Title: Building a model system to study capitulum development and evolution in the Asteraceae

Author: ***Reid Selby @ Auburn University***

Keywords: Asteraceae,Bidens,confocal imaging,Floral Development,flower,Meristem development,microscopy,reproductive biology,evolution of development,Development

Abstract:

With over 30,000 species, Asteraceae is the largest family of flowering plants. While the family displays remarkable ecological and morphological diversity, the highly compact inflorescence known as a capitulum is present in each species, forming a pseudanthium of many florets that functions as a single flower. These “false flowers” may be partially responsible for the family’s global expansion and success. While the evolutionary origin of this highly conserved structure is unclear, it is commonly thought to be derived from a raceme, with drastic reduction in inflorescence internode length. Understanding the developmental genetics underlying capitulum formation is key to understanding the Asteraceae; however, due to large genome sizes, resistance to stable genetic transformation, and lack of standardized lab protocols, relatively few genetic and genomic resources are available to researchers studying the Asteraceae. In the CapituLab at Auburn University, we are building a model system to explore the genetics of capitulum development using Bidens cv. Compact Yellow. Compact Yellow is a promising candidate model system as it has a compact growth habit and short generation times. Compact Yellow also has a relatively small genome, self-fertilizes, and easily propagates from cuttings. Here we present a highly contiguous, haplotype-resolved genome assembly of Compact Yellow using long-read PacBio HiFi sequencing coupled with Hi-C chromatin mapping. Along with these genome assemblies, we are identifying gene regulatory networks controlling flower development in Compact Yellow by using transcriptomics coupled with confocal microscopy targeting distinct stages of capitulum development. Finally, to test hypotheses about flower development via reverse genetics, we are also building reliable genetic transformation methods using in vitro tissue culture and Agrobacterium tumefaciens. A reference genome, transformation capabilities, and a foundational understanding of inflorescence development lay the groundwork for an exciting model system in which to study Asteraceae capitulum development.

652

Systematics

Topic: Poster

Title: Re-evaluating Sabal louisiana: Is the absence of an aboveground stem enough evidence to justify splitting two growth forms into different species?

Author: ***keily peralta @ Cornell university***

Keywords: Southeast US,systematics,Arecaceae

Abstract:

Sabal minor is a dwarf palmetto commonly found within the southeastern United States and it is described as being acaulescent. Along the Gulf Coast of the United States (most commonly in Louisiana), botanist have observed morphological variation of the stem, whereby S. minor can be acaulescent as well as caulescent. Historically, botanists have considered caulescent S. minor to be a distinct species from acaulescent S. minor known as Sabal louisiana. However, LH Bailey combined both the caulescent and acaulescent into one species, S. minor s.l. Nevertheless, the geographically restricted morphological variation of stem type within S. minor warrents taxonomic re-evaluation in light of recent population genetic sequencing efforts

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Development and Structure

Topic: Poster

Title: Intrafloral Variation in Stamens and Staminodes in Mentzelia (Loasaceae)

Author: ***Jenna McClure @ Ohio University***

Keywords: androecium,floral evolution,flowers,Loasaceae,Mentzelia,stamens,staminodes

Abstract:

Flowers evolve to optimize their reproductive output. Stamen, for example, should only be lost when the cost of building and maintaining them no longer benefits plant fitness. Staminodes, which are infertile stamen, no longer produce viable pollen but some have evolved a novel function that offers a different reproductive advantage. In Mentzelia section Bartonia (Loasaceae), petal-like staminodes have evolved repeatedly to increase the attractiveness of the flower to pollinators. Little is known, however, about whether staminodes evolve at the expense of stamens or in addition to stamens. Over half of the 51 species in Mentzelia section Bartonia have evolved at least one whorl of staminodes, and seven of those species have evolved multiple whorls. We hypothesized that flowers with staminodes would compensate for reduced male reproductive output by evolving additional whorls of fertile stamens. To determine how staminodes influence the number of stamens, we quantified androecial variation in flowers that had multiple whorls of staminodes. For some species, such as Mentzelia humilis, we found a negative relationship between staminodes and stamens—as the number of staminodes increased, the number of stamens decreased. Other species, such as Mentzelia collomiae and Mentzelia nuda, showed a consistent number of staminodes while the number of stamens varied within each species. We conclude that intrafloral variation in staminodes and stamens is dynamic across species—staminodes evolve at the expense of stamens in some flowers, but in others they evolve in addition to them.

658

Bryology and Lichenology

Topic: Poster

Title: Lichens of Iller Creek: A checklist for the Iller Creek Unit, a division of Dishman Hills Conservation Area, Spokane Valley, WA

Author: ***Devin Mumey @ Eastern Washington University***

Keywords: Checklist,Diversity,lichen,Lichenology

Abstract:

    The field of biodiversity documentation encompasses a broad range of research including new species discovery and description, compilation of species present in a given area, and investigation of interspecies interaction. In an era of increasingly devastating and rapid environmental change, documenting biodiversity has become increasingly important. Anthropogenic effects on urban-adjacent natural areas are especially significant, as they can cause numerous, often drastic, responses in ecosystem. Our objective here was to document the lichen biodiversity in a large urban-adjacent protected area: the Iller Creek Unit of the Dishman Hills Conservation Area in Spokane Valley, Washington. This unit encompasses a diversity of habitat types: Ponderosa pine savannah, riparian forests, mixed mesic coniferous forests, and xeric rocky outcrops. Despite conservation efforts, no formal checklists have been assembled for this unit. To compile this checklist, our methods include collecting voucher specimens of all species from each habitat type. The identification process used relevant literature and standard techniques, including thin layer chromatography, chemical spot tests, and microscopy. A selection of identifications were confirmed via DNA barcoding, using the nuclear Internal Transcribed Spacer region. A total of 75 species, spread throughout 44 genera of 23 families were identified. We identified 29 crustose, 39 foliose, and 7 fruticose. Moving forward, we intend to perform comprehensive searches of the less accessible areas without immediate trail access to compile a more complete checklist for use as a baseline for future lichen investigations of the inevitable anthropogenic effects that recreational use and expansion of the city will have on the lichen diversity.

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Hybrids and Hybridization

Topic: Poster

Title: Evaluating genetic intermediacy of a naturally occurring hybrid blueberry, Vaccinium x marianum

Author: ***Laura George @ Old Dominion University***

Keywords: Vaccinium,hybrid

Abstract:

Hybridization is common in plants and is a mechanism for increasing plant biodiversity and vigor. Detecting hybrids in nature can be accomplished by genetic data. The basis of this research is to evaluate if the highbush blueberry, Vaccinium x marianum, is a hybrid between the parental species, Vaccinium fuscatum and Vaccinium formosum. Morphological data suggests V. x marianum has traits intermediate to the parental species, and this research project used genetic data to evaluate differences between the parents that are expected in V. x marianum if it is a hybrid. Leaf samples of the three forms were collected from four locations in Virginia. They were identified in the field using a diagnostic key. Fourteen microsatellite loci were selected to test with the samples. Data from seven loci were evaluated for this study, although one locus was not found to be consistently scorable and thus was removed prior to analysis. Our preliminary analysis suggests that Vaccinium x marianum is genetically intermediate to the parental species. The parental species are genetically distinguishable from one another and little evidence of introgression was found in these samples. Samples of V. x marianum show extensive variation among samples, suggesting that it may represent multiple hybrid generations and diverse origins. More work is needed to examine the genetic variation of the three forms, and this semester I will use chloroplast markers to evaluate the maternal origin(s) of V. x marianum. Hybridization between blueberry species is common in nature and studying hybrids can further the understanding of genetic diversity, adaptation, and evolution of blueberries species.

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Paleobotany

Topic: Poster

Title: A new North American calibration for predicting canopy structure in deep time using epidermal phytolith morphology

Author: ***Brielle Ann Canares @ University of Washington***

Keywords: canopy ecology,Epidermal cells ,Epidermal morphology,Miocene,North America,Paleoecology,canopy,Leaf Area Index,phytoliths

Abstract:

Degree of canopy cover is linked to transpiration, carbon cycling and primary productivity of an ecosystem. In modern ecology, canopy structure is often quantified as Leaf Area Index (LAI), which is the amount of overstory leaf coverage relative to ground area. Although a key aspect of vegetation, the degree of canopy cover has proven difficult to reconstruct in deep time. One method, Reconstructed Leaf Area Index (rLAI), was developed to infer canopy structure using the relationship between non-grass leaf epidermal phytolith (plant biosilica) morphology, and leaf coverage in modern forests. This method leverages the observed correlation between epidermal phytolith size, shape (margin undulation), and light availability. When more light is available in a canopy, epidermal phytoliths tend to be smaller and less undulate, whereas less light availability is linked to larger and more undulate epidermal phytoliths. However, the calibration set used to develop this method was compiled from field sites and samples from localities in Costa Rica and it remains unclear how applicable it is to temperate North American fossil sites due to lack of data from relevant vegetation types and taxonomic differences between plant communities in the Neotropics vs. mid-latitude North America. For example, preliminary results measuring rLAI in phytolith assemblages from the Miocene of the North American Great Plains have yielded surprisingly high degrees of canopy density despite containing high relative abundances of open-habitat grasses. To test whether vegetational and taxonomic differences impact the calibration set, we constructed a new North American calibration using 24 quadrats from six sites, representing reasonable modern analogs for Miocene vegetation in eastern North America. Specifically, we sampled in Bennett Springs State Park in Lebanon, MO; Mark Twain National Forest in Rolla, MO; Tellico in Franklin, NC and Congaree National Park in Hopkins, SC. All sites include a range of canopy covers and vegetation types, from oak savannas and oak woodlands to mixed hardwood forests, pine savannas, and old growth bottomland forests. From each quadrat, we collected a soil sample and took hemispherical photos of the local canopy. From modern soil samples, biosilica was extracted in the lab, yielding phytolith assemblages which were scanned for epidermal phytoliths using a compound microscope. Recovered epidermal phytoliths size and margin undulation were measured and assemblage averages were used to predict measured LAI at each quadrat. Hemispherical photographs were processed using the software Gap Light Analyzer to obtain LAI values. We hypothesize there will be a linear relationship between actual LAI and LAI calculated from epidermal phytolith morphology, but its relationship will differ from that found in South America. Results will be used to reevaluate canopy coverage in sites within the Great Plains Miocene as well as applied to Pacific Northwest Miocene sites, both to understand changes to vegetation during global climatic events in their respective regions.

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Ecology

Topic: Poster

Title: Community-scale trends in leaf traits across ecological succession in three forest types: implications for inferring functional composition of ancient plant communities

Author: ***Alexander Lowe @ University of Washington***

Keywords: community assembly,functional trait,Paleoecology,succession

Abstract:

Paleobotanical records provide opportunity to deepen an understanding of plant community ecology by reconstructing the outcome of large-scale ecological 'experiments' in Earth's past. However, limited ability to describe ancient communities via plant functional traits and ecological strategies, rather than (para)taxonomic composition, can hinder the relevance of constructed datasets. Many functional traits are not measurable on fossil leaves and the link between leaf morphology and ecological strategy are currently unresolved. To help fill this gap, we analyze leaf traits applicable to fossil leaves (i.e., morphology, vein density, leaf mass per area) sampled at the community-scale from modern plots spanning successional gradients, where plant function and ecological strategies are expected to vary, in three different forest types: temperate deciduous forest (North Carolina, USA), tropical rainforest (Malaysian Borneo), and a tropical dry forest (Minas Gerais, Brazil). Preliminary results will be presented to draw empirical links between morphological leaf traits and ecological strategy.

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Biodiversity Informatics & Herbarium Digitization

Topic: Poster

Title: Can environmental DNA generate additional data from herbarium specimens and contribute to the extended specimen network?

Author: ***Brenda Molano-Flores @ University of Illinois***

Keywords: carnivorous plant,eDNA,extended specimens,herbarium specimen

Abstract:

Herbaria represent a vast and often untapped wealth of information. Data from herbarium specimens and their associated labels have provided invaluable information for the fields of ecology and systematics. For example, locality and phenological data from labels have allowed the assessment of changes to species distributions over time due to climate change. Also, sampling leaf material from herbarium specimens for DNA extraction is the backbone of plant systematics. Novel methodologies and emergent technologies and analyses to obtain additional data from herbarium specimens are opening new avenues of research. The growing field of environmental DNA (eDNA) has emerged as a promising method for facilitating the assessment of biodiversity. By incorporating eDNA with a metabarcoding analysis it is possible to identify whole communities from a single sample. Here, we explored eDNA analysis to further expand the use of herbarium specimens to assess plant-organismal interactions and contribute to the extended specimen network. As a proof-of-concept, we swabbed carnivorous plants, in particular from the genera Pinguicula and Drosera. No detectable damage was done to any of the specimens that were sampled. We successfully detected plant, insect, and microbial eDNA though the vast majority of the detected taxa were from other plants. These plant taxa included a wide variety of plant species from both natural/historical sources and contamination within the herbarium. While contamination must be accounted for, it was clear that eDNA from herbarium specimens can effectively characterize historical plant communities. As this method advances, herbarium specimens of non-carnivorous plants should also be sampled. It is possible that due to powerful enzymes released by carnivorous plants, insects and microbes were too degraded, or their DNA too fragmented to be detected. We believe that eDNA sampling of herbarium specimens is a promising tool to explore changes in plant communities, plant-insect interactions, and microbial communities across time and space.

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Phylogenomics

Topic: Poster

Title: Nuclear Hyb-Seq sequences and plastid genome data reveal ancient hybridization events in the evolutionary history of Carex (Cyperaceae)

Author: ***Se-eun Jung @ Sungshin Women's University***

Keywords: Carex,chloroplast,Cyperaceae,Hyb-Seq,phylogenomics,ancient hybridization,Global Carex Group

Abstract:

With around 2,000 species, Carex (Cyperaceae) is the second-largest genus of monocots. The Global Carex Group (GCG) has recently updated the traditional classification system of Carex, which contains six subgenera and 111 groups (62 formally named Linnean sections plus 49 informal groups). The system was suggested based on two detailed molecular studies: 1) an analysis that sampled many species (996 species) using a few genetic markers (matK, ITS, ETS-1f), and 2) a study that sampled fewer species (88 species) but used a considerable amount of data (308 nuclear exons, 543 introns, and 66 plastid exon regions) obtained via a Hyb-Seq technique. More extensive sampling and genome-scale data will allow us to understand the detailed evolutionary history of Carex, which will also allow us to evaluate the new classification system of Carex. In this study, we constructed both nuclear and plastid trees based on genome-scale data using 152 representative taxa: 490 nuclear single-copy gene loci were determined using the Carex-specific probes by the Hyb-Seq technique, and 71 coding plastid genes were determined by genome skimming. Results showed that four out of the six subgenera proposed in the new classification system were highly supported (BS=95%) in both nuclear and plastid trees. However, the phylogenetic position of subgenus Carex in the plastid tree differs from the nuclear tree, suggesting a possible hybrid origin for this subgenus. Of the 38 groups (19 Linnean sections plus 19 informal groups) included in the analyses, 100% of the groups in the nuclear tree and 90% of the groups in the plastid tree had high support (BS>90). Additionally, we observed many conflicting relationships among sections and informally recognized groups suggesting that these lineages may also have ancient hybrid origins. Our study reveals that our result largely supports the new classification system proposed for Carex but highlights conflicting relationships among some subgroups that could be due to the different evolutionary histories of plastid and nuclear genomes.

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Physiology

Topic: Poster

Title: EFFECTS OF SUPER ABSORBENT POLYMERS (SAPS) ON GROWTH AND YIELD OF LETTUCE (Lactuca Sativa)

Author: ***Aliyu Ahmad Nuhu @ Yusuf Maitama Sule University, Kano, Nigeria***

Keywords: drylands,physiology,hydrogel,super absorbent polymer

Abstract:

Superabsorbent hydrogels are used in agriculture as water and nutrient storage and retention materials, as well as additives that improve soil properties. They are of great interest for agricultural applications, especially in arid regions such as Nigeria, also because they can be used to create systems for the slow release of nutrients into the soil, which are necessary to increase crop yields using environmentally friendly technologies. The aim of the research is to evaluate the effect of super absorbent polymer on growth and yield of Lettuce in Kano, Nigeria The experiment was conducted in a completely randomized design factorial of 3×3 factorial design in the greenhouse of Kano Botanic Garden in Kano State Nigeria. The results showed that the use of super absorbent and drought stress has a significant effect on yield of the lettuce and the highest performance (5g) was obtained and application of 5g super absorbent hydrogel per kilogram of soil. The use of hydrogel at 5g/Kg of soil is therefore recommended for attainment of optimum yield and performance of lettuce.

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Conservation Biology

Topic: Poster

Title: Using comparative genomics to elucidate the distribution and life histories of Jamesianthus alabamensis and related genera

Author: ***Brannan Cliver @ Auburn University***

Keywords: _{conservation biology},Asteraceae,comparative genomics,genome assembly,Tageteae

Abstract:

Jamesianthus alabamensis (Blake and Sherff), is an Alabama endemic Asteraceae species first described in 1940 in Franklin County, Alabama. J. alabamensis has a limited distribution across Alabama, mainly found in the northern parts of the state with the majority of herbarium specimen coming from northwestern Alabama.Nested within the Tageteae (marigold tribe), J. alabamensis is closely related to Arnicastrum (Greenman), a genus containing two species found in Central Mexico, and Clappia suaedifolia (Gray), a monotypic genus found in the southern tip of Texas and adjacent areas of Mexico. All three genera have been placed within different tribes throughout history, with Arnicastrum and Jamesianthus often placed in the same tribes but Clappia being placed in separate tribes until more recent ITS sequencing data grouped all three in the Tageteae. Interestingly, both Jamesianthus and Clappia have unusual chromosome numbers (n = 16) for Tageteae species while Arnicastrum's chromosome numbers have not been determined yet. Here we present chromosome-scale haplotype resolved genome assemblies of J. alabamensis. These assemblies will help us to gain a better understanding of this species position within the Tageteae. Using comparative genomics, we aim to identify genome-scale changes or events shared by these three genera that could explain their similar life histories. This study has a particular focus on Jamesianthus alabamensis, where we plan on leveraging population-level data to understand its restricted distribution across Alabama as a part of a focused conservation effort.

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Paleobotany

Topic: Poster

Title: An Estimate for Mean Annual Temperature of the Florissant Formation using Digital Leaf Physiognomy

Author: ***Fletcher Levy @ Wesleyan University***

Keywords: digital leaf physiognomy,Mean annual temperature,florissant

Abstract:

The ancient lake-bed of the Florissant Formation in Colorado, which closely precedes the Eocene-Oligocene climatic transition (~34.1 Ma), preserves a diverse assemblage of flora and fauna. There are many published estimates of mean annual temperature (MAT) for Florissant, including over 15 based on the taxonomy and leaf physiognomy of plants, which range from ~10-18 °C. Here we use digital leaf physiognomy (DiLP) to reconstruct MAT. DiLP is based on traits related to leaf dissection, including the size and frequency of teeth. Similar to other leaf physiognomy-based climate proxies, DiLP tacitly assumes a convergent morphological adaptation within woody dicotyledons to a shared climate space. Our analysis is based on 174 fossil leaves from 64 species and five paleobotany collections across the United States, highlighting the importance of historic collections and their critical role in ongoing research. We estimate a MAT for Florissant of 12.4 ± 4 °C, which falls between the lower temperatures predicted by Climate-Leaf Analysis Multivariate Program (CLAMP) and the generally higher estimates based on taxonomy (nearest living relatives). Our estimate provides context for understanding the Florissant ecosystem and more generally for the Colorado region just before the onset of the Eocene-Oligocene transition.

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Ecology

Topic: Poster

Title: Fruit Traits of Palicoureeae, a Tribe of Tropical Flowering Plants

Author: ***Aislinn Mumford @ Louisiana State University***

Keywords: fruit color,Fruits,Neotropics,seed dispersal

Abstract:

This review will discuss the range of fruit traits in the tribe Palicoureeae, a group of flowering plants. Multivariate analyses plots will be used to illustrate corrlations between fruit traits and compare suits of traits between the major Neotropical genera of the tribe. Ideas for future research building upon this review will be presented as well.

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Ecology

Topic: Poster

Title: Plant biodiversity and marsh migration in the coastal forest area of South Carolina

Author: ***Siddhartha Regmi @ Clemson University***

Keywords: Forest structure,Transgression,species diversity

Abstract:

Coastal forests are under direct threat of drowning due to sea level rise. This causes gradual changes in the vegetation composition in the area, and mortality may also be high. This research aims to collect and analyze the vegetation database that can be used to assess plant biodiversity in the coastal ecotone region to provide baseline information to develop strategies for their preservation and management. Also, this project aims to aware the as much as people through different educational outreach plans. In this project, a systematic plant biodiversity data survey based on a standard design in numerous sample plots along the transects in the Hobcaw Barony, a 7,100- hectare forested area in the coastal area of South Carolina. Herbaceous, Shrubs, and Trees data will be collected in a sample plot of different sizes. The plant species composition, diversity, regeneration, and identification of plant species of ecological conservation value (threatened and endemic) found within this forest will be derived from this survey. Moreover, we will also combine the forest data collected from more than 27 years to model the changes in the forest structure, mortality rates and marsh transgression. Different analytical software like Excel, Arc GIS, R, etc. will be used to analyze and present the data. Social media posts, publications in journals, Brochures, Blogs, Vlogs, etc. will be the final products of the research. Moreover, presentations at conferences and local schools in the coastal area will also be done as an educational outreach.

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Phylogenomics

Topic: Poster

Title: A New Recipe for Echinacea Phylogenetic Analysis Utilizing Nuclear Data

Author: ***Chazz Jordan @ University of Georgia***

Keywords: molecular phylogenetics,Nuclear genome,plastid genome,Echinacea,ASTRAL

Abstract:

The Echinacea genus is an outcrossing taxon that is well known for its medicinal properties and bright pink ray flowers. Indigenous peoples used the roots and leaves as a cure all for allergies and allergic reactions (USDA NRCS). Echinacea species are typically found in prairie and glade ecosystems, which are threatened in the United States (Wagenius et al. 2010, Center for Cedar Glade Studies). The most broadly distributed Echinacea species is E. purpurea with a range expanding across the eastern half of the United States (Kindscher 2006). In contrast, E. tennesseensis is confined to only six counties in Tennessee (TN DNR).

I am aiming to 1) reconstruct the Echinacea species tree using 100s of nuclear genes and compare it with a plastid genome tree and 2) test for species radiations in the evolutionary history of Echinacea. While the Echinacea plastome tree includes a polytomy, my species tree analysis will test whether a polytomy is also seen in a species tree based on nuclear genes. In any case, a species tree for Echinacea will be foundational for my future investigation into the drivers of rarity for all species native to the southeastern U.S. (E. purpurea, E. laevigata, E. tennesseensis, and E. simulata).

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Bryology and Lichenology

Topic: Poster

Title: A New Understanding of Vinealobryum eckeliae (Pottiaceae: Bryophyta)

Author: ***John McLaughlin @ San Jose State University***

Keywords: bryophytes,distributions,ecological niche,mediterranean,phenology,Pottiaceae,Didymodon,Vinealobryum,moprphology

Abstract:

Vinealobryum eckeliae (R.H. Zander) R.H. Zander is a poorly understood moss species native to the west coast of North America and Spain. Since its description in 2007, the number of collections in North America has more than doubled, providing valuable data regarding the species' phenology, morphology, ecology, and distribution. An analysis of 78 specimens has confirmed the plant to be dioicous with sporophytes maturing predominantly in the spring and summer. Reproductive specimens were used to produce ranges for sporophyte characters, and non-reproductive specimens were used to investigate gametophyte morphological patterns that were not previously reported. Micrographs were captured to present both gametophytic and sporophytic features of the moss. Label data extracted from the Consortium of North American Bryophyte Herbaria were used to update the species' habitat preferences and distribution.

698

Crops and Wild Relatives

Topic: Poster

Title: Discovering the Genetic Basis of Rice Grain Shape

Author: ***UZEZI OKINEDO @ University of Massachusetts Boston***

Keywords: crop,genomics,Biotechnology

Abstract:

Breeding for high-quality rice can be accelerated by high-throughput phenotyping, leading to the identification and assessment of the genetic basis of rice grain structure. In this study, we used a recently described phenotyping pipeline to analyze rice grain size and shape, which are essential components of rice quality, in the diverse USDA rice mini-core collection. We measured nine grain phenotypes and identified significant differences among the five sub-populations represented in the mini core only for solidity, with aus sub-populations exhibiting substantially lower solidity values.

Solidity measures the ratio of grain area to the area of a convex hull surrounding the grain. These ratios vary from 0–1, where values closer to one indicate rounder seeds and smaller values signify curved or abnormal shapes. We identified genome-wide associations for variation in solidity on chromosomes 3, 7, 8, and 9, with 913 candidate genes within 1 MB upstream and downstream of these associated loci. Seven of these candidate genes have known functions in seed-related traits and 38 genes have no known function. These candidate genes for solidity may provide novel insight into the genetic control of rice grain shape and assist future breeding efforts. Our ongoing work focuses on characterizing haplotype diversity at these loci across rice varieties.

702

Biodiversity Informatics & Herbarium Digitization

Topic: Poster

Title: Harnessing the Power of Community Science to Digitize the Plants of Texas: The Armchair Botanist Program

Author: ***Ashley Bordelon @ FWBG|BRIT Philecology Herbarium***

Keywords: Citizen Science,Community science,digitization,Herbarium,Herbarium Digitization,Oklahoma,Texas,Zooniverse,NSF,Notes from Nature

Abstract:

Community science is a powerful tool to engage the public as contributors and as advocates for natural history collections. We developed the Armchair Botany program in 2020 to engage with community scientists for the purpose of digitizing herbarium specimens utilizing remote video-conferencing software, a digital transcription platform, and in-person events. The main focus of our program has been the digitization of specimens collected in Texas, as part of our National Science Foundation funded “American Crossroads: Digitizing the Vascular Flora of the South Central United States”. In 3 years, over 2479 unique users have transcribed >58,000 Texas-collected herbarium specimen labels through 31 expeditions launched in the online Notes from Nature platform. Since the Armchair Botany program’s inception, herbarium staff have hosted over 120 virtual events, and delivered in-person events out of the herbarium or at community partner events –the Texas Master Naturalist Program being of particular note. Recruiting and engaging plant-enthusiast organizations has proven rewarding and successful in engaging community scientists with specimens to address resource and space limitations in herbaria.

712

Ethnobotany

Topic: Poster

Title: Toward Genomic Resource for Ethnobotany of Lakota: Complete Chloroplast Genome of Artemisia ludoviciana subspecies ludoviciana (Asteraceae)

Author: ***Madhav Nepal @ South Dakota State University***

Keywords: Chloroplast genome,Ethnobotany of Lakota,White Sagebrush,Medicinal Plant,Artemisia Phylogenomics

Abstract:

Artemisia ludoviciana subspecies ludoviciana, commonly known as white sagebrush or prairie sage, is a perennial wild plant important to Native American communities for ceremonial and medicinal values. The chloroplast (cp) genome of the white sagebrush has not been reported to date. The main objective of this research was to sequence the chloroplast genome of A. ludoviciana subspecies ludoviciana to address taxonomic challenges among the six subspecies and within the genus as a whole. In this study, total genomic DNA of the leaf tissue was extracted and sequenced using the 2nd generation sequencing technology. The sequencing produced over 20 GB of short clean reads. The reads were assembled and annotated. We found that the chloroplast genome of A. ludoviciana is 156,824 bp in size and includes 92 coding genes, 36 tRNAs and 7 rRNA. The genome components include the inverted repeat B (IRB) of 27,481 bp (129,344-156,824), small single copy (SSC) of 18,006 bp (111,337-129,343), inverted repeat A (IRA) region of 27,481bp (83,857-111,337) and large single copy (LSC) region of 83,856 bp (1-83856). We are currently conducting a phylogenomic analysis of all available Artemisia chloroplast genomes, and we will share the major findings on phylogenetic relationships during our presentation.

716

Ecology

Topic: Poster

Title: Assessing fitness of a rare plant, buffalo clover (Trifolium reflexum), in response to environmental factors

Author: ***Ingrid Felsl @ Southern Illinois University Carbondale***

Keywords: ecology,fitness,functional traits,rare plants,Reproduction,threatened species,environmental variables

Abstract:

The conservation of Threatened and Endangered (T&E) plants is important for preserving global biodiversity and supporting ecosystem function. The largest threats to T&E plant species are anthropogenic climate change, habitat destruction and fragmentation, and the spread of invasive species. Understanding the habitat requirements of T&E species is vital to their conservation, as it informs management decisions. Trifolium reflexum L. (Fabaceae), also known as buffalo clover, is state threatened in Illinois and North Carolina and state endangered in Kentucky and Ohio. T. reflexum historically occurred across much of eastern North America along bison paths, where trampling would scarify seeds and reduce interspecific competition. The primary habitats in which T. reflexum historically occurred were tallgrass prairie, oak savanna, and dry open woods, all of which experienced natural fire disturbance. With the near elimination of wild bison populations and fire suppression across eastern North America, T. reflexum habitat has been reduced and degraded. However, the species persists in high quality open woods and along trails such as rights-of-way and mountain bike paths. Populations of T. reflexum within Illinois offer an excellent opportunity to research the species in all three habitats where it occurs, as well as at the edge and center of its north-south geographic distribution. Additionally, the growth rates of populations within the state range from positive to negative, offering a unique opportunity to identify environmental variables related to T. reflexum fitness. In an attempt to determine the optimal habitat for T. reflexum restoration in Illinois, we visited extant and extirpated populations during spring and summer 2022. Through measuring microsite environmental variables and vegetation composition, as well as functional traits of T. reflexum related to growth and reproduction, we aimed to determine how T. reflexum fitness was impacted by its environment. Extant populations exhibited greater soil temperatures and photosynthetic active radiation than extirpated populations, and vegetation composition differed between populations and microsites. Shorter T. reflexum individuals exhibited higher rates of reproduction, though fitness was variable between populations. Implications of this research will include management recommendations for extant populations as well as for identifying possible sites for reintroduction.

718

Paleobotany

Topic: Poster

Title: Palynology of the Dennis Formation (Upper Pennsylvanian, Missouri, USA): proposal and preliminary data.

Author: ***Jonas May @ William Jewell College***

Keywords: climate,Diversity,fossil,paleobotany,Paleozoic,Palynology,Pennsylvanian

Abstract:

The Middle-Late Pennsylvanian transition is marked by major change in coal floras across Tropical Pangea, but changes in the more heterogeneous clastic floras not associated with coals are less clear. To help clarify vegetation patterns through time in the Western Interior Basin, we propose an investigation of the palynology of the Dennis Formation in Missouri from 8–10 sample sites. The Dennis Formation is a unit of early Missourian (early Late Pennsylvanian) age in the midcontinent depositional basin with plant fossils preserved in carbonate mudstones in its upper part. Previous research on the Dennis Formation has focused on the macrofossil diversity, which primarily includes cordaitalean and medullosan foliage. Preliminary analysis of one site shows a dominance of monosaccate grains, with smaller quantities of bisaccate pollen, monolete spores, and trilete spores, which will serve as a guide for identifying grains from other sites The abundance of monosaccate and bisaccate grains (~50%) suggests cordaites and/or conifers were an important part of forest canopies, and the remaining spores capture elements of plant diversity that have not yet been detected among the macrofossils.

721

Symbioses: Plant, Animal, and Microbe Interactions

Topic: Poster

Title: Exploring Plant-Bee Relationships in Desert Biomes for Biodiversity Conservation and Ecosystem Services

Author: ***Jared Miller @ University of Florida***

Keywords: Bees,Chihuahuan Desert,desert annuals,life history,Mojave Desert,Pollinators,solitary bees,Sonoran Desert,desert ecology

Abstract:

The shared biogeographic trends between plants and bees in global scale analysis remain unclear. Understanding these trends is crucial for biodiversity conservation and ecosystem services, particularly in desert biomes facing climate change and habitat loss. One hypothesis for high bee diversity in deserts is the specialization in life-history strategies shared by desert plants and bees, such as delayed emergence triggered by precipitation. Variability in precipitation in desert regions may explain the success of specialization and increase overall bee species richness. However, this hypothesis lacks sufficient evidence from other host-specialist distributions. Furthermore, the relationship between bee species richness and plant species richness in desert communities is not well-established. A large-scale analysis of specimen records for bees and angiosperms in the major North American deserts (Mojave, Sonoran, and Chihuahuan) is proposed to address this knowledge gap. This analysis will assess data quality, species richness, and precipitation regimes to better understand the diversity of bee and plant assemblages in these regions.

724

Paleobotany

Topic: Poster

Title: Using Leaf δ13C to Assess Water Use Efficiency within Plant Communities Across a Successional Gradient in Temperate and Tropical Forests

Author: ***Josephine Meier @ University of Washington***

Keywords: disturbance ecology,stable isotopes,temperate forest,water use efficiency,tropical forest,carbon isotope

Abstract:

Understanding how plant communities of the past have responded to disturbance events can provide valuable insights when managing our natural resources and assessing human impacts on ecosystems. The geologic record has the potential to reflect these responses through the analysis of functional traits, which relate directly to plant function and ecosystem strategy. There is currently little evidence of how functional traits measurable in fossil leaves vary across succession in different forest types. Because of this, there is a limited ability to identify disturbance as the primary driver of vegetation change within the fossil record. To improve this ability, this study analyzes the carbon stable isotopic composition (δ13C) of bulk organic matter sampled at the community-scale across successional gradients in a temperate deciduous forest (North Carolina, USA) and compares them against values from a previous study across succession in a tropical evergreen forest (Malaysian Borneo). Leaf δ13C is representative of a plant's water use efficiency (WUE), an important axis of ecological strategy representing the carbon assimilated per water lost in a plant during photosynthesis. Leaf δ13C as a functional trait has the advantage that it is often preserved during leaf fossilization and, integrated across a plant community, can be informative about prevalent ecological strategies, functional diversity , and community assembly dynamics. In Borneo, the community-weighted mean of leaf δ13C to be highest in early-succession plots, indicative of a higher WUE in plant communities closely following a disturbance event. Old growth plots were found to have a lower δ13C, and thus a more conservative WUE. This study will further investigate if this trend is followed within temperate forests, which is important as many mid-late Cenozoic plant assemblages come from what would have been temperate regions. Developing a method of identifying disturbances within the geologic record, will improve the ability to discern drivers of plant community change in the past. This improved knowledge will help guide management decisions across a range of ecosystems.

726

Comparative Genomics/Transcriptomics

Topic: Poster

Title: A haplotype-resolved chromosomal genome assembly reveals the sex determination region in the dioecious watermelon relative Citrullus naudinianus

Author: ***Jim Leebens-Mack @ University of Georgia***

Keywords: Cucurbitaceae,Dioecy,genome assembly

Abstract:

A haplotype resolved genome assembly for the dioecious watermelon relative Citrullus naudinianus was generated using PacBio HiFi and Hi-C sequencing technologies. Shotgun sequence reads from male and female plants were mapped to the genome to facilitate identification of the sex determination system (XY or ZW) and the extent of the non-recombining sex determination region. We explore whether orthologs of genes influenicng male and female flower sex determination in monoecious Citrullus species including watermelon (C. lanatus) are sex-linked in C. naudinianus.

727

Development and Structure

Topic: Poster

Title: Parallel evolution of corolla tube width shifts in Penstemon

Author: ***Haylee Nedblake @ University of Kansas***

Keywords: Penstemon,convergent evolution,Pollination syndrome,QTL mapping,floral trait evolution

Abstract:

Pollination syndromes are an excellent area to study convergent evolution and to test whether genetic and developmental parallelism complement this striking phenotypic parallelism. Flower corolla width is a particular pollination syndrome trait that plays a role in determining which pollinators are able to "fit" the flower from a pollinator's perspective and efficiently move pollen between conspecifics. Narrow corolla tubes, which are specialized to transfer pollen to and from a hummingbird's forehead as its bill reaches for nectar, can exclude bees through preventing them to enter the flower. In Penstemon, shifts from bee pollination syndrome to hummingbird pollination syndrome often leads to a significant narrowing of the corolla tube. Penstemon is an exceptionally ideal system to study genetic and developmental parallelism in convergent evolution because within this ancestrally bee-pollinated genus of around 300 species, hummingbird pollination has evolved 11-20 times. Through quantitative trait loci (QTL) mapping, I aim to identify the genomic locations underlying the parallel floral corolla width differences in two independent origins of hummingbird pollination in Penstemon: P. amphorellae and its close relative P. kunthii, and in P. neomexicanus (bee pollinated) and its close relative P. barbatus (hummingbird pollinated). Once genomic regions are identified, I will determine whether a similar genetic basis for the independent origins of this parallel hummingbird pollination trait exists through assessment of QTL correspondence. Testing for QTL correspondence between the two distinct Penstemon mapping populations will reveal whether parallel evolutionary shifts are likely responsible for the striking parallel shifts in floral width traits we see.

728

Bryology and Lichenology

Topic: Poster

Title: DNA barcoding the bryophyte flora of British Columbia (Canada)

Author: ***Edward Sun @ University of British Columbia***

Keywords: bryophytes,Biodiversity,DNA barcoding,liverworts,mosses

Abstract:

We present on progress in developing a DNA barcode reference library for the bryophyte flora of British Columbia (BC). DNA barcoding is a method used to quickly identify species based on standardized molecular markers. Ideally, a barcode sequence is highly similar in all conspecifics and distinct from close relatives. The technique is useful for accurately identifying cryptic taxa or fragmentary samples, where morphology-based identifications may not be conclusive. Bryophytes can be more difficult to identify morphologically than vascular plants and may be underrepresented in regional floristic studies. As such, there exists a need to produce high-quality voucher-backed DNA barcode reference libraries to enable efficient identification and surveying of bryophyte taxa, particularly in British Columbia (BC) within Canada, which possesses the richest bryophyte diversity of any province. We assess sequence recoverability for common barcode markers and compare marker effectiveness in identifying individual species. Our reference library provides a useful resource for metagenomic and ecological genetic research in BC, and more broadly in North America and other temperate regions, and so will also contribute to national and international barcoding efforts.

740

Ecophysiology

Topic: Poster

Title: Predicting common bean yield using remote sensing in soils with phosphorus restriction in the highlands of Colombia

Author: ***Manuel Guzman @ AGROSAVIA***

Keywords: climbing plants,Crop yield,nutrient limitation,NDVI,maturity

Abstract:

Common bean (Phaseolus vulgaris L.) yield modeling using remote sensing is an emerging method in Colombia´s production regions where landraces are used. In general, these landraces are climbing plants with dissimilarities in phenological phases such as flowering and grain maturity. This condition is challenging to predict due to vertical biomass distribution, heterogeneous production and soil chemical conditions. The Normalized Difference Vegetation Index (NDVI) is useful to evaluate plant biomass and nutrient content in different growth stages. A field experiment was conducted with eight common bean landraces and climbing type and three Phosphorus restriction levels (25, 50, and 75% of P-relative to the control), according to the recommended dose. NDVI was measured using a GreenSeeker® canopy sensor, with a two-week frequency, from the V4 up to the R8 growth stages. P-restriction were laid out in a randomized complete block design with a split-plot arrangement and three replications, where P-doses were the main plots and landraces subplots. Biomass production was higher at the 50% P-restriction level. For the NDVI, an interaction between the P-restriction and days to flowering was observed. NDVI values increased from 0.92 at 25% restriction to 0.79 at 75% P-restriction. The common bean yield was linear and positively correlated with NDVI values ($P < 0.05$). Our results indicated that the NDVI can be used for estimating biomass production and P uptake in the early growth stages of common bean crops

741

Phytochemical

Topic: Poster

Title: Convergence and constraint in glucosinolate evolution across the Brassicaceae

Amanda Agosto Ramos1, Odinaka Okegbe2, Daniel J. Kliebenstein1
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Author: ***Amanda Agosto Ramos @ University of California, Davis***

Keywords: Brassica rapa,Brassicaceae,Brassicales,convergent evolution,glucosinolates,specialized metabolism,gene family evolution

Abstract:

Specialized metabolite genes can arise by gene duplication and neofunctionalization where one copy retains the ancestral function while the other changes to a new function. This process is at the core of chemical diversity across species. These duplicates also enable variation within species often from presence-absence-variation (PAV). The combination of PAV in reference genomes and the potential for convergent evolution could greatly complicate the use of sequence homology to identify enzymes across a plant family. To explore this potential, I use the GSL-OH enzyme in the glucosinolate biosynthetic pathway as a case study. Glucosinolates are a class of specialized metabolites with the most diverse representation in the order Brassicales. They play roles in plant environment interactions and humans perceive them as the flavor compounds in broccoli, wasabi, mustard, amongst other vegetables. GSL-OH catalyzes a terminal structural modification reaction that converts the AOP2 created but-3-enyl into S-2-hydroxy-but-3-enyl (S2HB3) and R-2-hydroxy-but-3-enyl (R2HB3). To identify GSL-OH in non-model species I first identified potential homology based GSL-OH candidate genes across the Brassicacea family. To test for potential convergent evolution where a non-homologous enzyme evolved the GSL-OH reaction, I used a transcriptomics genetic covariation approach. This consists of using transcriptomics in Brassica rapa and Brassica oleracea accessions with PAV for 2-hydroxy-but-3-enyl presence. Given the potential for the reference genome to be missing the GSL-OH gene we are developing a kmer approach to identify genes that correlate with the 2HB3 metabolite data for these Brassica accessions. The candidate genes from both approaches have been cloned and are being used to test for complementation in Arabidopsis thaliana lines that are natural knockouts for GSL-OH. If the transgenic lines produce 2-hydroxy-but-3-enyl, we can conclude that the gene is responsible for the GSL-OH activity. Thus far I have identified two previously uncharacterized GSL-OH genes from the plant Descurainia pinnata that have evolved novel sterochemistries. One produces a 5R:1S ratio of the enantiomers while the other enzyme results in a 1R:5S enantiomer ratio. Analyzing Descurainia plant tissue, showed a 4:1 ratio of R: S suggesting that the enzymes functions may both function and unequally contribute to the pool of 2-hydroxy-but-3-enyl enantiomers. Moving forward using the method I have developed I will continue to characterize candidate genes for the glucosinolate pathway to help inform our construction of phylogenetic tree for genes of this metabolic pathway as a way to explore the evolutionary patterns that have shaped this branch of specialized metabolism.

743

Biodiversity Informatics & Herbarium Digitization

Topic: Poster

Title: Lomatium & Friends: An Online Monograph of the Perennial Endemic North American (PENA) clade of Apiaceae.

Author: ***Mary Ann Feist @ University of Wisconsin***

Keywords: Apiaceae,Lomatium,Monograph

Abstract:

The Lomatium & Friends website brings together the results of an NSF-funded project to study the diversification of a large clade of Apiaceae from primarily the western United States. This clade, known as the Perennial Endemic North American (PENA) clade of Apiaceae, contains 18 genera and over 200 species (and still counting). Despite its size and importance in the western flora, the evolution of the PENA clade is poorly understood, a fact reflected in the artificiality of its genera. We are developing molecular-phylogenetic hypotheses of the PENA clade using comprehensive sampling of all known species and infraspecific taxa. Our work utilizes molecular, ecological, morphological, and climatic data to clarify the taxonomy and relationships of species within the PENA clade which we will use to provide a revised and updated classification for this group. Given the rampant examples of para- and polyphyly in the PENA clade, extensive reshuffling and renaming of genera and species will be necessary (including new names and many new combinations). The results of this project will be presented in the form of an electronic monograph that will include the updated nomenclature, species descriptions, photographs, specimen records, distribution maps, phylogenetic trees, and links to DNA sequence data, as well as identification guides and keys. The identification tools and species-specific environmental and ecological data provided on this website will aid in future research and in the conservation of the many rare species found within this group. On line approaches allow for numerous digital images, more detailed and updatable distribution data, and range maps generated from geo-reference data. Interactive and multi-access keys are also more feasible and more user-friendly than traditional keys — an important advantage in a group as challenging to identify as Apiaceae.

747

Ecology

Topic: Poster

Title: The importance of ‘enemy release’, competition and intrinsic plant characteristics in the invasion success of Phragmites australis

Author: ***Martina Koniger @ Wellesley College***

Keywords: Stomata,biological invasions,Competitive interaction,Photosynthetic capacity,Plant Growth,Phragmites,Arthropods,Enemy release hypothesis

Abstract:

Phragmites australis, an invasive reed species from Europe is spreading rapidly throughout North America. In the last few decades, Phragmites has also been spreading on Wellesley College’s campus, located 14 miles west of Boston, MA. Here Phragmites has formed dense stands in a wet meadow and in a lacustrine wetland, displacing other plant species as a consequence. This has potentially adverse consequences for the biodiversity and the functioning of these ecosystems. The goal of our study is to better understand the drivers behind the invasion success of Phragmites in this managed landscape. We collected data over two consecutive growing seasons (2021/2022) at three sites on campus, monitoring the arthropod and plant communities associated with marked Phragmites ramets along the edges of these stands. Additionally, we determined parameters related to the photosynthetic behavior and stress tolerance of Phragmites, and monitored ramet growth and leaf damage due to herbivory. (1) Our results show that aphids and stem borers introduced from Europe regularly affect Phragmites. A phloem feeder, the mealy plum aphid (Hyalopterus pruni), causes chlorosis, followed by fungal infections and premature senescence of leaves, while stem borers reduce flowering and induce side shoot formation. However, many of the other natural enemies found in the native range of Phragmites are missing. Hence ‘enemy release’ may in part explain the invasion success of Phragmites. While, generally considered a pest, Phragmites forms the basis of a robust food web of arthropods that includes aphids, parasitoids and predators. The arthropods that we collected on Phragmites were diverse, belonging to 17 different orders, and various guilds such as phloem feeder, chewers, predators, parasitoids, and detritivores. Most of them were probably incidentals and not dependent on the presence of Phragmites. (2) Phragmites co-exists with over 60 plant species along the edges of the stands. These species include trees, shrubs, herbs and grasses. Several species, like Rhamnus cathartica and Convolvulus arvensis are invasive species themselves, and many others thrive in disturbed areas. Several vine species use ramets as support (e.g. C. arvensis) and often affect Phragmites’ ability to unfold their leaves or even bind several ramets into a tangle. Trees mechanically hindered Phragmites growth as the reeds were touching branches. Hence some of these species may limit the spread of Phragmites, while others are poor competitors and were not found further inside the stands. (3 Our data on the morphology and physiology of Phragmites show that its invasion success is in part facilitated by the ability to increase in height and produce new leaves throughout the growing season into late October. This growth behavior goes along with high stomatal densities on both leaf surfaces, high photosynthetic capacities late into the growing season (even during the severe drought of ‘22), and a high stress tolerance, as indicated by high photochemical efficiency. Overall, invasion success of Phragmites seems to be the consequence of an intricate interplay between partial enemy release, limited competition and intrinsic plant characteristics.

754

Macroevolution

Topic: Poster

Title: Investigating the evolution of floral traits and fusion using herbarium specimens in Lonicera (Caprifoliaceae)

Author: ***Leann Janzekovich @ The College of New Jersey***

Keywords: Ancestral state reconstruction,floral evolution,honeysuckle,Pollination syndromes,animal pollination

Abstract:

The clade Lonicera is distributed throughout the northern hemisphere and comprises ca.140 species that are united by flowers with tubular corollas. Lonicera species are known to be pollinated by bees, hummingbirds, and hawkmoths, and adaptations to animal pollination may have contributed to the evolution of differences in flower shape and corolla tube among the Lonicera species we observe today. To date, there has not been a comprehensive study of floral traits across the entire clade, largely owing to the lack of a well-resolved phylogeny. Here we use a RAD-seq tree of 127 species of Lonicera to describe the evolution of Lonicera flowers. We explored 23 floral traits including corolla width and length, flower position, ovary width, flower color, anther position, and more in addition to fusion of extra floral organs such as bracts and bracteoles. Ancestral character state reconstructions of discrete traits were examined using three models of morphological evolution to determine the best fit of describing the evolutionary history of these character traits. First, we describe the evolutionary history of floral features using a near-complete species sample tree. Then, we will discuss possible correlated shifts in floral traits such as changes in floral tube length and width and flower color as well as variously fused structures that correspond to possible pollinator shifts and/or parallel shifts in floral traits. This research provides an important foundation for future studies of fusion across the clade as well as the pollination ecology and possible pollinator shifts among species of Lonicera.

758

Conservation Biology

Topic: Poster

Title: Who's your daddy? - finding the parents of cultivated Bidens

Author: ***Evie Moellering @ Auburn University***

Keywords: Bidens,Chloroplast genome,comparative genomics

Abstract:

Cultivated Bidens (Coreopsideae) is a common ornamental flower bedding plant from the Asteraceae. Currently, our lab is utilizing a cultivar of Bidens called "Compact Yellow" as a new model system to study flower development and genetics in the Asteraceae. Ornamental bidens have been historically classified as the species Bidens ferulifolia; however, it is unclear if this name has precedent as many herbarium collections use the name Bidens aurea interchangeably. Recent phylogenetic studies found B. ferulifolia specimen to be more closely related to the species B. andicola than B. aurea. To better determine the true parentage of B. ferulifolia we are utilizing our recently assembled genome of Bidens cv. "Compact Yellow" to compare to whole genome sequence data of B. aurea, B. ferulifolia, and B. andicola herbarium specimens. While collecting tissue we noted that the specimen looked very different under the same species classification. In this same study we are also comparing outwards toward this entire Bidens genus by analyzing whole chloroplast genome data via comparative genomics.

759

Ecology

Topic: Poster

Title: Management Short-Term Implications on Lupinus perennis, Duff, and Supporting Vegetation in the Concord Pine Bush

Author: ***Helena Mieras @ University of New Mexico***

Keywords: endangered species,habitat fragmentation,Habitat Restoration,management,Habitat loss

Abstract:

Protecting threatened and endangered species has become increasingly important under accelerating environmental and land use changes. Among the greatest threats to biodiversity are habitat loss and fragmentation, which can be mitigated with restoration and habitat management. Here we focus on the case of Concord Pine Bush habitat in Concord, New Hampshire, which is characterized by low-growth pine trees and exposed sandy soil. This unique habitat covers 223 ha of northeastern North America and supports 26 species of greatest conservation need, including the federally endangered Karner blue butterfly (Lycaeides melissa samuelis). Larvae of the Karner blue butterfly feed obligately on wild blue lupine (Lupinus perennis), thus protection requires not only consideration of the ecology of the butterfly, but also of its sole food plant. We compared the management practices of burning, herbicide, and mowing on fitness metrics of lupine plants and lupine habitat suitability. We asked (1) what management practices increase lupine fitness metrics, including abundance, size, and reproduction? and (2) how do management practices alter lupine habitat properties, including duff depth, supporting vegetation, and ground cover? The number of flowering stems was significantly lower when treated with herbicide versus when mowed and under control conditions. Average duff depth was found to be significantly greater under herbicide and burn conditions versus under mow and burn conditions. The mean percent of fern species cover was significantly less when treated with one burn and the treatments herbicide and burn and mow and burn. Understanding management practices that increase the number of flowering stems is vital for larval health and development of the Karner blue butterfly. Additionally, characterizing the conditions in which less duff is present may be used to maintain the habitat structure of exposed sandy soil. Finally, identifying conditions that impact competitors of L. perennis can be utilized in management decisions. Our results demonstrate the impacts of management practices on L. perennis fitness metrics and important habitat properties present in the Concord Pine Bush. These findings may have important implications on the successful recovery of the Karner Blue butterfly.

761

Systematics

Topic: Poster

Title: Reading between, across, and under the lines: how to interpret molecular data in a group that resists straightforward interpretation

Author: ***Alexa DiNicola @ University of Wisconsin***

Keywords: molecular phylogenetics,phylogenomics

Abstract:

The Potentilla breweri complex (Rosaceae) has been giving systematists headaches since at least 1940, and introducing molecular data has not especially smoothed out the problems. This group's rampant putative hybridization, geographically fragmented distribution, and bizarre karyology are well reflected in our GBS results — that is to say, despite analysis with several different phylogenetic approaches, the resulting trees fail to make very much sense at all. Even so, though, patterns do begin to emerge. We will discuss the interpretation of the most interesting morphological, cytological, and biogeographic themes that appear in our work so far, with an eye to future inference from larger (but probably equally odd) datasets still being developed.

770

Biogeography

Topic: Poster

Title: Phenotypic plasticity in widespread plant species in the Neotropics: The case of Cavendishia bracteata (Ericaceae)

Author: ***Katherin Arango-Gómez @ Louisiana State University***

Keywords: morphology,Endemic Species,ericaceae,Plasticity,widespread species

Abstract:

A lot of plant genera in the Neotropics usually consist of species that could exhibit narrow distributions and one to a few species with broader distributions; for this last case, those widespread species are usually characterized by a noticeable morphological variation. Answering questions regarding how much (if so) of this variation is due to phenotypic plasticity vs. genetic diversity (e.g. intra and/or interspecific hybridization), is important to understand the identity and dynamics in these groups.

Here, I will aim to explore this using the species Cavendishia bracteata as a case study. This widely distributed species is part of the plant family Ericaceae, and exhibit a highly variable morphology, something that seems unusual in a group mostly represented by endemic species

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Population Genetics/Genomics

Topic: Poster

Title: Extreme clonality across space and time in edge-of-range populations of the seagrass, Halodule wrightii

Author: ***Meghan Ford @ Northeastern University***

Keywords: population genetics,plant genetics,clonality,Cymodoceaceae

Abstract:

The genetic diversity of a population has wide-ranging and often positive impacts on ecosystem functioning. Seagrass meadows are highly productive marine plant ecosystems and reproduce both sexually and asexually, yielding different levels of genetic diversity which can influence responses to anthropogenic change. Here we investigate the genetic diversity, via microsatellite amplification, of the shoalgrass, Halodule wrightii across three different sites, in two different years, in North Carolina. H. wrightii is a tropical seagrass that has expanded northward as water temperatures increased. We found that H. wrightii was extremely clonal: of the 149 shoots sampled, 145 (97.3%) belonged to the same clone and this clone remained unchanged between years. These patterns indicate that edge-of-range seagrass populations harbor less genetic diversity and reproduce primarily asexually. Thus suggesting that the most well-adapted genotype has been maintained over time. Understanding the genetic composition of these key habitat-forming organisms can strengthen restoration and conservation practices.

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Ecophysiology

Topic: Poster

Title: The effect of flooding duration on aerenchyma formation in winter wheat roots

Author: ***Joshua Brandel @ Saginaw Valley State University***

Keywords: Triticum,Waterlogging

Abstract:

Crops often undergo flooding stress, thus reducing the amount of oxygen available for respiration within roots. Flooding-tolerant plants have the ability to produce aerenchyma, which occurs as large intercellular air spaces in root cortex to allow for aeration of submerged tissues. It was hypothesized that winter wheat under flooding conditions would grow a greater amount of aerenchyma than wheat under drained conditions. To investigate plant responses, winter wheat was grown in flooding and drained conditions, with roots harvested at 0, 1, 3, 7, 14, and 21 days of treatment. When assessed microscopically, root sections of flooded plants had more aerenchyma than roots in drained conditions. Aerenchyma development increased over time, appearing around 3 days of flooding and reaching a maximum between 7 and 14 days of treatment. Air spaces in aerenchyma function to ventilate root systems, allowing the plants to tolerate hypoxic soil conditions typical of flooding. Flooded conditions were correlated with an increased amount of aerenchyma in winter wheat. Future work repeating these methods with other crop species could be beneficial. This work would allow for informed agricultural decisions to be made, regarding the selection of crops best fit for environmental conditions.

791

Physiology

Topic: Poster

Title: Genome size variation among Rhododendron (Ericaceae) and implications for leaf anatomy and function

Author: ***Arezoo Dastpak @ Florida International University***

Keywords: genome size,Leaf anatomy,Stomata,vein density

Abstract:

Genome size, the amount of DNA contained in the nucleus, is a biodiversity trait that displays astonishing diversity in land plants and influences various plant traits from the subcellular to the organismal levels, as well as community, ecosystem, and evolutionary processes. Correlations between genome size variation and nuclear volume, duration of the cell cycle, minimum cell volume, cell packing densities, leaf vein density, and photosynthetic capacity, has been revealed in many studies. However, most studies linking genome size variation to phenotypic traits have focused on broad taxonomic diversity with little fine-scale phylogenetic sampling. Here, we sampled ~120 Rhododendron accessions of over 50 taxa, including both temperate and tropical species from the wild and in botanical gardens, along with leaf morphological and anatomical traits. We found multiple occurrences of naturally occurring interploidy hybrids among Rhododendron sect. Pentanthera. Additionally, genome size was correlated with guard cell size, stomatal density, epidermal cell area, leaf vein density. However, genome size and cell- and tissue-level anatomical traits were largely unrelated to leaf morphological traits, such as leaf water content, leaf mass per area, and leaf thickness. While both anatomical and morphological traits can influence maximum photosynthetic rates, our results show that anatomical and morphological traits are largely orthogonal to each other. Thus, while changes in ploidy and genome size can be important drivers of lineage diversification and can have direct impacts on leaf anatomical and photosynthetic function, how cells and tissues are arranged, and the allocation of biomass and water can also influence leaf construction costs independent of genome size variation.

793

Topic: Poster

Title: Classifying soil microbial community composition across cytotypes of Galax urceolata (Diapensiaceae)

Author: ***Nico Andrade @***

Keywords: plant-soil interactions,polyploidy,soil microbes,plant-fungal interactions,Galax,Galax urceolata

Abstract:

Galax urceolata (Diapensiaceae) is a flowering plant endemic to the southern Appalachian Mountains in North America and includes diploid, triploid, and autotetraploid cytotypes. Populations of G. urceolata may include only a single cytotype but are often a mix of multiple cytotypes. Population conditions dictating cytotype coexistence and separation are poorly understood but may be driven by interactions with other organisms in the community. The soil environment surrounding the roots of plants is diverse and ecologically complex. Soil microbes are responsible for maintenance of rhizosphere properties such as nutrient transport and storage, nitrogen fixation, and decomposition. The aim of this study is to investigate soil microbial community composition across populations of of Galax urceolata, specifically to (1) investigate if microbial and fungal community composition is associated with ploidal level, and (2) identify if community composition differs among single cytotype and mixed-cytotype populations. Soil samples were gathered around the root zone of G. urceolata from 22 populations for a total of 64 soil samples, and DNA was extracted from each. We then amplified and sequenced the bacterial 23S-16S-ITS and fungal ITS regions of nuclear rDNA to determine bacterial and fungal species composition, as well as relative abundance, for each sample. We found the majority of bacterial species were shared among cytotypes, but all three cytotypes had indicator species, which could indicate competition or niche partitioning within the soil microbial community. Overall, we found latitude, climatic conditions, and population cytotype composition all influenced bacterial community composition.

815

Topic: Poster

Title: Predicting maladaptation in crop landraces following a global climate catastrophe

Author: ***Chloee McLaughlin @ Pennsylvania State University***

Keywords: Biogeogrpaphy,landraces,Maladaptation,Crop Modeling

Abstract:

Global climate catastrophes such as a nuclear war, super volcano eruption, or asteroid strike, although rare, pose a serious threat to human survival. The reduction in solar radiation and temperatures would dramatically impact food security from decreased crop productivity. One method for increased agricultural resilience may include the identification of existing beneficial genetic and trait variation present in crop traditional species (landraces). Landraces account for the majority of crop genetic diversity, are still widely cultivated in the developing world, and are adapted to diverse geographic and climatic regimes. These locally adapted varieties may carry beneficial alleles for crop adaptation following cooling events. Using broadly distributed landraces of globally important cereal crops (sorghum, maize, barley, and rice), we identify the degree of disruption to current landrace adaptation and aim to identify natural resilience alleles for post-catastrophic agriculture. We simulate growth and stress parameters using the ecophysiological crop growth model, Cycles, for genotyped and georeferenced landrace accessions' point of origin under modeled control and post-catastrophe conditions. From this crop growth model, we infer emergent climatic, growth, and stress values experienced during key phenological stages of crop development, characterizing differences in stress that drive local adaptation in landrace populations. We identified climate associated SNPs and then used gradient forest offset (GF-offset) methods to predict maladaptation through time under different nuclear war scenarios. We find strong concordance between GF-offset and disruptions in climate; adaptation is predicted to be most disrupted where climate is the most perturbed. We find that stress experienced during specific growth stages contributes differently to GF-offset, indicating changes in maladaptation throughout a crop's lifetime. We further used our GF genotype-stress models to identify landrace varieties best matched to specific post-catastrophic conditions, indicating potential substitutions for resilience. Through leveraging untapped landrace genetic diversity, we aim to assess and identify strategies that increase food resilience in the case of global cooling scenarios.

818

Topic: Poster

Title: Biochemical regulation of photosynthesis: Not a limiting factor for net photosynthesis of plants grown under elevated temperature

Author: ***Chinedu Eze @ Smithsonian Tropical Research Institute***

Keywords: relative humidity,Elevated temperature,ACi,Vcmax,Jmax

Abstract:

Elevated temperatures are predicted to become more frequent and intense, posing potential challenges to plant growth and development. Understanding the response of photosynthesis to elevated temperature is crucial for predicting the future of plant productivity and ecosystem functioning. We investigated the effects of elevated temperature and low relative humidity (RH) on biochemical controls over photosynthesis (Vcmax and Jmax) for tropical forest species in a greenhouse-experiment in Gamboa, Panama. Seedlings of six species were grown at ambient conditions (control), elevated temperature with increased RH, and at elevated temperature with decreased RH. Vcmax and Jmax values were estimated from the dynamic assimilation technique (DAT) CO2-response curves measured at 31°C and 38°C. The values were generally higher at 38°C compared to 31°C, suggesting photosynthesis was unlimited by biochemical constraints at high temperature. Most species acclimated to elevated temperature exhibit similar or higher Vcmax and Jmax values compared to the control plants. However, two species demonstrate lower parameter values for the warm-acclimated plants. The effects of different RH levels on photosynthesis were consistently small, despite large differences in drought-tolerance of the target species. These preliminary findings provide insights into the factors that limit photosynthesis under the predicted climate change

819

Topic: Poster

Title: Comparative leaf micromorphology of Drypetes Vahl and Putranjiva Wall (Putranjivaceae) and its taxonomic significance

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2Leipzig University,

Author: ***Akeem Kadiri @ University of Lagos***

Keywords: morphology,Africa,Anatomy,leaf,putranjivaceae

Abstract:

Putranjivaceae are a pantropically distributed but poorly known glucosinulate-producing family of three genera (Drypetes, Putranjiva and Sibangea), previously included in Euphorbiaceae subfamily Phyllanthoideae. Characters of the leaf epidermis were previously suggested as being of infrafamilial taxonomic relevance, but epidermal features of the three genera have not so far been compared in the light of the phylogenetic relationships recovered by molecular data. Therefore, we compared the leaf micromorphology of 44 (out of c. 200) Drypetes spp. and two (out of three) Putranjiva spp. using light microscopy. Our findings revealed that there are more stomata types than previously reported in both genera. We also present a new record of stomatal complexes and epidermal cell characteristics.
The cell wall ornamentation character on both surfaces of the epidermis is useful for distinguishing D. aframensis subsp. aframensis. Based on a combination of the studied characters, doubtful species of Drypetes and Putranjiva are recognizable as belonging to the two genera, and this will require taxonomic and nomenclatural adjustments.
Other taxonomically useful characters are trichome distribution and types and leaf areole shape and tertiary veins branching patterns that appear to be relatively constant across the two genera. Oil droplets located within the cell lumen in Putranjiva differentiates it from Drypetes, where they inwardly streak the epidermal walls among other features. Thus, our study provides evidence that the investigated leaf micromorphological characters are useful for distinguishing the species of the two genera, and they corroborate the existing infrageneric classification of Drypetes that was based on exomorphology.

821

Topic: Poster

Title: Vegetative anatomical characteristics and trichome morphology of the monotypic Martynia annua L. (Martyniaceae) for use in identification and crude drug search

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Department of Botany, Faculty

Author: ***Akeem Kadiri @ University of Lagos***

Keywords: martynia

Abstract:

Leaf epidermis and indumenta structure of M. annua were studied with the aid of microscopy for easy identification of the plant materials when in fragments and for crude drug search. Stomata and trichome morphology appear significant in identifying the species. Paracytic and anomocytic stomatal types are basic but polocytic is additional on the abaxial surface of the epidermis.The overwhelming reports on the folkloric uses of Martynia annua L. (Martyniaceae) and the sole reliance on exo-morphology for its identification which gives room to error form the basis for this study. Moreso, the need to utilize as many data as possible for accurate identification of the plant is another important reason for its choice for investigation. A total of 20 plant samples were examined. 100 leaves and 40 stems, petioles and midribs obtained from both herbarium samples of the plant were examined. The epidermis was recovered after treatment with concentrated trioxonitrate (v) acid (HNO) in capped specimen bottles for about 3 8–24hrs to macerate the mesophyll. Samples were stained with acidified phloroglucinol and then one drop of toluidine blue. They were mounted on glass slides and examined under the microscope (XSZ-170BN Olympus) and photomicrographs were taken with microscope eyepiece camera (Toupview 3.7). Line drawings were made with camera lucida drawing instrument. Interesting folia epidermal features were encountered. These include 3 stomatal types, two main types of trichomes namely: - Type 1: Long to short multicellular-glandular trichomes with globular heads and Type 2: Unicellular non-glandular globular-headed trichomes with stalk or no stalk. The report of leaf teeth in M. annua which is the begonioid type is novel and cell shape of the perivascular structures is oval to polyhedral. A suite of these characters will aid identification of M.annua when a whole fresh plant specimen is absent.

822

Topic: Poster

Title: Discovery and Validation of Conserved Cold Transcriptional Regulators

Author: ***Xiaojin Wang @ Purdue University***

Keywords: tomato,Transcriptomics,cold tolerance

Abstract:

Plant stress, particularly abiotic stress caused by non-living factors such as flooding, droughts, heavy metals, salinity, and extreme high or low temperatures, can negatively impact plant growth, development, and productivity. The recent decades have seen an increase in unpredictable precipitation and temperature changes, attributable to climate change. Cold stress is one of the major abiotic stresses that limits plant geographical distribution and adversely affects crop growth. Although extensive molecular studies on cold tolerance have been conducted in Arabidopsis, a temperate species adapted to cold, the response of a tropical species, such as Tomato, to cold stress remains poorly understood. This study aims to compare the cold-responsive genes in both species, identify early response regulators, validate their role in cold response, and enhance tomato cold tolerance by manipulating these regulators. If the basic mechanisms of cold response are conserved between this temperate rosid and the tropical asterid plant, these findings can be applied to other tropical crop plants. Our hypothesis is that altering the expression of conserved cold responsive TFs will change the cold tolerance in both species. In this project, we combine computational approaches, such as regulatory network inference, with molecular approaches, including gene editing, to predict and validate key TFs involved in cold stress response. Specifically, we exploit the public transcriptome datasets of Arabidopsis cold response and compared them with our Tomato cold response transcriptome data to identify a list of differentially expressed transcription factors under low temperature in both species. CRISPR technology was then utilized to generate tomato mutant lines for these TFs, and the phenotypes of transgenic plants will be experimentally validated. Furthermore, a gene regulatory network for tomato under cold stress will be established based on the perturbations caused by the disruption of these major regulators. Enhancing plant cold tolerance will mitigate yield loss caused by sudden temperature drops and expand the geographical distribution and growing season of tropical crop species.

827

Topic: Poster

Title: Development of Integrative Taxonomic Resources for the Global Composite Database: a case study in the ironweed tribe, Vernonieae (Compositae)

Author: ***Morgan Gostel @ Botanical Research Institute of Texas***

Keywords: Biodiversity Database,Collections management,nomenclature,the International Compositae Alliance,World Flora Online

Abstract:

A key challenge for biological sciences in the 21st century is the necessary coordination and integration of biological collections and their associated data. Collections-based research is in the process of undergoing a renaissance that is driven largely by the mobilization of worldwide digitization efforts. The development of online databases to share plant taxonomic information with the public and link this information to digital collections resources is a priority for biodiversity research and conservation. Decades of international plant conservation expertise culminated in 2002 with the establishment of the Global Strategy for Plant Conservation (GSPC), which was adopted by the United Nations' Convention on Biological Diversity and has included 16 targets – the first of which was to establish "a widely accessible working list of all known plant species." The GSPC has led to a number of breakthroughs for the systematics community, including the World Flora Online (WFO). To mobilize taxonomic expertise, the WFO recognizes taxonomic expert networks (TENs), that contribute to this international effort. One of these TENs, the International Compositae Alliance (TICA) has recently launched the Global Compositae Database (GCD). The GCD is an expert-curated repository of taxonomic information that is publicly accessible through an expansive, permanent, and integrative online platform and helps to facilitate collections management, train the next generation of taxonomists, and advance collective knowledge regarding the diversity and evolution of these enigmatic plants. Here, we present the development of taxonomic reference data using the GCD and a case study in one of the largest tribes in this family, the "ironweed tribe" (Vernonieae). The "ironweeds" comprise approximately 1,500 species, a broad geographic distribution, and until recently, most species in the tribe (>1,000) were placed into a single, broadly defined genus, Vernonia. While this genus has been reduced to include only 21 species restricted to the Americas, in the Eastern Hemisphere, more than 200 species still remain in Vernonia, awaiting placement in segregate genera. The convoluted taxonomic history of the ironweeds has resulted from many factors, including high species richness distributed across a broad geographic range. Moreover, taxonomists who have specialized in this group historically have spanned vast geographic and generational distances, which has led to various disagreements and/or the perpetuation of taxonomic errors, likely due to unintentional mistakes. We are developing resource-rich taxonomic reference pages using the GCD to clarify the challenging taxonomic history of this tribe and here present some examples of dynamic content and features that this public database can provide. As TICA continues to refine and improve the GCD, we hope to recruit additional taxonomic specialists as contributors and inspire other TENs to develop similar databases

829

Topic: Poster

Title: Invasive Plant Species Monitored by the Northern Research Station Forest Inventory and Analysis Program: Comparing the 2009, 2014, and 2019 Inventories

Author: **Cassie Kurtz @**

Keywords: biological invasions,community ecology,disturbance ecology,invasive species,plant ecology

Abstract:

Invasive plant species (IPS) are causing vast changes across the landscape and costing billions of dollars to mitigate. They impact aesthetics and agriculture but are still widely used for erosion control. The same characteristics that promote their spread, quick colonization and ability to withstand harsh environments, are qualities that are valued for site reclamation. These species are also used for various pharmaceutical uses and new cultivars are bred for landscaping. To monitor the spread and cover of these species, the USDA Forest Service (FIA) program collects invasive plant data on all forest ownerships, public and private. A new revised report was created to update the previous report (Kurtz 2013) which was from 2005 through 2010. These new data are a comparison of the 2009 data to 2014 and 2019 and looks at change for the 44 IPS monitored by the 24 states of the Midwest and Northeast that comprise the region monitored by the Northern Research Station (NRS).

830

Topic: Poster

Title: Building an Inclusive Botany: The “Radicle” Dream

Author: **Makenzie Mabry @ University of Florida**

Keywords: Accessibility,Colonialism,Community science,Digitized Biocollections,traditional knowledge,History of botany

Abstract:

Driven by the national conversation on systemic racism, ongoing inequities, appeals to decolonize science, and the many recent calls for diversity, equity, accessibility, and inclusion, we use stories of plants to discuss the history of bias and exclusionary practices in scientific botany, particularly regarding access to scientific spaces, and the exploitation of marginalized peoples. We discuss the many opportunities and challenges presented by the age of information technology as we seek to create a more inclusive botany that recognizes and acknowledges the contributions of historically marginalized groups, including Black and Indigenous communities. We hope this article can be used as a conversation starter to raise awareness, encourage reflection, and promote action toward creating a more equitable and just scientific practice.

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Topic: Poster

Title: Morphological and Structural Responses of Albizia lebbeck to Different Lead and Nickel Stress Levels

Iram Ijaz1,2, Amir Bibi2, Syed Riaz Ahmed2and Daniel K. Y. Tan3 et al

1Laboratory of Molecular Systematics and Evolution Genetics, Florida Museu

Author: **iram ijaz @ University of Florida**

Keywords: Albizia lebbeck; lead nitrate; nickel nitrate; structural modifications; phytoremediation

Abstract:

Lead (Pb) and nickel (Ni) are serious soil pollutants that adversely affect plant growth and development and need to be removed through phytoremediation. The present study aimed to assess the morphological indices of Albizia lebbeck (L.) (Benth.) in relation to anatomical modifications for survival under both Pb and Ni stress. The seedlings of A. lebbeck were established and then subjected to four different concentrations, viz. 0 mM, 25 mM, 50 mM and 75 mM, of Pb and Ni for 14 days in two phases. Morphological traits such as shoot length (70.93%), fresh weight (79.27%), dry weight (83.9%), number of root hairs (65.7%), number of leaves per plant (67.4%) and number of leaflets per plant were greatly reduced under Pb or Ni stress. Surprisingly, root length increased rather than decreased with the increase in Pb or Ni concentrations, along with an increase in leaflet width, leaflet length and leaflet area. Moreover, root cortical cell area, metaxylem area and phloem area decreased at 75 mM of Pb and Ni while epidermal thickness and cell area increased. Stem epidermal thickness, cell area and phloem area significantly decreased with the consistent increase in metaxylem area and cortical region thickness under both Pb and Ni stress. Leaf anatomical traits such as midrib thickness, abaxial epidermal thickness and stomatal density and adaxial epidermal thickness and stomatal area significantly increased with increasing Pb or Ni stress. Correlation analysis revealed close relations among morphological and anatomical traits (such as root length with cortical region thickness) for better plant survival under Pb or Ni stress, and a PCA-biplot further verified these correlation analyses. Cluster analyses demonstrated the associations among the morphological and anatomical traits based on different stress levels. Furthermore, we found that longer exposure (from phase 1 to phase 2) to heavy metal stress is more dangerous for plant survival and can ultimately lead to plant death. Moreover, our results also confirmed that Ni is more harmful or dangerous to plants than Pb at high and moderate concentrations. The anatomical modifications ensured the survival of A. lebbeck in extreme heavy metal stress and therefore unlocked its potential to be used as a natural source of phytoremediation. We also recommend that the genetic potential of A. lebbeck associated with its survival under heavy metal stress be investigated.

833

Topic: Poster

Title: Testing an origin hypothesis for the Costa Rican tetraploid Polystichum talamancanum Barrington with the Hybphaser pipeline

Author: ***Julia McClafferty @ University of Vermont***

Keywords: Allele phasing,allopolyploidy,hybridization,Pteridology

Abstract:

The product of speciation via an allopolyploid derivative of a sterile hybrid is a genetically distinct lineage combining the genomes of its progenitors. Conventional phylogenetic analyses representing divergence histories cannot accurately capture the relationships in allopolyploid complexes. The tropical Andes and southern Central America harbor an unusually intricate complex of Polystichum Roth (Dryopteridaceae) species, hybrids, and polyploids whose relationships have proved refractory to standard analysis. Here we use target-sequence capture and read-to-reference phasing with the bioinformatics workflow Hybphaser to approximate phased haplotypes of Polystichum talamancanum Barrington, an allotetraploid fern endemic to Costa Rica and Panamá, as a test of Hybphaser's ability to detect hybrid species and determine their parentage. Phased haplotypes were used in downstream phylogenetic analyses alongside accessions of species judged to be possible parents from previous phylogenetic work. The resulting measures of locus heterozygosity and allele divergence were consistent with the hybrid status of P. talamancanum and the highest proportion of reads phasing unambiguously matched the accessions of its progenitors as hypothesized in previous studies. This outcome corroborates a history comprising hybridization of a Polystichum species with tropical North American relationships endemic to southern Central America with a species now endemic to the northern Andes followed by in situ polyploidization. This history requires that the Northern-Andean endemic species previously occurred in southern Central America, a scenario possible given the substantially expanded open-alpine habitat in Central America at the height of the Pleistocene. Overall, we accomplished two goals. First, our study corroborates the usefulness of the Hybphaser workflow in resolving hybridization events and accurately identifying parentage in complex reticulate lineages. Second, it demonstrates the power of combining modern genomic techniques with ecological, geographic, and historical data to reconstruct integrated histories of reticulate evolution.

836

Topic: Poster

Title: Inferring the Evolutionary History of YABBY Transcription Factors across Monocot Species

Author: ***Irene Liao @ University of California, Los Angeles***

Keywords:

Abstract:

As part of a high school internship project offered through Big Picture High School in Bellevue, WA, we worked together to explore data collection, analysis, and interpretation in scientific research. The goal of this internship was to gain experience in a career involved in biology and to learn about aspects of laboratory research.

In this project, we examined the evolutionary history of YABBY transcription factors at the genome level. YABBY transcription factors play important roles in plant leaf and floral development. There have been extensive studies of YABBY genes in Arabidopsis thaliana, with targeted studies in grasses, poppies, and gymnosperms. However, besides grasses and tropical gingers, little is known about YABBY genes across monocots, including the number of gene copies and their putative gene functions. To examine YABBY genes across monocot species, we searched for YABBY genes using BLAST across 11 species representing major monocot lineages: Acorus americanus, Ananas comosus, Asparagus officinalis, Brachypodium distachyon, Dioscorea alata, Musa acuminata, Musa balbisiana, Oryza sativa, Phoenix dactylifera, Zea mays, and Zostera marina. We then ran the results in MAFFT to align sequences, visually assessed the alignment using AliView, and built a gene tree using RAxML. Our results show similar patterns of gene loss and gene duplication compared to previous studies using monocot species: 1) there is an expansion of YABBY2 gene copies compared to other YABBY clades, and 2) only YABBY2 and YABBY1/YABBY3 clades have all monocots studied represented. We also compared these results with outputs from running OrthoFinder, an orthology inference program, which also showed similar results. This study will serve as the basis for downstream analyses into the functional consequences of duplication and loss of YABBY gene copies in monocots.

837

Topic: Poster

Title: The Effects Nematode Interactions have on the Relative Growth Rate of Hericium erinaceus.

Author: ***wyatt tindall @ University of Idaho***

Keywords: relative growth rate,Hericium erinaceus,lion's mane,Acrobeloides,Panagrolaimus,nematophagy,wood decomposer,medicinal fungi

Abstract:

Lion's mane (Hericium erinaceus, family Hericiaceae) fungi are important forest decomposers in addition to being widely consumed by humans for nutritive and medicinal purposes. Many species of fungal wood decomposers are thought to be opportunistic by evolving nematophagous mechanisms to trap and consume nematodes to acquire additional, often limited, nutrients (i.e., nitrogen). The interaction between nematodes and H. erinaceus is not well documented and it is currently unknown whether H. erinaceus can demonstrate nematophagy. This project explored this topic and demonstrated reduced growth of H. erinaceus when paired against five different species of nematodes (e.g., Acrobeloides spp. and Panagrolaimus spp.) in a nutrient poor environment (i.e., water agar). Further research is being conducted to conclude whether nematophagous mechanisms were utilized in these interactions. And additional research will be conducted to determine the impact various nematode species (e.g., Caenorhabditis elegans, family Rhabditidae) has on the growth rate o H. erinaceus and the decomposition rate on various tree hosts (e.g., Acer sp., Fagus sp., Fraxinus sp., and Quercus sp.). This information could potentially be used by commercial growers and forest ecologists to boost fungal production for agricultural, forestry, and medical research purposes

839

Topic: Poster

Title:

Emerging trends in parasitic plant evolution

Author: ***Liming Cai @ UT Austin***

Keywords: convergent evolution,Parasitic,systematics

Abstract:

840

Topic: Poster

Title:

Loss of the plastid genes ndhJ and ycf4 in one population of Fritillaria affinis (Liliaceae).

Author: ***Emily Johnson @ Oregon State University***

Keywords:

Abstract:

Fritillaria is a genus of photosynthetic plants native to western North America and characterized by bulbs and showy flowers. While the loss (including pseudogenization and partial or full deletion) of plastid genes is well-documented in many parasitic and mycotrophic plants, these phenomena are uncommon in autotrophic lineages like Fritillaria. The plastid genes cemA, infA, and ycf15 are pseudogenes in the 33 species of Fritillaria sequenced to date. Sequencing of the plastid genome of individuals from three populations of Fritillaria affinis (Liliaceae) revealed the loss of two additional genes in one individual. The genes ndhJ and ycf4 have a single base pair insertion or deletion that changes the reading frame and creates a premature stop codon, rendering them pseudogenes. This result is noteworthy for several reasons: 1) Examples of intraspecific variation in plastid gene loss are rare, and none encompassing two genes was found via NCBI. 2) This is the first known instance of ndhJ and ycf4 loss in Liliaceae. 3) While one or more of the 11 ndh genes are known to be lost in several autotrophic plants, it is rare for only a single ndh gene to be impacted. 4) The loss of ycf4 in autotrophic plants is rare, and is previously only known from Fabaceae and Bignoniaceae. We are currently conducting Sanger sequencing of the ndhJ and ycf4 loci in additional populations of F. affinis to determine if its loss is truly restricted to a single population.

848

Topic: Poster

Title:

Frost Flash: the Effects of Abrupt Freezing Events on Bromus tectorum and Elymus elymoides

Author: ***Jon Mai @***

Keywords: Cheatgrass,freezing tolerance,Germination,invasive species,native species

Abstract:

As global climate shifts, the emergence of new temperature extremes test physiological tolerances of both invasive and native grass species. With the occurrence of aseasonal and more intense cold snaps, variation in frost tolerance could shift the current population dynamics between native and invasive grasses. To elicit this phenomena, we tested cheatgrass (Bromus tectorum), an invasive winter annual grass, and bottlebrush squirreltail (Elymus elymoides), a native Great Basin perennial species. Treatments consisted of the two grass species subjected to dry ice applications that varied during the timing of application (½ hr, 2 hr, 7 hr, 15 hr, and 24 hr) targeting different developmental stages of the germinating seed. Each dry ice application was replicated seven times for each species: 84 experimental units. For each replicate, twenty five seeds were planted in pots (9x9 cm). To quantify the effect of abrupt cold via dry ice, emergence and aboveground biomass were measured. We found that on average, both species emerge at a proportion of 65.81% at the ½ hour application window; however, as dry ice is applied at 2 hours, the proportion of emergence drops to 18.4% in cheatgrass as opposed to 43.5% in squirreltail. Cheatgrass also exhibited diminished above-ground biomass as the hour of dry ice application increased from time of imbibition, following a negative exponential regression (y=0.916 · 0.9338x r=-0.9945, r2=0.989). Where cheatgrass exhibits a continuous decline, squirreltail displays variation: average biomass decreases from by 26.14% from ½ hour application to 2 hour application, yet increases by 54% from 7 hour application to 15 hour application. Given the difference in emergence and biomass, cheatgrass was more susceptible to the effects of extreme cold stress than the native squirreltail. Though cheatgrass's invasion displays a competitive advantage, its early emergence under developmental cold stress proves disadvantageous when compared with native species.

849

Topic: Poster

Title: Investigating Corrplot and Interaction Analysis of Varied Phenolic Acids in Withania somnifera (L.) across Summer and Winter Seasons

Author: ***Ayesha Siddiqui @ University of Agriculture, Faisalabad***

Keywords: medicinal compounds,Medicinal Plants,phenolic compounds

Abstract:

This research study investigates the correlation patterns and two way interactions among different phenolic acids present in Withania somnifera, a medicinal plant, during the contrasting seasons of summer and winter. The objective is to gain insights into how these phenolic acids vary and interact across seasons, shedding light on the plant's biochemical dynamics. To study this objective plant samples were obtained from three distinct sites within the Salt Range region. Which were chosen based on variations in soil properties, altitude, and dominant plant communities. High Performance Liquid Chromatography (HPLC) was employed to quantify the levels of phenolic acid in different plant tissues, including fruits, leaves, and roots. Corrplot analysis is employed to visually represent the correlations and identify potential patterns. During the summer season, phenolic acids showed varying quantities across different plant tissues, with higher levels of ferulic, vanilic, and m. coumaric acids in leaves, while syringic and benzoic acids were more abundant in roots. Sinapic, p. coumaric, and caffeic acid remained relatively stable. In contrast, during the winter season, higher quantities of benzoic, caffeic, syringic, and gallic acids were found in roots. A correlation analysis during winter indicated positive correlations among chlorogenic, syringic, p coumaric, m-coumaric, caffeic, benzoic, and vanillic acids. Negative correlations among phenolic acids were less definitive, possibly due to a lack of interaction or values below the HPLC's detection limit.The findings contribute to a deeper understanding of the phenolic acid composition of this plant and offer valuable insights for future research on its bioactive properties. Moreover, this study underscores the importance of considering seasonal variations in the analysis of phenolic acids and their potential applications in herbal medicine and drug development.

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Topic: Poster

Title: Examining the Resilience of Squirreltail Grass (Elymus elymoides) Against a Zinc Gradient

Author: ***Connor Robitaille @ Gonzaga University***

Keywords: Abiotic stress,Heavy Metal,native plants,tolerance,zinc

Abstract:

Squirreltail grass (Elymus elymoides) has demonstrated promising capabilities in heavy metal accumulation and tolerance. The Inland Northwest, which encompasses Eastern Washington, Idaho, and Montana, has a notoriously long history of heavy metal mining, resulting in high levels of zinc contamination within the region. Studying the tolerance of native grasses to zinc provides a sustainable and cost-effective approach to restoration efforts within polluted areas. In this study, we aimed to evaluate the tolerance of squirreltail grass by subjecting it to various concentrations of zinc. The experimental treatment consisted of 7 zinc concentrations 0, 0.5, 1, 10, 20, 50, and 100 mM. There were 5 seeds planted in containers (long narrow pots; 4cm x 20.2cm). The setup was housed in a controlled greenhouse with 10 reps of each of the concentrations. One initial zinc treatment (250 mL) was applied to the seeds. To assess the effects of zinc stress on Squirreltail grass we measured plant height, root length, above-ground biomass, and below-ground biomass. Our results showed that mean shoot height was highest at 1mM Zn in comparison to the other concentrations (8% higher than control and 25% higher than 100mM), indicating a small fertilizer effect on squirreltail grass. However, the mean height of shoots decreased at the 10 mM concentration and contained a steady decrease throughout. Similarly, plant biomass showed a 3-fold decrease in below-ground biomass and a 2-fold decrease in above-ground biomass. These results suggest that squirreltail grass can tolerate heavy metal stressors such as zinc, demonstrating a broad tolerance to zinc concentrations, with declines occurring around the 50mM range. Further investigation into the tolerance of Zinc within the plant itself is still needed to fully understand its potential applications in ecological restoration efforts.

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Topic: Poster

Title: Identification of novel transcription factor regulators of fatty acid biosynthesis in Arabidopsis seeds

Author: ***Rajeev Ranjan @ Purdue University***

Keywords:

Abstract:

Vegetable oils are an important natural resource consumed by human and also serves as feedstock for biofuel production. Plant oils which are derived from fatty acids are stored in the form of triacylglycerol (TAG) in the seeds of oil crops. Extensive research has been done to understand the process of lipid biosynthesis and modifications in the seed. However, its regulatory network driven by transcription factors (TFs) is largely unknown and needs further investigation. Arabidopsis serves as an excellent model to study the regulation of lipid biosynthesis due to the availability of curated genomic resources and the accumulation high amount of oil in its seed. By using over 1500 RNAseq gene expression an Organ-Delimited Gene Regulatory Network (OD-GRN) was built and by inferring this OD-GRN, potential candidate TF regulators of lipid biosynthesis was identified. We obtained 11 previously uncharacterized TF regulators of seed oil biosynthesis. The role of these TFs was experimentally validated by analyzing fatty acid content and composition in the knock-out mutant and overexpression lines. Results suggested a high accuracy of (75%) of this gene discovery pipeline as two-thirds (7/11) of the predicted TFs exhibited phenotypes affecting seed oil content or composition. Among the most promising TFs, we observed that CESTA and bHLH93 control the initial step of lipid biosynthesis as they affected total seed oil content while HB25 altered seed oil composition reflecting its action during the chain elongation process. However, SRM1 is possibly involved in multiple steps, as it influences both oil content and composition. These findings not only enhance our understanding of the intricate mechanisms of fatty acid biosynthesis but also provides valuable insights into the potential manipulation of lipid content and composition in oil crops through targeted TF regulation.

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Topic: Special Lecture

Title: Plants: a natural history of resilience

Author: ***Jacquelyn Gill @ University of Maine***

Keywords:

Abstract:

For half a billion years, land plants have played a foundational role as the life support system for Earth’s terrestrial biodiversity. After overcoming the challenges of life on dry land, plants rapidly evolved a wondrous array of morphologies and strategies to thrive in nearly every terrestrial environment across the globe. What happened next is one of the greatest success stories in evolutionary history, recorded in rock, mud, and in the genomes of modern-day plants. From the long duration of many lineages, to plants’ ability to survive mass extinctions, the paleobotanical record is an impressive—and inspiring—lesson in resilience. In this talk, I’ll first explore the fossil record of plants and their ability to withstand the dramatic environmental and climatic upheavals of Earth’s history. I’ll then identify some of the mechanisms that have facilitated their success and explore the horizon of emerging botanical research on plants as agents of ecological resilience. Finally, I’ll draw on these examples to explore the ways that plants – and the people who research and love them – have a critical role to play as we tackle the challenges of the modern-day biodiversity and climate crises.

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Topic: Special Lecture

Supporting inclusive and sustainable research infrastructure for systematics (SISRIS) by connecting scientists and their specimens

Title: Discovering together "who dunnit?": building a borderless knowledge community

Author: ***Deborah Paul @ University of Illinois Urbana Champaign***

Keywords: Biodiversity Informatics,museum,Data Standards,Underrepresented Groups,Bionomia,Wikidata,ORCiD,People Identifiers,Shared Knowledge Management,Collection Metrics,Culture Change

Abstract:

Knowing definitively who collects or identifies a vouchered museum specimen offers new benefits for both individuals and groups. Usually, digitized data for collection objects (e.g. herbarium sheets) pivot around the “what” and include where and when. The who information ends up as unstandardized “text strings” making it difficult to index or search, which limits usefulness for everyone. If we know more about the who, we gain a searchable data asset offering unique insights for many groups including: collectors, researchers, collections staff, students, underrepresented groups, organizations, and the public.

Unique identifiers for people provide the means to do this (e.g. Wikidata “Q numbers”, ORCiD “IDs”). Of course, not everyone associated with specimen vouchering has an identifier like this (yet). For current and historical collections, it turns out we can all work together to assign these people identifiers. Using Wikidata as a shared knowledge management tool means we can all contribute to implement effective knowledge transfer and reduce duplication of effort. Doing this work openly allows anyone who wants to, the chance to help. Then, using Bionomia software (Bionomia.net), anyone can work to link specimen records definitively to a person with a globally unique identifier. This work makes all sorts of new discoveries and impact metrics possible both for an individual and any organizations housing these materials who also steward and publish the related factual data to aggregators such as the Global Biodiversity Information Facility (GBIF). For example, scientists taking part in this work often discover uses of their specimen data in research papers they did not know about.

To uncover tacit people information and its power, we need to find ways to promote identifiers, engage more people to do this work worldwide, store these IDs in our collection databases, and increase Wikidata entries for people associated with vouchered collections (Groom, et al 2022). Once these data exist, we can reveal hidden individuals and their contributions to science and compile individual and institution-level metrics. At the cross-domain level, this work and the tools used to do it, foster culture change in our worldwide biodiversity data and collections communities. Individuals gain the power to contribute expertise across domain disciplines and outside the walls of a physical collection or local collection database. Everyone gets the equally valuable gifts of discovering who (and what) makes their collections unique or where they have much in common with others they can share. It becomes easier to find the research, novel uses, outreach, education, and policy development made possible through people collecting and identifying these specimens. Organizations and administrators find a new window with which to look at the positive and long-lasting impact of their support for collections and the people who create and curate them.

In this symposium, you will discover who is doing this work, how it is being done, who benefits and how, along with outstanding community needs and opportunities for you. With these data we can better understand our past, and illuminate the future, for people, the specimens, and the data.

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Topic: Special Lecture

Title: People in the biodiversity knowledge graph and their roles in building the data connections we need

Author: ***Erica Krimmel @***

Keywords: Wikidata,Shared Knowledge Management

Abstract:

Herbaria are connected to each other by intricate and deep-rooted social histories. A student trained at one collection moves on and eventually becomes the curator of another. A prolific amateur collector donates specimens to multiple herbaria over the course of their lifetime. Rival systematists wage a decades-long battle documented by annotations back-and-forth on specimen labels. Although 21st-century data management in herbaria has not prioritized information about the people associated with specimens, people are often a critical link to data beyond the basic specimen occurrence record. Capturing and sharing more data about the “who” of specimens can improve connections across institutions and individuals, augment local data records, and encourage expertise-sharing. Typically, data about people are digitized and managed individually by each herbarium or institution, or at best by a consortia of institutions using the same collections management system. Not only does this lead to redundant time spent, but it also results in isolated knowledge management. Shared knowledge management, in contrast, can improve knowledge completeness, raise the visibility of the work required to manage knowledge, and make data more accessible to the linked open data ecosphere. Ultimately, these benefits lead to improved discoverability for specimens by increasing their data connectivity in the biodiversity knowledge graph.

Over the past few years, Wikidata has gained visibility in the biodiversity collections community as a centralized, accessible platform for working collaboratively to disambiguate entities, e.g., people associated with herbaria, and to mobilize information about them. In this way, Wikidata is a tool for shared knowledge management, and we can use it to support inclusive and sustainable research infrastructure. Such research infrastructure depends on social systems as much as on information systems for successful knowledge management. Wikidata also provides an established social system with its collaborative, community-oriented approach to curation. This approach may be initially uncomfortable to many herbarium professionals, but relinquishing total control over “our” data promotes inclusivity by recognizing that we may not be the ultimate authorities on every aspect of our collections data. This is especially true of data related to people, who are frequently important to domains other than herbaria. Even within the herbarium community, many individuals involved with collections are not fully acknowledged for their work or have been misrepresented, especially those who are women, non-White, and/or Indigenous. Tools like Wikidata offer the opportunity for data to be augmented and/or corrected, and for this work to be done in a shared knowledge managemen context that benefits all herbaria and specimens connected to an individual.

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Supporting inclusive and sustainable research infrastructure for sys

Topic: Special Lecture Supporting inclusive and sustainable research infrastructure for systematics (SISRIS) by connecting scientists and their specimens

Title: The State of Herbarium Backlogs: Perspectives from Bryophyte Collections

Author: ***Jessica Budke @ University of Tennessee***

Keywords: Accessions ,bryophytes,Collections,Collections management,herbaria,herbarium specimens,Specimen processing,SISRIS,staff,survey

Abstract:

In order to fulfill its role in the botanical community, an herbarium must have its specimens processed, identified, and accessioned so that botanists can consult these materials during their research. Many herbaria, however, struggle to keep up with the influx of specimens. As a result, specimens may accumulate while awaiting further processing, leaving the institutions with what is known as a ‘backlog’; yet we know little about the content of such backlogs. In this study, we surveyed herbarium staff about their institution's backlog of unaccessioned specimens, focusing on the number and taxonomic lineage of backlogged specimens as well as the challenges associated with curating these specimens. We asked additional questions about unaccessioned bryophyte specimens in order to explore these collections in more depth. Eighty-seven staff members responded to our survey and 65 of these responses were complete and thus able to be analyzed. Approximately 92.0% of these staff indicated that their herbarium had a backlog with an average of approximately 30,372 unaccessioned specimens per herbarium. According to Index Herbariorum there were 3,426 active herbaria in 2020, and thus we estimate that ~104 million specimens are present in herbarium backlogs. While bryophytes only represent 9% of the accessioned specimens reported by our study participants, they are overrepresented in the backlog, comprising 16% of all unaccessioned specimens. According to our staff respondents, slightly more than half of backlogged bryophyte specimens are stored in field packets without labels, and approximately three-quarters of the unaccessioned bryophytes are not yet identified to species. In addition to describing the challenges associated with the integration of partially curated materials into an herbarium, staff also discussed other limitations. These obstacles included competing institutional priorities, labor shortages, and insufficient bryological expertise. Drawing on the answers provided by our survey respondents, we offer suggestions regarding how best to accession specimens currently in herbarium backlogs.

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Supporting inclusive and sustainable research infrastructure for sys

Topic: Special Lecture

Title: An exception proves the rule: Lena Artz (1891–1976) and her legacy of botanical specimens.

Author: ***Andrea Weeks @ George Mason University***

Keywords: herbaria,SISRIS

Abstract:

Lena Artz is one of many thousands of individuals who documented the plant biodiversity of the southeastern United States in the mid-20th century. But her accomplishments as a pioneering explorer of the Massanutten Mountains, which were uncovered only because of ongoing herbarium digitization in Virginia, is a case study of how interrogating the legacies of poorly known collectors can advance botanical research in the present day. In 2019, the collection notebooks and professional papers of Lena Artz were discovered during the salvage of the Lord Fairfax Community College Herbarium. Despite being occasionally acknowledged in print as an early contributor to knowledge about Central Appalachian shale barren ecosystems, Lena Artz's biography and her professional accomplishments were largely undocumented at the time of the discovery. This presentation describes how archival research gumshoe detective work, and the curation of Artz’s ca. 2000 sheet exsiccatae across multiple institutions have worked synergistically to uncover the life and life’s work of this hidden figure in botany. The results provide insight on why she, like many other collectors whose collections inhabit museums and databases, become forgotten. The results also reveal the time-value of her collections for contemporary studies of rare, threatened and endangered plant species, for capturing the biodiversity of landscapes long since destroyed, and for informing studies of global climate change. Lastly, I show how Bionomia can be used as a tool to improve digital data about specimens across institutions using the curation of Artz’s exsiccatae as an example. I argue that assigning universal unique ID’s to historical collectors and appending these to their digitized specimen records is a tractable challenge for the herbarium community to meet that not only will help us achieve the vision of the extended specimen concept but will make collections-based research more inclusive in the 21st century.

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Supporting inclusive and sustainable research infrastructure for sys

Topic: Special Lecture

Title: Prolific plant collectors and the HBCU legacy: Charles Parker as a case study

Author: ***Janelle Burke @ Howard University***

Keywords: Collections,Herbarium Digitization,SISRIS

Abstract:

Charles S. Parker Ph.D., a botanist and former Chairperson at Howard University, was a prolific plant collector. Over his career, Parker collected over 2,000 specimens which included over 900 different species. He collected all over North America, though most of his collections were concentrated in the Pacific Northwest, Mid-Atlantic, and Southeast regions of the United States. His collections in Idaho and Washington contributed greatly to the “Flora of Southeastern Washington and of Adjacent Idaho”. Notably, Harold St. John named two new taxa after Parker’s collections: Lathyrus parkeri H.St.John and Rosa spaldingii var. parkeri H.St.John. After moving to Washington, DC in the 1930s, Parker continued his collecting and expeditions, building the collection of specimens at the Howard University herbarium (HUDC). Our study documents Parker’s contributions to floristic work, and locations of the specimens of this pioneering Black botanist.

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Population Genetics/Genomics

Topic: Symposium From theory to practice: New innovations and their application in conservation biology

Title: Translating RADseq data into genetically informed conservation strategies for functionally extinct in the wild cycads

Author: ***Maia Jones @ California Academy of Sciences***

Keywords: Cycads,RADseq,conservation genetics

Abstract:

Cycads in the genus Encephalartos (Zamiaceae) have been poached for decades, leading to the extirpation of wild populations. For our research, we have focused on the species in the most dire situations, classified as critically endangered or functionally extinct in the wild, and are using RADseq data to evaluate their remaining genetic diversity and population structure. The known individuals of these species are held in private and botanical garden collections in South Africa, and our main objective in this project is to translate the results of our analyses into management strategies that can be implemented by conservation horticulture practitioners. The botanical gardens stewarding the living collections of these species will make up a broader meta-collection within which germplasm can be exchanged, to maintain the genetic diversity and longevity of these species.

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Conservation Biology

Topic: Symposium

Title: One is the loneliest number: identifying and prioritizing plants of one known occurrence for conservation action

Author: ***Wesley Knapp @ NatureServe***

Keywords: _{conservation biology},ex situ,extinction,in situ,OKO,prioritization

Abstract:

Our new geologic era requires modern approaches for preventing extinction events. Previous work on plant extinctions in the United States and Canada discovered that 64% were single-site endemics (Knapp et al. 2021). This agrees with a recent global analysis of plant extinctions that showed taxa from one area/or with extremely limited geographic ranges are the most common trait shared for all extinct plants (Humphreys et al. 2020). Current methodologies used by the International Union for the Conservation of Nature (IUCN) and NatureServe do not explicitly identify or prioritize taxa of One Known Occurrence (OKO) for conservation action. NatureServe has assessed the entire flora of the United States and Canada. Of these assessments, ca. 1250 taxa are given the highest assessment rank, G1 - Critically Imperiled with Extinction. Given the lack of funding available for plant conservation, it is obvious additional prioritizations are needed to meaningly prevent extinctions. In situ and ex situ conservation methods should be employed for all OKO plants if such actions haven't already occurred. The Endangered Species Act (ESA) is the mechanism for the protection of plants under Federal law. There is a common misconception that such extremely rare organisms must already be protected under the ESA, but that is not correct. In one case, the U.S. Fish and Wildlife Service was petitioned to list an OKO, but the petition was eventually denied. We will present our preliminary findings on the OKO plants in the USA and Canada. In partnership with the Laukahi Network, we are also conducting a parallel analysis for Hawai'i.

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Hybrids and Hybridization

Topic: Symposium Whole genome duplications and impact on angiosperm character evolution

Title: From dark to light: the genetic basis of flower color evolution in Nicotiana tabacum allopolyploids

Author: ***Elizabeth McCarthy @ SUNY Cortland***

Keywords: Nicotiana,allopolyploidy,Anthocyanins,Evolution,Flower color,homeolog expression bias

Abstract:

Allopolyploidy can result in genomic shock as divergent progenitor genomes adjust to cohabitation in the same nucleus. We are interested in how allopolypoidy affects the evolution of biosynthetic pathways, comparing natural and synthetic Nicotiana tabacum allopolyploids with their diploid progenitors. We examine how divergent flower color phenotypes and underlying pigment compositions arose in N. tabacum allopolyploids, using transcriptome analyses across flower development with a focus on differential expression of genes involved in the flavonoid biosynthetic pathway, a branched pathway that produces both anthocyanin an flavonol pigments. Differences in the composition of these pigments underlie the light pink and dark pink flower phenotypes observed in natural and synthetic N. tabacum accessions. We investigate whether reciprocal homeolog bias drives flower color differences, assess expression patterns across the flavonoid biosynthetic pathway, and correlate those patterns with pigment composition. We observe no reciprocal homeolog bias associated with flower color differences, but do find that natural allopolyploids have stronger homeolog bias than synthetic allopolyploids, suggesting the importance of trans-regulatory differences at allopolyploid origin, followed by the evolution of cis-regulatory differences between progenitor subgenomes as allopolyploids age. The maternal N. sylvestris copy of DIHYDROFLAVONOL 4-REDUCTASE (DFR), which encodes for the first enzyme in the flavonoid biosynthetic pathway that drives the flux toward anthocyanin pigments, appears to be becoming a pseudogene in natural N. tabacum accessions due to the fact that it has a frameshift, which results in the production of a nonfunctional protein. Overall expression of flavonoid biosynthetic genes correlates with flower color differences in N. tabacum allopolyploids. Specifically, a high ratio of FLAVONOL SYNTHASE (FLS), the gene encoding the enzyme that produces flavonols, to DFR, which is due to delayed activation of DFR in flower development, results in the light pink flower phenotype in N. tabacum allopolyploids. Pigment composition differences seem to involve both transcript level differences and changes in enzyme efficiency.

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Topic: Symposium

Whole genome duplications and impact on angiosperm character evolution

Title: Evolution of flooding tolerance in maize relatives

Author: ***Sontosh Deb @ The University of Alabama***

Keywords: crop,flooding,gene expression,leaf,polyploidy,stress,Wild relatives,Root,paralog,traits

Abstract:

Maize (Zea mays L.) is an economically valuable crop grown widely across the world. It is very sensitive to soil flooding and submergence/waterlogging which leads to yield loss and can result in death of the plant. Variation in precipitation patterns and increased flooding due to climate change may result in lower overall maize productivity in afflicted areas. Since maize is one of the world's most planted crops and a staple for millions, it is very important to develop improved varieties of maize to cope with the increasing stress. Maize is an ancient allopolyploid and shares this event with other members of the genus Zea and the genus Tripsacum. Recently, Vossia cuspidata (Roxb.) Griff. (hippo grass) was suggested as a putative, extant relative of one of Zea/Tripsacum's diploid progenitors. The parental relative Vossia cuspidata and close relatives Zea nicaraguensis H.H.Iltis and B.F. Benz and Tripsacum dactyloides L. show increased tolerance to submergence/waterlogging stress compared to cultivated maize, which are all likely independently evolved traits. Several flood tolerant quantitative trait loci have been identified in maize inbred lines suggesting maize may have the capacity for flooding-tolerance. The study aims to examine the evolution of flooding tolerance in maize using extant parental and wild relatives. To do this, we designed a greenhouse experiment using one flooding-sensitive maize inbred line and three flooding-tolerant wild relatives. The studied species were subjected to three different flooding treatments and a total of 72 root and leaf tissue samples were collected for RNA extraction, transcriptome library preparation, and sequencing. We have used the sequencing data to investigate whether gene expression and recruited molecular pathways differ in maize compared to wild relatives in response to flooding, specifically focusing on how paralog retention and usage differs between species of varying responses. We also conducted phylogenetic analysis of the differentially expressed genes to answer how the flooding response traits evolved in maize. Initial results suggest that these species have very different responses to prolonged flooding, with the aquatic Vossia having the most distinction. The identification of flooding tolerance genes will potentially help to develop flooding-tolerant cultivars, while the comparison of a crop to wild relatives demonstrates the need for crop scientists to look to nature for solutions to agricultural problems.

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Topic: Workshop

Title: Rekindle your creativity: Unifying art and science for personal and professional wellbeing

Author: ***Johanne Stogran @ Botanical Society of America***

Keywords:

Abstract:

Are you curious about integrating art and science but not sure where to start? Do you love to create but feel intimidated by the gap between doodles and a completed project? Feeling isolated from your creative spark amidst academic pressure? Join us for panelist presentations, open-circle discussions, and guided activities on how art and science can strengthen each other in our professional and personal lives.

Throughout the workshop, we will explore our intrinsic motivations and celebrate bringing our whole selves to our work. Whether you are a veteran artist-scientist or new to the scene, we hope you'll come out of this experience with a deeper connection to your creative process.

In the first portion of this workshop, we will see examples of projects that integrate art and science in teaching, research storytelling, personal growth, and more. Our invited panelists create diverse media for a range of audiences. They will bring us on a "behind the scenes" tour of their creative process, showing not just the final product but also the progress and pitfalls along the way. In the second portion of the workshop, we will embark on a guided exploration of how you personally approach art, from the emotional impetus to expression. We will also discuss our approaches and relationships to art with fellow attendees. This is a space to envision the role that creativity can play in your science and to develop ideas collaboratively.

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Topic: Workshop

Title: What Makes Botanical Illustration Science

Author: ***Johanne Stogran @ Botanical Society of America***

Keywords:

Abstract:

Accurate, quality botanical illustrations have been a primary component of floras, monographs, and descriptions of new species and infraspecific taxa for decades. The quality of illustrations is based upon the artistic ability of the illustrator, the standards used for illustration style, the specimens used as a basis for illustration, and the quality of the author's work in the publication to be illustrated. In this two-hour workshop, botanical illustrator and Ph.D. botanist Linda Ann Vorobik presents standards she has used in her 30-plus years as an illustrator, followed by an open discussion as to what standards should be used for scientific illustration for publications in this century, as well as how to most effectively set up and edit illustrations. Examples of topics discussed are as follows. 1) Voucher specimens for illustrations make these illustrations science. 2) Parallel illustrations are as important as parallel key construction. 3) Use of photographic resources may present the problem of lens distortion and questionable reference to voucher specimens. 4) Simplified measurements for scale bars (ex multiples of 1, 2, and 5) more readily communicates the size of the subject illustrated. 5) Labelling within an illustration (as well as included in illustration caption) more readily communicates illustration information to the reader. The workshop will conclude with a discussion of rates for illustration, copyright, limits to use of student illustration, and the ethics of illustration internship.

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Topic: Workshop

Title: Introduction to Phylogenetic Comparative Methods in R

Author: ***Johanne Stogran @ Botanical Society of America***

Keywords:

Abstract:

Advances in phylogenetic comparative methods have allowed biologists to robustly and objectively test macroevolutionary hypotheses, leading to a greater understanding of the processes of species diversification. Although the potential to answer numerous hypotheses across clades has invigorated macroevolutionary studies, learning how to apply phylogenetic comparative methodology remains a significant impediment. The Introduction to Phylogenetic Comparative Methods in R workshop will provide foundational knowledge of phylogenetic comparative methods and how to apply them using the statistical program R. Attendees will gain hands-on experience in applying methods, such as phylogenetic independent contrasts; phylogenetic generalized least squares; ancestral character estimations; constructing, fitting, and testing evolutionary models; fitting Brownian motion and Ornstein–Uhlenbeck models of evolution; lineage through time plots; and estimating phylogenetic signal in trait data. Participants will gain a theoretical understanding of the phylogenetic comparative methodology and be able to apply even the most rigorous analyses to their own study systems. Prior experience applying phylogenetic comparative methods or using R is not expected or required Early career scientists are especially encouraged to attend.

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Biodiversity data wrangling: Linking large phylogenies with species

Topic: Workshop — Biodiversity data wrangling: Linking large phylogenies with species traits and ecologies

Title: **Biodiversity data wrangling: Linking large phylogenies with species traits and ecologies**

Author: ***Johanne Stogran @ Botanical Society of America***

Keywords:

Abstract:

Botany has seen a massive growth in “big data” resources ranging from DNA to plant distributions and morphological traits. Databases like GenBank and GBIF have accordingly become household words among meeting attendees, reflecting the impact data resources have had on today’s research landscape. BSA has seen productive workshop series focused on each of these data streams in isolation, such as the popular iDigBio and phylogenomics workshops. Based on sheer data scale, we are at the threshold of using these data as platforms for assessing species traits and ecologies at the kinds of truly continental and global levels needed to test fundamental theories and to produce the applied outcomes needed for environmental action. Yet biodiversity researchers are only beginning to tap the potential that these datasets have when employed in synergy. Needed is a relatively new set of skills to perform analytical integration: bringing distributions and phylogenetic trees together, bringing traits and distributions together, and other typical yet challenging tasks. We propose a crash course in performing an essential component of integrative science—Data Wrangling—that meets the increasing needs of students and academics.The purpose of this workshop is to showcase novel methods and applications of biodiversity data in a phylogenetic and spatial context, exposing attendees to several typical workflows and hopefully inspiring them with new ideas for their own scientific systems and datasets. We will cover diverse research topics representing the future of the field, and instructors will include early-career individuals. We will offer hands-on instruction in each analysis topic, including assessing trait history and evolutionary rate, ancestral niche reconstruction, trait-associated diversification, phylodiversity, and other popular topics. We will focus our coverage on strategies to test popular hypotheses using publicly available data. Advanced and novice users are both encouraged to attend and will be divided into separate working groups. We aim particularly for those who have or are in the process of acquiring datasets and looking for ideas for analytical applications, and we refer to other BSA workshops those attendees who primarily seek instruction in data acquisition. Prepared datasets will be used for this workshop; attendees who are able to bring their own diverse datasets are enthusiastically encouraged to do so, but should contact workshop leaders several days in advance of the workshop date to make the most of the workshop experience. Users should plan to bring a computer that is set up with an R environment.

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Decolonizing Botany Discussion + Workshop

Topic: Workshop — Decolonizing Botany Discussion + Workshop

Title: **Decolonizing Botany Discussion + Workshop**

Author: ***Johanne Stogran @ Botanical Society of America***

Keywords:

Abstract:

The history of the botanical sciences is deeply intertwined with histories of colonization and resource extraction, which have resulted in the continuous disenfranchisement of peoples across the globe, especially Black and Indigenous peoples. This workshop will aim to discuss how this history and the assumptions embedded in the culture of the botanical sciences today engage with and perpetuate harms through colonization, and how we as researchers can critically examine our own work and how we can work to reduce, remove, and reverse colonial violence in our own work and the work of our institutions.

Aims of the workshop:

Address questions from participants about what is colonization and decolonization, how botanical research perpetuates colonization, the scope of the impacts of colonization
Brainstorm and share reading lists/resources on the subject, particularly as it relates to botany
Discuss and share experiences and strategies of how researchers in our community have been working to address colonization and decolonization in their own work

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Methodological advances in reticulate evolution

Topic: Workshop — Methodological advances in reticulate evolution

Title: **Methodological advances in reticulate evolution**

Author: ***Johanne Stogran @ Botanical Society of America***

Keywords:

Abstract:

The rapid development of phylogenetic network methods allows evolutionary biologists to infer reticulate relationships between species or their common ancestors. Given the notable levels of hybridization in plants relative to other groups, phylogenetic networks have the potential to elucidate complex evolutionary histories of speciation and trait evolution in addition to explaining historically contentious nodes in the Tree of Life despite increasing genomic data. This workshop will connect method developers with empirical botanists to discuss models, misconceptions, and best practices on network estimation and downstream applications. A combination of theoretical lectures and hands-on computational exercises will provide an overview of the field and exposure to cutting-edge tools. Workshop participants are encouraged to bring their own data as there will be opportunities for analysis and discussion with speakers outside of guided activities.

Specific topics include estimating networks using multi-locus nuclear data, evaluating the robustness of networks to different sources of error, and testing hypotheses of trait evolution on networks. Software used during the workshop includes FastNet, PhyNEST, PhyloNetworks, BPP, and PhyNetPy. This brief survey of the many existing methods will demonstrate a range of strategies that fit different data types and taxon sampling scenarios. The assumptions and limitations of various methods will be discussed. No prior experience is expected and speakers will be available to provide real-time guidance through exercises.

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National Science Foundation Proposal Writing Workshop

Topic: Workshop — National Science Foundation Proposal Writing Workshop

Title: **National Science Foundation Proposal Writing Workshop**

Author: ***Judy Stone @ National Science Foundation***

Keywords:

Abstract:

What makes a compelling, potentially-fundable grant proposal? In the first part of this workshop, NSF program officers will provide a quick overview of best practices and common pitfalls. In the second part, program officers will host mock proposal review panels in small groups, allowing participants to experience how proposals are evaluated and what makes a successful proposal. Participants will be provided with two proposals to review, along with instructions, ahead of the workshop. This workshop is limited to early-career researchers, e.g., postdocs, assistant professors, or equivalent.

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Topic: Workshop Navigating deep learning with digitized herbarium specimen image data

Title: Navigating deep learning with digitized herbarium specimen image data

Author: ***Johanne Stogran @ Botanical Society of America***

Keywords:

Abstract:

The rapid increase in digitized herbarium specimens available in natural history collections has enabled us to study many aspects of plant biology, such as morphological comparisons, shifts in phenology, and changes in species distributions. Currently, tens of millions of herbarium specimen images are available via online databases, with more image data added every day. In recent years, machine learning methods have shown promise in efficiently extracting data from herbarium specimens. Deep learning analyses, such as convolutional neural networks, leverage computer vision to automate analyses of herbarium sheet images. Researchers can use deep learning methods to classify digitized herbarium specimens by species or other user-specified categories.

Even relatively simple neural networks can contain hundreds of billions of parameters and require the use of graphical processing units (GPUs), which can process multiple computations simultaneously. Accessing and interfacing with GPUs can represent a barrier to entry for some users. This workshop will help participants to vault past the initial technical challenges of using deep learning on herbarium sheets to conduct analyses for object detection, image segmentation, and taxonomic classification.

Participants will work with curated sets of images, or they can use their own datasets--although this will require some advance preparation by the participant to organize their images. The workshop will be conducted in Jupyter notebooks, and some knowledge of Python will be helpful, but not required. A laptop computer and a Google account will be required.

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Workshop

Topic: Workshop Workshop

Title: A Workshop to Form a Working Group to Summarize New Taxa of Vascular Plants and Bryophytes in North America, 1995-2019.

Author: ***Neil Snow @ Pittsburg State University***

Keywords:

Abstract:

In 1998 R.L. Hartman and B.E. Nelson published a comprehensive summary of newly described vascular plant taxa in North America (north of Mexico) covering the years 1975–1994. In so doing they helped illuminate the fact that many vascular plant taxa continue to be described, despite over 250 years of plant collecting and taxonomic research in this expansive and widely explored area. Not surprisingly, discoveries of new plant diversity have continued steadily since that time. However, interest in (and even awareness of) taxonomy as a field of study, area of expertise, and career path continues its general decline, with increasingly fewer students acquiring basic skills in plant identification and fieldwork. This is unsurprising given that many universities under-prioritize offering taxonomic and systematics coursework and field opportunities. The decline likely is further aggravated by the fact that the visibility of this work to the average student is minimal. For example, easily found and digestible summaries of such work are difficult to find. A simple online search for plant species described in North America in 2020 yielded only a few of the highlights considered interesting by popular science writers. Although it is satisfying to see a few studies highlighted, it is regretful that the bulk of the discoveries remain obscured. This open workshop will bring together interested plant taxonomists and systematists to collaboratively create a Working Group with the goal of publishing a summary of new taxa of vascular plants and bryophytes described over the 25-year period of 1995-2019. The project will include analytics summarizing various aspects of taxonomic, geographic, and phylogenetic significance. We propose the creation in concert of useful on-line and interactive resources (perhaps hosted on ASPT or BSA websites) to allow interested users to explore the new taxa, where they occur, and other aspects of their biology, ecology, and phylogeny. The tentative goal will be to review the results at BOTANY 2024 and submit them as a publication soon thereafter. Additional goals include raising the profile and importance of ongoing taxonomic work, biodiversity exploration, recruiting a diversity of new students to the field of taxonomy, and highlighting the project’s value to ongoing conservation efforts.

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Topic: Workshop Workshop

Title: 3D Printing for Plant Science: Design to Optimize

Author: ***Johanne Stogran @ Botanical Society of America***

Keywords:

Abstract:

The methods used to collect data vary greatly between different research programs. Standardized equipment rarely accounts for nuances relating to study system or resource limitations, creating a need for inexpensive, custom solutions. Bespoke equipment has historically been limited to well-funded research programs, but advances in 3D printing are making it possible for nearly all labs to design and manufacture their own research tools using the current generation of inexpensive and reliable printers.
The goal of this workshop is to demonstrate the problem-solving potential of open-source hardware and 3D printing for plant scientists. 3D printing facilitates the adoption of custom equipment that can increase the rate and quality of data collection.
3D printing in plant sciences is a relatively new subfield, but it is rapidly growing. Multiple peer-reviewed articles outlining potential uses of 3D printing in the sciences exist, but relatively few involve plant sciences.

Microfluidics (https://doi.org/10.1016/j.addma.2018.10.028),
microscopy (https://www.preprints.org/manuscript/202105.0352/v1),
phenomics (https://doi.org/10.34133/2020/8640215), and
education and outreach initiatives
(https://doi.org/10.1016/j.revpalbo.2023.104860; https://doi.org/10.1016/j.addma.2018.1
.028) are all areas that have successfully demonstrated the potential impact of 3D printing.

To introduce and promote 3D printing in the plant sciences, this workshop is part of a series of in-person and online workshops that guide researchers through the process of designing custom tools for their research questions, setting up and using 3D printers, and performing maintenance on their machines. While the organizers will not receive any benefits from 3D printing companies or suppliers through this workshop, we will be contacting 3D printing companies and suppliers to request discount codes, supplies, and assistance in creating workshop teaching materials to give to participants and offset workshop costs.
3D printing can positively impact plant science research and is worth adopting as part of your research methods. This workshop aims to provide participants with the knowledge needed to successfully incorporate 3D printing into their research.

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Topic: Workshop

Title:

Author: ***Deborah Paul @ University of Illinois Urbana Champaign***

Keywords:

Abstract:

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Topic: Workshop Writing your CV and translating it into a public-facing website

Title: Writing your CV and translating it into public-facing website

Author: ***Johanne Stogran @ Botanical Society of America***

Keywords:

Abstract:

Let's work together to create a comprehensive description of your career in a CV format and then create a website that will highlight those achievements for the world to see. We will first organize your skills and accomplishments in a CV that you can use for job, funding and nomination applications. Then we will use these highlights of your career history to design a website that can showcase your research, teaching, publications, speaking engagements and service. At the end of this workshop you will have the tools to write a well developed CV and to create your own website. You will also leave with a working draft of a CV and a basic academic website that you will be able to build up further in the weeks to come.

This workshop is for students and early career professionals. Please bring a draft of your current CV to edit in class, a computer and any previous attempts at making a website.

In this workshop, you will:
1. Learn the basic structure of a CV and best practices for writing it
2. Receive feedback on your CV from peers and instructors
3. Learn the steps to create your own website
    a. Why create a website? Define your audience and intentions for having a website
    b. Discover possible content to include and see good examples
    c. Create a structure for your personalized website content (using your CV as a starting point)
    d. Work together to build a free website

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