BioSyst.EU 2013
Global systematics!

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18-22 February 2013

Abstract volume

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BioSyst.EU 2013
Global systematics!
18–22 February 2013

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Abstract-Volume

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Preface

The umbrella organisation BioSyst.EU is intended to bring together and strengthen communication between the various national systematic societies of Europe. Thus, NOBIS Austria as the host society of the second joint meeting is proud to welcome members and representatives of the Gesellschaft für Biologische Systematik (DE), the Société Française de Systématique (FRA), the Systematics Association (GB), the Swiss Systematics Society (CH) and the Svenska Systematikföreningen (SE). The motto of the 2nd BioSyst.EU 2013 meeting in Vienna, however, is "Global systematics!" – clearly insinuating a global perspective not only in science but also in respect to scientists. Therefore, we are very happy that more than 420 participants from 36 countries, including representatives from all continents, document the enormous interest of the scientific community in systematics.

A strong group of convenors came up with more than 20 symposia and workshops with 381 oral and poster presentations. We even managed to cross the border between life- and earth-sciences as geological deep time considerations are frequently found in the abstracts. Consequently, our meeting covers a very broad range of themes and topics ranging from protists to metazoans, and from the Cambrian to the Recent.

We are looking forward to four days of intensive and stimulating discussions, controversies and new insights. On behalf of the organising committee we wish you all a pleasant and fruitful stay in Vienna.

Mathias Harzhauser

President of NOBIS Austria

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How to assign species status to cryptic lineages: the case of *Troglodrius galarzai* (Annelida, Clitellata, Tubificinae) [Talk]

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Cryptic species based on molecular evidence are accumulating in the literature, becoming a problem in taxonomy and affecting all fields of biology *e.g.* applied ecology and conservation. The main reason may be that resolving the incongruence between morphology and DNA data is not attempted in most cases. Here, we show how a detailed re-evaluation of the morphological characters supported the recognition of two cryptic lineages as species. *Troglodrilus galarzai* (Giani and Rodriguez, 1988) is a groundwater limited oligochaete species from south-western Europe. Mitochondrial gene data revealed a maximum genetic distance of 18 % (p) in the species, which led to consider it as cryptic. In the light of the molecular results, we evaluated 23 morphological characters and compared the ranges of the trait values across populations. For this purpose, we calculated the coefficient of difference by Mayr (CD), which evaluates the overlapping of characters between populations. Higher CD values correspond to lower overlap in trait values. A character was considered to be diagnostic if it showed no overlap in trait values. We applied the statistical method by Wiens and Servedio to estimate whether or not we had examined sufficient individuals to delimit a species by one or more diagnostic traits. The test was applied only to characters that showed no correlation. Results separated two metapopulations based on five diagnostic characters and showed that the total number of analysed specimens was high enough (>15) to assume fixation of the five diagnostic characters. Therefore, a new species was proposed for the French metapopulation, *Troglodrilus jugeti* Achurra *et al.*, 2012, while *T. galarzai* was retained for the Iberian metapopulation. The recognition of two *Troglodrilus* species has direct consequences on regional conservation plans of groundwaters since both species show a narrow endemism and in addition, groundwater-limited taxa are vulnerable to environmental oscillations due to their high specialization for the subterranean medium.

Cell morphology and SSrRNA data contradict the lorica-based classification of tintinnid ciliates (Protista, Ciliophora) [Talk]

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Tintinnids are mainly marine planktonic ciliates. They form vase-shaped or tube-shaped loricae (houses), which might be hyaline or agglomerated with biogenic and abiogenic particles on the whole surface or only the posterior portion. The classification of the about 1,000 extant tintinnid species is entirely based on lorica features, although they are known to vary with environmental conditions and the cell cycle.

Recent small subunit ribosomal RNA (SSrRNA) phylogenies and cladistic analyses of mostly cytological data are congruent in the main points, *i.e.*, they (i) contradict the lorica-based classification, clearly showing that hyaline and agglomerated loricae are not separate taxonomic entities and (ii) indicate that the development of the somatic ciliary patterns appropriately reflects the evolution in tintinnids. Besides this feature complex, the ultrastructure of the lorica walls and capsules (minute harpoons) and the presence of a lorica sac (membranous sac with a foldable closing apparatus lining the lorica) seem to be valuable for the reconstruction of the phylogenetic relationships. Apparently, tintinnids originated from marine planktonic ciliates and entered twice freshwater, viz., at the beginning of their evolution and later with species characterized by the most complex somatic ciliary pattern. At the moment, some genera and families are non-monophyletic in both kinds of trees. Occasionally, apomorphies could be used for some improvement of the tintinnid classification. For instance, conspicuous differences in the ultrastructure of the lorica walls and the somatic ciliary patterns resulted in the split of a non-monophyletic genus and the establishment of a new one in a different family. Furthermore, the interpretation of the lorica sac as synapomorphy of four genera necessitated the removal of two families. A far-reaching revision, however, is currently impossible due to the restricted knowledge of the cytological features (studied in only 27 species) and the SSrRNA gene sequences (analysed in about 60 species), especially, in the type species. Supported by the Austrian Science Fund (FWF, Project P20461).

Climate-change driven shift of *Tegula atra*: Late Pleistocene Patagonian biostratigraphical-palaeoceanographical marker [Talk]

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Molluscs predominate in Late Quaternary (MIS11-1) beach ridges along Patagonia (Argentina, Southwestern Atlantic, SWA). Among gastropods, *Tegula atra* (Lesson) is particularly interesting from biostratigraphical/palaeoclimate standpoints: excellently preserved along ca. 1000km, abundant, with all dimensions/ontogenetic stages, reliable as an autochthonous macrobenthic element of the original nearshore associations, curiously absent in the SWA today but living in the Southeastern Pacific (SEP) as a typical intertidal, free-epifaunal herbivorous species along the cold Humboldt system. We aimed at defining its taxonomy and distribution (stratigraphical-geographical) and its regional palaeobiogeographical context in South America, in order to assess possible explanations for its extinction. A systematic review including field observations, own collections, museum collections, records from oceanographic expeditions along the SWA, bibliographic compilations, and morphometric analysis (Relative Warps) of fossil (SWA) and modern (SEP) shell specimens from different geographical areas confirms: no shape differences between fossil Patagonian and modern SEP specimens, its value as a Late Pleistocene biostratigraphical tool exclusive for Patagonia and for Marine Isotope Stages (MIS) 9, 7 and 5. Multivariate (CA, cluster analysis; PCO, Principal Coordinate analysis) and cladistic (Parsimony analysis of endemicity) methods applied to a large dataset of 382 gastropod records from localities between Surinam and Tierra del Fuego

(49 Pleistocene, 28 fossil Holocene, 35 modern) allowed to define areas of endemism (AE) and patterns between localities through time. All methods yielded similar between areas patterns, the PAE more objectively and clearly showed Patagonia as an AE since the Pleistocene, during MIS9-5 the dominance of *T. atra* associated with other cold taxa and northern sites linked to southern Patagonian localities suggest dominantly colder nearshore scenarios with enhanced Malvinas (Falkland) current. Its extinction during MIS1 and mid-Holocene (southern) shifts of warm taxa represent a biotic response to atmospheric-circulation changes in the SWA post-Pleistocene/Holocene transition: activated thermal/salinity fronts, intensified Brazilian current, lower wind velocities, higher drainage pattern, less nutrient availability, altering growing and floating capabilities of kelps (macroalgae) responsible for the dispersal by rafting of *T. atra* along the SWA.

Developing Bayesian and Maximum likelihood supertrees [Talk]

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Supertrees can be used to combine partially overalapping trees and generate more inclusive phylogenies. It has been proposed that Maximum Likelihood supertrees could be developed using an exponential probability distribution to model errors in the input trees (given a proposed supertree). When the tree-to-tree distances used in the ML computation are Symmetric Differences, the ML supertree has been shown to be equivalent to a Majority Rule Consensus Supertree, and hence, exactly as the latter, it has the desirable property of being a median tree (with reference to the set of input trees). The ability to estimate the likelihood of supertrees, allows implementing Bayesian MCMC approaches, which have the advantage to allow the support for the clades in a supertree to be properly estimated. We developed the first software for the estimation of Maximum Likelihood and Bayesian supertrees, and used it to reanalyse a variety of datasets the datasets for the Metazoa, the Carnivora and we also recovered the first Bayesian supertree-based phylogeny of the Eubacteria and the Archaebacteria. Here, results from these analyses will be presented and properties of these new supertree methods discussed, with refernce to other, well known supertree methods like Matrix Representation with Parsimony.

Molecular phylogeny and biogeography of the fern genus *Microgramma* C. Presl (Polypodiaceae – Polypodiopsida) [Poster]

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Microgramma C. Presl (Polypodiaceae) has about 30 species occurring in tropical America, Africa and Indian Ocean islands. Recent phylogenetic studies using molecular data show that the genus is monophyletic and closely related to *Campyloneurum* and *Niphidium*; however, these studies did not present a large and sufficient sampling, not allowing thus elucidate the relationships among species and groups within the genus. Moreover, the inclusion of some species in the genus, as *Microgramma chrysolepis*, *M. percussa* and *M. dictyophylla*, as wells as the species previously treated in the genus *Solanopteris*, is still contentious. The disjunction between Africa and South America also raises questions about the historical events and biogeographical patterns involved in its current diversity and distribution. In this context, this project goals are to, through the development of a molecular phylogeny of *Microgramma* based on chloroplast sequences and including almost all species of the genus, test its monophyly; to help clarify relationships among its subgroups and to trace a possible evolution of morphological characters and biogeographic history within the genus. Our sampling comprises 65 specimens regarding 48 species, from which 25 are *Microgramma*, 23 are *Campyloneurum* and two are *Niphidium*. Total genomic DNA was extract from field-collected or from cultivated specimens silica-dried leaf samples. Four plastid regions (cpDNA) were used: rbcL, rps4, trnL–trnF IGS region and the rps4–trnS IGS. As outgroups, species of the closely related genera *Campyloneurum* and *Niphidium* were used, as well as sequences obtained from GenBank for the following: *Adenophorus, Pleopeltis, Polypodium* and *Serpocaulon*. The raw sequences will be generated, aligned and the resultant data set will be analyzed using parsimony, maximum likelihood and Bayesian methods. As a result, we expect to clarify the phylogenetic relationships among the species of the genus *Microgramma*, giving support to further evolutionary and biogeographic studies in the genus and in Polypodiaceae. This study is part of a larger PhD project that also includes taxonomic and nomenclatural studies in the genus.

Genes, fossils, occurrences, and the printed article paradigm: Biogeography and systematics in the era of Big Data [Talk]

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The amount of biological data made publically available has exploded in the last few years. GenBank grows exponentially; doubling its size every 18 months and currently comprising c. 300,000 sequenced organisms and over 156 million sequences. There are over 340 million geo-referenced species occurrences available through GBIF, and over a million taxonomic occurrences of fossils in the Paleobiology Database. There are serious pitfalls concerning uneven quality and uneven geographic, temporal and taxonomic representation in these databases, yet all these data hold a tremendous and largely unexploited scientific potential. In this talk I will present our initiative termed SUPERSMART (Self-Updating Platform for Estimating Rates of Speciation and Migration, Ages and Relationships of Taxa), which aims at merging data from major biological databases and providing users with a flexible, open-source platform for a wide range of evolutionary and biogeographical questions and analyses. More specifically, we are 1) further developing the PhyLoTa browser in order to produce genus-level, fossil calibrated mega-chronograms for plants, animals and fungi; 2) from these trees, producing hundreds of species-level, multi-gene datasets of directly comparable crown ages; 3) applying a newly developed Bayesian meta-analysis approach to estimate rates of speciation, extinction, and migration within and among user-defined operational areas; and 4) testing for correlations between diversification, migration, and environmental niche evolution. The bioinformatics pipeline developed for this purpose is distinctly modular and can easily be modified and extended as new methods and software become available. The data handled for each step will be continuously and automatically updated, and the results will be made public online. User-defined analyses resulting in publications will be continually updated and made available, thus keeping the recognised value of scientific publications but at the same time solving the ‘printed article paradigm’ (implying that scientific results become out-dated as soon as new source data is produced by the scientific community).

Climatic niche divergence in old sister lineage splits of Caricaceae, but not young species pairs [Talk]

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We have combined a dated phylogeny for the 34 species of Caricaceae (Brassicales) with species distribution modelling based on 1979 collections from the Neotropics (6 to 280 per species), with the geo-referenced data coming from the first author’s ongoing monograph of the family. The family’s two African species, which are the sister clade to the neotropical ones, were not included. Sixteen species occur in the northern Andes, one along the coast of Chile, one from Mexico to northern South America, one in the Atlantic forest, one in Amazonia, and six are widespread in South America. Seven species, including the wild form of *Carica papaya*, occur in Central America and Mexico. Bioclim niches were modeled for 18 well-supported neotropical sister clades including 9 sister species pairs to test whether species divergences are associated with divergence in climate niches. Results show that 3 of the species pairs have divergent climate niches and date from the Miocene (6.5–15 Ma); 5 species pairs with similar climate niches date from the Pleistocene (0.5–3 Ma) and one from late Miocene (10 Ma). Four of the sister pairs with similar climate niches occur in the Andes. Thus, members of young divergences occur in the same climate conditions, while 9 of 12 older (> 6 Ma) splits involve climate niche change. Climate niche divergence thus seems to have played a limited role in the Andean Caricaceae; allopatric speciation may be more important in montane habitats.

Historical biogeography of *Artemia* (Anostraca): some intriguing aspects of diversification [Talk]

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Biodiversity is a result of historical processes of species diversification, speciation, migrations and their complementarily integration in whole biotic systems which are coupling with geological and climate changes. Most halotolerant animal *Artemia* (Anostraca) is a good model object for understanding of many difficult issues in biology, including for going to better understanding of how current biogeography can gives us a key to paleoreconstruction of history. A short description of biological peculiarities, taxonomy and biogeography of *Artemia* is given. Biogeography of *Artemia* itself can not give us insight on its history, but taking into account data on historical geology, paleoclimates, molecular genetics, cariology, ecology of *Artemia* we can image history, causes and rate of diversification of it. Distant ancestors of *Parartemia* and *Artemia*, probably lived in lagoons of Panthalassa, Tethys Sea, in lakes of the supercontinent Pangaea 300–400 Ma. Pangaea split into the Gondwana and Eurasia at about 150–220 Ma, it gave rise to the tectonic plate drift, which caused the most significant events in the evolution of protoartemies. Last common ancestor for *Parartemia* (Parartemiidae), *Artemia* (Artemiidae) and *A. persimilis* existed about 85 million years ago – the isolation of Australia in the late Mesozoic – a result of the Indo-Australian Plate drift. The lineage leading to *A. persimilis* diverged from the common ancestor of all *Artemia-Parartemia* species at the same time caused by separation of South America from Gondwana. The question arises: Is not *A. persimilis* a representative of a particular genus or family, not *Artemia* (Artemiidae?)? Considering all available data on historical geology, cytogenetics, and molecular genetics, we tend to the view that it should be isolated from the genus *Artemia*, as a new genus at least. Probably some predecessor gave rise to the formation of genus *Artemia* in lagoons of the northwestern coast of the Tethys 50–60 Ma. At the time of the Late Miocene (15 Ma) Tethys broke up into the Mediterranean Sea and Paratethys. A later diversification of *A. salina* associated with the evolution of the Mediterranean Basin, but the Asian *Artemi*a bisexual line – more with Paratethys and its subdivisions later, and had last shared a common ancestor with *A. franciscana* 32 Ma. Data argue that *A. franciscana* is really genus with several species. The possibility of strengthening the bridge between biogeography and systematics will be discussed.

Enrolling high-tech farmers in functional biodiversity assessment: A practical experience of technology development and transfer between researchers and agricultural sector players in France [Poster]

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We have developed a reliable, convenient and fast method accessible to non-specialists to monitor predominant functional guilds of arthropods (pollinators, predators, parasitoids and herbivores) in French horticultural agrosystems. The methodological framework is partly based on species classification by morpho-species according to the Rapid Biodiversity Assessment (RBA) method which allows monitoring average local species richness and related ecosystem services. Our final aim is to provide professional end-users from the agricultural sector (experimenters, chambers of agriculture advisors, observers and producers) with an innovative android tablet application that facilitates data collection and calculation of indicators for biodiversity monitoring.

Whatever the spatial scale considered, arthropods largely contribute to species richness and are thus more representative for organismal biodiversity than any other group of organisms. Their abundance and diversity can also inform on the sustainability of some key ecosystem services such as pollination, pest control and prevention of invasive species. However, their identification at the species level, usually required to estimate relevant biodiversity trends, is often unreachable to non-specialists whose professional activities depend on the quality of local ecosystem services.

The objective of our project is to meet this demand by developing and transferring a scientifically robust biodiversity evaluation method that is easily manageable by non-specialists in field conditions. At first we have built a methodological framework based on the RBA method (Obrist and Duelli, 2010) that differentiates arthropods in parataxonomic groups (morpho-species). These groups were then gathered according to their ecological roles (herbivores, predators, parasites, pollinators). Our classification scheme for morpho-species determination was integrated into an android tablet application for a rapid using in field conditions. The generated tool is currently being tested for its performance in realistic conditions of use in French horticulture centers of Region Centre. The preliminary feed-back is very positive and supportive and opens the possibility of an adaption of the tool to a wider typology of agrosystems. This innovative project brings together biologists, computer scientists, sociologists and horticultural professionals.

Winter is coming: Cenozoic climate shifts shaped diversification of Western-Mediterranean *Harpactocrates* spiders [Talk]

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Past climate shifts played a major role in shaping and generating biodiversity. Quaternary glacial cycles are among the best-known examples of dramatic climatic change in temperate regions. Although still a matter of debate, most authors agree that glaciations shaped species ranges and structured populations and, in some cases, also prompted speciation. However, studies have revealed that time divergences among some temperate lineages preceded the Quaternary glaciations, suggesting that older geological events drove their diversification. Here we investigate the effect of past climatic changes on the generation of terrestrial fauna of the Mediterranean region by examining the patterns of geographic diversity and inferring the time frame of diversification of a low-vagility, ground-dweller spider, distributed across the major mountain ranges of the western Mediterranean, the genus *Harpactocrates*. Our results suggest that *Harpactocrates* diversification followed a classic geographic isolation model closely linked to major Cenozoic climate shifts undergone by the Mediterranean region. Concatenated and species tree analysis of multiple mitochondrial and nuclear loci combined with the use of fossil and biogeographical calibration points reveal a Miocene origin of most nominal species but also identify several cryptic lineages that originated during the Pleistocene. We hypothesize that the Miocene Climatic Transition triggered major extinction events in the genus, but also promoted its subsequent diversification. Under this scenario, the Iberian mountains acted as sky-islands, providing shelter to *Harpactocrates* lineages during climate shifts and favouring isolation between mountain ranges. Quaternary glacial cycles further contributed to the diversification of the group by isolating lineages in peripheral refugia within mountain ranges. In addition, we recovered some unique biogeographic patterns, such as the colonization of the Alps and the Apennines from the Iberian Peninsula.

Evidence for cryptic species in a small-scale Alpine sample of the Holarctic harvestman *Mitopus morio* [Talk]

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Mitopus morio is a widespread harvestman occurring in most parts of Europe, and in moderate and cold-moderate climate zones of Asia and North America. The species is characterised by extreme variability in body size and leg length, and recent observations for a single Alpine location in Tyrol, Austria, indicated the absence of mating between short- and long-legged individuals of *M. morio*. We explored this putative reproductive barrier using an integrative approach that combined data from mating trials, amplified-fragment-length-polymorphism whole-genome scans, mitochondrial sequences and morphometrics. Unexpectedly, the mating trials did not stringently corroborate the initial, leg-size based hypothesis, and both types of genetic data revealed the existence of three distinct groups incongruent with leg morphology. This three-entities grouping was in line with the results from mating and with novel morphometric characters which we identified using a supervised approach. Of methodological relevance, we made the first-time discovery of nuclear-mitochondrial pseudogenes in harvestmen, underscoring the need for vigilance for and management of this potential source of distortion of inferences also when studying Opiliones. We infer from all data together the existence of cryptic species among the analysed individuals originating from two Tyrolean valleys. However, due to the unexpected amount of differentiation found within a geographical scale and elevation range very small compared to the distribution of *M. morio*, we suggest a thorough revision of the genus prior to the implementation of taxonomic consequences.

Biogeography and systematics: The genesis of the distribution of Raphidioptera in the world [Talk]

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Raphidioptera (snakeflies) – with altogether about 240 described valid species in two families (Raphidiidae: ca. 200 species, Inocelliidae: ca. 40 species) – one of the smallest insect orders, often addressed as living fossils, is presently confined to the northern hemisphere inhabiting large parts of the arboreal biome in the Palaearctic on one hand and in the Nearctic on the other hand. The southernmost records are from high altitudes in transgression zones of the Holarctic to the Oriental and to the Neotropical region respectively. In the Nearctic they are restricted to the western and southern parts of North America, and they do not occur in the north, while, in the Palaearctic they are to be found in Northern Scandinavia and northern parts in Asia. In the Mesozoic Raphidioptera occurred in large numbers of species also in tropical regions and also in the southern hemisphere. It is hypothesised that the K/T impact led almost to an extinction of the Raphidioptera and that only those lines survived which were adapted to a colder climate with a significant decrease of temperature in winter. Both families occur in the Palaearctic as well as in the Nearctic, but Nearctic and Palaearctic snakeflies are systematically entirely different and belong to different clades (genera, genus groups). Recent results of molecular studies on the phylogeny of Raphidioptera as well as substantial chorological findings are in contrast to previous hypotheses on the genesis of the distribution of snakeflies in the world so that new concepts on the biogeography of Raphidioptera have to be developed. The formerly proposed hypothesis that the Nearctic snakeflies are the descendants of early immigrations to the Americas before the formation of the Atlantic Ocean must probably be left. It seems that the colonisation of large parts of the Holarctic took place from the high north very early (perhaps soon after the K/T impact, perhaps even shortly before) with subsequent separation into Nearctic and Palaearctic clades.

Beaded lacewings – a new phylogenetic start-up (Insecta: Neuroptera: Berothidae) [Talk]

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The Berothidae are a small neuropteran family comprising about 120 known species. They are part of the dilarid clade which is constituted by Dilaridae + (Mantispidae + (Berothidae + Rhachiberothidae)). In a previously performed cladistic analysis six subfamilies have been recognized: 1) the Nyrminae, hitherto monotypic and restricted to Anatolia, 2) the Cyrenoberothinae, known from southern South America and southern Africa, 3) the Protobiellinae from New Zealand and from southeastern Australia, 4) the Trichomatinae, endemic to Australia, 5) the Nosybinae in the Afrotropical region and South America and 6) the heterogenous worldwide distributed Berothinae. Some distribution patterns are peculiar indeed. The rediscovery of the enigmatic genus *Ormiscocerus* in South America and its relationship to Nyrma from Anatolia, representing the Nyrminae, remains a biogeographic challenge. Also the Cyrenoberothinae, the Nosybinae and the *Podallea* clade within the Berothinae apparently evolved with Gondwanean background. In order to provide an update to the phylogenetic relationships within Berothidae and to gain a better understanding of the biogeographical patterns, an analysis has been started combining the published holomorphological character matrix with newly homologized genital sclerites in both sexes, and a new interpretation of the heterogeneous heads of the adults.

Pseudo-cryptic diversity in planktonic foraminifera: a rule with exceptions [Talk]

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Planktonic foraminifera are pelagic protists that secrete calcareous shells. Extracted from sediments, these shells are of great assistance for paleoceanographers to reconstruct past climate changes. Such reconstructions assume that each species has its own ecological preferences and can be identified based on shell morphology. Therefore, the use of these organisms in paleoceanography requires a high degree of taxonomic consistency. Molecular analyses have shown that the classical, morphological definition of species in planktonic foraminifera hides higher levels of genetic and ecological differentiation. Analyses of rDNA allowed the systematic recognition of distinct eco-genotypes among morphospecies, which can be distinguished on the basis of subtle differences in shell morphology. Such apparently generalized "rule" has important repercussions: the pseudo-cryptic species of planktonic foraminifera can be recognized back into the fossil record and it is possible to transfer the biological information acquired through genetic analysis to paleoceanography. Here, based on single-specimen morpho-genetic analyses of living material collected from the plankton, we show two examples where this apparent "rule" of pseudo-cryptic diversity is violated. First, we report on the first case in planktonic foraminifera where biodiversity has been over-estimated. The morphologically diverse plexus of *Globigerinoides sacculifer* s.l. exhibits a worldwide lack of SSU and ITS rDNA differentiation. This was unexpected considering both its partly disjunct range in the tropical oceans and its old age (20 Ma). Second, in the subpolar *Neogloboquadrina pachyderma*, we report on the first case of "true" cryptic diversity in planktonic foraminifera. Specimens collected from an environmentally well-extended transect in the Austral Ocean exhibit a high differentiation within the SSU. Searching for a connection with morphology, we find that the morphological variability in *N. pachyderma* is purely ecophenotypic. Both these examples show that in planktonic foraminifera, the assumption of congruence between morphological and biological species can be violated in different ways. In these organisms, not only the morphological taxonomy does not reflect genetic differentiation, but also the scaling between the two may be inconsistent. Such inconsistent scaling complicates the interpretation of diversity patterns in the foraminiferal fossil record and subsequent use in paleoceanography.

Geographic and taxonomic disparities in species diversity: dispersal and diversification rates across Wallace's Line [Talk]

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Broad-scale patterns of species diversity have received much attention in the literature, yet the mechanisms behind their formation may not explain species-richness disparities across small spatial scales. Few taxa display high species diversity on either side of Wallace's Line and our understanding of the processes causing this bimodal pattern remains limited, particularly in plant lineages. To understand the evolution of this biogeographical pattern, a time-calibrated molecular phylogeny of Livistoninae palms (Arecaceae) was used to infer the colonization history of the Sahul tectonic plate region and to test for disparities in diversification rates across taxa and across each side of Wallace's Line. Our analyses allowed us to examine how timing, migration history, and shifts in diversification rates have contributed to shape the bimodal pattern observed in Livistoninae. We inferred that each of the three genera found in Sahul crossed Wallace's Line only once and relatively recently at about 8.5 Ma. In addition, at least two of the three dispersing genera underwent an elevation in their diversification rate leading to high species richness on each side of Wallacea. The correspondence of our results with Southeast Asian geologic and climatic history show how palms emerge as excellent models for understanding the historical formation of fine-scale biogeographic patterns in a phylogenetic framework.

DNA methylation pattern analysis in the symbiosis between *Apis mellifera* and its parasitic mite *Varroa destructor* [Poster]

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DNA methylation is a key epigenetic modification which consist in the addition of a methyl group on a cytosine in a CG dinucleotide. The mechanism of DNA methylation is shared among all organisms and provides a source for the switching off of gene activities, the maintenance of stable phenotypes and the integration of environmental and genomic signals. In honey bees DNA methylation is found exclusively in transcribed regions and predominantly in exons with low G+C content and few CpGs overall. Moreover in honey bees the major functional role of DNA methylation is the regulation of splice variants diversity rather than silencing gene transcription. The honeybee (*Apis mellifera*, Insecta: Hymenoptera) has become an important model for genetic study, specially as its genome has been sequenced. It also an important economic insect as it is the world's principal crop pollinator and honey producer. These activities have bee threaten by the spread of the mite *Varroa destructor* (Acari: Parasitiformes). *Varroa* mites are ectoparasites of honey bees, parasitising both immature and adult bees and reproducing in cells in the honeycomb that contains brood. *Varroa* mites impair the honey bee immune system and in some cases boost the amplification of bee viruses. In this study we are exploring the hypothesis that *Varroa* mite infestation might modify DNA methylation pattern of honey bee pupae infested. DNA methylation pattern are studied using sodium bisufite treatment that convert methylated cytosine into uracil whereas unmethylated cytosines remains as cytosine in the sequence. Allowing a discrimination between methylated and non methylated nucleotides, sodium bisulfite treatment provides a reliable and detailed picture of the methylation state of DNA.

First demonstration of interspecific hybridisation in *Myrmica* ants by geometric morphometrics (Hymenoptera: Formicidae) [Poster]

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A case of hybridisation between *Myrmica scabrinodis* Nylander, 1846 and *M. vandeli* Bondroit, 1919 is demonstrated by means of geometric morphometrics in a nest sample found in Baden-Württemberg/Germany. 41 Landmarks and 252 semilandmarks were fixed in four anatomical aspects in 299 worker ants – dorsal head, frontodorsal clypeus, dorsal mesosoma and lateral petiole. 316 relative warps (RWs) were extracted from the shape variables. Shape differences between these very similar species are well-exposed by mean deformation grids exaggerated by the factor of 3. Among a number of differences already known, geometric morphometrics revealed also differences not discovered so far by conventional morphometrics or subjective character assessment. A full separation of the parental species was already given by the first two RWs of the head and clypeus aspect but this approach was not sufficient to reliably demonstrate hybrid identities on individual level. A stepwise linear discriminant analysis (LDA) using the RWs as characters and reducing character number from 316 to 25, offered a very powerful separation of the 291 workers of the parental species (F=6735.1, ANOVA) and placed the eight workers of the hybrid sample in a coherent cluster exactly in the empty space between the parental species. Basically similar results were achieved with conventional linear morphometrics (CLM) considering 16 characters but this system was less powerful (F=3108.0, ANOVA) and placed two specimens of parental species close to the hybrids. There was no directional asymmetry detectable in the whole material and the hybrid sample did not show increased fluctuating asymmetry. With the current methodology applied, data acquisition time was 45 minutes per specimen in CLM but as much as 165 minutes in geometric morphometrics. The main problems of the latter method are the slowness of the automatic z-stack imaging methods and the absent software for automatic or semiautomatic landmark recognition. A considerable reduction of total data acquisition time to 62 minutes per specimen is predicted if a grid-and-sector system assisting landmark fixation is automatically projected on the screen and if already available software packages for symmetrizing will be used. The overall hybridisation frequency for the region of Baden-Württemberg is estimated as 0.44 % from the side of *M. vandeli* and 0.03 % from the side of *M. scabrinodis*. Despite apparently strong reproductive barriers between *M. scabrinodis*

Big thistle eats the little thistle: introgressive hybridization and demographic swamping in *Onopordum hinojense* [Talk]

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Hybridization is known to have a creative role in plant evolution and may lead to speciation events. However hybridization and introgression can also have negative effects on the parental species and can even result in their extinction due to genetic and demographic swamping; such harmful effects may be particularly evident in the case of rare species. *Onopordum* L. (Asteraceae) is a large genus with several weedy species, which frequently hybridize with congeners around the world. In the SW Iberian Peninsula, the rare *O. hinojense* Talavera *et al.* co-occurs with the invasive and widely distributed *O. nervosum* Boiss., and hybrids between these two taxa have been described as *O.* × *onubense* González-Sierra *et al.* To determine the extinction risk in the hybrid zone, both for hybrids and the parentals, we used analyses of morphological and cytogenetic traits as well as genetic markers and demographic models. In addition, we used AFLP markers, Bayesian analyses and a novel genome scan method to investigate the introgression process. Morphological characters, genome size and molecular markers confirmed homoploid hybridization. However, the hybrid population showed an abundance of F1 individuals (recognized as the hybrid species *O.* × *onubense*) and BxNERV (*i.e.* F1 × *O. nervosum* backcrosses) but, remarkably, F2 hybrids and subsequent generations were absent as well as BxHINJ plants (*i.e.* F1 × *O. hinojense* backcrosses). These results indicated unidirectional introgression through *O. nervosum*, the parental with the highest flower and fruit-set. In addition, the introgression pattern was mostly neutral although some loci significantly deviated from neutrality in spite of the conservativeness of our novel genome-scan method. Finally, our demographic models suggested, in most of the simulations, a high extinction risk (in less than four generations) for *O. hinojense* after contacting with *O. nervosum* because of introgressive hybridization towards the latter (which showed the highest fitness too). If conservation actions are not taken, all individuals in the hybrid zone will become eventually an almost pure *O. nervosum* population after not many successive generations of backcrosses.

Lineage diversification and speciation across the Australasian Archipelago – from tropical shores to sky islands [Talk]

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The Australasian Archipelago and neighbouring areas feature some of the world's most diverse biota across geologically highly complex island and terrane systems. This setting has intrigued naturalists ever since Wallace, and many important concepts in evolutionary biology and ecology were born here – such as for example the whole discipline of biogeography. We pair molecular phylogenetic work with some of the most extensive field collecting campaigns to date and focus on hyperdiverse arthropods which researchers

usually avoid due to their hardly manageable species diversity. We report discovery, and peu a peu formal description, of hundrets of new species. Here, we present recent results on weevils (beetles with "long noses") which defy biogeographical lines and colonize islands *e.g.* in the Sunda Arc in mysterious ways. We show complex peripheral speciation patterns of diving beetles in Melanesian sky islands, turning New Guinea into a diversity pump for tropico alpine taxa; we describe speciation patterns of diving beetles in SE Australian mountain ranges and link their diversification to global climate change and then provide recent insights into Oceanian biogeography.

Anatomy of slime glands and biochemical composition of glue secretion among velvet worms (Onychophora) [Poster]

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Velvet worms use a unique hunting and defence strategy, which involves the ejection of an adhesive, glue-like slime secretion produced by a pair of specialised glands. So far, comparative studies on the structure of these glands and their slime secretion are missing among different onychophoran species. We therefore analysed the anatomy of slime glands and the protein composition of slime secretion in representatives of the two major onychophoran subgroups, Peripatidae and Peripatopsidae, from different parts of the world. Our data show that the musculature of the reservoir is conserved among onychophorans, whereas the composition of the secretory duct displays taxon-specific variation. Major differences concern the arrangement of glandular endpieces, which are distributed along the duct in Peripatopsidae but condensed in numerous repeated rosettes in Peripatidae. In addition, there are differences in the attachment pattern of slime glands within the body. A structure with a putative valve-like function occurs at the transition of the secretory duct and the reservoir in Peripatopsidae but is absent in Peripatidae. Our findings suggest that the arrangement of musculature in the reservoir of the slime gland has remained unchanged since the divergence of Peripatidae and Peripatopsidae, while the composition of the secretory duct has been altered in one of these groups. However, the direction of evolutionary changes in duct composition cannot be determined unambiguously due to current uncertainty regarding the phylogenetic relationships of the onychophoran subgroups. Our ongoing studies using protein separation techniques revealed that despite remarkable intraspecific conservation of the onychophoran slime secretion there are remarkable differences in protein composition even between closely related sympatric species. We therefore suggest that an analysis of slime composition in additional species would help develop a method of non-invasive species identification for Onychophora.

Developments in botanical nomenclature [Talk]

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The primary goal of the International Code of Nomenclature for algae, fungi and plants is (ICNafp) to provide for stability and consistency in the interpretation of the names of organisms that fall under its aegis. Changes, both those that have been made and those under consideration, are designed to enable the ICNafp to achieve this goal more effectively even as new technologies lead to changes in understanding and changes in methods of disseminating information. Changes to the ICN can only be made once every six years, because they have to be approved at an International Botanical Congress. There were many changes made at the 2011 botanical congress. Some hit the headlines (*e.g.*, dropping of Latin as a requirement, permitting electronic only publication; mandatory registration for fungal names); most did not. The six year interval between Congresses provides lots of opportunity for discussion prior to the final vote. The2011 International Botanical Congress established five special committees, each of which was charged with considering whether changes should be made in particular aspects of botanical nomenclature for consideration including one to identify how the ICN could be modified to make registration of new names and combinations mandatory for algae and plants (including their fossils), as has been done for fungi. Some of the other committees are charged with looking at possible changes in the procedures governing the processes botanists use to make nomenclatural decisions.

The radiation of six legs: How it all began – A phylogenomic approach within the 1 kite project [Talk]

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Going ashore more than 400 million years ago, the hexapods started the most impressive success story in the evolution of animals in terms of species richness, diversification and adaptive radiation. While insects generally display a high morphological diversity, differences become puzzling when comparing entognathous groups with ectognathous lineages. The resulting disparity is even more perplexing when adding crustacean subgroups, discussed as the potential sister group of Hexapoda, to the comparison. Allowing for no clear polarization of phylogenetic characters, these factors impede the reconstruction of the early splits and consequently of the early evolution of hexapods. Five primarily wingless groups are traditionally subsumed in an assemblage denominated “apterygotes” or “basal hexapods”: Collembola, Protura, Diplura, Archaeognatha, and Zygentoma. The advent of phylogenomics, is characterized by an underrepresentation of basal hexapods. Embedded into the recently started 1KITE project which aims to sequence and analyze 1000 insect transcriptoms, working groups of 3 universities (Austria, Germany, and Japan) focus on the relationships and evolution of primarily wingless insects. With about 100 taxa final aim of this project is to analyze the largest taxon sampling concerning the basal hexapod lineages. Phylogenetic questions to be tested encompass: (i) monophyly of Hexapoda and Entognatha, (ii) sister group relationships among the entognathous groups (Collembola, Protura, Diplura) (iii) the sister group of the Hexapoda, and (iv) the phylogenetic position of the living fossil Tricholepidion gertschi. We will analyze not only molecular data sets but also investigate the reliability of these results with new data from developmental, embryological and morphological studies. First results will be presented along with focus, aims and workflow.

Conditioned branching processes and species' evolution [Talk]

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Conditioned branching processes have recently received a lot of attention in the biomathematical literature. They are useful for modelling and developing software in the field of phylogenetic tree inference. However on top of this they can also be combined with continuous stochastic processes to describe the evolution of character traits without the need to use a fixed phylogeny. This makes them an appealing tool for the field of phylogenetic comparative methods where often there can be great uncertainty attached to the underlying evolutionary relationships. By using them we can predict how much we expect species to diverge (in the trait of interest) and include uncertainty due to phylogeny in our conclusions. Morphological characteristics are an important factor in the field of systematics, for example for the delimitation of species, and therefore the framework of phylogenetic comparative models on top of branching processes offers an attractive application of stochastics in biology. We will also show how one can analytically, which is important for software development, connect models for hybridization events with branching process tree models

Using molecular and complementary techniques to detect and characterise elusive protist lineages [Talk]

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Continuing the trend started by environmental clone library analyses over the past decade, next generation sequencing investigations of eukaryotic microbial diversity are currently revealing very high levels of diversity within established protist groups and are also detecting highly novel lineages that can be difficult to place phylogenetically. Making sense of these data presents a range of challenges and opportunities for integrating other molecular techniques such as fluorescence in situ hybridisation microscopy, metagenomics and transcriptomics. However, the value of specimen/culture-based methods should not be overlooked, as these provide access to studies of living organisms and their ecological interactions. This talk presents in-progress reports of work on several enigmatic protist groups, both parasitic (phytomyxids, haplosporidia), and free-living (network-forming amoebae, vampyrellids, other rhizarian groups).

A role for epigenetic inheritance in plant ecology and evolution? [Talk]

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Our laboratory is interested in unravelling the molecular and genetic bases of plant reproduction, studying processes that span the range from the cellular, over the organismic, to the ecosystems level. While we mostly focus on Arabidopsis thaliana as our model system, the use of other study organisms has proven instrumental to address specific questions. The work I will present is based on observations on Mimulus spp. populations that show an unexpected behaviour, implicating a role of epigenetics in reproductive isolation and, thus, possibly speciation. Until recently, epigenetic variation was not thought to play a significant role in evolution and most text books on Evolutionary Biology lack any reference to epigenetic processes. Indeed, many biologists have difficulties to see how epigenetic variation could contribute to evolutionary change, as exemplified by the statement: "… it is hard to see its [epigenetic's] possible evolutionary significance, …" (1). Nevertheless, over the last years epigenetic research has taken centre stage and several scientists have argued that a possible role of epigenetic variation in evolution should be considered (2–4). I will present a model system that may allow us to analyze epigenetic changes and their possible role in evolution at the genetic and molecular level. We will provide evidence that different taxa of Mimulus spp. with distinct pollinator syndromes are in fact epigenetic variants. An insect-pollinated plant with yellow flowers can change, over the course of several years, into a plant producing bird-pollinated, red flowers. Since the acquired epigenetic state affects the morphology, colour, and scent of the flower and leads to reproductive isolation, it is expected to have a strong effect on population structure and eventually the evolutionary trajectory of this taxon, if we consider a change in epiallele frequency to contribute to evolutionary change.

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Combining landmarks with multivariate ratio analysis: extracting new character ratios for separating cryptic species [Talk]

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Morphometrics plays an important role in the differentiation of cryptic species, as they usually can be recognized only by gaps in quantitative characters. Two morphometric approaches are commonly used in this respect, that is, multivariate morphometrics of distance measurements and geometric morphometrics of landmark data. The latter came as the revolution in morphometrics during the past two decades and is generally considered superior, also for taxonomic purposes. For instance, it is claimed to uncover subtle differences not detectable by traditional methods and to offer unparalleled graphical output. While this last issue is undeniable, I will demonstrate that both, distance as well as landmark data, have actually comparable statistical power and that it depends mainly on the nature of the study which one is preferred. In order to be fully comparable, multivariate morphometrics should be done by applying the recently developed technique of Multivariate Ratio Analysis (MVR). With MVR, however, it is possible to extract from a set of distance variables the most significant shape differences in terms of character ratios, that can then be directly used for keys, diagnoses, and descriptions, the core elements of a taxonomic study. In contrast, the most commonly used landmark method, that is, generalized least squares Procrustes superimposition, does neither offer this possibility nor does it allow to distill the essence of geometric shape differences. It furthermore can be applied only to single, rigid structures, such as a skull or the body of a fish. Hence, it is not possible to investigate simultaneously an arthropod body including its articulated extremities. For MVR, this posses no difficulties, as this method can embrace distances of any body part. As an example, distances calculated from landmark configurations of fore and hind wing may be combined with measurements obtained from the head, thorax, abdomen, and legs. The shape of specimen can thus be analyzed as an abstract whole, which demonstrably enhances the power of the analysis. The results of MVR can finally be combined in a fruitful manner with the graphical output from Procrustes superimposition. Hence, the two approaches may be used in combination rather than exclusively.

Speciation-related events in plant genome: repetitive DNA and chromosomal rearrangements [Talk]

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Considerable restructuring of highly repetitive DNA fraction is one of the important components of speciation process. The major fractions of repetitive DNA are transposable elements (TEs), rDNA, and tandem repeats. Long-term monitoring of wild diploid *Aegilops* and allopolyploid wheat *Triticum dicoccoides* (Triticeae, Poaceae) species genomes reveal considerable quantitative and qualitative differences between central-marginal populations of the entire species area. Combination of 454-sequencing, molecular fingerprinting, and molecular-cytogenetics methods were used to achieve the comprehensive goals. It was found that in small peripheral populations, which are first to suffer the impact of global warming, several important processes occur, namely: enchased mobility of rDNA clusters, depletion of species-specific tandem repeats, and numerous chromosomal rearrangements. But the most significant changes attributed to TEs fraction which is the main internal factor for genome variability. Tracing TEs dynamics in time revealed bursts of various TEs families in several genotypes of small peripheral populations. With their capacity to drive non-adaptive host evolution, mobilized TEs can restructure the genome and displace populations from adaptive peaks, thus providing an escape from stasis and generating genetic innovations required for rapid diversification. Thus, in marginal populations under the influence of unusual ecology, intensive processes of genome rebuilding are taking place and some models assume marginal populations to play an important role in the maintenance and generation of biological diversity.

Morphological and molecular phylogeny of the subfamilies of Ichneumonidae (Hymenoptera) [Talk]

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The parasitoid wasp family Ichneumonidae is the most speciose family of parasitic organisms on earth. The relationships of the 40 subfamilies of Ichneumonidae were investigated using a combined morphological and molecular phylogenetic analysis. Most subfamilies were recovered as monophyletic, but a few

were not. A discussion is made of the subfamily groupings within the family (Ophioniformes, Pimpliformes and Ichneumoniformes) and the ground state plan for the family in terms of ecto- versus endoparasitism and idio- versus koinobiosis is considered.

Nomenclator Ciliophorum and Monograph of the Hypotricha, two works documenting the biodiversity of ciliates (Ciliophora) [Poster]

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Recent estimates about numbers of ciliate species range from 3,000 (free-living only) over at least 8,000 (including 200 fossil forms and 3,000 symbiotic species) to about 40,000 (free-living only). The wide range demonstrates that we are far away from knowing the "true" number of ciliate species. Unfortunately, we do not even know the exact number of species described so far and, more important, we do not have serious estimates about the number of valid species due to lack of detailed revisions in many groups of ciliates. To overcome the first problem, the Nomenclator Ciliophorum is prepared. This catalogue will contain all ciliate names ever published: (i) basionyms of species; (ii) infrasubspecific taxa; (iii) combinations; (iv) genera; and (v) suprageneric taxa. Furthermore, important taxonomic papers are listed for each taxon, so that the nomenclator will be useful not only for taxonomists, but also for ecologists and molecular biologists who will benefit from such an index, for example, in that they can find the updated name (combination) of a certain organism easily. To estimate the valid number of species it is necessary to revise a group in detail. The Monograph of the Hypotricha (Springer) deals with a major group of ciliates, the hypotrichs, which are a core-group of the spirotrichs. Hypotrichs are widely distributed in limnetic and marine habitats, but also in soil. About 1,000 nominal species have been described and it is estimated that 700 to 800 of them are valid. Four volumes are available (Oxytrichidae; Urostyloidea; Amphisiellidae and Trachelostylidae; Gonostomatidae and Kahliellidae) and volume 5 (Uroleptidae) will be published in 2013. The final volume is in preparation and deals, inter alia, with the "spiralled" genera, for example, *Hypotrichidium, Strongylidium, Spiretella, Chaetospira.* A key to all taxa revised in volumes 1–6 will be a major part of volume 6. When the monograph is complete, the hypotrichs will be the sole very large group of ciliates which is revised in detail. For further details, see www.protozoology.com/monograph. The Monograph (vol. 6) and the Hypotricha part of the Nomenclator are supported by the Austrian Science Fund (FWF), project P23415-B17.

Bayesian species delimitation reveals specialist parasitic wasps in coevolution with chrysomelid beetles [Talk]

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To understand the ecological and evolutionary consequences of species interactions in food webs necessitates that interactions are properly identified. Genetic analyses have shown that many supposedly generalist parasitoid species have a much more narrow diet, reducing the probability that such species may mediate indirect interactions such as apparent competition among hosts. A recent set of studies showed that the parasitoid *Asecodes lucens* (Chalcidoidea: Eulophidae) mediate apparent competition between two hosts, *Galerucella tenella* and *G. calmariensis*, affecting both interaction strengths and evolutionary feedbacks. The same parasitoid was also recorded from other species in the genus *Galerucella*, suggesting that similar indirect effects may also occur for other species pairs. To explore the possibility of such interactions, we used mitochondrial and nuclear genetic markers to resolve the phylogeny of both host and parasitoid and to test the number of parasitoid species involved. The analysis of the *Galerucella* data verified the five species previously documented as reciprocally monophyletic, but the bayesian species delimitation for A. lucens suggested 3–4 cryptic taxa with a more specialised host use than previously suggested. The gene data analyzed under the multispecies coalescent model allowed us to reconstruct the species tree phylogeny for both host and parasitoid and we found a fully congruent coevolutionary pattern suggesting that parasitoid speciation followed upon host speciation.

Intraorganismal phenotypic variability and polymorphism: bryozoans as potential model organisms for evolutionary studies [Talk]

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In comparison with solitary organisms, the modular nature of clonal organisms enables, from a single genome, the evolution of two or more morphologically and functionally differentiated “individuals” (polymorphic zooids) within a colony. Natural selection as well as changes in the genome/proteome thus act upon and affect at least three distinct yet interdependent entities: the normal feeding zooid (structural equivalent of a solitary organism), the polymorphic zooid(s), and the entire colony. Moreover, varying degrees of intrinsic (genetic) and extrinsic (in response to changing environmental conditions) phenotypic variability are expressed in all these entities. Species in the phylum Bryozoa (Ectoprocta) are exclusively colonial. With feeding zooids rarely exceeding 1 mm in size, and with colonies consisting of a few to several thousand zooids, they show an enormous range of polymorphism with functionally specialised zooids and highly integrated colonies. Their small colony size, easy rearing in seawater tanks, continuous budding of new zooid generations, and easy propagation of clones render bryozoans an ideal marine laboratory rat. Another prime advantage of bryozoans is their excellent fossil record, preserving morphological change in all skeletal features, which allows testing the origin of traits and their evolution through time. In this talk the peculiarities of the phylum Bryozoa are presented and the potential of bryozoans as model organism for a wide range of evolutionary studies is highlighted.

Phylogenetic network for a high ploidy series in *Fumaria* (Papaveraceae s.l.) [Talk]

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The genus *Fumaria* (Papaveraceae s.l.) accommodates 50 species within a distribution concentrated in the Mediterranean basin. The group forms a complete polyploidy series with ploidal level covering the entire 2x-14x range and is thus ideal to study polyploid speciation. Our aim was to reconstruct the reticulated evolution within the genus based on sequences of the low-copy nuclear gene NRPB2 combined with four chloroplast markers. Combining sub-cloning technique with direct sequencing relying on clade specific primers, we managed to recover nearly all homoeologs corresponding to known ploidy in 35 species. Phylogenetic reconstructions showed evidence of a missing homoeolog in one specific clade, which gene loss thus represents an apomorphic trait defining this clade. Incongruence between nuclear and chloroplast trees was investigated using a hierarchical parametric bootstrapping strategy which allows to disentangle discordances due to phylogenetic stochasticity, incomplete lineage sorting and introgressive hybridization. After accounting for the factor causing gene tree discordance, the two marker types were combined to infer a multi-labels species tree that was subsequently folded to produce a species network. Using all technical and analytical tools in our armory, we have demonstrated that speciation through allopolyploidization is phylogenetically tractable even in the most difficult cases of a high polyploid series.

Annelids – introduction into a neglected taxon of venomous animals [Talk]

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Venom systems evolved in a broad phylogenetic range of animals and are used for defence or predation. Typically, the venom is produced in exocrine glands which are coupled to a delivery system. Venoms consist of mixtures of bioactive molecules and active components are usually described as toxins. More than 100,000 venomous animals are known and these include the well-studied snakes, scorpions, and spiders, as well as various other invertebrate taxa like molluscs, echinoderms, insects, and cnidarians. Even though venoms evolved independently in these taxa, it is obvious that throughout evolution, many protein families have been recruited convergently into the venoms. However, venomous annelids remain largely unstudied. Annelids comprise a group of highly diverse taxa with over 15,000 described species and are one of the dominant benthic macrofauna from the intertidal down to the deep sea. Here we give a broad overview of this group with a focus on potential venomous taxa. Descriptions of venomous species are reported from members of Aphroditiformia and Glyceridae, including putatively more than 1000 annelid species. More specifically, we provide Illumina based data, derived from glands of the venomous annelids taxon Glyceridae. Glyceridae are well known to be equipped with a teeth-bearing pharynx, which is connected to a venom gland. Searching for putative secretory proteins which have been also recruited into venoms of other animals, our study identified a range of potential venom proteins for Glyceridae, including CRISP-proteins, lectins, peptidases, phospholipases, and a range of protease inhibitors. Besides this, we provide a view on a toxin uniquely known from Glyceridae, the α-glycerotoxin. This toxin acts selectively on N-type calcium channels and is able to stimulate an increase in miniature potentials which is fully reversible.

Immunocytochemical investigations of anterior muscle regeneration in *Eurythoe complanata* (Amphinomidae, Annelida) [Poster]

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One of the most fascinating characteristics of annelids is their ability to regenerate lost body parts in cause of injury. Although this feature is common within most annelid taxa, there is a lack of investigations dealing with the re-development of organ systems, especially the musculature. In order to gain more data regarding patterns of muscular re-development in annelids, we analyzed different stages of anterior regeneration in *Eurythoe complanata* (Amphinomidae, Annelida) by using immunocytochemical staining techniques combined with subsequent confocal laser scanning microscopy (cLSM). With focus on different stages of anterior regeneration in adult specimens, we used a muscular marker (rhodamine phalloidin) to reconstruct the process of tissue and body formation after decapitation. Our investigations help to understand basic patterns of reorganization within annelid organ systems and provide fundamental knowledge for further investigations. Here we present a summary of our findings and draw conclusions regarding regenerative patterns of Annelida.

Herbivory-mediated fitness along an elevational gradient of three *Senecio* species (Compositae) and their hybrids [Talk]

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The three C European species (*S. hercynicus, S. ovatus*, and *S. germanicus*) exhibit a distinct distribution pattern showing vertical vicariance, with preferences of lower elevations and more continental climatic conditions by *S. germanicus*, intermediate ones with more oceanic conditions by *S. ovatus*, and high elevations with a high montane or subalpine climate by *S. hercynicus* and hybridisation occurring in overlap zones between the first and second two species pairs. We here report on the results of (a) transplantation experiments with representatives of the three species and their reciprocal F1 hybrids along an elevational/climatological transect in order to infer if herbivory-mediated fitness proxies (*i.e.*, consumed leaf area, CLA) explain the vertical vicariance and of (b) food choice (cafeteria) experiments in order to

search for dependencies between the phytochemical constitution of plants (pyrrolizidine alkaloids, PA) and their palatability to herbivores. To address the first question, we transplanted *S. hercynicus, S. ovatus, S. germanicus*, and F1-hybrids of *S. ovatus* and *S. germanicus* at four elevations (300–1200 m a.s.l.) in the Bavarian Forest National Park. The statistical analysis shows significant dependencies of CLA on elevation, time, the elevation-time interaction, and the taxon-elevation-time interaction. The higher palatability of the montane species *S. hercynicus* may explain the genetic assimilation the species is suffering from caused by fitness disadvantages compared to *S. ovatus*, which was once distributed at lower elevations but now introgresses into higher elevations. In food choice experiments with the slug *Arion fuscus, S. hercynicus* and *S. germanicus* were significantly favoured over *S. ovatus* despite the fact that *S. hercynicus* showed the highest PA content, indicating that PA content has no relevance for the palatability of the *Senecio* taxa to this slug species. Testing parental species against their reciprocally formed hybrid genotypes, in both species combinations (*i.e.*, *S. hercynicus/S. ovatus; S. germanicus/S. ovatus*) we observed tendencies towards a higher palatability of hybrids compared to the parental genotypes. These hybrid disadvantages, however, may be not severe enough in the wild (as indicated in the transect analyses) to put a reinforcement process into operation that could inhibit the hybridogenic fusion of species and the eventual loss of taxonomic diversity.

Population genomic analyses along elevational transects through a hybrid zone of two *Senecio* species (Compositae) [Poster]

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Senecio hercynicus and *S. ovatus* are two central European representatives of the *S. nemorensis* group showing vertical vicariance, with *S. hercynicus* growing in montane to subalpine regions and *S. ovatus* growing in colline to montane environments. Although the species show differences in their flowering time, natural hybridisation is a common phenomenon and leads to introgressive hybrid swarms. We have used a population genomic approach to (a) infer the intensity of hybridisation in a hybrid zone along elevational transects in the Bavarian Forest National Park and (b) to determine whether there are hints for the acting of a reinforcement process that may lead to the completion of the speciation process through the selection against maladaptive hybrid genotypes. Using AFLP fingerprinting, 689 individuals from 38 populations of the two species along four elevational transects (ca. 650–1350 m) in the Bavarian Forest National Park were genotyped for 618 anonymous loci. Based on Bayesian cluster algorithms implemented in Structure (Falush *et al.* 2007) and NewHybrids (Anderson, Thompson 2002), all populations were identified as being hybrid swarms with different admixture proportions of both parental genotypes, indicating the intense introgressive hybridisation realised in this hybrid zone. To check for a reinforcement process in action, we searched for loci under selection by using either FST-based (BayeScan v2.1, Foll M. 2012) or logistic regression model-based techniques (MatSAM v1, Joost *et al.* 2007). As results, we identified four AFLP markers under selection, which showed a significant correlation with some environmental variables along the transects. Furthermore, two of these loci under selection turned out to be species-specific. The low number of species-specific markers under selection compared to the high number of neutrally evolving ones makes it quite questionable that a reinforcement mechanism is acting, which is strong enough for an enforcement of prezygotic barriers (*e.g.*, flowering-time differences) that would allow the two species to escape their eventual merging.

OpenUp! – Discovering quality data and images of Europe’s natural history heritage [Talk]

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European Natural History collections manage and give access to over 1.5 billion objects from the world´s biodiversity heritage, covering most species described worldwide. These are reference objects for common and famous species in the world. These collections of Europe´s scientific heritage are distributed in institutions across Europe. The OpenUp! project is bringing them together, providing a single point of access for digitized multimedia objects, and a support for checked quality metadata. For this purpose, OpenUp! is taking advantage of the existing infrastructures in the Global Biodiversity Information Facility (GBIF). OpenUp! provides a central aggregation facility, translating local database schemas into the ABCD (Access to Biological Data) standard and adding enrichment measures to metadata before channelling them into Europeana, the cross-domain portal to Europe´s cultural and scientific heritage.

Up to now (end of October 2012), OpenUp! displays nearly 775.000 objects via Europeana. The content mobilized by OpenUp! consists of botanical and zoological specimen, as well as paleontological and mineralogical objects, artworks, sound and text files, videos *etc.* What OpenUp! addresses besides providing a broad spectrum of multimedia objects are data quality and enrichment measures to achieve a high level of completeness and correctness of metadata associated with the multimedia objects. A dedicated Collections Data Quality Toolkit is developed which integrates a number of quality services *e.g.* scientific name catalogues for botany and zoology. It also validates information on taxonomy, geography, language and type of multimedia. The enhancement of scientific names by multilingual common names is yet another feature of OpenUp!'s working programme.

OpenUp! introduces a new system for data quality control and semantic enrichment of scientific biological multimedia data [Poster]

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Multimedia data held by European natural history museums and botanical gardens cover most of the world's described organisms, ranging from common and famous species to those that have already gone extinct. A lot of this data, however, is presently not readily accessible even within the natural history community itself. The EU-project OpenUp! (www.open-up.eu) is an effort to mobilize scientific biological multimedia resources and open them to a wider audience via the European digital library Europeana (www.europeana.eu). Content served includes specimen images, animal sound files, and movies – all with a reference to an observation or collection event.

The main objective of OpenUp! is to implement a sustainable pipeline from natural history collections to Europeana (and potentially to other portals using the Europeana standards). This connection between natural history and Europeana is accomplished using well established BioCASe and GBIF technologies and it is complemented with a system for (1) data quality control, (2) data transformation, and (3) semantic enrichment. (1) With the OpenUp! Collections Data Quality Toolkit, data providers are now able to critically assess the completeness, correctness, and compliance of their data and to correct and enrich them according to their needs. (2) The OpenUp! Harvesting and Transformation Component realizes the harvesting of ABCD metadata and transforming of this metadata into the Europeana standards ESE and EDM. (3) The OpenUp! Metadata Enrichment Services are collecting a substantial amount of multilingual reference information (scientific names, common names, person names, and geographical names) that will greatly improve the scope of semantic linking of natural history content with other domains in Europeana.

With this approach, OpenUp! will provide at least 1.1 million multimedia objects from the natural history domain to Europeana by 2014. Its lean infrastructure is sustainable within the natural history community and will remain functional and effective in the post-project phase.

Brain evolution in cephalopods: a matter of ganglionic differential maturation? [Talk]

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Studying the nervous system development in cephalopods is not just a developmental but also an evolutionary issue. First, cephalopod species are famous for their brain, the most developed and centralized central nervous system among invertebrates, but the proximate causes of such a peculiarity among molluscs are still unknown. Second, the fact that cephalopod species have a direct development whereas most mollusc species show larval stages and metamorphosis raises the question of nervous developmental homology between cephalopods and other molluscs. The lobes of the adult cephalopod brain are issued from a few ganglia, typical of molluscs, but contrary to most of them these ganglia never become part of a larval functional nervous system. Proneural cells early and simultaneously emerge from ectodermic placodes and form clusters that are called “ganglia”, but actually, nothing is known about when these “ganglia” add differentiated neurons and when they become functional. We intended to evaluate the chronology of neuron differentiation during the embryogenesis of the cuttlefish Sepia officinalis. We searched for members of the elav/hu family in the cuttlefish genome, since they are known to be among the first genetic markers of post-mitotic neural cells in metazoans. Two paralogs have been identified and one of them, Sof-elav1, is expressed in all ganglia and all nervous cells at one time of embryogenesis, which provides the first genetic map of neurogenesis in a cephalopod. We observed that the cerebral ganglia, that give rise to the over-developed learning centres of the brain, are among the latest ganglia to add differentiating neurons suggesting a higher cell proliferation. In other molluscs, where a larval nervous system predates the development of the definitive adult nervous system, cerebral ganglia are among the first to mature. Thus, such a difference may constitute a first cue in understanding the specific brain evolution of cephalopods among molluscs. We also discovered that some nervous elements differentiate in very early stages of organogenesis: the palliovisceral ganglia and the future olfactory organs. These results provide an interesting parallel with what is known about the larval nervous system in other molluscs, where olfactory neurons early appear and are involved in detecting environmental cues inducing metamorphosis.

Nervous system evolution: how to integrate novel data from an unconventional species, *Sepia officinalis*? [Poster]

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The nervous system of cephalopods presents an exceptionally high degree of centralization, which makes it analogous to that of insects and vertebrates. However, these different nervous systems are not homologous: cephalopods belong to the mollusk family and major developmental differences exist. First, nervous system does not emerge from a unique anlage, and neural induction gives rise to a set of distant ganglia which join later to form the brain. Second, it is not organized as a nerve chain or a neural tube, like in model species (*Drosophila* and mouse), in which these structures are metamerized and disposed along clear A/P and D/V axes. Therefore, since the cephalopods exhibit a complex nervous system but no evident embryonic body axes, they constitute important models to correctly investigate the evolutionary origin of convergent complex nervous systems as well as the regionalization process. Nervous regionalization process is known to be under the control of genes expressed in similar patterns during development along the nerve chain of insects and the neural tube of vertebrates. Among them, we have chosen to study otx2/otd, pax3/7 and pax2/5/8 of the pax family and gsx/ind, a parahox columnar gene. In order to know if the acknowledged regionalizing and nervous roles of these genes are conserved in an organism devoid of nervous axes and of “metamerized” organization, we have investigated their expression during *Sepia officinalis* embryogenesis. Some expression patterns seem to be consistent with those of other model species. Otx2 (anterior regionalizing gene) is expressed in specific embryonic nervous structures leading to the hypothetical anterior brain of the adult. These results enlighten the orientation of the cephalopods embryos. But we also evidenced some differences for other gene expressions regarding vertebrate and insect development. Pax3/7, for instance, is expressed in sensory areas in *S. officinalis* embryo, without clear involvement in the D/V axis as in the central nervous system of vertebrates. These data point out the difficulty to conclude homology of gene roles between species with totally different body plan organization. If the A/P and D/V neural patterning makes sense in insects and vertebrates, we start to measure the limit of these classical “metamerized” models when studying mollusks. Such an Evo-Devo approach underlines the interest of also studying models with developmental derived peculiarities and different body plans.

Turn-over of clones in a sexual-asexual ostracod species complex [Talk]

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The freshwater ostracod, *Eucypris virens*, is widespread throughout Europe and shows a striking pattern of geographical parthenogenesis. We have shown that there are many distinct sexual and asexual lineages within this species complex, including triploid clones that appear to be more successful in the north. Here we examine mutation accumulation in clonal lineages and compare origination and extinction rates between sexual and asexual lineages.

Phylogenetic position of the helicid species *Cylindrus obtusus* based on nuclear and mitochondrial DNA marker sequences [Poster]

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Cylindrus obtusus is an endemic of the eastern Alps. Besides many interesting peculiarities in biology, ecology and anatomy, its systematic position seems enigmatic and has been discussed controversially in the past. Its genital anatomy, highly consistent with the genus Arianta, has led to placing the species within the family Helicidae, subfamily Ariantinae. However, *C. obtusus* shows a conspicuous aberrant shell form within this group – all other representatives display globular or more or less depressed shells – and it has a geographically and ecologically rather restricted distribution. This raises questions about the age of the species, its evolutionary history and its relationships within Ariantinae. No genetic analyses to ascertain the phylogenetic position of *C. obtusus* have been performed so far. Moreover, no fossils have been found, except some rare and probably young findings within the extant distribution range in the Eastern Alps, with no reliable age dating available. Here we tested the presumed sister group relationship of *Arianta* and *Cylindrus* using phylogenetic methods, including additional genera of Ariantinae and of some other subfamilies of Helicidae. Five molecular markers were used: partial sequences of three mitochondrial genes, cytochrome oxidase subunit 1 (COI), 12S rRNA (12S) and 16S rRNA (16S), and two nuclear genes for histone 3 (H3) and histone 4 (H4). Phylogenetic trees calculated using Bayesian methods show that the closest relative of *C. obtusus* is indeed the genus *Arianta*. Furthermore, the analyses provided further insight regarding phylogenetic relationships within Ariantinae. Our findings underline the relevance of genital anatomical characters for taxonomic issues, opening the question as to why the shell morphology in this species is so different from its closest relatives, and whether its restricted distribution, habitat preferences and ecological requirements, along with its evolutionary history, can explain this phenotypic difference.

Unravelling the complex *Ulota crispa* [Talk]

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We present here a case study on the diversity of the moss genus *Ulota* Mohr. This is a moss genus distributed along the word and especially present in temperate areas. Still, there are several taxonomic problems that await to be solved. The target of this work is *Ulota crispa* (Hedw.) Brid., one of the most widely distributed species in the Holarctic. This taxon is today interpreted as a single very variable species. However, its morphological variability leads to the recognition of different taxa in older times. In this study we combine the morphological studies with molecular analyses of several nuclear and chloroplast markers to clarify its taxonomy. Both the morphology and the molecular analyses show that several taxa have been included under this name.

A phylogenomics approach for selecting robust sets of phylogenetic markers [Talk]

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Reconstructing the evolutionary relationships of species is a major goal in biology. Despite the increasing number of completely sequenced genomes, a large number of phylogenetic projects rely on the targeted sequencing and analysis of a relatively small sample of marker genes. The selection of these phylogenetic markers should ideally be based on accurate predictions of their combined, rather than individual, potential to accurately resolve the phylogeny of interest. Here we present and validate a new phylogenomics strategy to efficiently select a minimal set of stable markers able to accurately reconstruct the underlying species phylogeny. In contrast to previous approaches, our methodology does not only rely on the ability of individual genes to reconstruct a known phylogeny, but it also explores the combined power of sets of concatenated genes to accurately reconstruct trees of species not previously analyzed. We applied our approach to two broad sets of cyanobacterial and fungal species, and provide two minimal sets of seven and four genes, respectively, necessary to fully resolve the target phylogenies. This approach paves the way for the informed selection of phylogenetic markers in the effort of reconstructing the Tree of Life.

Habitat segregation and population structure in incipient species of *Anopheles gambiae* s.s. in Gambia and Guinea Bissau [Talk]

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The main Afrotropical malaria vector, *Anopheles gambiae* s.s., is undergoing a process of sympatric ecological diversification leading to at least two incipient species (the M and S molecular forms) showing heterogeneous levels of divergence across the genome. In most of their west-African range, M and S forms are strongly reproductively isolated and clearly identified based on SNPs in the IGS rDNA region, which co-segregate with the insertion of a SINE element about 1 Mb apart from the IGS-SNP. Unusual high rate of putative M/S hybrids have been, however, recorded in The Gambia (up to 7%) and in Guinea Bissau (>20%). It has been hypothesized that in these westernmost African regions represent a secondary contact zone between the two molecular forms, where asymmetrical introgression from M to S is occurring. We collected *An. gambiae* samples in a west to east transect about 400 km long was conducted along the Gambia River from the western coastal region of The Gambia (16°45'W) to south-eastern Senegal (12°07'W). Samples have been identified to the molecular form level and a subsample of 507 individuals from 14 villages along the transect were genotyped by 10 microsatellite loci on chromosome-X and 10 on chromosome-3. In addition, over 1.500 half-gravid females were karyotyped. Interestingly, the results of the analyses of 10 X-linked loci strongly support M and S partitioning also in this area of high inter-form hybridization, while the 10 loci on chromosome-3 clearly reveal habitat segregation. Moreover, results from Bayesian and Factorial Correspondence analyses of the microsatellite dataset show the existence of 4 genetically distinct clusters. Two of these largely correspond to 2 S-form populations eastern and western of the central rice-cultivated area, where only M-form has been found. The two S-populations show very distinct paracentric inversion polymorphism configuration on chromosome-2, the eastern one more closely resembling the typical S-form population from eastern dry savannah areas. The two remaining clusters, showing similar inversion pattern, correspond to M-form populations from the coast and from the inner rice-cultivated areas, respectively. Our results will be described in detail and discussed in relation to the possible ecological determinants of this further population structuring within *An. gambiae* s.s. at the western extreme of its range.

What remains after 2 months starving? – Analysis of sequestered algae in a photosynthetic slug, *Plakobranchus ocellatus* [Talk]

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The sacoglossan sea slug, *Plakobranchus ocellatus*, incorporates chloroplasts from its algal food for several months and is able to starve without losing photosynthetic activity. Little is known concerning its food sources, but it is suggested that *P. ocellatus* feeds on a broad variety of Ulvophyceae. This raises the question which, if not all, chloroplast types ingested contribute to photosynthetic performance. We therefore investigated specimens of *P. ocellatus* from the Philippines kept without any food supply and under various light regimes to identify chloroplast types using the algal chloroplast barcoding markers rbcL and tufA during the starvation period. Results show that *P. ocellatus* feeds mainly on *Halimeda macroloba* but also on further members of the genera *Halimeda, Caulerpa, Udotea, Acetabularia* and unidentified algae. Independent of light treatment and starvation period several chloroplast types survive and probably contribute to photosynthetic performance. This raises a statistical question: How many chloroplasts of which algal species were incorporated, and which of these chloroplasts are we able to detect? The detection of cryptic speciation in *Plakobranchus ocellatus* and comparison with recent literature indicating geographic variances concerning algal food items also raises the question, whether ecological adaptations to available food has occurred in this species.

Cryptic bird species on a remote archipelago of the Pacific Ocean [Talk]

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Remote oceanic islands often provide good illustrations of adaptive radiations, but phylogenetic studies have also demonstrated unexpected multiple colonization events for a given archipelago. In this study we investigate the relationships among endemic populations of the Marquesas reed-warblers (genus *Acrocephalus*, Acrocephalidae, Passeriformes), which have colonized nearly all islands of this remote Polynesian archipelago. Because of their very uniform plumage pattern, all populations in the Marquesas were originally treated as a single species, but molecular data suggest that the Marquesas reed-warblers constitute in fact a polyphyletic taxon including two independent lineages, one on the northern islands of the archipelago and the other on the southern islands. These two taxa are not closely related within the Pacific reed-warblers radiation, although we found evidence of rare introgression between them. Analyses of morphological characters show that the size and shape features of the Marquesas reed-warblers exhibit high plasticity linked to adaptation to ecological factors, particularly habitat richness, and preliminary plumage coloration analyses using spectrometry suggest a very uniform type of coloration for the two Marquesas taxa (possibly related to a relatively homogeneous environment). This example provides thus an amazing case of convergent phenotypic evolution consecutive to the double colonization of one of the most remote archipelagos in the Pacific Ocean. Relaxed molecular clock analyses show that both colonization events occurred more or less simultaneously at ca. 0.6 Ma, and are more recent than the islands' formation, suggesting a relatively fast convergent evolution.

Uncharted Waters: Characterizing Sodium Channel Diversity in Spiders (Araneae) [Poster]

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Voltage-gated sodium channels are not only vital to the function of animal nervous systems, but are also involved in numerous unique aspects of animal behavior and chemical ecology. The voltage-gated sodium channels of spiders (Araneae) are virtually unknown, despite the fact that some spider venom peptides target arthropod sodium channels, while spider sodium channels themselves are targeted by venom components of other predators and parasites. We have been focusing on Domain IV of the voltage-gated sodium channel in a diverse sample of spider taxa in order to determine whether amino acid diversity exists at certain known receptor sites that are critical for the binding of neurotoxins – such as those found in arachnid and other arthropod venoms.

An extreme case of plant-insect co-diversification: figs and fig-pollinating wasps [Talk]

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The paradigm that attributes speciation in phytophagous insects to colonization of novel host plants is predicated on the asynchronous radiation of plant and insect lineages. Recent phylogenetic comparisons have supported this model of diversification for insect herbivores and specialized pollinators alike. Among the few outstanding cases where contemporaneous plant-insect diversification might be expected is the obligate mutualism between fig trees (*Ficus* species, Moraceae) and their pollinating wasps (Agaonidae, Hymenoptera). The ubiquity and ecological significance of this mutualism in tropical and subtropical ecosystems has long intrigued biologists but the systematic challenge posed by >750 interacting species pairs has hindered progress toward understanding its' evolutionary history. In particular, taxon sampling and analytical tools have been insufficient for co-phylogenetic analysis of such a large problem until now. We obtained ~6 kb of DNA sequence from a global sample of nearly 200 interacting species pairs and we developed a new analytical tool, Jane 2, for event-based phylogenetic reconciliation analysis of extremely large data sets. Separate Bayesian phylogenetic analyses for figs and fig wasps under relaxed molecular clock assumptions suggested the Cretaceous diversification of crown groups and contemporaneous divergence for nearly half of all fig and pollinator lineages. Event-based co-phylogenetic analyses further supported the co-diversification hypothesis. Biogeographic analyses indicated that the present-day distribution of fig and pollinator lineages is consistent with a Eurasian origin and subsequent dispersal rather than with Gondwanan vicariance. These findings suggest that the fig-pollinator mutualism represents an extreme case among plant-insect interactions of coordinated dispersal and long-term co-diversification.

Another kind of preservation issue: digitisation of literature for biosystematic studies [Talk]

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Not only collections of plants and animals but also taxonomic literature are important tools for studies of biodiversity. 1753 was the starting point of modern nomenclature with Linné's "Species Plantarum" – since then journal articles with descriptions of life on earth were consulted. Scientific journals of the 18th and 19th century very often consist of only a few volumes, published by different small societies and spread over several libraries. Frequently access to literature is difficult and the paper of the journals is threatened by decay. The "Biodiversity Heritage Library" aims to change this situation: the scientific historic literature should be digitised, collected, preserved and presented in one portal – accessible worldwide and for free. BHL-Europe is the "European wing" of this effort and our collection is the German botanical contribution: The University Library Frankfurt and the Library of the Botanic Garden and Botanical Museum Berlin-Dahlem (Germany) are digitising ca. 180 German botanical journals from the period 1753 through 1914 – together with another 25 libraries (http://sammlungen.ub.uni-frankfurt.de/botanik). The journals are indexed at article level. The talk will present examples of the content and further information about the project, funded by the German Research Foundation (DFG). The collection is also accessible via vifabio, the Virtual Library of Biology (www.vifabio.de/?lang=en) which combines high-quality scientific sources from libraries, article databases and the Internet. vifabio offers additional services such as an overview of digitisation projects for historical literature.

A cryptic species of *Orchestia mediterranea* Costa, 1853 (Amphipoda) revealed by DNA sequence-based phylogenetic analysis [Poster]

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The limited data resulting from an insufficient characterization of cryptic species may affect the estimates of species diversification rates. In this regard, the analysis of DNA sequences has proved to be an important means of understanding evolutionary relationships at different taxonomic levels, even of revealing speciation events among morphologically similar species. In our ongoing study on talitrid amphipods, we focus on DNA sequences from the mitochondrial (mt) region between the cytochrome oxidase I and II genes (COI and COII), which showed a peculiar rearrangement in relation to mt genomes of other amphipod crustaceans. Our analysis of mt COI and COII gene sequences confirmed that a taxon from Lanzarote, Canary Islands, morphologically ascribable to *Orchestia mediterranea* Costa, 1853, is most closely related to, but genetically distinct from, *O. mediterranea* of NE Atlantic and Mediterranean areas. The level of genetic divergence between this putative cryptic species and *O. mediterranea* is consistent with the range of interspecific distance values found between morphologically recognised *Orchestia* species, including

O. canariensis, O. cavimana, O. gammarellus, O. garbinii, O. gomeri, O. guancha, O. mediterranea, O. montagui, O. stephenseni, among others. A phylogenetic modelling for the examined *Orchestia* species has been conducted on the DNA sequences of this peculiar mt region, revealing an interesting clustering with a clear separation between morphologically recognised species and cryptic taxa as well. Notably, inferred evolutionary relationships are in agreement with that previously we observed for some of these *Orchestia* species by means of allozymes encoded by nuclear loci. Our efforts, integrating of data from different sources, such as morphology, DNA sequences (which is now a relevant part of the biosystematic approach) and biogeography, provide crucial information to resolve evolutionary relationships of known and newly identified species within *Orchestia* and other genera of the Talitridae family.

Phylogenetic assessment of taxonomic and ecological biodiversity of herbivore beetles in the dry tropical forest [Poster]

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The dry tropical forest is the most threatened ecosystem in the tropical areas and any effort towards understanding its function and composition is critical in order to implement conservation measures. In this study we explored, using molecular tools, two aspects of the biodiversity of the Mesoamerican dry forest: species inventories of herbivore beetles (Coleoptera, Chrysomelidae) and their ecological interactions with angiosperms. Specifically, we intended to: (1) Assess species diversity of three subfamilies of Chrysomelidae – Cassidinae, Eumolpinae and Galerucinae – in the dry tropical forests of Nicaragua; and (2) infer these species' diet using molecular forensic tools. Total DNA was extracted from 371 specimens of Cassidinae, 251 of Eumolpinae, and 632 of Galerucinae, collected in 14 dry forest areas distributed along de Pacific Coast of Nicaragua. For animal species delimitation, we used phylogenies of the cox1 mitochondrial gene and the Generalized Mixed Yule Coalescent model to establish independent evolutionary lineages, which we validated by comparison with morphospecies designations. Inference of food plant associations was obtained by amplifying the chloroplastic psbA-trnH intergenic spacer from plant tissue remains in the beetle DNA extraction and each sequence was contrasted with GenBank data and our own reference database using the BLAST algorithm and phylogenetic methods. For Cassidinae we obtained 79 species and 388 food inferences that correspond to 35 botanical families, for Eumolpinae we obtained 51 species and some 130 food associations in 21 plant families; finally, for the Galerucinae, we obtained 194 species and 310 diet sequences that correspond to 40 botanical families. These data allowed us to evaluate aspects on the biodiversity of interactions of beetle and plant communities, including the degree of trophic specialization of each beetle assemblage, diet overlap among beetle groups, and seasonal or local ecological adaptations. This study, with relatively low cost and time effort has generated a lot of valuable and novel information about the diversity of herbivore beetles and their interactions with host plants in the dry tropical forest. In the future, we hope that this approach will allow us to understand the ecological niche of these species and their role in the food-web structure of this highly threatened ecosystem.

DNA barcoding reveals unexpected biodiversity patterns in earthworm communities at the Nouragues Research Station (FG) [Poster]

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Earthworms comprise about 3700 described species, a number thought to represent less than half of the actual biodiversity of this group. The taxonomy of the group is poorly resolved in most regions of the world, especially in the inter-tropical area which hosts most of the described and expected biodiversity of the group. This represents a serious constraint for any ecological study requiring species identifications and/or reliable species lists. DNA barcoding using Cytochrome Oxidase subunit 1 (COI) represents an efficient approach to counter this taxonomic deficit. This tool can be used for rapid species discrimination without requiring time consuming morphological identifications, allowing further analyses of community structure and biodiversity estimations using the number of COI lineages (MOTUs) as a proxy for species richness. We used this approach to describe earthworm community patterns in the Nouragues research station (French Guyana). We sampled earthworms using a qualitative protocol in 10 different habitats of the station ranging from lowland forests and stream banks to rocky savannas and hilltop forests. In each habitat, all microhabitats available were prospected from the ground level to epiphytic soils. A total of 750 earthworms were collected, and we obtained COI sequences for more than 600 of them. A neighbour joining tree allowed the discrimination of 48 MOTUs with inter-lineages divergences higher than 15 %. Forty of these MOTUs were found at the ground level in soil and litter, while 21 and 22 were found in decaying trunks and epiphytes, respectively. Habitat richness ranged from 2 in rocky savannas to 28 MOTUs in stream banks with a high level of MOTUs turnover between them. Earthworms were recorded in epiphytes up to 40m in epiphytes, but most of these “arboricolous” lineages were also found at the ground level, suggesting an unexpectedly high vertical niche range of these MOTUs. Estimated species richness using the ACE index suggests that more than 60 species may occur at the study site, representing the highest local earthworm diversity ever recorded.

Hands-on DNA barcoding: Engaging students for rapid invertebrate diversity assessment in the Lopé National Park, Gabon [Talk]

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The natural ecosystems of Gabon are considered among the most emblematic from a biodiversity conservation perspective. The forest block of central Africa represents the second largest area of pristine forest worldwide, and the patchwork of forests and savannas covering most of Gabon are renowned for their charismatic species of vertebrates and plants. By contrast, invertebrates are poorly known and are generally absent from conservation plans and strategies, despite the important part of biodiversity they represent in these ecosystems. In this situation, DNA barcodes can help documenting the basic descriptive metrics of invertebrate diversity, providing a unique educational tool to raise students' awareness and hopefully promote the future surveying and description of this diversity. In February 2011 and March 2012, two editions of the "field school in tropical ecology and palaeoecology" (ECO-TROP) were organized in the National Park of La Lopé (Ogoué Ivindo region) with the participation of several universities and institutions from Gabon, France and Cameroon. Students were trained to the main invertebrate sampling methods routinely used in biodiversity, ecology and palaeoecology studies in intertropical environments. Questions relating to the description and conservation of invertebrate biodiversity emphasized the potential of DNA barcoding. Students participated in the successive steps of a classic field survey, from specimen collecting to sorting of morphospecies, tissue sampling and voucher fixation and labelling. The diversity of the sampling methods implemented in the field was highly stimulating for both students and scientists, allowing the discovery of an outstanding diversity of invertebrates to illustrate taxonomic classes. In total more than 3500 Lepidoptera, 500 soil arthropods, 350 earthworms and 100 mantids were sampled for DNA barcoding. Preliminary examination of the material suggests the presence of a high number of new taxa in several taxonomic groups, especially in soil invertebrates. For instance, we found more than 30 lineages of earthworms and more than 40 lineages of collembolans, the majority of which are likely to be new to science.

Study of Tardigrada biodiversity in Maritime Alps – A new *Echiniscus* species from Italy [Poster]

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Tardigrades can be found in a variety of habitats including marine, brackish, freshwater and terrestrial ecosystems, ranging from the deep sea to the highest mountains, as well as in many extreme environments ranging from the coldest to the hottest and driest places. However, there are only few biodiversity assessments and many tardigrades might remain undiscovered. Within the “All Taxa Biodiversity Inventories+Monitoring” (ATBI+M) in the Parc national du Mercantour (France) and Parco Naturale delle Alpi Marittime (Italy) we collected more than 300 moss cushions and extracted tardigrades. Two samples contained specimens of a new *Echiniscus* species. It belongs to the reticulatus species group. Species of this group have the only trunk appendages (in the position A) and plate ornamentation composed of a system of round or polygonal units (depressions of thickenings) while space between them has an appearance of more or less distinct reticulation. The surface of these structural units themselves is covered by granulation which is different in different species. The new species differs from other members of the reticulatus group mainly by unique cuticular pattern on its plates – a system of darker polygonal patches delimited from each other by a rosette of several dark spots on their perimeters and with or without central spot. More differences between the new species and others having same number of trunk appendages and similar character of a cuticular ornamentation are also discussed. This study was partly supported by the Slovak Scientific Grant Agency (VEGA) as a Project No. 1/0294/09 to P. Degma, and partly supported by the German Federal Ministry of Education and Research, BMBF (0313838) as project FUNCRYPTA to R.O. Schill.

The challenging revision of Alpine-endemic diversity in the jumping-bristletail genus *Machilis* (Insecta, Microcoryphia) [Talk]

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According to a recent survey, jumping bristletails – and herein specifically the genus *Machilis* – stand out as the taxon with the highest portion of endemic animal species in Austria. The general knowledge on this ancient insect group is scarce, though, and the degree of endemism could potentially be attributed to overlooked synonymies and incomplete sampling rather than biological diversification. Our goal is to revise the nominal species described from the Eastern Alps using integrative taxonomy (i.e., the evaluation of accordances and discordances between different disciplines, in this case morphology, molecular markers, karyology and ecology) for accurate species delimitation and thus to reassess the endemic status of the included species. So far, our results indicate (1) the presence of several hitherto unnoticed synonymies, (2) increased distribution ranges in some small-scale endemics and (3) a rather complex evolutionary history of the genus *Machilis* due to putative hybridisation and polyploidisation.

ITS-2 Barcode supports the systematics in *Microglena* (Chlorophyceae), a genus investigated by an integrative approach [Poster]

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Recently the genus *Microglena* Ehrenberg has been revised using an integrative approach. Phylogenetic analyses of SSU and ITS rDNA sequences revealed that freshwater strains previously assigned as *Chlamydomonas monadina* belong to *Microglena* and represent eleven species. Morphologically three different morphotypes could be recognized. Strains belonging to type I have a cup-shaped chloroplast with a massive basal part, in which a large, single, ellipsoidal pyrenoid is located. The members of type II also have a cup-shaped chloroplast, which is partly lobed and has a thinner basal part than type I; here the pyrenoid is half-ring or horseshoe-shaped and occupies different positions in the chloroplast depending on the strain. The strains of type III have multiple pyrenoids, which appear to have developed from the subdivision of a single ring-shaped pyrenoid into several parts. The eleven species have been confirmed by morphology and ITS-2 DNA Barcode. Closely related to these freshwater species are two marine species and unidentified strains isolated from Arctic and Antarctic regions, which all have chloroplast of morphotype I. The latter strains are all obligate psychrophilic and can be identified as species previously assigned as *Chlamydomonas* or represent new species. Comparison of the ITS-1 and ITS-2 secondary structures confirmed the species delineations in *Microglena*. All species have characteristic compensatory base changes in their ITS secondary structures and are supported by ITS-2 DNA barcodes. Summarizing species of *Microglena* showed similar morphology with respect to cell shape and size, but showed differences in chloroplast and pyrenoid structures. Some freshwater representatives of this group have the same type of sexual reproduction (advanced anisogamy). Surprizingly, recent investigations of the coccoid genus *Tetracystis* have discovered that two authentic strains of *Tetracystis* (*T. pampae* and *T. vinatzeri*) also belong to *Microglena* showing the high phenotypic and genetic variability among this widely distributed genus.

Maximum polyphyly: A new delimitation of *Minuartia* (Caryophyllaceae) [Poster]

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Minuartia L. is one of the larger genera in the Caryophyllaceae with about 200 described species. The genus contains annual and perennial species with usually white and entire petals. *Minuartia* is delimited morphologically by a combination of three styles and three capsule valves/teeth from the other genera of the family. *Minuartia* is divided into four subgenera, twelve sections, five subsections and 21 series. Molecular studies of the past decade of the Caryophyllaceae revealed that the subgenera of *Minuartia* do not form a monophyletic group. Even the subgenus *Minuartia* – the largest subgenus with more than 90 % of the species – was not resolved as monophyletic. We analyzed the phylogeny of *Minuartia* using DNA sequences of nrITS and two plastid markers (matK-trnK, trnQ-rps16) of ca. 90 species of *Minuartia* and numerous outgroup samples. The sampling covers all sections, subsections and all except one series. Our results show clearly that *Minuartia* is highly polyphyletic. The previously published phylogenies could be confirmed by our study. The subgenus *Rhodalsine* (J. Gay) Graebner is closely related to *Spergularia* (Pers.) J.Presl & C.Presl, *Spergula* L. and *Thylacospermum* Fenzl; the subgenus *Hymenella* (Moc. & Sessé ex Ser.) McNeill is part of a group of New World taxa (including *Schiedea* Cham. & Schltdl., *Wilhelmsia* Rchb. and *Geocarpon* Mack.); and the subgenus *Spergella* (Fenzl) McNeill seems to be sister to the subgenus *Eremogone* (Fenzl) Fenzl of *Arenaria* L. The subgenus *Minuartia* is polyphyletic, as well. It is divided into six to seven clades. The type species of *Minuartia, M. dichotoma* L., is part of a group containing the sections Minuartia, Plurinerviae McNeill and the series Graminifoliae Mattf. We propose to keep this group as the genus *Minuartia* s. str. and to transfer the remaining species to independent genera. In some cases these groups are well defined by chromosome number or morphology; for others further morphological and cytological investigation is needed.

Arctic-alpine lichens of the Tatry Mountains, their ecological indicator values and life history traits [Poster]

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In the study the arctic-alpine lichens of the Tatra Mountains were examined. The study was carried out under the umbrella of the Visegrad Fund 5120138. A number of 1175 lichen taxa are reported from the Tatra Mountains, of these 148 are with arctic-alpine geographical elements. Listed in the local Red list are *e.g.* Alectoria nigricans (EN), *Cetraria ericetorum* (VU), *Cetrariella delisei* (EN), *Cladonia carneola* (EN), *C. ecmocyna* (EN), *C. macrophylla* (EN), *C. macrophyllodes* (EN), *C. strepsilis* (CR), *C. sulphurina* (EN), *Stereocaulon alpinum* (VU) and others have not been recorded in the area for more than twenty years. There are taxa on hardly reachable sites which are still needed to be discovered. Knowledge not only about the lichen diversity, but also indicator values for light conditions, climate, substratum and about the species traits such as ecological and geographic values were reviewed or modified, and original values were established for taxa with missing informations. As well as higher plants, the distribution of lichens are primarily related to the ecological conditions, therefore ecological indicator values of terricolous lichens will be a valuable tools for analyzing Alpine lichen rich plant communities.

Inference and distribution of reproductive modes in the Potentilleae (Rosaceae) applying the flow cytometric seed screen [Talk]

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The flow cytometric seed screen (FCSS) is an accurate and effective tool for the inference of reproductive modes in the angiosperms, but its applicability depends on a sufficient amount of endosperm and a conserved bi-nucleate female contribution to this tissue. In addition, accompanying cyto-embryological analyses or other approaches to infer reproductive modes are necessary for a comprehensive understanding of the cytology of reproductive pathways. We aimed at i) testing the applicability of the FCSS to the rosaceous tribe of the Potentilleae, a group rich in polyphenolics – known to interfere with the fluorescence stain of nuclei – and reported to have seeds with minor amounts or even no endosperm, ii) inferring reproductive pathways in this group as well as their (iii) phylogenetic, taxonomic and geographic distribution. Analysing 60 species from eight genera, we could demonstrate that the basic prerequisites for the application of the FCSS are met. However, low numbers of endosperm nuclei in apomictically-derived seeds as well as strong dependence of gamete ploidy inference on accuracy of peak index estimation were identified as methodological limits of the FCSS. Furthermore, for the series Tormentillae from the genus *Potentilla* the number of polar nuclei contributing to the endosperm remained uncertain. Applying the established method, apomixis and sexuality are shown to be the predominant reproductive pathways in *Potentilla*, whereas the segregate genera *Argentina, Dasiphora, Drymocallis, Comarum, Farinopsis, Horkeliella*, and *Sibbaldia* were exclusively sexual. The phylogenetic distribution of reproductive modes suggested – including literature data – that apomixis independently arose at least two times in the Potentilleae. Apomixis is shown to be widespread in the whole northern hemispheric distribution range of the genus *Potentilla*.

The case of *Chroococcidiopsis*: New phylogenetic and morphological insights of an ecologically important Cyanobacterium [Talk]

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Cyanobacteria are the oldest prokaryotes performing photosynthesis; they caused a sharp rise in the oxygen of the atmosphere about 2.45–2.32 billion years ago, and gave the basis for the evolution of complex lifeforms. Morphological data were traditionally used for their classification, which often did not reflect their evolutionary history. The unicellular genus *Chroococcidiopsis* is known as a globally distributed component of desert photoautotrophic communities, and thus the evolution of the genus is of major interest. Based on morphological traits, the genus *Chroococcidiopsis* has been traditionally classified within the Pleurocapsales; whose members share the same unique reproduction modus by so called baeocytes. Recent molecular studies indicate that the Pleurocapsales are paraphyletic, and that *Chroococcidiopsis* is a sister group to heterocyte-forming Cyanobacteria. This is in strong contrast to the close morphological similarity of *Chroococcidiopsis* with other members of the Pleurocapsales. In this talk we present an approach to the evolutionary relationships within *Chroococcidiopsis* using three lines of evidence. First, we present a multi-locus sequence analysis using three genes (16S rDNA, rpoC1 and gyrB) for approx. 100 strains of Pleurocapsales, *Chroococcidiopsis*, and heterocyte-forming Cyanobacteria. Available data from GenBank and completed genomes were combined with new sequences and analysed using Maximum Likelihood and Bayesian methods. Second, thylakoid structures as a morphological character of 65 selected taxa are analysed using low temperature scanning electron microscopy. Third, biogeographical distribution patterns are correlated to the phylogenetic relationships, in order to understand distribution patterns of *Chroococcidiopsis*. Our phylogenetic results support the hypothesis that *Chroococcidiopsis* is more closely related to heterocyte-forming Cyanobacteria, and confirm the non-monophyly of the Pleurocapsales. Microscopy revealed three types of thylakoid structures which cannot be unambiguously linked to the phylogenetic findings. Our biogeographical analysis does not show any clear patterns, a result that is discussed in the context with recent literature. The consequences of the conceptual view of the evolutionary relationships of *Chroococcidiopsis* are highlighted and future research perspectives are discussed.

Molecular and morphological circumscription of *Brachythecium coruscum* I. Hagen [Talk]

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Within bryophytes, the taxonomy and species circumscription is still under study for several groups. One of the families regarded as taxonomically problematic is Brachytheciaceae. In this study we aim to increase the knowledge on this family, focusing on the complex around *Brachythecium albicans*. For this purpose, we have combined morphological studies and molecular data from three markers, one nuclear (ITS) and two chloroplasts (rpl16 and trnG). Our results suggest that *Brachythecium coruscum*, which has recently been treated either as a separate species, as a variety or subspecies of *Brachythecium salebrosum*, or as a variety of *B. albicans* should be considered as distinct at species level.

New assessment for an old species: the Austrian endemic *Trochulus oreinos* (Gastropoda: Pulmonata: Hygromiidae) [Poster]

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In the last decade, the connection of classic gastropod determination by shell and genital traits in combination with new molecular biological methods opened new ways of species delimitation, which led to a “re-discovery” of forgotten or fairly unknown Pulmonata species in Europe. One of them is *Trochulus oreinos*, an endemic of the Austrian North Eastern Alps with two subspecies (*T. o. oreinos, T. o. scheerpeltzi*) which were originally described as a local subspecies of the wide-spread *T. hispidus*. Its reassessment was based on the combination of morphology, habitat preferences and phylogeny. *T. oreinos* can be unambiguously differentiated by its hair morphology and the specific arrangement of penial folds from related species. Other traits, like shell measures and the number of whorls separate this species by trend, although values overlap partially. *T. oreinos* prefers to live in remarkably cool and dry alpine areas like rocks and *Carex firma* meadows with patchy structure above 1400 m asl in an area supposed to be ice-free during the last glaciation. It was probably always a stenoecious dweller of a very narrow ecological niche, a fact, which accelerated its development as endemic species. These results accord with the distribution pattern and habitat needs of other endemic invertebrates and vascular plants reconfirming the Austrian north eastern Alps as a hot spot of endemic species. A phylogenetic tree of *Trochulus* established from concatenated mitochondrial sequences shows that *T. oreinos* is only distantly related to other species in this genus and splits from a basal node. Also the subspecies of *T. oreinos* could be re-validated, as they were well separated genetically, geographically and also to some extent morphologically.

The expansion of woody species on the abandoned subalpine grasslands of the Western Bieszczady Mts [Poster]

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On abandoned grasslands in the mountains we can observe shifting the timberline in European montane ranges. The Western Bieszczady subalpine grasslands in the Polish part of the Eastern Carpathian were cultivated for hundred of years. Since 1960s they became protected areas and since 1973 they are protected in Bieszczady National Park (part of the "Eastern Carpathian" International Biosphere Reserve). We studied overgrowing of subalpine grasslands of Mała Rawka and Wielka Rawka with woody vegetation. Those grasslands were used in the past as reaped meadows and pastures. Now, the tree species which dominate in process of overgrowing of this area is *Sorbus aucuparia*, but some other woody species are also present *e.g. Alnus viridis* and *Acer pseudoplatanus*. We used cartographic data from year 1980, 1994 and 2009 to determine area of *S. aucuparia* thickets of Mała Rawka and Wielka Rawka. Moreover in regular net of 57 plots established on subalpine meadows we analysed tree species composition, density, diameter and height structure of trees. The obtained results indicated that during the last dozens of years overgrowing of subalpine meadows of Mała Rawka and Wielka Rawka by thickets of trees has been a continuous process and is still continuing. In 1980–1994 area of brushwood increased 4.3 times and in years 1994–2009 it increased 7.1 times. Density of trees was from 0 to 100 individuals per 100 m^2 and decreased with increasing altitude. *S. aucuparia* constitute 99% of woody species individuals present in subalpine meadows. Most *S. aucuparia* individuals consisted of more than one stem and the highest number of stems per individual was 67. Diameter of *S. aucuparia* was from 0.5 cm to 25 cm. Height of *S. aucuparia* trees was up to 9 m. Both diameter and height of trees decreased with increasing altitude.

Chromosomal evolution and taxa diversification in *Prospero* (Hyacinthaceae) [Talk]

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Changes in chromosome number and structure are recognized as important aspects of plant evolution and speciation. A group well-suited to investigate the evolutionary role of chromosome number changes in plant speciation is circum-Mediterranean genus *Prospero* (Hyacinthaceae). Three species are commonly recognized in the genus: *Prospero hanburyi* (eastern part of the range; $2n=2x=14$), *P. obtusifolium* (western part of the genus range; $2n=2x=8$), and *P. autumnale* complex distributed thoughtout the whole Medditerannean basin. *P. autumnale* complex possesses at least four distinct diploid cytotypes with three basic chromosome numbers (A, B7, both $x=7$; B6 $x=6$, and B5 $x=5$) and distinct karyotypes. *Prospero autumnale* complex exhibits a spectacular array of genomic and chromosomal variation which contrasts with its very poor morphological differentiation. Chromosomal changes commonly encoutered in the complex include auto- and allopolyploidy, presence of B chromosomes and supernumerary segments, inversions, and dynamic changes in the repetitive DNA fraction. Previous hypotheses on origin and karyotype evolution of individual cytotypes and species of genus *Prospero* have been tested in robust phylogenetic context. Phylogenetic relationships among basic diploid cytotypes of *Prospero autumnale* complex and allied species ($x=4$, 5, 6, 7) have been inferred using three nrDNA markers: 5S rDNA spacer

(NTS, non-transcribed spacer), 35S rDNA (ITS, internal transcribed spacer), and low copy nuclear gene (MS, malate synthase). Phylogenetic analyses of all the markers confirm evolutionary distinctiveness of each of the species and cytotypes. Independent origin of cytotypes B5 (x=5) and B6 (x=6), in line with cytogenetic data suggests the descending dysploidy with independent basic chromosome number reduction from x=7 to 6 and from 7 to 5 rather previously hypothesized step-wise chromosome number reduction and common origin of B5 and B6 cytoraces. Sister relationship of cytotype A (x=7) to other cytotypes has been suggested reflecting its geographical isolation during last glaciation. Molecular phylogenetic analyses allow insight into the role of chromosomal changes and rearrangements in speciation, evolution, and diversification within *Prospero*.

Multiple gene analyses provide insight into the phylogenetic relationships of the "South African Clade" of Lacertidae [Talk]

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Lacertidae are a successful widely distributed lizard family. They consist of three subfmailies: Gallotinae, Lacertinae and Eremiadinae. The latter group, which is subject of the current study, is predominantly distributed throughout Asia and Africa. Previous phylogenetic studies tried to clarify the phylogenetic relationships within the subfamily, but did not result in a highly supported topology, especially with respect to one group of Eremiadinae which we designated "South African Clade" because of its main geographical distribution. It includes the genera *Pedioplanis*, *Meroles*, *Ichnotropis*, *Tropidosaura* and *Australolacerta*. For this group support value was quite low. In the present study we wanted to test the monophyly of this group and tried to obtain good support for the relationships among the five above mentioned genera. We also included representatives of "East African" Eremiadinae (genera *Nucras*, *Heliobolus* and *Latastia*) and some distantly related genera (*Atlantolacerta*, *Ophisops*, and *Lacerta*). We sequenced sections of the widely used mitochondrial genes for 16S rRNA, 12S rRNA and cytochrome b as well as the nuclear genes c-mos and RAG-1. To obtain more sequence information we also tested four new nuclear markers which were already used for other reptiles, but so far have not been widely tested: PRLR, KIF24, EXPH5 and RAG-2. Altogether, the sequence information was 4473 bp for nuclear and 2045 bp for mitochondrial marker sequences. The combined data set increased the support values for several nodes considerably. However, the relationships among the five major lineages within the "South African clade" could not be clearly resolved. We interpret this result as a "hard polytomy" caused by a fast radiation within the South African lacertids. The phylogenetic tree based on nine marker genes provides strong support for the "South African Clade" and its sister group relationship with the "East African Clade". Our results confirm the genus *Tropidosaura* as a monophylum, while *Ichnotropis* is paraphyletic in our trees: *Ichnotropis squamulosa* appears more closely related to *Meroles* than to *Ichnotropis capensis*. Furthermore, the monophyly of *Meroles* is questionable as well. Based on our results, I. squamulosa should be transferred from *Ichnotropis* into the genus *Meroles*. Also, the two species of *Australolacerta* (*A. australis* and *A. rupicola*) are very distantly related and the genus is possibly paraphyletic, too.

Gomphonema parvulum revisited: A critical assessment of the taxonomic concept [Talk]

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Due to the morphological variation found in specimens ascribed to *Gomphonema parvulum* (Kützing) Kützing and the uncertainty regarding the delineation of the species complex, 22 cultures from Europe, Meso-America and Asia were studied in morphological detail as well as molecularly which led to an emendation of the current taxonomic concept. Initially the cultures were morphologically assigned to four different taxa from *G. parvulum* s.l.: *G. parvulum*, *G. lagenula* Kützing, *G. parvulum* var. *exilissimum* Grunow, and *G. parvulum* f. *saprophilum* Lange-Bertalot & Reichardt. Detailed morphometric analyses (incl. characters such as width and shape of the valve, density of fibulae, striae, alveoli, areolae, raphe characters, and structure of the stigma) showed overlaps between most strains, except for two groups consisting of two Mexican respectively two Korean strains. Three molecular markers (18S V4, rbcL, ITS) were used to clarify patterns of molecular relations between the 22 cultured strains. Here four different, statistically supported clades were retrieved from the concatenated data set (incl. the morphometric data) corresponding to their geographic origin: the Mexican and Korean clade were separated as well as a continental European clade with strains from Southern Sweden and Northern Germany. The fourth clade comprised species from three different Faroe Islands in the North Atlantic. The taxonomic consequences drawn from this analysis are: The Mexican strains correspond to *G. lagenula*, the continental European clade corresponds to *G. parvulum* f. *saprophilum*, the Faroe Island strains comprise the morphodeme “exilissimum” but are taxonomically *G. parvulum* var. *parvulum* and some additional unassignable variants. The Korean strains belong to a species to be described as new.

Possible ancient hybridization in *Medicago* [Poster]

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In the genus *Medicago*, incongruence has been observed between gene trees, but the cause of this is not clear. In the nuclear genes CNGC5 and B-cop, two species, *M. cretacea* and *M. prostrata*, may contain evidence of hybridization several million years ago between the *M. sativa* complex and *M. arborea*. In the nuclear gene CNGC5, *M. arborea* was sister to *M. cretacea*, whereas *M. prostrata* was nested in the *M. sativa* complex with strong support. Conversely, in B-cop, *M. arborea* and *M. prostrata* formed a clade, whereas *M. cretacea* was nested in the *M. sativa* complex. In other genes *M. cretacea* and *M. prostrata* are almost always grouped with *M. sativa* complex taxa. *M. prostrata* has been found to have 2n = 16 and 2n = 32 chromosomes, which seem to be locality specific. Nicoloff, 1961, found that the diploids are located in Italy-Sicily, whereas the tetraploids are located in former Czechoslovakia. In *M. cretacea* there have also been reports of 2n = 16 and 2n = 32 chromosomes, but not if they are locality specific. Are the differences in gene trees due to an ancient hybridization between *M. arborea* and the *M. sativa* complex giving rise to *M. prostrata* and *M. cretacea*? Or might incomplete lineage sorting be the cause behind the incongruent gene trees? Another possibility is that the two ploidy levels within *M. prostrata* may indicate the presence of two different taxa, and therefore may be cryptic species. To approach these questions we will sample many unlinked genes and specimens from different localities to see if additional loci show a pattern consistent with introgression. And by sampling the specimen in a gradient we might see if there is a split between the diploid and the tetraploid *M. prostrata.* We will also examine chromosome number differences across the range of *M. prostrata.*

Barcoding sponges – much more than just barcodes [Talk]

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DNA taxonomic approaches (*e.g.*, DNA barcoding) became important tools for unambiguous identification of species and subsequent assessment of biodiversity, identification of cryptic speciation, understanding of biogeography, and numerous other applications in the recent years. Sponges (Porifera) are excellent subjects for DNA barcoding approaches due to their difficult taxonomy and strong morphological plasticity in combination with high ecological importance as filter feeders in almost all aquatic habitats, their evolutionary pivotal position as first branching metazoan phylum, and their importance for biotechnological, biochemical and pharmaceutical purposes. The Sponge Barcoding Project (www.spongebarcoding.org) aims to facilitate such unambiguous species identification for sponges on grounds of the standard barcoding and other molecular markers. More than five years after its foundation, the Sponge Barcoding Project is in progress to establish a reference backbone database based on 17,000 samples of the Queensland Museum (Brisbane, Australia) and other sources. Data originating from the Sponge Barcoding Project is in the past and present successfully applied to a wide range of evolutionary research: 1) Identification of sponge colonization patterns in freshwater habitats; 2) Detection of endemism among marine and freshwater taxa; 3) Phylogenies of pivotal demosponge taxa; 4) Reconstruction of skeleton evolution; 5) Identification of sponge chemotypes; 6) Unravelling cryptic shallow and deep-sea taxa. We demonstrate in several cases to what extent DNA barcoding of this important metazoan phylum provides a powerful tool not only for taxon discrimination but also for multiple other applications in evolutionary research, biochemistry and biotechnology.

Cryptic speciation in clitellate annelids [Talk]

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Clitellates (oligochaetes and leeches) are segmented worms that are well represented in aquatic as well as terrestrial habitats. Many morphospecies are widely distributed in the world, including some considered as more or less cosmopolitan. Among these are popular as model organisms in biology and toxicology. Recent DNA work on a number of taxa, however, has revealed complex genetic patterns suggesting cryptic speciation. This presentation will give an overview of such studies among micro-oligochaetes, such as Enchytraeus albidus, Limnodrilus hoffmeisteri and Branchiura sowerbyi, and lumbricid earthworms and well-known. The importance of multiple criteria for species delimitation will be emphasized (i.e., in particular, mitochondrial and nuclear gene data, and morphological characters). Moreover, the relative nature of the concept of "cryptic" species will be discussed.

Using the morphometric values for identification of most common cultivated infraspecific taxa of *Tilia platyphyllos* [Poster]

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During the study, morphometric measurements were made for the four taxa of *Tilia platyphyllos* Scop., which are most frequently found in Latvia: *T. platyphyllos* subsp. *platyphyllos*, *T. platyphyllos* subsp. *cordifolia* (Besser) C.K.Schneid., *T. platyphyllos* 'Rubra', *T. platyphyllos* 'Obliqua'. Ten most typical our collected herbarium material samples were selected (from DAU herbarium collected in Latvia). In turn, five typical leaf samples were measured from each herbaria. Some selected morphologic parameters were measured and analyzed: width of leaves, length of leaves, pubescence and margin of leaves. Unfortunately, generative parameters are not available in all herbaria, therefore we use only vegetative features. Statistical analysis was performed by SPSS (version 20.0) software using descriptive statistic tools, one – way ANOVA with Sidak post hoc multiple comparison, and Kruskal – Wallis with Mann – Whitney post hoc multiple comparison, for which it was designed new critical level of significance 0.0085.

The comparison between taxonomic group showed significant difference of leaf length F3, 177.25=2.872 P=0.038; pubescence of leaves x2=102.84 df=3 P<0.000 and margin of leaves x2=15.47 df=3 P=0.001. Mainly difference was between *T. platyphyllos* subsp. *cordifolia* and *T. platyphyllos* 'Obliqua' (length of leaves, pubescence of leaves); *T. platyphyllos* subsp. *cordifolia* and *T. platyphyllos* subsp. *platyphyllos* (pubescence of leaves; margin of leaves; *T. platyphyllos* subsp. *cordifolia* and *T. platyphyllos* 'Rubra' (pubescence of leaves); *T. platyphyllos* subsp. *platyphyllos* and *T. platyphyllos* 'Rubra' (pubescence of leaves); *T. platyphyllos* subsp. *platyphyllos* and *T. platyphyllos* 'Obliqua' (pubescence of leaves; margin of leaves). There are no taxonomically significant difference between such morphometric parameters as width of leaflet and length of petiole.

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Chiral instability as an important driver of speciation in the Carpathian rock-dwelling gastropod genus *Alopia* [Talk]

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While the vast majority of snails (Gastropoda) possess dextral shell and body organization, members of the Clausiliidae family are almost exclusively sinistral. Within this group Alopia, an endemic genus of the Carpathian Mountains, is unique by the comparable representation of sinistral and dextral taxa, and the existence of enantiomorph taxon pairs that seemingly differ only in their chirality. Chirality is known to be determined by a maternally inherited dominant cytoplasmic factor encoded by a single gene, mutations of which can have considerable evolutionary consequences. The anatomical difference between the individuals of opposite coiling considerably restricts interchiral mating, thereby leading to reproductive isolation. Occasionally, reversed individuals of the same offspring succeed in establishing stable subpopulations. As reproductive success of each chiral morph is ensured by the availability of surrounding mating partners of the same chirality, this gradually leads to territorial separation and, in time, the formation of isolated sinistral and dextral populations. These inversely coiled populations are considered to belong to distinct taxa, however, the possible evolution and systematic significance of coil inversions in *Alopia* have long been disputed, preventing consistent classification at the species level. Therefore the aim of our study was to find out whether the unusually high number of dextral forms descended monophyletically, which would imply extreme convergence in the cases of enantiomorph taxon pairs, or resulted from multiple independent inversions, indicating that in *Alopia* the genetic fixation of chiral stability is much weaker than in any other genera of the Clausiliidae. Our molecular phylogram that was inferred from mitochondrial cytochrome oxidase (COI) gene sequences revealed multiple inversion events and in each case very close evolutionary relationships between the enantiomorph pairs. The COI phylogeny is well supported by apomorphic morphological traits, and these together provide reliable basis for a comprehensive taxonomic revision of Alopia species. The deduced phylogenetic lineages gave important clues for reconstructing the zoogeographical history of the genus. Furthermore, our results also suggest that due to the relatively unstable inheritance of coil direction Alopia species might become attractive experimental models for genetic studies aimed at elucidating the molecular basis of chiral stability.

Evolutionarily successful asexuals: examples from plants and lichens [Talk]

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Most switches to asexual reproduction are independent, evolutionarily young events that are sometimes connected with environmental change. The performance of a range of organisms representing various forms of asexuality is assessed here. *Potamogeton*, the largest genus of the pondweed family (Potamogetonaceae), has worldwide distribution. Many hybrid taxa are known; most of them are sterile and propagate vegetatively. Some of these genotypes may date back to post-glacial times when hybrid establishment was facilitated by the colonization of new habitats. Although they are evolutionary dead ends, due to their abundance and longevity, *Potamogeton* hybrids represent a non-negligible part of aquatic plant biodiversity. *Hieracium* and *Pilosella* (Asteraceae), two closely related hawkweed genera with mainly European distribution, are characterized by few diploids and large numbers of polyploids.

Different kinds of apomixis emerged in these groups. In *Hieracium* (diplospory), only diploids are sexual; most are rare and confined to un-glaciated refugia. Polyploids are most likely obligate apomicts; many are widespread. The emergence of polyploidy/apomixis may be connected with abundant hybridization when isolated lineages that survived in different glacial refugia came into secondary contact. Although apomicts do not seem to produce additional variation nowadays, due to their high species numbers and wide distribution, they are mainly responsible for the survival and spread of the genus. In *Pilosella* (apospory), apomixis is a facultative trait. Apomicts are strongly involved in the recurrent formation of new genotypes as male or female parents and produce an even higher diversity of different progeny than sexuals. Favorable genotypes with a high degree of apomictically produced offspring can spread over large distances. As a result, many apomictic *Pilosellas* are invasive on other continents. *Lepraria* (Stereocaulaceae) is a genus of sterile lichens with worldwide distribution. As there are no indications of sexual reproduction, these haploid ascomycetes might represent ancient asexuals. Their speciation was accompanied by large genetic diversification, comparable to the level of variation within (sub)tribes or even families in plants. While it is unclear how such a high diversity can be generated in the apparent absence of recombination, asexual reproduction as such obviously does not diminish the evolutionary success of this group.

Genome size evolution in the family Zingiberaceae [Talk]

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Genome size is an important characteristic of a species and is often correlated with diverse life traits. However, there is little known about evolutionary trends in genome size change, especially at the family level. Several mechanisms of genome size change during evolution were proposed but there is scarce knowledge whether up- or downsizing of the genome size is prevalent throughout phylogeny. Furthermore, mostly temperate groups of plants were investigated and almost nothing is known about genome size evolution of plants in tropical and subtropical climate zone. Zingiberaceae is the largest (ca 1,500 species in ca. 55 genera) and the most complex family of Zingiberales order and is distributed in the tropical and subtropical zones on three continents (Asia, Africa and Southern America). It comprises of four subfamilies from which two are monotypic or very small (Tamijioideae and Siphonochiloideae, respectively). The Alpinioideae is most diverse in evergreen tropics forests and members of this group are continuously growing with more or less obvious peaks of rapid growth and flowering. In contrast members of Zingiberoideae are most common in areas of monsoon climate. Life cycle of the majority of the species include a dormant period to overcome dry season. Such contrasting life strategies make Zingiberaceae an ideal group to study whether tempo, mode and directional trends of genome size changes are influenced by seasonality. We measured absolute genome size (2C) of more than 250 species from all Zingiberaceae genera and correlated this with phylogeny based on the sequencing (ITS and matK) of the same specimens. Phylogenetic association, mode and tempo of genome size evolution were tested using lambda, kappa and delta parameters, respectively, using a Bayesian framework in BayesTraits. Higher variation of genome sizes was found within Zingiberoideae with several polyploid genera (*e.g.*, *Curcuma*, *Globba*).

However, different evolution of genome size was observed in both families. In Alpinioideae, genome size evolution is correlated with phylogeny but not completely in Zingiberoideae. There is a gradual change of genome size in Alpinioideae and a tendency to punctuational evolution in Zingiberoideae. Moreover, a signature of accelerating evolution as time progresses was detected in Zingiberoideae.

Phylogeography and speciation of the Spot-backed Antbird (*Hylophylax naevius*) in lowland Amazonia [Talk]

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Phylogeography of species distributed across barriers such as rivers and mountains may help to understand speciation in the Neotropical region. The phylogeography of the Spot-backed Antbird complex (*Hylophylax naevius*; Aves, Thamnophilidae) was investigated throughout its range in the Amazon basin and in trans-Andean South. The sampling of a total of ~100 individuals encompassed opposite banks of the major Amazonian rivers and both sides of the Andes. Nucleotide sequences from two mtDNA genes (1015 bp of cyt b and 1023 bp of ND2), and one nuclear gene (539 bp of BF5) were obtained. Allopatric/parapatric well-supported lineages were uncovered within the *H. naevius* complex with high levels of genetic differentiation, on opposite sides of major Amazonian rivers (0.6–7.1 %) and across the Andes (6.9 %). A striking result was the observed paraphyly of Cis-Andean populations (*H. naevius*) with respect to the Trans-Andean populations (*H. naevioides*), indicating the former taxon ought to be separated into distinct species. A second instance of paraphyly was observed in the *H. n. theresae* subspecies, demonstrating the existence of a yet undescribed new taxa which can also be diagnosed morphologically and vocaly. Molecular dating indicating speciation at different periods and associated with distinct vicariant events suggest that biodiversity in the Amazon was shaped by very distinct historical processes.

Exploring slime mould diversity in high-altitude forests and grasslands by environmental RNA analysis [Talk]

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Myxomycetes, the plasmodial slime-moulds, a monophyletic taxon (ca. 900 species) in the phylum Amoebozoa, are distinctive amoebae with a complex life cycle culminating in the formation of mostly macroscopic fruiting bodies. They are found in nearly every terrestrial biome and as amoeboflagellates in aquatic environments where they cannot form fruiting bodies. Recently it has been shown that they are one of the major components of the soil protistan community. Despite this, they are absent from nearly all environmental sampling studies, probably because of their highly diverging SSU rDNA gene sequences. For the first time, *Myxomycetes* partial SSU rDNA sequences have been obtained from soil-extracted RNA by using specific primers. Soil samples were collected in three ranges of mountains (French Alps, Scotland and Hokkaido), next to remaining snow patches in spring, a habitat particularly rich in *Myxomycetes* that have very narrow ecological requirements, the nivicolous species. Seventy-three genotypes were retrieved, the majority (74%) had less than 98% percent similarity with known *Myxomycetes* sequences; only few genotypes were common to all sites. Our study provides insights into the community composition of an important group of protists and marks a direction for generalized studies about their distribution and abundance.

Stay high or get low: exploring epigenetic correlates of altitudinal variants in *Heliosperma pusillum* (Caryophyllaceae) [Talk]

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Adaptation is a fundamental property of living organisms and can be viewed as a process continuously moving a population towards a best fit phenotype in its current environment. Adaptation can take place on different temporal levels. Short-term variation within the reaction norm involves time frames shorter than individual life spans; it comprises labile epigenetic modifications and other mechanisms of short-term transcription regulation. Long-term, across-generation adaptation is based on natural selection acting on heritable variation (*i.e.*, segregating [epi]allelic variants) caused by processes such as mutation, alteration of (meta)stable epigenetic states, recombination and genetic drift. Across heterogeneous environment, variation in biotic and abiotic conditions and in the resulting selective pressures often leads to the formation of "ecotypes", *i.e.* distinct populations adapted to their specific habitat. Whereas they are usually still inter-fertile with other conspecific ecotypes, limited gene flow, *e.g.* via habitat isolation, may result over time in speciation. An interesting example for a multiple independent formation of ecotypes is found in the species complex of the Southeastern European mountain plant *Heliosperma pusillum* s.l., which comprises i) a widespread group of alpine plants occurring on the banks of creeks and moist calcareous screes as well as ii) several lowland representatives with smaller distribution ranges inhabiting gorges and rock overhangs in the Southeastern Alps and on the Balkan Peninsula. Results from AFLP fingerprints indicate that there is no overall genetic differentiation between altitudinal variants of H. pusillum s.l. that would parallel the conspicuous morphological and ecological differences. Nevertheless, morphology of the two types remains stable in offspring grown from seeds of high- and low altitude accessions in a common garden. In a current study, we use methylation sensitive amplified polymorphism (MSAP) to test for genome-wide differences in DNA methylation correlated with the striking phenotypic differentiation between high- and low altitude populations and discuss the possible role of epigenetics in the initial phase of divergent evolution of ecotypes.

Testing molecular markers for phylogenetic signal – A case study in opisthobranch Gastropoda [Poster]

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Molecular systematics has entered the genomic era – however, malacologists are still utilizing datasets of standard nuclear and mitochondrial genes to infer phylogenetic hypotheses due to the lack of adequate genomic data. Albeit, these standard markers (nuclear markers H3, 18S rRNA and 28S rRNA, mitochondrial markers 16S rRNA and COI) have produced inconclusive results with regards to phylogenetic relationships. This holds true for Mollusca in general but even more so for Gastropoda and their subgroups. The aim of our study is to test different molecular markers for phylogenetic signal at different taxonomic levels. Our study group are opisthobranch Gastropoda. We will subject sequence datasets to a battery of a priori tests (e. g. alignment masking, split decomposition, networks). Tree reconstruction will utilize optimized datasets integrating phylogenetic signal at the respective taxonomic level. Moreover, based on mitogenomic data available we search for potential novel markers which are amplified in a set of species of opisthobranchs and are likewise rigorously tested for phylogenetic signal prior to tree reconstruction.

Champuru, SeqPHASE and FFRhunter: an online software suite for phasing heterozygotes and using them to delineate species [Software Bazar]

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Here I present three online programs that I have developed to facilitate species delimitation using nuclear sequence markers. Direct sequencing of nuclear markers yields homozygotes (that have no double peaks in their chromatograms), heterozygotes with only one base difference between their alleles (one double peak), length-variant heterozygotes (many double peaks) and heterozygotes with multiple SNPs (several double peaks). Phasing in the first two cases is trivial, the third case can be solved automatically using Champuru (that reconstructs the two alleles using the information available in the forward and reverse chromatograms) and the fourth case can be solved in a Baysesian framework using SeqPHASE and PHASE (that compares the genotypes of the individuals sequenced in order to infer their most probable haplotypes). As a last step, FFRhunter finds reproductively isolated gene pools in the resulting alignment of phased sequences and delineates species using the criterion of mutual allelic exclusivity.

Delimiting cryptic species using haplowebs and the criterion of mutual allelic exclusivity [Talk]

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Common molecular approaches to delineate cryptic species fall in either of two categories. On the one hand, population genetic approaches rely on restrictive assumptions on the population and genome structure of the organisms under scrutiny and necessitate data from large numbers of individuals and of independent markers. On the other hand, phylogenetic approaches can yield meaningful conclusions from just a handful of individuals and markers but only delineate taxa that are reciprocally monophyletic. The latter limitation is particularly problematic since one-fourth of well-documented animal species turn out to be non-monophyletic in phylogenetic trees obtained from mitochondrial DNA. To solve this dilemma, I propose to abandon the criterion of reciprocal allelic monophyly and replace it with the more sensitive criterion of mutual allelic exclusivity, and will illustrate this approach with practical examples of its application to various phyla.

Genomic signatures of ameiotic evolution in the bdelloid rotifer *Adineta vaga* [Poster]

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Bdelloid rotifers are considered as “something of an evolutionary scandal” because of their apparent persistence for more than 40 million years without sex, which contradicts the common assumption that strict asexual reproduction represents an evolutionary “dead end” for metazoans. Indeed, bdelloid rotifers not only appear to have survived without sex for a very long time, but have even diversified into more than 460 currently recognized species. Moreover, bdelloids are extremely resistant to radiations and desiccation, which allows them to survive in semi-terrestrial environments that dry out frequently. To investigate the genomic consequences of a long-term absence of meiosis, 454 shotgun sequencing of the genome of the bdelloid *Adineta vaga* (a degenerate tetraploid) was performed using three different libraries with insert sizes of 3kb, 8kb and 20kb, respectively. Assembly proved very challenging due to the moderate heterozygosity of this organism, which was at the same time too high for allelic regions to be fused together and too low for them to be assembled separately. This was unexpected, as theory predicts that allelic regions of ameiotic organisms should become more and more divergent with time (the so-called “Meselson effect”). The apparent absence of Meselson effect in *Adineta vaga* may be explained by the occurrence of mitotic recombination.

Morphology, phylogeny and ecology of ciliates (Protists, Ciliophora) from tank bromeliads [Talk]

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Bromeliads are rosette plants occurring mainly in Central and South America. They collect rainwater and particulate materials in tanks (cisterns) formed by the coalescing leaf axils. The tanks are inhabited by many ordinary and endemic organisms, ranging from small insect larvae to large crustaceans and amphibians. Protists, in contrast, have been poorly researched. Thus, it was easy to discover about 40 new ciliate species in the tanks, many representing new genera and families. Here, we report on two outstanding species: *Bromeliothrix metopoides* and *Glaucomides bromelicola*. The first is a small (~ 20–40 × 15–30 µm) colpodid ciliate that likely evolved from the very common soil ciliate *Paracolpoda steinii*. Basically, *B. metopoides* is a bacteria feeder but when their abundance decreases under a certain level, large (~ 55 × 30 µm) macrostome specimens develop, feeding specifically on a heterotrophic, 20–40 µm-sized flagellate of the genus Polytomella. When the environmental conditions become unfavourable, B. metopoides produces resting cysts. Experiments showed that *B. metopoides* needs an unusually high food threshold (> 1.4 mg C/L). Its maximum growth rates (6.8 doubling/d!) belong to the highest one recorded thus far for freshwater ciliates. Glaucomides bromelicola is about 60 × 40 µm in size and belongs to the order Tetrahymenida. Its life cycle is similar to that of B. metopoides but it cannot make resting cysts. *Glaucomides bromelicola* belongs to a group of species that evolved in bromeliad tanks. The ancestor is *Glaucoma scintillans*, a cosmopolite in running and stagnant freshwaters. (Supported by FWF project 20360-B17 and DFG grant STO 414/3-2.)

Expression patterns of segment polarity genes in an onychophoran suggest that parasegments evolved in arthropods [Talk]

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Body organisation into serially repeated units or segments is found in several distantly related animal groups, including chordates, annelids and arthropods. The evolutionary origin of body segmentation in these groups has been discussed controversially. Among segmented bilaterian taxa, only arthropods show two types of segmentation: the embryonic parasegments and the adult segments. Based on gene expression data, the arthropod parasegments have been homologised with the adult segments of annelids, suggesting that the adult segments are a derived feature of arthropods. However, such a dual nature of body segmentation has not been described from Onychophora (velvet worms), one of the closest relatives of arthropods, and therefore it is unclear whether onychophorans show segments, parasegments or both. To address this issue and to contribute to the discussion on the evolution of animal body segmentation, we analysed the expression patterns of the segment polarity genes engrailed, wingless, hedgehog and cubitus interruptus in embryos of the onychophoran *Euperipatoides rowelli*. Our data show that the antero-posterior order of expression domains of these genes corresponds in onychophorans and arthropods, suggesting that the subdivision of the body into repeated genetic units predated the evolution of externally visible segmental boundaries in panarthropods. The analysed gene expression patterns revealed only one type of segmentation in onychophorans, which is homologous to the adult segmentation in arthropods. This suggests that the embryonic parasegments are a derived feature of arthropods, which contradicts the proposed homology of the arthropod parasegments with the adult segments of annelids.

The biogeography and phylogeny of Lymnaeidae (Gastropoda: Pulmonata) in Southeast Asia – Insights from new data [Poster]

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Southeast (SE) Asia is one of the most interesting and probably the world‘s second largest freshwater fauna hotspot. However, previous research on SE Asian biota is limited and does not encompass a variety of freshwater fauna, including family Lymnaeidae. Malacological interest aside, species from this family are also of high parasitological importance as they act as intermediate hosts to numerous trematode species. However, combined shell and anatomical plasticity have contributed to the long and controversial systematic history of the lymnaeids. Thus, recent studies have involved the use of several molecular methods to reveal deeper (interspecific) relationships among this family. Recent studies have distinguished three deeply-rooted clades of Lymnaeidae by geographic origin: namely Eurasian, American and Indo-Pacific species, the latter including all Australasian and *Radix* species. Based on chromosome numbers the basal clade tends to encompass species from Europe and North American. Radix seems to have arisen in Eurasia through chromosome reduction following the split of Nearctic and Palearctic. A separate chromosome reduction event may have led to the evolution of the genus *Austropeplea*. This was subsequent to the dispersal of ancestors from Eurasia to Australia due to the convergence of Australian and Gondwanan fragments. European *Radix* species seem to be more closely related to Australian lymnaeids than Asian *Radix* species. Depending on molecular markers used, *Radix* appears to be either mono- (combined 16S and ITS) or paraphyletic (16S). Here, we present a phylogeny of SE Asian lymnaeids based on DNA sequence data from mitochondrial 16S and nuclear internal transcribed spacer (ITS) markers. We will also discuss biogeographic patterns based on recent findings on the regions complex and dynamic geological and climatic history. In addition, we performed a molecular clock analysis to examine the diversification and distribution of lymnaeids across SE Asia and neighbouring regions through time.

Molecular determination of larval Digenea as basis for epidemiology, biodiversity and medical data [Poster]

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Digenean trematodes (= Digenea) comprise numerous species of medical and veterinary importance. They have complicated life cycles with molluscs serving as obligate first intermediate hosts, inhabiting sporocysts, rediae and cercariae. Often, those stages are morphologically indistinct and therefore not determinable at the species level. Cercarial monitorings therefore frequently face the problem of unconfident species determination. Since DNA data of many economic important species are available in databases, molecular methods are advantageous for species assignment. During a repeated cercarial screening in Eastern Austria – focused on several pulmonate aquatic snail species (more than 15,000 specimens), a number of digenean trematodes were recorded. Species in focus of the study have been the invasive American Liver Fluke *Fascioloides magna*, as well as species of the family Schistosomatidae, parasites of birds, the cercariae of which may cause dermatitis in humans and animals. The samples from affected snails were tested by PCR for both, the presence of trematodes in general and the identification of several species of economic importance. For this purpose, several primers were developed to enable the specific detection of relevant pathogens like *Fascioloides magna*, *Fasciola hepatica*, *Trichobilharzia* spp. and *Bilharziella polonica*. By subsequent sequencing of the PCR products and alignment with reference sequences, a species-specific identification of the digenetic specimens could be achieved. As a result we gain more reliable species lists and therewith proper epidemiological data of the species mentioned above. Host-parasite species lists and prevalence data are given here. Besides the taxa mentioned, we found other digeneans of several families, so that further determinations are to be conducted. Thorough tools for species delimitation of parasitic organisms warrant reliable epidemiological analyses, proper ecological evaluations, enhanced biodiversity data and significant medical risk assessments.

Biodiversity of Austrian recent ostracods [Talk]

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The last species list of recent ostracods of Austria done by Löffler dates from 1963 and includes 80 species and subspecies. During the subsequent years and due to the intensive research on ground waters and lakes of the Salzkammergut, 5 species were added to the list. Taxonomical research done on the ostracod fauna of Danube River, the backwaters of March and Danube River, two lakes of Upper Austria and one of Tyrol and of several ponds in Lower Austria (Gaviria, unpubl. reports), resulted in records of 5 supplementary species for the country and extended the distribution of known species to new departments. *Fabaeformiscandona balatonica*, *F. brevicornis* and *Physiocypria kraepelini* within the

Candidonidae, *Prionocypris zenkeri* and *Heterocypris reptans* within the Cyprididae are new for the country. Thus, the present biodiversity of ostracods reaches 90 species and subspecies. The modern taxonomy of the order *Podocopida* has included creation of new genera (*e.g. Fabaeformiscandona*, *Mixtacandona*, *Brandleystrandesia*) and recognition of cases of synonimies, not clearly recognized before 2000. In the national aquatic animal catalogue Fauna Acuatica Austriaca, this crustacean group has not been treated. This speech pretends to show the present inventory of the ostracod species, their distribution in the country and remarks on the taxonomy of some species that still remain to be clarified applying morphological and probably genetic characters.

Systematics and evolution within the hyperdiverse lichen family Teloschistaceae (Ascomycota, Fungi) [Talk]

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Using a cumulative supermatrix approach to generate a comprehensive multi-locus phylogeny, we have recently re-circumscribed and proposed a new classification for the orders Caliciales and Teloschistales. Within the Teloschistales, the family Teloschistaceae outstands by being the most specious group (more than 600 species) and encompassing an extraordinary phenotypic diversity. The resolution of its phylogenetic relationships has been hindered by the limitation in the resolving power that a single-locus or two-locus phylogenetic studies have provided up do date. In our previous studies, we conducted the most exhaustive phylogenetic survey of species within the Teloschistaceae by restricting the sequencing to ITS. The expected consequence in adding more taxa without adding characters was the loss of significant support for deep internodes. In this context, an extensive taxon sampling within the Teloschistaceae with more loci (especially nuclear protein-coding genes) were needed to confront the current taxonomic delimitations and to improve our understanding of evolutionary trends within this family. The present study assessed this issue using eight loci, including several protein-coding genes apart from nuclear and mitochondrial ribosomal loci. We also used this study to validate some of the newly designed primers by the AFTOL2 phylogenomic approach to develop new genes for phylogenetic studies of fungi. We tested EFT2, KRR1, FAL1, CTK1, and RET1_2. CTK1 and RET1_2 seem to perform the best within the Teloschistaceae. We predict these two markers will be useful in other phylogenetic studies of fungi. Mcm7 was also tested within the context of the Teloschistaceae and resulted sufficiently phylogenetically informative. Additionally, we are presenting a first reconstruction of the evolution of several phenotypic traits, especially secondary compounds, the evolution of substrate preferences in relation to land plant evolution, and an in-depth characterization for a major taxonomic redelimitation of genera within this family. Populating the Teloschistaceae tree with representatives of all types of growth habits, substrates,

secondary compounds, habitats, we will be able to reconstruct the evolution of major traits that have shaped this diverse group of lichens. Finally, we are also exploring the effect of including or not ambiguous regions in such a large dataset with the method PICS-Ord and a morphology-based phylogenetic binning method.

Introducing the Fredie Project with notes on the freshwater fish diversity of the Mediterranean hot-spot [Talk + Poster]

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FREDIE stands for ‘Freshwater Diversity Identification for Europe’ and is a nationally funded project aimed at bringing together DNA barcoding with taxonomic expertise for European freshwater organisms (www.fredie.eu). Included are freshwater fishes, mayflies and freshwater molluscs, and we aim to develop an online available identification system for species diversity of these groups in Europe. Although DNA barcoding offers the possibility to accelerate detection and monitoring of biodiversity, its quality and significance is strictly bound to availability and quality of underlying reference data, especially reliable species determinations. Resources and expertise of three core institutes and a web of associated partners are combined to create a reliable and sustainable reference system. Representatives of nearly all species of the three groups occurring between Portugal and the Ural are collected, identified by experts and sequenced to become barcode references. In selected cases a refined identification system is planned including morphological characters and other genetic markers with better taxonomical resolution. We will provide the respective voucher specimens and a DNA collection as permanent references available to the scientific community. FREDIE generates molecular and morphological estimations of species numbers of the three organism groups for Europe, as well as deeper insights into their spatial structure on a large scale. In a first sub-project we focused on the freshwater fish diversity of the Mediterranean hot-spot, which harbors about 557 extant species. We were able to obtain so far more than 95% of these species, represented by >3,500 individuals by own collecting efforts and support by European colleagues. Through intensive sampling of widely distributed taxa from several major European drainages, some possessing different levels of morphological divergence and specific designation, we evaluated the performance of barcoding in distinguishing sister-species. The analysis of geographic variation revealed both, previously known but also underappreciated phylogeographic breaks among different taxa. This has important conservation implications for those species and populations and further enhances our understanding of the biogeography and evolution of European freshwater fish diversity.

Diversity and habitat partitioning of the ectomycorrhizal *Cortinarius* in boreal forest and arctic tundra ecosystems [Talk]

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Mycorrhizal fungi play crucial roles in the functioning of ecosystems at cold-dominated habitats, such as the arctic tundra and the boreal forest, because these fungi greatly enhance their host plants' access to nutrients that are otherwise scarcely available. *Cortinarius* is considered to be among the most species-rich fungal genera in boreal and arctic regions, yet very little known about the diversity of *Cortinarius* species and their distribution among various vegetation types. In this paper, we analyzed ITS rDNA sequences from both curated sporocarp collections and soil PCR clone libraries sampled in the arctic tundra and boreal forests of Alaska. Our genetic diversity assessment, based on various phylogenetic methods and operational taxonomic unit (OTU) delimitations, suggests that the genus *Cortinarius* is very diverse in Alaska, including both known species and possibly novel and/or previously unsequenced groups. Many *Cortinarius* taxa show strong habitat preference to certain vegetation types as well as strong soil horizon preference, as supported by statistical analyses, such as non-metric multidimensional scaling (NMS). Together, our data robustly demonstrate great diversity and non-random ecological partitioning in an important boreal ectomycorrhizal genus within a relatively small geographic region.

Molecular differentiation and ecology in cryptic bumblebee species of the *Bombus lucorum* complex [Poster]

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Bumblebees are among the most important pollinators in the high mountain regions. Within the *Bombus lucorum*-complex at least two cryptic species (*Bombus lucorum*, *B. cryptarum*) inhabit the Alps; a third one (*B. magnus*) cannot be excluded to occur. Recent taxonomic studies using molecular markers to investigate the *B. lucorum*-complex, found that colour patterns traditionally used for species identification do not correspond with the distinct molecular operational taxonomic units. Furthermore, no characteristic colour pattern for any of these species was found and some traits showed gradual variation across the species. Hence, a reliable identification of females based on morphological characters alone seems impossible. DNA-barcoding represents an objective and reproducible method for species determination in the challenging *Bombus lucorum*-complex and provides a basis to study altitudinal preferences, ecological and morphological characters. The present study comprises nine regions in the Austrian Alps ranging from

the Silvretta in the west to the Schneeberg in the east. Along altitudinal transects of 1900 m – ranging from 1000 to 2900 m a.s.l. where possible – bumblebees belonging to the *B. lucorum*-complex were collected. The geographical and altitudinal range of the area under investigation will provide sufficient data to answer following research questions: – Are there differences in the occurrence of the species in various geographical expositions and elevations in the Austrian Alps? – Do the species show different flower preferences? – How reliable are morphological characters for species determination by re-evaluation using DNA-barcoded specimens? We present current findings and first conclusions of our ongoing study.

Advancing the Biodiversity Exploratories Information System (BExIS) [Software Bazar]

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The Biodiversity Exploratories Information System (BExIS) is a virtual environment for interdisciplinary, collaborative research. Starting in 2006 the system has been developed as a long-term data repository, resource management and information exchange platform for the Biodiversity Exploratories project. Currently, the Exploratories comprise around 40 sub-projects and more than 300 users from disciplines ranging from soil science to remote sensing and from genetics to landscape ecology. The system supports this diversity by allowing flexible, user-defined data structures for primary data. BExIS is accessed through a web interface containing functionality for data storage and management (upload, download, update of primary data; creating and publishing metadata, fieldbook) and for viewing and processing data (*e.g.* merging data, statistics). Based on additional funding by the German Science Foundation (DFG), BExIS is currently being redesigned and reengineered to become a generic biodiversity repository software (BExIS++) that is modular, scalable and adaptable to other use cases. During this 3 year process existing features are being enhanced (*e.g.* security, authorization, geospatial data support, visualization) and new feature are added (*e.g.* Lucene search engine with faceted search interface, mobile client support). The BExIS++ system builds on Microsoft .NET technology and will be provided under a creative commons licence.

Investigating horizontal *Wolbachia* transmission between bees (Anthophila) and their kleptoparasites [Talk]

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Wolbachia is a maternally inherited intracellular symbiont that is found in most terrestrial arthropods and in filarial nematodes. Some aspects of *Wolbachia* biology are fairly well understood and much research has been focussed on how the bacteria alter their hosts' reproduction to enhance the rate of their vertical transmission. It is mainly unclear however, how *Wolbachia* spreads between hosts laterally. Indirect (phylogenetic) evidence suggests that such interspecific transfer occurs between closely and distantly related hosts; proposed mechanisms include shared food sources, ectoparasites and parasitoids. In our study, we aim to contribute to the understanding of horizontal *Wolbachia* transmission among bees (Anthophila). Specifically, we hypothesize that the bacteria are transmitted between bees and corresponding kleptoparasites via saliva present in provisions provided by bees for their offspring. After establishing that *Wolbachia* may invade salivary glands of bees using antibody-staining, we performed a MLST typing of Wolbachia strains from bee hosts. The sampling focussed on kleptoparasite-host pairs and enabled us to test if those bear *Wolbachia* more often than expected by chance. We found that transmission via saliva in provisions is not the predominant mechanism by which *Wolbachia* spreads among bees. Based on a phylogeny of bees that bear Wolbachia we were able to identify instances of co-speciation between bees and Wolbachia. Although such cases are generally regarded to be rare, we argue that vertical transmission may be a major determining factor of *Wolbachia*'s distribution patterns among arthropods.

Taxonomic revision and phylogeny of *Corticium* s.l. (Corticiales, Basidiomycota) in Europe [Poster]

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Resupinate basidiomycetes collectively referred to as 'corticioids' are a form group of basidiomycetes which have been largely neglected in mycological inventories due to their inconspicuous fruiting bodies, and also because of their problematic identification and classification. The pinkish resupinate genus

Corticium is the core genus of this group and comprises several satellite genera with similar morphological characteristics, viz. *Dendrocorticium*, *Laeticorticium*, *Dentocorticium etc.* Taxonomy of *Corticium*-like taxa is poorly understood and they have never been subject to a comprehensive phylogenetic study. The majority of the species in *Corticium* have been described from Europe. *Corticium* is the type genus of the recently recognized order Corticiales. Recent studies by the author and colleagues in the order Corticiales presented a preliminary refinement of the family arrangements for this order, and gave insights into the taxonomic resolution for entities included in *Corticium* sensu lato. Notably, it was shown that unlike the earlier presumptions, *Corticium* in strict sense and *Dendrocorticium* are distantly related, nesting in two different families in the Corticiales, Corticiaceae s.s. and Punctulariaceae, respectively. The results were however calling for a comprehensive sampling of the taxa in question. In this project we aimed to elucidate the species diversity, phylogeny and taxonomy of the corticioid genus *Corticium* in Europe for the first time, using extensive morphological examinations and molecular markers. Attempts were made to study type and additional specimens of all species morphologically, to provide support for the correct application of species names, and to obtain and analyse sequences of nuclear and mitochondrial genes for the species.

Diversity of lichens on the Tomb of Cyrus the Great, Pasargadae, Iran [Poster]

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Lichens are intimate and long-term stable symbiotic relationships between two or more organisms joined to form a new biological entity different from its individual components including photosynthetic, unicellular algae and or cyanobacteria and heterotrophic fungi. They survive in extreme environments which are intolerable for many other organisms. Lichens have important role in the nature as a part of biogenic weathering of rocks and soil production, but when this natural process occurs on stone monuments with historical value, it becomes a serious threat. Biodeterioration of the Tomb of Cyrus the Great in Pasargadae, one of Iran's cultural heritages, because of lichens growth, is an important problem for preservation of this ancient monument. The amount and rate of deterioration depends on several factors such as species involved, type of substrate, climate and many others, so techniques to prevent or remove lichens are selected by considering these factors. With this approach, biodiversity of destructive lichens in the Tomb was studied. Macroscopic and microscopic morphology and biochemical characteristics of species were carefully evaluated. The results indicate the presence of about 25 species of lichens growing on the stone work. Most of these species belong to *Caloplaca* spp., *Acarospora* spp, *Lecanora* spp. *Polysporina* spp. and *Verrucaria* spp. Our Study also showed that almost all of the studied species are crustose, and *Caloplaca* erodens effectively involved in substrate destruction. Another result of this study is that the used cleaning techniques applied do not have a good efficiency. The results of this study can be used for the selection of appropriate control methods and investigation of environmental factors influencing the lichens variety.

Natural history collections today: within the limits of raw data for basic research and objects of cultural heritage [Talk]

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Natural history collections in Europe, some with collection histories spanning more than two centuries, are and have been the basis for fundamental research typically in the fields of taxonomy, biodiversity, biogeography and evolution. As for any research collection, the roles to fulfil are manifold – individuals of the collection as part of a larger series of specimens in this or other collections can serve to obtain a data point to answer an overarching question, to test a hypothesis *etc.* At the same time, the specimen itself can, due to its history and accompanying data, be of cultural importance. This double function of natural history collections as a research tool and an object of the cultural heritage that needs to be protected must be kept in mind, when research interests of users demand the violation of the physical integrity of a specimen. One workaround to this problem may be of technical nature – modern imaging techniques for rare and fragile objects can provide the data needed without harming the specimen in question. This talk will explore various non-invasive approaches of sampling museum specimens for morphological research on zoological and paleontological specimens.

The orbital mosaic in mammals: characters and implications [Poster]

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The arrangement of bones forming the lateral part of the skull in the orbito-temporal region has variedly been used in mammalian systematics, both prior and after the general revision of higher mammalian phylogeny based on molecular data. Morphological characters from this region were used in primate or carnivore systematics and prior to the separation of the Afrosoricida (tenrecs and golden moles) from the former Lipotyphla, the latter were unified by a separation of the palatine and frontal bones by a caudally extended maxilla. Besides straightforward cases of easily assessed characters (*e.g.* sutures and Foramina), in some taxa the characters involved are obscured, thus impeding the examination. In a review, the obstacles for a correct analysis of the orbital mosaic are illustrated and some characters are further explored in this systematic context.

Tracing back the snail trail – What freshwater gastropods tell us about the colonization of "down under" [Talk]

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Due to their limited potential of dispersal in the face of wide distribution, ubiquity and high abundance, snails tend to preserve distribution patterns over long periods of time and are thus suitable organisms for studying phylogeography. We present here preliminary results of our ongoing study on freshwater Thiaridae (Caenogastropoda: Cerithioidea) with focus on Australia. Based on own collections, relevant type material and the comparison with material in major Australian museum collections we document their geographical distribution (with over 900 records) with references ranging from world-wide patterns to smaller scaled drainage-based characteristics. The origin of Australian faunal elements and the directionality and timing of colonizations are controversial. As to the thiarids we tested whether they are either an "appendage" of the SE Asian biota, or originated on the Australian continent since ancient times. We applied molecular phylogenetic techniques analyzing mitochondrial 16S rRNA and cytochrome oxidase I gene sequences as well as histone H3 subunit and 28S rRNA gene sequences for representative thiarids from all over the world. The resulting gene trees indicate multiple colonization of Australia by different lineages of these freshwater taxa and do not give reason to refute the hypothesis of Gondwanan origin of the family. By this means we identify a total of eleven distinct clades in Australia (corroborating the morphologically distinguished genera and species, respectively) of which four represent species being endemic to the continent. Concerning their reproductive biology we find two distinct viviparous modes within the Australian thiarids. While the live-bearing thiarids that release veligers are found to have very restricted occurrences, the more widely distributed thiarids of Australia all brood and release shelled juveniles. The role of the different viviparous modes as a dispersal factor remains to be evaluated according to their occurrences in the different river drainage systems. We use the Amplified fragment length polymorphism (AFLP) technique to assess genetic variation and population structuring with regard to the different river drainage systems. Our first AFLP results are largely congruent with the current geographic distribution and indicate that the technique could help to get a better insight into contemporary relationships between Australian taxa in order to finally illuminate the colonization history of the continent.

Free access to biodiversity data? How to contribute to GBIF – and why [Poster]

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The Global Biodiversity Information Facility (GBIF) is an international initiative of 57 countries and 47 organizations. GBIF has the overall mission of mobilizing the world's primary biodiversity data via the Internet. The GBIF network currently provides access to more than 388 million records. GBIF was established in 2001 and Germany is one of the founding nations. Currently GBIF Germany (GBIF-D, www.gbif.de) is funded as a 3-year project by the Federal Ministry of Education and Research (BMBF, 01LI 1001 A-F). Eight institutional nodes form the backbone of GBIF-D. The Botanic Garden and Botanical Museum Berlin-Dahlem is responsible for coordination as well as for plants and protists; the German Collection of Microorganisms and Cell Cultures in Braunschweig for bacteria and archaea. In Munich, the Botanische and the Zoologische Staatssammlung are in charge of fungi, lichens and invertebrates (molluscs, arachnids and myriapods), respectively. The Museum fuer Naturkunde in Berlin is responsible for insects and fossils, Senckenberg in Frankfurt for invertebrates (marine invertebrates) and the Forschungsmuseum Alexander Koenig in Bonn for vertebrates. Main objective of GBIF-D is the mobilization of suitable data from Germany's research community, focussing on "species occurrence data", *i.e.* from collections and observations. In addition, GBIF-D offers expertise on technical aspects of data capture and database networking. Stable workflows to support the provider from data entry to open and free online access are established. But GBIF is far more than the mobilization of natural history collections data. We call on scientists to integrate their data into the GBIF network and to start using GBIF data for their own work, in order to benefit from the global effort GBIF represents.

GBIF-D: The German contribution to the Global Biodiversity Information Facility (GBIF)-Overview and perspectives [Talk]

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The Global Biodiversity Information Facility (GBIF, www.gbif.org) is an international initiative of 57 countries and 47 organizations established in 2001 by governments. The overall mission of GBIF is to facilitate free and open access to biodiversity data worldwide via the Internet. Currently the GBIF network provides access to more than 388 million records from over 10,000 datasets from more than 400 publishers. These data span a wide range of geospatial, temporal and taxonomic coverages. As a founding member GBIF Germany (GBIF-D, www.gbif.de) contributes since 2001 to this largest biodiversity information initiative worldwide. Main objective is the focused gathering and mobilization of suitable data from Germany's research community and natural history collections. Available observation data are linked into GBIF, too. In addition, GBIF-D offers expertise on technical aspects of data capture and database networking. Stable workflows to support the provider from data entry to open and free online access are established. Since the end of 2010 GBIF Germany is funded as a 3-years joint research project by the Federal Ministry of Education and Research (BMBF, 01LI1001A-F). Eight institutional nodes form the backbone of GBIF-D. The Botanic Garden and Botanical Museum Berlin-Dahlem is responsible for coordination as well as for plants and protists; the German Collection of Microorganisms and Cell Cultures in Braunschweig for bacteria and archaea. In Munich, the Botanische Staatssammlung and the Zoologische Staatssammlung are in charge of fungi, lichens and invertebrates (molluscs, arachnids and myriapods), respectively. The Museum fuer Naturkunde in Berlin is responsible for insects and fossils, Senckenberg in Frankfurt for invertebrates (marine invertebrates) and the Forschungsmuseum Alexander Koenig in Bonn for vertebrates. The eight project partners of GBIF-D are organizing the sharing data but also develop and provide software tools for data mobilization. The talk gives a short review of the goals and the organization of GBIF from the first years to today’s achievements on global and on German scale. In a second step it will give a first overview of the current work program of the German GBIF Nodes. More details about the latter will be presented in the subsequent talks in this session.

The phylogeny of interstitial annelid taxa using Next Generation Sequencing: when morphological data is not enough [Talk]

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The marine interstitium is a typical habitat for certain annelid taxa (i.e, Dinophilidae, Diurodrilidae, Nerillidae, Polygordiidae, Protodrilidae, Protodriloidae, and Saccocirridae), which are characterized by a small body size, weak segmentation, few or no appendages, parapodia or chaetae, and ventral ciliary gliding bands. Based on these features some of them had been considered as primitive annelids and as part of the basal grade "Archiannelida". To date however, "Archiannelida" is regarded as a polyphyletic assemblage of highly derived but secondarily simplified annelid taxa adapted to the interstitial realm. Due to this adaption, these taxa lack several characters, which are typical for larger annelids, and this lack causes the problem to differentiate between primary and secondary absence. This problem is very well known for different metazoan taxa of supposedly paedomorphic origin, an evolutionary process which is also proposed for interstitial annelid taxa. Within Annelida, *i.e.* dorvilleids, exhibit the greatest number of paedomorphic taxa. Due to similarities to eunicidan larva and investigations of parasite-host relationships, the former archiannelidan taxon Dinophilidae was placed within "Dorvilleidae" assuming paedomorphosis. However, Dinophilidae completely lack the ventral jaw apparatus, which is typical of Eunicida. Another example is Diurodrilidae, also a former member of "Archiannelida". Their phylogeny is still unclear based on morphological data only, because they lack common annelid characteristics. If they are annelids, this would be an extreme case of paedomorphosis. To recover the phylogeny of the former archiannelidan taxa we are using Next Generation Sequencing-Methods (Illumina shot gun sequencing) to generate complete mitochondrial genomes of about 15–17 kb. With this method we are able to get nearly complete mitochondrial genomes respectively large mitochondrial fragments. The preliminary Maximum Likelihood analysis of the mitochondrial sequence data showed the potential of these data to address the phylogenetic position of former archiannelidan taxa.

Rapid biodiversity assessment in biodiversity hotspots: diversity and diversification of New Caledonian leaf beetles [Talk]

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Biodiversity hotspots attracted a lot of attention in recent years precisely to characterize their particularly rich, unique and relatively endangered biota. In this effort, DNA-based biodiversity surveys generally proved to be cost-effective in terms of species characterization, but also species discovery and, sometimes, to study the underlying diversification processes leading to the diversity we observe today. New Caledonia, the fragmented piece of Gondwana in the western Pacific, is one such hotspot profiting from this approach for several groups of organisms. In our case, we worked with leaf beetles in the subfamily Eumolpinae, which contemporary taxonomic work – 48 newly described species in only five years – reveals as far more diverse than expected. To estimate how many species of New Caledonian Eumolpinae still await discovery, we used rapid DNA-based biodiversity assessment tools, exploring mtDNA (cox1 and rrnS) diversity and phylogenetic structure in a sample of 840 specimens across the main island in the archipelago. A notable concordance of species delimited by phenetic (Automated Barcode Gap Discovery) and phylogenetic (Generalized mixed Yule-Coalescent models) algorithms with those informed by external and genitalic differences (morphospecies) revealed some 98–110 species in our sample, twice as many as were described so far and all of them almost certainly endemic. The study of sample-based rarefaction curves and species estimators using these species counts doubled this figure (up to 210 species), a plausible outcome based on information on taxonomic coverage, local endemism and characteristics of sampling design, among others. New Caledonia, compared with larger tropical islands, stands out as a hotspot for Eumolpinae biodiversity. MtDNA phylogenies were also exploited to illuminate on the origins of this diversity. Molecular clocks using leaf-beetle specific rates or internal tree calibration using the Pleistocene uplifting of nearby islands, dated the root of the neocaledonian Eumolpinae tree (not necessarily a monophyletic radiation) at 38.5 Ma, implying colonisations well after the Late Cretaceous breakage of Gondwana. The diversification mode was consistent with a reduction in diversification rates through time, also consistent with recent faunal origins, possibly reflecting niche occupancy after a rapid initial diversification. Environmental factors (*e.g.* soil characteristics) seemingly played a role in this diversification process.

Molecular systematics of the shieldtail snakes (Uropeltidae) of South Asia [Talk]

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Uropeltidae Müller, 1832 comprises 48 nominal species (8 genera) restricted to Sri Lanka and peninsular India. These "shieldtails" are generally small, montane snakes that burrow in soil. Superficially at least, uropeltid systematics appears stable, with very little taxonomic action having taken place in the last 50 years, but there is a suspicion that this reflects lack of study rather than a robust understanding of diversity. The vast majority of taxonomic actions within Uropeltidae occurred in the 1800s and lack of attention since has left a somewhat fragile foundation with many probably valid species hidden in synonymy. Species delimitation and generic monophyly is not adequately determined because of little study, few systematic characters (for which variation is not well understood), and a confusing literature. We inferred the phylogenetic relationships of 63 uropeltid specimens representing approximately 20 species (5 genera) using mitochondrial (mt) and nuclear (nu) markers. The results support those from previous analyses of albumin immunological and allozyme data and preliminary DNA sequence analyses in recovering Sri Lankan uropeltids as monophyletic and Indian uropeltids as paraphyletic. Within the Sri Lankan clade *Rhinophis* is paraphyletic with respect to Uropeltis and Pseudotyphlops such that Sri Lankan species of the latter two genera should be transferred to Rhinophis to make the classification natural. The inferred topology is consistent with a single origin of Sri Lankan uropeltids from southernmost Indian lowland forms. Nominal Sri Lankan species, including recently described taxa, are strongly supported as monophyletic, lending support to most of the current taxonomy of the uropeltids of this island, including the perceived lack of variability in colour pattern and generally narrow geographic ranges of especially the montane forms. Some possibly undescribed, cryptic Sri Lankan species are indicated. The taxonomy of Indian Uropeltis is much less well founded.

Three new species of *Drusus*: Adult genital and larval characterisation [Poster]

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The caddisfly genus *Drusus* STEPHENS comprises roughly 100 species that inhabit mountain ranges in Europe, Asia Minor and the Caucasus. Here we present three new species of the genus Drusus and a hitherto unknown larva of Drusus macedonicus. All these species are closely related to *Drusus discolor*, *Drusus romanicus romanicus* and *D. r. meridionalis*, with which they share distinct features in feeding ecology, larval head capsule shape and adult morphology. The new species are clearly distinguished in both the larval and adult stages by unique features. Larvae can be identified by examination of fronto-clypeal shape and surface structure. The adults can be separated from other species by details in the genital apparatus. Additionally all these species are clearly differentiated genetically from another and all previously known species of *Drusus*. *Drusus krpachi* n. sp., *D. macedonicus*, and *D. sutjeskae* n. sp. are micro-endemics of the western Balkan ranges; *D. bucegi* n. sp. is an endemic of the Bucegi Mts in the south-eastern Carpathians.

Enhancing integration within biology with theoretical modelling under the semantic conception paradigm [Talk]

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Bio-ontologies, which provide a structured controlled biological vocabulary, have become the tool for achieving integration within biology. They aim at linking genomics with phenotypic traits through the semantics of structured knowledge they gather. For that reason, they rely on semantic standards for computer representation which make them computationally intelligible and allow for data mining. The discussion I present here focuses on morpho-anatomical bio-ontologies, which gather and structure descriptive concepts. They are referred to as theoretical models, leading me to analyze them in terms of the semantic conception of theories which provides philosophical foundations for the modelling activity. The semantic conception recognizes a model as structured knowledge to which constraints are applied. Here, given the term “bio-ontology”, the required constraints are ontological, *i.e.* constraints about that which is; hence bio-ontology usefulness for integrating phylogenetics and morpho-anatomy. Indeed, the ontology of biological entities depends on the phylogenetic test. In this framework, I present the link

between bio-ontologies, descriptive models and phylogenetic models. In this demonstration, bio-ontologies are the structures underlying the modelling activity. I show that descriptive models and phylogenetic trees can be reduced to the same family of models. Since phylogenetic trees are an ontology (through epistemic commitment regarding their representation, and ontological commitment regarding their conceptual content), descriptive models convey ontology through their representation at the very least (even though not through their content). I illustrate my point of view with the interoperability of two programs developed in the field of informatics for biodiversity: Xper2 (implementing descriptive models) and LisBeth (implementing phylogenetic models). I regret that current descriptive model programs do not rely on semantic standards for computer representation. These models are intelligible for researchers but only partially for computers. I show that the creation of interoperability between them and bio-ontologies (allowing models to be benefit from semantic standards) would considerably enhance integrative studies. This issue emphasizes the need for collaborative work between the biology community and developers.

LisBeth: a new cladistic tool for phylogenetics and biogeography [Poster & Doftware Bazar]

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We present LisBeth, the first and only phylogenetic/biogeographic program freely available that uses the three-item analysis (3ia) approach and offer some insights into its theoretical propositions. LisBeth includes a user-friendly Graphical User Interface and is aimed to become an open platform for computing in 3ia. LisBeth development is moving forward so as to offer updated versions for download. As admitted within cladistics, "hypotheses of homology cannot be corroborated or refuted outside of a scheme of relationships". With LisBeth, character representation is based on homology relationships, *i.e.* rooted trees or easy to use Venn diagrams. For the sake of interoperability, LisBeth can also import characters from matrix in NEXUS format or from Xper2 knowledge bases, allowing for the faithfulness to the logical dependencies among characters. LisBeth performs branch and bound analyses based on maximum congruence of three-item statements and calculates the intersection tree (a summary tree much more than a consensus). Trees may be edited, *i.e.* relative positions of terminals may be modified, and/or saved in eps format (*i.e.* vectorial) for printing. LisBeth implements the 3ia method for character interpretation, based on the tree topology and character state distributions. For the first time in 3ia, synapomorphies are identified at nodes. LisBeth provides support values: overall and per-character retention index (RI) and completeness index (Compl, with no precedent in any other phylogenetic program). In biogeography, LisBeth applies the transparent method to handle widespread taxa and implements paralogy-free subtree analysis to remove redundant distributions. LisBeth is freely available: http://www.infosyslab.fr/lis/?q=en/resources/software/lisbeth/download

Our team is fully inclined to help users step by step at taking ownership of the 3ia approach.

Genome size in *Botrychium* species and their evolution in the monilophyte basal group [Poster]

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Botrychium s.s. has more polyploid than diploid species with polyploidization events numerous and misunderstood. Flow cytometric analyses were performed in order to assess genome size in seven species in *Botrychium* s.l. Our results indicate different genome sizes in evolutionary history and dynamic events accross the monilophyte basal groups. This study could be the first step to investigate the dynamics in the genomes in the basal groups of land plants.

Morph·D·Base – a Data Repository and Web Portal for Morphological Data [Software Bazar]

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Morph·D·Base is an online web portal and data repository. Morph·D·Base is the way for researchers to sustainable archive, share and disseminate data of biological species and morphological research. It manages entries about taxa, biological specimens, literature, morphological character matrices, and media, including 3D image stacks. Researchers can provide detailed documentation for each entry, interlink the different entries, and can efficiently collaborate with colleagues.

Streamlining material- and data flow within the German Barcode of Life Project, GBOL [Talk]

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The material- and dataflow constitutes a crucial point within the German Barcode of Life Project (GBOL). Within this large-scaled project, a network of interactions span the material- and dataflow, from collecting the physical specimen, to laboratory processing and finally providing the barcode sequence and metadata. The underlying data system allows tracking the sampled material from the tissue sample to the final barcode sequence and back to the original specimen from an exact geographic location in Germany. The web site 'www.bolgermany.de' provides a portal for the taxonomic experts collaborating with GBOL to check which species and regions still need to be sampled, to order collecting material, to enter and update associated metadata for the collected specimen, and to submit the specimen to GBOL. The DiversityWorkbench framework (www.diversityworkbench.net) functions as central data repository for the GBOL project, stores laboratory data and is further extended to provide the possibility for sharing data among the web portal, the taxon coordinators and curators at the involved institutions. The GBOL consortium, composed mostly of natural history collections, archive and procure the voucher material, house the laboratories and workers as well as various external data services. These provide additional information relevant for the workflow and disseminate the results back to the public. Images are archived and disseminated via the morphological data repository MorphDBase (www.morphdbase.de).

What makes a worm a worm? [Talk]

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Myxozoa are a group of endoparasitic organisms now considered to be a highly derived taxon within the Cnidaria. Myxozoans, like many other endoparasites, are characterised by extremely simplified morphologies but have evolved a complex life cycle involving alternation between two different animal hosts. All myxozoans lack gonads, gametes, intestinal tracts, nerve cells and centrioles. Members of the myxozoan high level subtaxon *Malacosporea*, that infect freshwater bryozoans as their primary hosts, exhibit two distinctly different body plans. The worm-like *Buddenbrockia plumatellae* is unique and has retained a bizarre form of longitudinal musculature that enables vigorous swimming movements. In contrast, the closely related malacosporeans *Buddenbrockia allmani* and *Tetracapsuloides brysalmonae* are spherical, non-motile and lack musculature and any recognisable body polarity. We analyse morphology and development in *B. plumatellae* and *T. bryosalmonae* using confocal microscopy, electron microscopy histology and developmental gene expression data to address two questions: How may differences in the early development of these species potentially account for the drastic morphological variation observed? How have basic animal body plan features become reduced?

Recent microfauna and -flora in the Gulf of Cádiz and W off Portugal: basis for actualistic paleoceanographic research [Talk]

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IODP Expedition 339 Scientists (Acton, G., Bahr, A., Ducassou. E., Flood, R., Furota, S., Jimenez-Espejo, F., Kim, J. K., Krissek, L., Kuroda, J., Li, B., Llave, E., Lofi, J., Lourens, L., Miller, M., Nanayama, F., Nishida, N., Richter, C., Roque, C., Sanchez Goñi, M., Sierro Sanchez, F., Singh, A., Sloss, C., Takashimizu, Y., Tzanova, A., Voelker, A., Williams, T., Xuan, C.)

Actualism is the fundamental principle of modern paleobiology. Understanding the composition and distribution of recent faunal and floral communities enables us to reasonably reconstruct past environments. The basis of any actualistic approach is a thorough taxonomic groundwork. IODP Expedition 339 recently drilled 5 sites in the Gulf of Cádiz and 2 west off Portugal, and recovered 5.5 km of core. The Gulf of Cádiz was targeted for drilling 1) to investigate the Mediterranean Outflow Water (MOW) and its influence on global circulation and climate, and 2) to understand the effects of tectonic activity on evolution of the Gibraltar Gateway and margin sedimentation. During the expedition samples from surface-waters and the seafloor were collected to evaluate recent communities of foraminifers, ostracods and calcareous nannoplankton. The results will serve as an important reference for future paleoceanographic work based on the actualistic approach in the Upper Miocene-Pleistocene deposits drilled during IODP Expedition 339. Preliminary results on benthic foraminifers show that living specimens are rare, which is most likely related to deep-sea patchiness; loss during the drilling process cannot be excluded for some samples. Composition of live and dead assemblages strongly depends on water depth and position along the pathway of MOW. Combined with ostracod and nannoplankton assemblages the results will provide insights into the effect of North Atlantic Deep Water, Antarctic Intermediate Water and MOW circulation on the microfauna and -flora. Moreover, $\delta^{13}C$, $\delta^{18}O$, Mg/Ca and Sr/Ca of foraminifers, ostracods and coccoliths will be determined and compared to seawater geochemistry to evaluate “vital effects”.

Using the morphometric values for identification of most common cultivated infraspecific taxa of *Tilia platyphyllos* [Poster]

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During the study, morphometric measurements were made for the four taxa of *Tilia platyphyllos* Scop., which are most frequently found in Latvia: *T. platyphyllos* subsp. *platyphyllos*, *T. platyphyllos* subsp. *cordifolia* (Besser) C.K. Schneid., *T. platyphyllos* ‘Rubra’, *T. platyphyllos* ‘Obliqua’. Ten most typical

our collected herbarium material samples were selected (from DAU herbarium collected in Latvia). In turn, five typical leaf samples were measured from each herbaria. Some selected morphologic parameters were measured and analyzed: width of leaves, length of leaves, pubescence and margin of leaves. Unfortunately, generative parameters are not available in all herbaria, therefore we use only vegetative features. Statistical analysis was performed by SPSS (version 20.0) software using descriptive statistic tools, one – way ANOVA with Sidak post hoc multiple comparison, and Kruskal – Wallis with Mann – Whitney post hoc multiple comparison, for which it was designed new critical level of significance 0.0085. The comparison between taxonomic group showed significant difference of leaf length F3, 177.25=2.872 P=0.038; pubescence of leaves x2=102.84 df=3 P

Resolving species complexes for conservation planning [Talk]

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The importance of accurate taxonomy for conservation planning is often overlooked. Using a genus of dung beetles, *Lepanus* (Scarabaeidae), as an exemplar approach, we examine the effect of cryptic species on distribution modelling, richness and endemism. Examination of the major holdings of *Lepanus* revealed over 60 new species already existed within museum collections and misidentified as belonging to the 23 described species. Species complexes were resolved using an integrative approach before all distributional data was examined. Results highlight the importance of unravelling species complexes for conservation planning.

What drives the coexistence of di- and tetraploids in the primary contact zone of relict serpentine *Knautia arvensis*? [Poster]

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Although the sympatric occurrence of different cytotypes within a plant population seems to be a much more common phenomenon than originally assumed, theoretical models usually predict a limited evolutionary stability of ploidy mixtures. This especially concerns the newly arisen polyploid derivatives growing together with their diploid progenitors. Understanding the patterns and processes surrounding polyploid establishment requires a suitable model system, in which polyploid lineages coexist in situ with their genetically close diploid progenitors (*i.e.*, the incidence of primary contact zones). A promising candidate for getting deeper insights into the evolutionary dynamics of mixed-ploidy systems are relict serpentine populations of *Knautia arvensis* agg. (Dipsacaceae). There are four spatially isolated serpentine outcrops inhabited by *Knautia* diploids in Central Europe, one of which (in the Slavkovský les, NW Bohemia, CZ) harbours also a tetraploid cytotype. Overall phenotypic similarity, ecological preferences and AFLP genotyping indicate autopolyploid origin of the tetraploids from the local diploid races and hence a primary contact of both cytotypes. We studied the mechanisms driving the di- and tetraploid coexistence using a combination of detailed ecological surveys conducted at different spatial scales and greenhouse cultivations. Tetraploid plants clearly predominated within the study site. Significantly better performance of tetraploids was found both in situ within mixed-ploidy populations and during greenhouse cultivations, which indicates the competitive superiority of tetraploids over their parental diploid race. The lack of inter-cytotype habitat differentiation along with unequal size-stage distribution of di- and tetraploids in mixed stands suggest a temporal nature of cytotype coexistence. The predicted tetraploid expansion at the expense of diploids is, however, slowed down by prevailing clonal reproduction and plant longevity of both cytotypes, resulting in a stable co-existence within a short time frame.

Phylogeography of the land snail genus *Orcula* Held 1837 with a special focus on the Alpine species group [Talk]

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Gastropoda are currently underrepresented in phylogenetic studies despite the huge number of species described. However, land snails in particular have generally low dispersal abilities and inhabit small areas, facilitating the study of speciation processes and dispersal and moreover, the extensive fossil record can provide insights into past distributional patterns. In our study we performed a phylogeographic analysis of the rock dwelling land snail genus *Orcula* Held 1837, including all currently accepted species, twelve of which show an Alpine-Carpathian-Dinaric distribution and one occurring in the Western Black Sea region. Using three marker genes (COI, 12S, 16S), we set up a reliable mitochondrial phylogeny and found that the genus can be divided into three major groups: 1) The eight species with purely Alpine distribution form one clade, which is the sister group of the widespread *Orcula dolium*. 2) The second group consists of the Dinaric species *O. wagneri* and *O. schmidtii* and the Southern Carpathian *O. jetschini*. 3) *Orcula zilchi*, finally, represents the third major lineage. The Alpine taxa exhibited by far the largest diversity. Speciation and distribution within this group seem to be strongly influenced by the extensive Pleistocene glaciations. Our data suggested that glacial refuges were located in the Western, North-Eastern and South-Eastern Alps and that especially parts of the Eastern Alps served as centers of diversification. In addition, a comparison of mitochondrial and nuclear (histone 3/4) sequences indicated that hybridisation took place between some of the species during the Pleistocene but probably even up to the present.

Environmental sampling uncovers hidden diversity of haplosporidian parasites [Talk]

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Haplosporidia are protist parasites in the supergroup Rhizaria that infect a wide diversity of marine invertebrates. They include the well-known causative agents of several oyster diseases, which threaten stocks of native species and cause severe economic impacts for shellfish farming and export/import businesses. Despite some haplosporidian lineages being well recognised and routinely monitored by agencies concerned with food security, the group as a whole remains very poorly known. We used a combination of group-specific PCR primers to intensively probe environmental DNA samples taken periodically from the benthos and plankton of neighbouring muddy brackish and rocky shore coastal sites near Weymouth, UK, and other marine and freshwater DNA samples from elsewhere in the UK, South Africa and Panama. We demonstrate an extensive diversity of haplosporidians, both related to known parasitic lineages and highly distinct novel clades that are highly and widely represented in planktonic and benthic samples from many localities. We present a significant increase in haplosporidian sequences from non-marine environments. Brackish, littoral, and freshwater haplosporidian communities are significantly different, but we detected no significant differences between planktonic and benthic communities. We show that most haplosporidian lineages are absent from many large online sequence datasets and emphasise the importance of lineage-specific approaches, both for molecular and morphological analysis, of the highly diverse haplosporidian parasites and their relatives.

Species delimitations by molecules – less or more problems with taxa? [Talk]

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There is no doubt that species delimitations (species descriptions and revisions) are genuine scientific hypotheses and thus should be cited as such like all other hypotheses. Nowadays these hypothetical frameworks can and should be improved by adding new genotypic (usually molecular) data in the sense of an "integrative taxonomy". Purely phenotypic descriptions as well as original DNA-barcoding approaches usually focus on or are restricted to the stated differences between closely related species, whereas statistic analyses have been comparatively rarely outlined in morphology. In contrast, there is a large number of recent papers concerning improvement of algorithms and analyses to proceed towards robust and repeatable hypotheses on species delimitations by means of molecular data and to improve phylogenetic aspects also under evolutionary processes of hybridization or lineage ingression. Whereas the methodology of analyses has been substantially improved during the last years, the nomenclatorical (“naming”) aspects usually are entirely ignored in respective examples. Typically, after inferring cryptic species, authors are faced with a large number of old names in the literature, often severely insufficiently described and coupled with incomplete or even unknown or lacking type specimens. The freshwater gastropod family Valvatidae in Europe will serve as an example for these conditions, and possible solutions with accompanied problems are presented: (1) Classic, detailed historical analyses including type studies of all old names will cause a delay in research for years and usually are not conclusive. (2) Application of pure MOTU numbers are difficult to compare worldwide and will cause chaos in the future. (3) Drastic reduction of available taxa due to insufficient description will need many decisions of the Nomenclature Commission, again is time-consuming, and will blame the old authorities. (4) Ad hoc erection of new species names causes the danger of producing synonyms. In conclusion specimens from type localities should be incorporated as far as possible to clear up the original name among species clades. Concerning old, possible synonyms new names are considered as the best available solution under the given circumstances.

The role of biogeographic barriers on the evolution and current distribution of *Dysoxylum* (Meliaceae) in South East Asia [Poster]

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Wallacea, a major distributional barrier for animals dividing South East Asia, comprises the islands between Lydekker’s line (1896) and Wallace’s line (modified by Huxley 1868). However, Wallacea exists in various modifications, particularly including or excluding islands like Java, Palawan, and the whole of Philippines from the area. Wallacea is supposed to have influenced organismic diversification and diversity patterns, including those of the speciose Sunda Shelf region and the Sahul Shelf region. Its significance for plants, however, is less clear than for animals. To shed light on the influence of Wallacea on plant diversification and distribution, dispersal routes and directions of distinct monophyletic taxa within and across Wallacea need to be investigated throughout the region’s complex geological history. We chose the overall tropical genus *Dysoxylum* (Meliaceae) as a suitable model group, as it often shows western (Sunda Shelf) and eastern (Sahul Shelf) variants of a single species, differing morphologically. The genus includes *c*. 90 species, most of them trees of different size and position (understory, mid-layer and canopy) within the forests. The genus’ distributional range covers the whole of South East Asia, but also Australia, New Zealand and the majority of the Pacific Islands. We sampled 85 species of *Dysoxylum* plus additional outgroup taxa from the tribe Guareeae to reconstruct the genus´ phylogenetic history. Special attention is given to the genus’ internal division (into the morphologically differentiated sections *Dysoxylum* and *Cyrtochiton*) as well as to the relation to *Chisocheton* and other members of Guareeae. The analyses were based on two sets of molecular markers: the internal transcribed spacers (ITS) of nuclear ribosomal DNA (nrDNA), and plastid regions (atpB-rbcL intergenic spacer, trnL intron and trnL-F intergenic spacer). Here we present preliminary results of our biogeographical analyses. Molecular dating was performed using BEAST v. 1.7.4, based on fossil data within the tribe Guareeae and beyond. The origin of *Dysoxylum* was calculated by two different models: statistical dispersal-vicariance-analysis (S-DIVA in RASP 2.1a) and Lagrange (in Python). The application of these methods also included the testing of our major dispersal hypotheses.

A major contribution of the ZSM to the genetic library of life: 35,000 insect species barcoded in 7 years [Talk]

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The Bavarian State Collection of Zoology (ZSM) is one of the major German natural history research institutions. It holds the world's largest collection of Lepidoptera and Germany's largest Hymenoptera and second largest Coleoptera collection. In 2006 the ZSM started a close alliance with the Biodiversity Institute of Ontario ('BIO', Guelph, Canada) to build up a genetic library in the framework of the International Barcode of Life Initiative ('iBOL'). In just seven years the ZSM submitted tissues of 100,000+ identified vouchers belonging to 35,000+ insect species. Sequencing was performed at the Canadian Centre for DNA Barcoding ('CCDB'). Major contributions were given to the campaigns 'Barcoding Fauna Bavarica ('BFB'; 10,000 barcoded species) and German Barcode of Life ('GBOL'; 2,000 sp.), Global Geometridae (15,000 sp.) and iBOL Lepidoptera (further 10,000 sp.). As taxon sampling in the lepidopteran campaigns is rapidly approaching a comprehensive coverage at a global scale, they already provide a model for worldwide biodiversity assessments, community analyses and a basis for taxonomic revisions. Despite a long tradition in faunistics and zootaxonomy, Germany still lacks a comprehensive faunistic monograph for its more than 40.000 metazoan species. As DNA barcoding is a rapid, cost-effective alternative strategy for the identification of described species, for challenging existing species concepts, and for the discovery of new species, the project Barcoding Fauna Bavarica was activated in January 2009. It was the first program to aim to create a DNA barcode library for all animal species in a whole country. In 2012 a second, even larger initiative was started targeting all metazoan species living in Germany (GBOL). The projects are currently supported by grants from the Bavarian State Government and the German Federal Ministry of Education and Research. The BFB project shows near-complete coverage for butterflies and moths, bees, grasshoppers and fishes of Bavaria. More than half of the known German species have been analyzed for the large groups of Coleoptera, Araneae, Heteroptera and Microlepidoptera. Comprehensive data releases of the Rhopalocera, Macroheterocera and Myriapoda are already published and several others are in progress. Our analyses have led to the discovery of unexpected faunal elements, cryptic species, and have also revealed interesting cases of barcode similarity, barcode sharing, and deep intraspecific splits.

Evidences for several species within the cosmopolitan eurybathic deep-sea lysianassoid amphipod *Eurythenes gryllus* s.l. [Poster]

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Eurythenes gryllus (Lichtenstein, 1822) is a presumed cosmopolitan eurybathic benthopelagic giant deep-sea amphipod. However, previous studies already highlighted genetically divergent lineages in the Atlantic and Pacific Oceans, which appeared to be vertically stratified, and minor morphological differences between populations were also recorded. With an aim to quantify the geographic and bathymetric patterns of genetic variations, the genetic diversity in *Eurythenes gryllus* was investigated at the global scale (Arctic, Atlantic, Pacific and Southern Oceans) using three different genes (COI, 16S rRNA, 285 rRNA). This genetic analysis was accompanied by a thorough morphological study. Phylogenetic and phylogeographic analyses revealed the existence of at least eight well-supported clades, two bathyal and six abyssal, which were separated by genetic distances at the level of usual interspecific divergences. A subsequent morphological analysis confirmed the genetic findings and revealed small but consistent differences between the different clades, which will be described as separate species. Furthermore, a clear genetic break was observed between specimens sampled above and below 3000 m. This bathymetric break below 3000 m has already been reported for several organisms and regions, suggesting its role as a ubiquitous phylogeographic barrier for barophysical tolerance. The Eurythenes clade, comprising specimens sampled at bathyal sites in the Arctic and Southern Oceans, is presumably the true *E. gryllus*. This represents, to our knowledge, the first molecular evidence for a bipolar distribution in a macro-benthic deep-sea organism. The present results clearly highlight the difficult nature of research on the systematics of deep-sea crustaceans and shows that the abyss is a more complex environment than previously assumed, likely to harbour an important hidden diversity.

SmartHerper Comoros, a free field guide to the herpetofauna of the Comoro archipelago as a mobile application [Software Bazar]

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We present SmartHerper Comoros, a free field guide to the reptiles and amphibians of the Comoros as a mobile application for smartphones. It includes an introduction to the Comoran environment and herpetofauna, an interactive key, and species accounts with text information, photographs, sounds, and a map with localities that can be viewed and are available for navigation via the GPS function of the smartphone. The app enables users to contribute photographs and locality data of the species included. This data is directly uploaded to the database for inspection by the administrator and will be made available to the user community in regular updates. The app is freely available for download at the website of the Zoologische Staatssammlung München (http://www.zsm.mwn.de/). It was programmed using Java and is currently available for the Android operating system. The development of versions runnig on iOS and Microsoft Windows Mobile is planned. In addition to the current English version, editions in other languages are planned. Since SmartHerper Comoros and planned future SmartHerpers are free, easily available and easy to use, we hope that they will contribute to the dissemination and generation of knowledge on biodiversity of their focus regions and thus stimulate interest in the observation and conservation of regional biodiversity in visitors, *e.g.*, ecotourists, and residents alike.

Speciation and species delimitation of Australian diving beetles: the impacts of glaciation and aridification [Talk]

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With a broad set of modern methodological approaches and over 30 published species concepts, the task of systematicists to delimit species has become increasingly complex. In cases in which species delimitation is complicated by conflicting evidence from morphological and molecular data, investigations into the possible modes of past speciation may shed light also on the differences between recent lineages of organisms. We present the cases of Australian diving beetles in which candidate species can be distinguished using morphological, but not molecular, data, or vice versa. Our results show that lineage diversification correlates with past climate change in Australia, from the onset of the Miocene aridification to the Pleistocene glaciations. We find that lineages with marked differences in genetic characters, but no detectable morphological difference, have most likely been geographically isolated by arid regions for millions of years. The morphological diversification of very young lineages that cannot be safely distinguished by their genotypes, on the other hand, was probably mediated as a mechanism of reproductive isolation, when the geographic ranges of lineages were repeatedly isolated and merged in the glacial cycles. In both cases, ecological niche modelling and qualitative ecological data detected differences in the responses of recent lineages to ecological variables, probably in part also mediated by past climate change. Species delimitation was then conducted using an integrative approach based on evidence from mitochondrial and nuclear molecular markers, morphological, and ecological data. We conclude that an investigation into the possible modes of speciation with an integrative approach using as many lines of evidence as possible was the safest approach toward species delimitation in our examples.

A phylogenetic hypothesis for Chalcidoidea, a hyperdiverse group of insect parasitoids [Talk]

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With the combination of morphological and molecular methods of phylogenetic analysis, we are beginning to get a much better understanding of the evolution of the order Hymenoptera, which includes all of the ants, bees and wasps. Within this group, the evolution of a parasitic lifestyle occurred only once in the Apocrita, followed by subsequent changes to other important lifestyles such as nest provisioning, pollination and phytophagy. Within the suborder Apocrita, the Chalcidoidea are an extremely diverse group of parasitic wasps. With over 500,000 estimated species, this superfamily represents one of the greatest post-Cretaceous radiations among the insects. Economically and ecologically, they are extremely important for the control of other insects in both natural and agricultural ecosystems. Because of their parasitic lifestyle, species are regularly used for the biological control of insect pests, and have resulted in more cases of successful pestiferous insect control than for any other insect group. Ranging in size from the smallest insect at 0.13 mm to veritable giants at over 20 mm, most species average 2–4 mm in size. Their morphological diversity is staggering. Convergent morphology is rampant, and many features are independently derived in very divergent taxonomic groups. Their extreme numerical and morphological diversity has resulted in a large number of higher taxa being described relative to other superfamilies of parasitic Hymenoptera, with 19 families and 85 subfamilies currently recognized. The results of a recent series of morphological and molecular approaches to understanding their phylogeny, evolution and diversity with a focus on ant parasitoids will be discussed.

Transcriptome analyses in representatives of Tardigrada and Onychophora suggest that colour vision evolved in arthropods [Poster]

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Phylogenetic analyses of gene sequences encoding c- and r-opsins, key proteins in animal photoreception, have provided useful insights into the evolution of animal vision. These studies revealed that multiple r-opsins are expressed in the eyes of arthropods, whereas c-opsins are mainly found in their brains and might be involved in circadian clock mechanisms. Despite numerous studies on arthropod opsins available to date, only little is known about the opsin genes in their closest relatives, the onychophorans (velvet worms) and tardigrades (water bears). We therefore analysed the opsin genes in five distantly related species of Onychophora and a species of Tardigrada using deep transcriptome sequencing and screening approaches. Our data revealed only one functional r-opsin gene in each onychophoran and tardigrade species studied. In our cladograms, the onychophoran and the tardigrade r-opsins comprise a monophyletic clade, which forms the sister group to the monophyletic clade of visual r-opsins of various arthropods. These findings provide evidence for monochromatic vision in Onychophora and Tardigrada, suggesting that the diversification of visual pigments and colour vision evolved in arthropods, along with the evolution of compound eyes. Our ongoing expression studies of opsin genes in onychophorans and tardigrades might provide insights into the visual system in the last common ancestor of Panarthropoda.

Microhabitat complexity as a promoter for speciation in habitat-specialized coral reef fishes [Talk]

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Speciation through adaptation of species/phenotypes to specific microhabitat characteristics (*e.g.* physical structure) may significantly contribute to biodiversity. While phenotypic traits (through morphometric measurements) and even the genetic structure behind those can be quantified by several modern methods, the physical structure of habitats may be much more difficult to capture. The extraordinarily high diversity of small marine fishes (represented by hundreds to thousands of species within the families gobiids, triple-fins, damselfishes and blenniids) is often attributed to the high diversity of the microhabitats in the ecosystems they live in (*i.e.* corals reefs). However, few studies have actually measured the structural complexity of habitats and related it to the diversity of the organisms that exploit these habitats. Coral-dwelling gobiids of the genus *Gobiodon* represent a highly interesting model for speciation through adaptation to their microhabitat. Apart from several unique behavioural and physiological adaptations of these tiny fishes to the spatially restricted microhabitat of coral colonies, it was proven that the physical structure of host corals also sets important limits for the phenotype evolution of associated fishes. Natural selection on the size and shape of these fishes acts mainly through intra- and interspecific competition and predation. This results in fish phenotypes varying with different levels of habitat specialization and adaptation to microhabitats with different physical structure. A molecular clock calculation of the most frequently occupied coral genus, *Acropora*, suggests, when compared with the molecular clock of speciation within *Gobiodon*, that the diversification of corals has very likely driven that of associated fishes.

Nematode Diversity – nightmare and paradise, problems and strategies [Talk]

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Without a doubt nematodes are the most species-rich taxon on earth. They are ubiquitous and numerous and a nematode free place is hard to find. Yet they are difficult to identify due to their tininess and their scarcity in morphologically informative characters. We work on the nematode family Diplogastridae. One member of this family is the species *Pristionchus pacificus*, a nematode established as satellite system for comparison with the model nematode *Caenorhabditis elegans*. After finding the ecological niche of the nematode (necromenic on scarab beetles) we did a large-scale search for new strains and species in the genus *Pristionchus*. Newly isolated nematodes have to be brought in culture and identified. For identification we use molecular markers, which give information on species identity and also help in calculating molecular phylogenies. Species identity is then confirmed with mating experiments. We formally describe new species combining morphological and molecular information and try to set a new standard for nematode species descriptions. World-wide sampling gave us a multitude of nematode taxa (not only from the genus *Pristionchus* but also from many other genera) which we all keep in live and frozen cultures and which help us understanding diversity patterns and phylogenetic relationships. We study biogeography and invasion/introduction in *Pristionchus* and also look at an example of coevolution of a diplogastrid genus with bark beetles. Taken together, nematodes might not be easy to work with initially but the amount of information and data we can get from that system is highly rewarding.

Neurogenesis in *Lineus albocinctus* (Nemertea) as inferred by immunocytochemistry and confocal laserscanning microscopy [Talk]

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Nemertea is one of the most neglected taxa concerning neurodevelopmental studies within the Lophotrochozoa and the sparse data available do not unambiguously allow for answering important questions concerning the neural groundplan of the phylum, such as, *e.g.*, the presence of an apical organ, a feature that is commonly found in most other trochozoan larvae. In order to contribute data to this issue, detailed studies on neurotransmitter distribution during neural development of the pilidiophoran *Lineus albocinctus* are presented herein. Two serotonin-like immunoreactive neurons occur in the anterior part of the apical plate and send numerous processes into all four lobes, where they form a complex subepithelial nerve net. All four larval lobes are surrounded by a marginal neurite bundle, which is associated with numerous serotonin-like immunoreactive monociliated perikarya. A serotonin-like immunoreactive oral nerve ring encircles the stomach sphincter and is associated with few serotonin-like immunoreactive conical-shaped cells. Two suboral neurites descend from the oral nerve ring and merge with the marginal neurite bundle. Of all neural structures investigated only two larval neural components are incorporated into the juvenile nervous system: the oral nerve ring and the two suboral neurites. In addition to the serotonergic components, a complex larval FMRFamide-like immunoreactive nervous system is described in detail for the first time for Nemertea. Interestingly, no FMRFamide-like immunoreactive structures are present within the larval apical region. Together with previous findings on *Micrura alaskensis*, the results of the present study show serotonin-like immunoreactive structures in the apical region in pilidiophoran Nemertea, and contradict an earlier study that did not reveal any neural structures in the apical region of *Lineus albocinctus*. In addition, our study shows that the nervous system, especially the FMRFamide-like components of pilidiophoran larvae, is much more complex than previously assumed.

Problems of automatic species delimitation by GMYC in protistan lineages [Talk]

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Next generation sequencing of environmental DNA results in masses of sequence data that often cannot be assigned to currently known protistan species. Restrictions in personnel, space and time on the other hand do not allow for an extensive cultivation of clonal strains facilitating a combination of morphological and molecular research that could keep up with the speed new sequences are generated by NGS. It is, thus, tempting to use methods for automatic species delimitation for protistan lineages to circumvent time-consuming work on cultured material. Automatic species delimitation methods usually originate from metazoan research on biodiversity. Unicellular organisms, however, differ from animals not only in size, but also in distribution patterns and propagation. Therefore, in addition to that morphological characters often proved to be unreliable and anyway cannot be assessed in metagenomics approaches, thus, fail to serve as a feedback control, a researcher faces problems when trying to apply automatic species delimation methods such as the general mixed Yule-coalescent model (GMYC) to protistan species. In this presentation some problems inherent in automatic species delimitation – focused on GMYC – are presented using the Cryptophyceae as a model system.

Metamorphosis in dwarf males and hermaphrodites of the barnacle *Scalpellum scalpellum*: How early do they diverge? [Talk]

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Metamorphosis in barnacles is conventionally viewed as involving the change from a settled cypris larva to a juvenile suspension feeding barnacle, but this view stems from taking hermaphroditic acorn barnacles (Thoracica Balanomorpha) as typical for the taxon. Within pedunculated barnacles (Thoracica Pedunculata) many species have a separate males sex that in the form of dwarf males are permanently attached to a large and suspension feeding partner. This partner can be either a hermaphrodite (androdieoecy) or a female (dioecy). In what is apparently an early evolutionary stage the dwarf males are just hermaphrodites arrested in development before female organs become mature. In such species the ontogeny of the male follows that of a hermaphrodite until growth and maturation is arrested. The situation is much more complex in species of the large family Scalpellidae. Here virtually all species carry dwarf males that are highly specialized, and the mature male does not resemble any ontogenetic stage passed through by their hermaphroditic or female partners. In the androdioecic species *Scalpellum scalpellum* I have followed both male and hermaphrodite ontogeny under controlled conditions in the laboratory. The cyprids are all morphologically similar, but those developing into males start to deviate from hermaphrodites as soon as 2–3 days after attachment. At 6–7 days the males are morphologically mature, while females need ca. 3 weeks to reach a stage, where they have developed the typical shell plate pattern and initiate suspension feeding. The first clear deviation in male and hermaphrodite ontogeny involves the formation, number and shape of the primordial shell plates. The results provide a tool for very early separation of males and hermaphrodites in settlement experiments and can applied to experiments on sex determination of the species. This again has important implications for the genetic control of the divergent ontogeny and for the general reproductive strategy of both *S. scalpellum* and other scalpellids, which are emerging models for testing the mathematical theories on the evolution of reproductive systems.

Biogeography and evolution of alpine apomictic plants [Talk]

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Geographical parthenogenesis describes the enigmatic phenomenon that asexual organisms have larger distribution areas than their sexual relatives, especially in colder climates and previously glaciated areas. Although apomixis has been reported for many species of the Alps, the biogeographical patterns are poorly documented. A review of alpine apomicts suggests that apomixis is prevalent in subalpine and alpine grasslands and pastures, while the phenomenon is scarce in subnivale species. Apomixis is correlated to polyploidy but not to extreme habitats. We present the model system of *Ranunculus kuepferi* to understand the causality of geographical parthenogenesis. We analyzed ploidy levels, population genetic structure and breeding systems of the plant species *R. kuepferi* on 59 populations from the whole distribution area (European Alps, Apennines, and Corsica). Amplified Fragment Length Polymorphisms (AFLPs) and five microsatellite loci revealed individual genotypes for all populations and mostly insignificant differences between diploid sexuals and tetraploid apomicts in all measures of genetic diversity. Low frequencies of private AFLP fragments / SSR alleles, and character incompatibility analyses suggest that facultative recombination explains best the unexpected high genotypic diversity of apomicts. Structure analysis using AFLPs revealed two regional gene pools for sexual populations in their southwestern glacial refugia; apomictic populations exhibited high admixture near the sexual area, but had just one rather uniform gene pool in remote areas. Bagging experiments and analysis of pollen-tube growth confirmed self-fertility for pollen-dependent apomicts, but self-sterility for diploid sexuals. We conclude that facultative apomixis combines advantages of both modes of reproduction: uniparental reproduction allows for colonization of remote areas, while facultative sexuality and polyploidy maintains genetic diversity within apomictic populations. The density-dependence of outcrossing limits range expansions of sexual populations. However, more studies are needed to understand the generality of the model.

The BioCASe Monitor Service v1.2 [Poster]

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The BioCASe Monitor Service is a tool for coordinators of networks of biodiversity databases that are based on the BioCASe Provider Software (BPS). The first part of the tool allows registration of BioCASe providers and their data sources and displays all relevant information in a compiled view, *e.g.* provider name (linking to the access point URL), list of data sources, total number of records and of unique values per concept (*i.e.* number of units, number of multimedia objects), date of last modification and other useful links including a mapping checker tool and the respective BPS instance. The relevant configurations can easily be set and modified in a user friendly administration interface. The second part of the tool is a service that checks the mapping of a provider to the ABCD (Access to Biological Collection Databases) and ABCDEFG (Access to Biological Collection Databases Extended for Geosciences) schema by displaying the mapped concepts, counts (total and unique) and sample values. It can also check the compliance of the ABCD/ABCDEFG mapping with other exchange schema. This part of the tool is also useful for the providers, as it offers a comprehensive overview of the mapping of their data and associated values, reports required data that are missing and lists their corresponding concepts in the destination schema. In the EU funded project OpenUp! the BioCASe Monitor Service is used to monitor the progress of the provision of multimedia objects to Europeana. Furthermore, it is a useful tool for the coordinators of the content-providing work packages as a quality check of the mapping of the associated metadata in the ABCD or ABCDEFG schema and its required compliance with the Europeana Sematic Elements (ESE), the Europeana standard. The tool is being developed in close collaboration between the OpenUp! team (Work Package 4 & 7) and the GBIF-D team at the Museum für Naturkunde Berlin, Germany. Links: BioCASe Monitor Service 1.2: http://edit.africamuseum.be/biocasemonitor/ BioCASe Provider Software (BPS): http://wiki.bgbm.org/bps/

Systematics, genomes, museum specimens and non-destructive sampling [Talk]

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Recent advances in DNA analyses such as the different next-generation-sequencing methods in combination with hybridisation capture approaches that allow targeting DNA sequences up to the megabase range have revolutionised all fields of evolutionary genetics. As these technologies are particularly suitable for degraded DNA, molecular analyses of museum specimens become increasingly attractive for various research fields, including phylogenetics, population genetics and functional genetics. Although such studies promise exciting insights into many aspects of the evolutionary processes that have shaped extant and recently species, this increasing interest in using museums specimens for genetic research also puts increasing pressures on museum collections, as most genetic studies at least to some extent damage the specimens investigated. At the same time, research has shown that under standard museum storage conditions, DNA continues to degrade arguing for sooner rather than later genetic analyses of the specimens involved, before the genetic information stored in them is irreversibly lost. I will discuss possibilities for minimally invasive DNA and protein analyses of museum specimens as well as the progress made in ancient DNA technologies, which now at least in some cases allows high-quality genomes to be obtained from minimal sample amounts. I will also suggest ways forward how the need to preserve the morphological integrity of museum specimens can be balanced with the possibility to obtain the genetic information stored in them.

Effects of hybridity, polyploidy and allelic divergence on functional development of apomixis in *Ranunculus auricomus* [Talk]

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Hybridization and polyploidy are major features contributing to plant evolution, and are often connected to shifts from sexuality to apomixis in angiosperm lineages. In natural populations, gametophytic apomixis is hypothesized to be a result of developmental asynchrony and alterations of gene expression in duplicated hybrid genomes. Here we analyze the consequences of interspecific hybridization, ploidy levels and allelic divergence on embryo sac development, embryogenesis and seed formation in the *Ranunculus auricomus* complex. High quality single nucleotide (SNP) and insertion-deletion (indel) polymorphisms were mined from sequence libraries of sexual and apomictic biotypes obtained through RNAseq transcriptomes. Reproductive development in natural, allohexaploid aposporous apomicts and their sexual parental taxa (4x *R. cassubicifolius* and 2x *R. carpaticola*) was compared to experimentally produced homoploid and heteroploid F1 hybrids with 2x sexual *R. notabilis*. Non-synonymous (dN) to synonymous (dS) substitution ratios between apomictic and sexual genotypes revealed outliers and diversifying selection for 324 genes, some associated with meiosis and gametogenesis. Flowers of natural 6x apomicts show a delay in megaspore development and high frequencies of apomixis in mature seeds. Diploid and triploid experimental hybrids as well show a delay on the timing of ovule development compared to sexual parental genotypes, and aposporous initial cells or active nucellar cells occur regularly but at lower frequencies. Mature functional seeds these experimental hybrids are mainly sexual though two seed derived from apomictic embryo sacs in F1 triploids were detected. Results suggest that diversifying selection on reproductive genes can drive the shift from sexuality to apomixis in natural populations. We confirm that

interspecific hybridization triggers the initiation of apospory, but successful embryo sac development and functional apomixis require a rise in ploidy level. Implication of functional apomixis on the establishment of newly formed polyploid individuals is discussed.

BiNHum: Access, alignment, and dissemination of established data repositories via a joint data portal [Talk]

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on behalf of the Humboldt-Ring
http://wiki.binhum.net

BiNHum – Biodiversity Network of the Humboldt-Ring – is a joint project of five natural history museums and research collections representing the Humboldt-Ring. The three-year project will enforce collaboration and consolidate collection data of the Humboldt-Ring institutes and their associates by development of a joint data portal and efforts in data mining, standardization, new data types (*e.g.* 3D images), or data digitized by the sub-project MORPHYLL at the SMNS, acquisition of ecophysiologically relevant morphometric data of fossil leaves, DFG RO 3250/21), and data porting to current IT standards. Additionally, the portal will provide all accessible data according to ABCD standards, compatible with international projects such as GBIF. But, in comparison, there will be several extensions to the GBIF functionality: – Indication of correlations between multiple organisms located on one collection object, – Correlations between objects and other data (*e.g.* multimedia, DNA samples), – Correlations between collection objects and their parts (*e.g.* tissue samples, specimen preparations), – Provision of different multimedia files as pictures, videos, and sounds together with thumbnails and file formats, – Search index also providing common names of organisms, – "Shopping cart" and Facetted search functionality, – Enrichment of data by the user community via annotations of the single datasets. The Humboldt-Ring institutes already use several established database systems for collections management and provision of digitized collection data. The most important ones are IMDAS (SMNS, SMNK); Systax; DNA-Bank, Virtual Herbar, BoGart (BGBM); Amibio, DORSA, MorphDBase (ZFMK); Diversity Workbench (SNSB, ZFMK, SMNK, SMNS), and Specify. The BiNHum portal will centralize these systems to a joint data pool considering the above-mentioned aspects and promote data quality in using automatic testing tools. Further information can be found on the wiki site: http://wiki.binhum.net. Involved institutions: – State Museums of Natural History Karlsruhe (SMNK) and Stuttgart (SMNS) – Zoological Research Museum Alexander Koenig in Bonn (ZFMK) – Bavarian Natural History Collections in Munich (SNSB) – Botanic Garden and Botanical Museum Berlin-Dahlem (BGBM) – The Museum of Natural History Berlin (BfN) was involved in the planning of BiNHum and is still an assisting partner.

Lessons from a nearly complete barcode library for European Gracillariidae leaf-miners [Poster]

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Moths in the family Gracillariidae constitute one of the primary groups of plant-mining microlepidoptera. While the majority of species are leaf miners, the family shows a diversity of other life-history strategies, such as fruit mining, stem mining, leaf rolling, boring, and galling. Many species are highly invasive and serious pests of agricultural and ornamental plants. Gracillariids include 1855 described species of which 257 have been recorded in Europe. Here we present barcode data for more than 2000 specimens for 230 species representing 89.5 % of the European fauna. On average seven specimens were barcoded per species. Morphology and DNA barcodes were carefully studied and compared. Preliminary results show that barcoding is capable of unambiguously discriminating ~97 % of the species investigated so far, including some of closely related species notoriously difficult to identify. We highlight some interesting cases of barcode similarity, barcode sharing, and deep intraspecific splits. DNA barcoding revealed divergent clusters within several described species when extending the study area to the whole continent of Europe calling attention for closer taxonomic scrutiny. Our comprehensive DNA barcode library for Gracillariidae leaf-mining micromoths will make identification more straightforward in particular larvae and light trapped specimens for which no host plant data is known. This research highlights the importance of international cooperation among European entomologists to complete the barcoding of all the Lepidoptera of Europe.

Do typhoons influence dispersal and speciation in the mega-diverse genus *Begonia*? [Talk]

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Begonia is a mega-diverse genus and has a hotspot of diversity in Malesia. The Malesian region is heterogenous in terms of the occurrence of large cyclonic weather systems, which are absent from a ca. 4 degree region north and south of the equator. The Philippines experiences a succession of tropical cyclones from June to October, some of which bring extremely high winds and engulf the entire archipelago. In contrast equatorial Sulawesi is never directly exposed to high-energy cyclonic systems and sustained high winds are rare. The dust-like seeds of *Begonia* are potentially wind-dispersed, although current phylogenies of the genus show a dearth of long-distance dispersal events. Here two phylogenies of *Begonia* are com-

pared, one from the Philippine archipelago and one from Sulawesi, and contrasting signals of dispersal looked for. The potential for weather patterms to shape wider patterns of biodiversity within the tropics will be discussed.

Celleporella hyalina as an experimental model in evolutionary ecology and physiology [Talk]

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The bryozoan *Celleporella hyalina* sensu lato occurs throughout north-temperate and arctic seas, extending more locally into the southern hemisphere. An ephemeral colonizer of algal and hard substrata, *C. hyalina* shows relatively little ecological variation despite prolific cryptic speciation. The short non-feeding larval phase, readiness to settle on plastic or glass and good post-metamorphic growth on cultured algae allow successive sexual generations of *C. hyalina* to be reared in the laboratory. Although they do not divide naturally and seldom survive more than a few months in the field, colonies may be propagated from cuttings and continual repetition of the process allows successive generations of ramets to be maintained free of senescence for at least a decade. Establishment of a clone bank allows genotype to be factored into experimental designs, greatly increasing statistical power to investigate a wide range of problems in evolutionary ecology and physiology. Experiments using this model system to test hypotheses on mate choice and sex allocation are reviewed here.

Partitioning the factors explaining the eco-geography in the amphi-apomictic species *Potentilla puberula* (Rosaceae) [Talk]

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Ecological site conditions and migration history are major determinants of the spatial distribution of plants. In addition, reproductive interactions among individuals of different ploidy and/or reproductive mode (*i.e.* sexuality or apomixis) may co-determine the presence/absence of cytotypes within populations. However, the relative contribution of these three factors has never been assessed for a single model system. We quantified the effects of abiotic site conditions, migration distance to the border of the last glacial maximum and the co-occurrence of heteroploid individuals on the distribution pattern of five ploidy levels (tetra- to octoploids) of *Potentilla puberula* at 244 sampling sites in the Eastern Alps ranging from the southern border to central parts of the Pleistocene ice-shield. The spatial distribution of cytotypes was more affected by the co-occurrence pattern of cytoypes than by the migration history and ecological preferences. In detail, sexual tetraploids were strongly separated from high-polyploid apomicts, while the latter neither attracted nor avoided each other. Thus, reproductive interactions played a significant role in determining the distribution of cytotypes.

Evolution of diversity above the species [Talk]

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In this talk we will consider how biodiversity is patterned above the species and how such patterns evolve. Nature abounds with distinct higher taxa: roses, orchids, hummingbirds and cats are all well known examples. Higher taxa were historically considered to constitute natural entities, but in contrast to species, no modern theory describing the evolution and maintenance of higher taxa exists. As a consequence, there are no objective criteria for delimiting higher taxa and they are generally dismissed as arbitrary, with no reality beyond shared ancestry. However, some of the processes that cause evolution of the discrete entities we call species could lead to evolution of significant units above the species as well. This view requires that the diversity of higher clades is limited, *e.g.* due to occupation of a finite geographical region or ecological niche, and that clades that have reached their diversity limit persist over time in dynamical equilibrium, governed by turnover of species through speciation and extinction. Such a view of higher clades is gaining empirical support but the units within which these processes operate and the implications of such a view for understanding how biodiversity is patterned at broad scales have not been explored. We investigate this using simulations and will demonstrate under which circumstances discrete units of diversity above the species can evolve. Empirical analyses of densely sampled gene trees reveal the existence of such units across a diverse sample of the Tree of Life. The analytical framework and the findings we will present offer a new realm for studying diversity at broad scales and provide a crossroads between taxonomy and evolution currently lacking above the species.

On interpreting the ghost shrimp (Crustacea: Decapoda: Callianassidae and Ctenochelidae) fossil record [Talk]

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One of the greatest challenges of modern decapod crustacean paleontology is the interpretation, both systematic and ecological, of the ghost shrimp remains. Ghost shrimps (Crustacea: Decapoda: Axiidea: Callianassidae and Ctenochelidae) are fossorial animals inhabiting predominantly shallow intertidal and subtidal marine habitats (or habitats under seawater influence) mainly in tropics and subtropics (Dworschak 2005) and belonging to major substrate bioturbators. Ghost shrimp remains are among the most commonly found decapod fossils and they are present in most Cenozoic decapod crustacean associations described so far. Yet, the understanding of the ghost shrimp fossil record is limited because most of the fossil material has not been re-examined with respect to modern classifications. There are nearly 300 named fossil ghost shrimp species; more than half of them have been described under the collective taxon *"Callianassa"* (Schweitzer *et al.* 2010) which, in fact, represents a heterogeneous mixture of several independent genera (or even families). Thus, the callianassoid fossil record is in a need of revision. More than forty extant callianassid and ctenochelid genera are currently recognized. However, less than a quarter of these have a fossil record that extends back before the Pliocene (Hyžný & Müller 2010). This can be ascribed to preservational, collecting, and reporting (fragmentary chelipeds often remain undescribed) biases. Moreover, as many extant genera are differentiated on the basis of soft-part morphology only, then if not re-diagnosed they will remain unrecognized in the fossil record. In this respect, looking for proxy characters present on chelipeds (commonly found as fossils) that are consistent throughout the biologically defined genera may help in better classifying their remains in older stratigraphical levels. Comparative studies using the extant material proved to provide a basis for more reliable generic assignment of the fossil ghost strimp remains (Hyžný 2012; Hyžný & Hudá?ková 2012; Hyžný & Karasawa 2012; Hyžný & Müller 2012; Hyžný & Muñiz 2012). The identification of still extant genera in geologically old strata can shed new light on the phylogeny and adaptive radiation of the entire group. Moreover, the fossil record, if interpreted correctly, is a perfect tool for independent testing of the results from the phylogenetic studies based on molecular characters (*e.g.* Felder & Robles 2009).

The International Committee on Bionomenclature: its mandate, achievements and future [Poster]

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The International Committee on Bionomenclature (ICB) was created to explore ways and means to harmonize the various sets of international rules governing the creation and use of scientific names of organisms. To this end, the International Union of Biological Sciences (IUBS) funded the Programme BioCode from 2010–2012. As a result, the Draft BioCode – Principles and Rules Regulating the Naming of Organisms – was published. In the meantime it has been changed to a BioCode Framework open for future implementation after harmonization of terms. As a first step, ICB published a paper in 2012 on Biological nomenclature terms for facilitating communication in the naming of organisms which proposes harmonized terms between the recommended Bionomenclature and the six codes (ICN, ICNCP, ICNP, ICVCN, ICZN, Phylocode). For the term 2013–2015, ICB is now working on the IUBS funded project 'Naming organisms in an age of molecular-based biodiversity discovery'. The project will drive forward an international agenda on nomenclatural activities in a world in which discovery of biodiversity is increasingly based on molecular tools. This discovery process is currently not compatible with type-based naming and we are in need of a unified system of naming and registering these new entities and integrating our knowledge of them with that of currently named diversity.

Biodiversity homemade?! – *Clausilia dubia* and its various subspecies [Talk]

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Clausilids are one of the most species-rich groups among land snails. In Austria they are very abundant in the alpine region. As the conditions in different alpine habitats vary, also the morphology of the clausilids varies strongly. In this study the subspecies classification of *Clausilia dubia* Draparnaud, 1805 was reassessed by morphological analyses (various shell characters) and for the first time by molecular analyses (partial sequences of the mitochondrial gene for COI). In Austria 17 subspecies of *C. dubia* are described, 13 of them occur in the investigated area of the Northern Calcareous Alps of eastern Austria. The individual distribution areas of these subspecies often overlap and some of them occur even syntopically in this region. We wanted to find out whether the described subspecies are genetically and/or morphologically differentiated. Moreover we wanted to find out whether the morphological and the genetic results are in accordance. The determination of the subspecies proved to be very difficult, but there are some subtle characters, which allowed to distinguish them. For an easier classification the subspecies were merged into four morphogroups. Based on our results a separation of any of the described subspecies or morphogroups was possible, neither with the morphometric data, nor with the molecular analyses. Hence, the validity of the described subspecies appears doubtful.

Evolution of genomes of allopolyploids is more dynamic than of diploid homoploid hybrids [Talk]

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Prospero autumnale complex is chromosomally very variable and comprises four distinct diploid cytotypes (AA: 2n=14, B5B5: 2n=10, B6B6: 2n=12, and B7B7: 2n=14) differing in basic chromosome number, karyotype structure and DNA amount. Diploid cytotypes hybridize in nature and produce diploid homoploid hybrids and allopolyploids. We have examined three diploid hybrids (AB5, B5B7 and B6B7) and two allopolyploid groups: (1) allopolyploids of B6 and B7 origin (3x, 4x, 5x, 6x); and (2) allopolyploids of A and B7 origin (4x and 6x). Fluorescence in situ hybridization (FISH) with 5S and 35S rDNA, and novel tandem repeat PaB6 (454 pyrosequencing) as probes enabled identification of the parental sets of chromosomes in all hybrids. Comparative genomic in situ hybridization (GISH) confirmed genomic constitution of allopolyploids of A and B7 origin, but was less successful in allopolyploids of B6 and B7 origin. All diploid hybrids exhibited additive or near-additive genome size values, and additivity of the number and localization of 5S and 35S rDNA, and satellite DNA PaB6 loci in comparison to diploid progenitors. In contrast, genome size of allopolyploids was slightly higher than expected, while the number and localization of both rDNA types and satellite DNA loci among and within cytotypes/polyploid lineages most often deviated from expected additive pattern. The changes in rDNA loci number and localization were allopolyploid-specific (A-B7 vs. B6-B7). The evolution of rDNA and satellite DNA loci in allopolyploid genomes has proven to be more dynamic than in homoploid diploid hybrids. Cytogenetic data were interpreted in phylogenetic framework (nrITS sequence data) and revealed several trends in the evolution of hybrid genomes: (1) changes in rDNA loci number and localization were detected in allopolyploids but not in diploid hybrids; (2) loss of 35S rDNA loci and gain of 5S rDNA loci were observed in allopolyploids and frequency of changes increased with increase of ploidy level; (3) Intra-cytotype variation of genome size was greater in allopolyploids than in corresponding parental diploid cytotypes; (4) allopolyploids of genomic constitution B6-B7 were genomically more variable than allopolyploids of A-B7 origin; (5) The satellite DNA PaB6 showed tendency to spread from genome B6 (PaB6 abundant) to all B7 chromosomes (PaB6 scarce) in allopolyploids B6-B7, regardless of their ploidy level, in contrast to diploid homoploid hybrids of these two genomes.

Gender specialisation and control of female investment in sessile colonial invertebrates [Talk]

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Mating systems of sessile colonial invertebrates can be characterised by: simultaneous hermaphroditism, at either the level of the individual module or the colony as a whole; internal fertilisation of a retained egg by water-borne sperm (spermcast mating); and the brooding of offspring (often with ongoing maternal investment). The phylum Bryozoa exemplifies the polymorphism between modules often exhibited by colonial invertebrates. Zooidal polymorphism facilitates division of labour in these modular organisms, with specialised modules for feeding, support, defence and reproduction. Spatial constraints may influence development of these zooidal polymorphs but other external cues may also determine their fate. The receipt of conspecific allosperm is known to trigger the development of female zooids in the bryozoan *Celleporella hyalina*. This trigger of female investment is also observed in the colonial ascidian *Diplosoma listerianum*, although without clear zooidal polymorphism. Research presented here reveals the same cue controlling the allocation of resources to female investment in a cyclostome bryozoan. The order Cyclostomata are characterised by enlarged zooids for the brooding of multiple embryos produced by polyembryony. These gonozooids or 'brood chambers' were taken here as a measure of female investment, and a greater degree of female investment was observed in the presence of allosperm in *Tubulipora plumosa*. Similar investigations with the cyclostome *Filicrisia geniculata* produced evidence of separate-sex colonies. 'Female' colonies are comprised of regular autozooids (feeding zooids) and gonozooids, which were aborted at an early developmental stage in the absence of allosperm. Sperm was only produced by 'male' colonies, comprising solely autozooids. This example of gender specialisation, a concept identified in plants, is perhaps rare in colonial invertebrates. However, further investigations into mating systems of these organisms, may yet reveal more examples, with implications for our understanding of hermaphroditism and its related traits.

Imagining ancestors: the changing role of phylogenetic's oldest principle [Talk]

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Phylogenetics is, and always has been, the study of evolutionary origins, embodied in the concept of evolutionary ancestors. In this talk I will follow the changing epistemological role of 'imagining ancestors' in phylogenetics. I trace the origin of the concept of ancestors back to attempts to establish the 'unity of type' in the work of pre-Darwinian morphologists, notably Johann Wolfgang von Goethe, Étienne Geoffroy Saint-Hilaire, and Richard Owen. Darwin's thinking subsequently gave birth to the concept of ancestors as concrete organisms by reifying the abstract archetypes of his predecessors, and in so doing placing all of biology on a new metaphysical basis. No one embraced this ontological revolution more swiftly or with more enthusiasm than the young Ernst Haeckel, the 'German Darwin.' For Haeckel the criterion of progress for advances in Darwin's theory of evolutionary descent was the increasingly precise inference of the nature and number of ancestors. Consequently, the main objective of much of Haeckel's work and that of many other pre-cladistic phylogeneticists was to trace the origins of organismal body plans across all taxonomic levels. Efforts to imagine the nature of ancient ancestors had a central epistemological role in this phylogenetic research, to the extent that certain ancestral themes or fashions can be seen to hold sway at certain times or places. The influential German archicoelomate theory and the conception of embryonic stages as thinly veiled reincarnations of ancestors are just two examples. However, the advent of cladistics removed ancestors from their epistemological pedestal, relegating ancestral imaginings to the lowly status of phylogenetic inferential by-product. This epistemological demotion of ancestors was not sufficient to content pattern cladists, however. For them phylogenetics can only retain its scientific credentials if all talk of ancestors is banished wholesale. Yet, for most contemporary phylogeneticists understanding the origins of organismal diversity is still a major objective of their work. This is nowhere more clearly on display than in some recent evo-devo research. Here the strong desire to understand evolutionary origins is conspiring with the use of a faux phylogenetic framework almost exclusively based on model organisms to produce highly speculative inferences about ancestors that would not be out of place in the company of some of the worst speculative excesses of the late 19th century.

Back to the sea? First ontogenetic data of limnic slugs (Acochlidia, Heterobranchia) [Poster]

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Among slugs, Acochlidia uniquely have conquered the limnic habitat. Based on our current phylogenetic hypothesis on the evolution of Acochlidia there is strong support that the limnic lineages even arose twice independently – in the Western Atlantic and the Indo-Pacific – from marine, meiofaunal ancestors. Dispersal and biogeographic patterns among Indo-Pacific islands in these taxa are however still largely unknown. We collected egg masses of *Acochlidium sutteri* (Acochlidiidae) from the underside of stones together with adult specimens in freshwater streams on Flores Island (Indonesia). Conspecifity of the egg masses was confirmed by barcoding. Egg masses are gelatinous and amorphous, having a varying amount of up to several hundred egg capsules loosely embedded. Egg capsules are oval; no extracapsular yolk could be detected. Serial semithin sections (0.5 µm) were prepared to characterise early veliger stages. Hatching veliger larvae were actively swimming for up to two days, all larvae kept in freshwater died after a maximum of 48 hours. Scanning electron micrographs of the free veliger stage are provided. Even though comparably small (approx. 95 µm), lecithotrophy is likely based on histology and light-microscopy. Experimentally transferred to sea water, larvae stopped swimming, closed the larval shell and attached to the substratum. Completely inactive they survived for several weeks glued to the bottom of the petri-dish or a sand grain. When removed they reglued themselves. Based on the incapability of survival in freshwater but under marine conditions, amphidromy in limnic Acochlidiidae is likely, as reported for other co-occurring gastropods (*e.g.* Neritidae). The observed long-living 'adhesive larva' might serve as protective stage not to be swamped out in the open ocean or present a dispersal stage by attaching to larger mobile organisms as vectors of dispersal.

Struggling with uniformity and rarity – molecular species delineation and DNA taxonomy in elusive meiofaunal slugs [Talk]

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Due to frequently low dispersal abilities, many meiofaunal taxa are prone to cryptic speciation. Barcoding and molecular species delineation have been advocated to uncover theses cryptic species. But in addition to the striking uniformity in meiofaunal slugs, these groups are rare and hard to sample and sampling efforts frequently result in singletons from distant localities. To our knowledge, none of the proposed methods of molecular species delineation is specifically designed to deal with the common phenomenon of rarity. We struggled with a workflow to nevertheless receive reliable diversity estimates and species delineations hypothesis for elusive taxa as a basis for *e.g.* biogeography or conservation biology approaches. Our workflow was performed on a worldwide sampling Pontohedyle (Acochlidia, Heterobranchia). Combing sequence data from three gene regions (mitochondrial COI and 16S rRNA and nuclear 28S rRNA), we constructed a molecular phylogeny of the genus Pontohedyle and determined preliminary molecular operational taxonomic units (MOTUs) based on the criterion of reciprocal monophyly in concatenated and single gene trees. We performed four independent methods of molecular species delineation: General Mixed Yule Coalescent model (GMYC), statistical parsimony, Bayesian Species Delineation (BP&P) and Automatic Barcode Gap Discovery (ABGD). To choose the conservative approach in species delineation, we rely only on uncontradicted results from the different approaches resulting in a minimum of twelve candidate species (compared to two valid species described on morphology). In our opinion, DNA taxonomy remains incomplete with the discovery of species only. An increasing amount of detected but unnamed candidate species, which lack minimum voucher information, float around in taxonomic no-man's land. In the present study, all identified candidate species were objected to morphological analyses of characters traditionally used for species delineation (*e.g.* SEM of radulae) and combined with micro-anatomical comparison based on histological semithin sections of the major clades. In absence of any reliable diagnostic characters, species descriptions were based on diagnostic molecular characters, retrieved using the Character Attribute Organization System (CAOS). Necessary consideration and putative pitfalls when integrating DNA taxonomy into the Linnaean system are evaluated.

Prey choice and molecular evolution in parasitic spider-wasps (Pompilidae) and their larval hosts [Talk]

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Randy Coryell (presenter)
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Our group is studying the molecular interactions and evolutionary histories of host-parasite relationships between North American spider-wasps (Hymenoptera: Pompilidae) and the spiders (Araneae) they sting and utilize as living food provisions for their own parasitic larvae. Approximately 90 species from 26 genera of pompilid wasps are known to occur in the state of New Mexico. Some are host generalists and prey upon a wide diversity of host spiders, while others are more specialized and target specific spider taxa such as tarantulas (Mygalomorphae), wolf spiders (Lycosidae), or orb weavers (Araneidae). Pompilid wasp venoms contain short neurotoxic peptides (pompilidotoxins) that bind to a known receptor site on voltage-gated sodium channels, apparently resulting in extended paralysis (but not death) of the host. By using a diverse sample of species, phylogenetic estimates, and the sequencing of spider sodium channels and wasp venom peptides, we are testing the hypothesis that pompilid wasp venoms and host spider sodium channels have co-evolved via an antagonistic selective process such as an evolutionary arms race.

Evolutionary convergence of sodium channel neurotoxins and receptor sites [Talk]

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Venom fractions and endogenous toxins that affect voltage-gated sodium channel function are remarkably widespread, having been identified and studied in arthropods, cnidarians, molluscs, and vertebrates including venomous snakes and certain fishes and amphibians. Sodium channel neurotoxins are structurally diverse, but often bind to and impair the voltage-gated sodium channel in analogous ways. This presentation examines 2 systems we are working on that both address molecular convergence in sodium channel neurotoxins and/or their receptor sites. First: known venom fractions from scorpions, sea anemones, and spider-wasps (Pompilidae) show little structural homology, but all bind to the same site in Domain IV of the sodium channel, inhibiting channel inactivation. We have been examining whether prey spiders that are utilized by parasitic spider-wasps have acquired mutations that confer resistance to this type of venom toxin. Second: parallel evolution has also occurred in sodium channels that have fixed mutations conferring neurotoxin resistance in venomous/toxic animals and/or their prey. Using phylogenetics, site-directed mutagenesis, and electrophysiology, we have demonstrated that guanidinium neurotoxin resistance has evolved multiple times in teleost fish genomes via a diverse suite of amino acid replacements at the otherwise conserved pore region of voltage-gated sodium channels.

Key habitats of large grey mongoose, *Herpestes ichneumon*, in Djurdjura national park, North Algeria [Poster]

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The use of space and feeding habits of large gray Mongooses (*Herpestes ichneumon*), was studied in Djurdjura national park North Algeria, between March 2010 to Fabruary 2011. The space occupation assigns model to Herpestidae, formed of mosaic landscapes containing a mixture of cultures and scrub. Circadian activity patterns can be crepuscular, Mongoose daily activity time adapted with activity time of its staple prey. The diet was studied through the analysis of 360 faeces monthly collected, show the predominance of wood mice (*Apodemus sylvaticus*), the importance of plants and the regular presence of insects. Evidences of correlations between the dietary variations and environmental factors emphasized the influence of environmental variable on the space use and the feeding ecology of Herpestes.

Towards a phylogeny of the oldest metazoans builders (Archaeocyatha, Lower Cambrian) [Talk]

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Archaeocyaths are a key-group of marine sessile organisms, almost entirely early Cambrian and with some relicts during middle and late Cambrian. Reef dweller and often modular, they are substrate for calcified cyanobacteria and seldom produced a true framework to reef. Discovered in 1845 by the captain Bayfield, in the oldest fossiliferous rocks of Labrador (Canada), they have been assigned to various phyla: Cnidaria, Porifera, independent phylum convergent to many groups without dominant affinities… For a long time, the affinities of this enigmatic group were the main topic of research. The discovery of recent calcified aspiculate sponges in sub-marine caves demonstrated that the sponge model is consistent with archaeocyaths structural organization. They are now recognized as an extinct class of the phylum Porifera, close to the Demospongiae. This renews interest in the biology and phylogeny of related fossils with previously problematic status, such as Archaeocyatha. Despite, specialists never found enough arguments to propose outgroups to have a coherent phylogenetic approach. They established the modern systematics, following Zhuravleva's work on ontogenetical principles. The different ranks are defined as follows: Orders by cup architecture, Suborders by the growth pattern, Superfamilies by the outer wall types, Families by the inner wall types, Genera by variations in walls, intervallar primary types and distribution of pores in each element, and Species by different numerical coefficients. Presently, the class consists of 6 orders, 120 families and 308 genera, whose diagnoses have been updated in different recent synthetic works. They were used to establish a XPER^2 knowledge base on Archaeocyatha (http://www.infosyslab.fr/archaeocyatha). It comprises the 308 valid genera described with 123 descriptors (88

morphological and ontogenetical, 8 stratigraphical and geographical and 27 refer to traditional classification data). Initially produced to provide a flexible tool to identify archaeocyaths genera, the knowledge base and the standardization work to instantiate it become precious tools for phylogenetic approach. We propose evolutionary hypotheses for 48 characters: 11 are binary and 37 multistates (some have up to 9 states). Character-state graphs (transform into stepmatrix) allow fulfilling a cladistics analysis using parsimony with a hypothetical ancestor. The first phylogeny of Archaeocyatha is presented and discussed here.

Phylogeographic analysis of Alpine populations of *Pyramidula pusilla* (Gastropoda: Pulmonata: Pyramidulidae) [Talk]

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Even though the alpine land snail *Pyramidula pusilla* (Vallot, 1801) is the most widespread species of the monotypic family Pyramidulidae, it often remains unnoticed due to its small size. Its distribution ranges from the Mediterranean area to Western and Central Europe where it inhabits sunlit calciferous rock and feeds on endolithic lichens. Although it is quite common, nobody has taken a closer look into its phylogeography so far. To gather first insights, we per-formed genetic and morphometric analysis in respect to its geographic distribution. We investi-gated 357 individuals genetically, whereof 143 were also used for morphometric analysis. The individuals were collected at 98 different sampling sites located mainly in the Eastern Alps. First, we extracted DNA and sequenced a ~650 bp section of the mitochondrial cytochrome c oxidase subunit 1 (COI) gene. The phylogenetic tree obtained from the sequence data reveals at least two distinct clades, which appear differentiated in the morphometric analysis. Whether those findings indicate the division into two separate species or merely express a high degree of genetic variation within the Alpine population of *P. pusilla* has to be investigated by further studies on gene flow and reproductive barriers.

Parasitofauna of carps in fish farms of Latvia [Poster]

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Investigations of carp parasites from fish farms (ponds) during the period from 1955 till now show sixty parasite species of following groups: Protista – 17 species, Myxosporea – 7, Diginea – 8, Monogenea – 10, Cestoda – 9, Nematoda – 4, Acanthocephala – 2, Hirudinida – 1, Mollusca – 1, Crustacea – 1. Last investigations were mainly focused on carp Mixosporea and helmints studies, obecause fish for examination were delivered fresh (not a live) and ectoparasitic Protozoa determination was problematic. Results of study show that from one to six parasite species simultaneously parasite on the carp. More common were – *Dactylogyrus achmerowi*, *D. anchoratus*, *D. extensus*, *D. minutus*, *Caryophyllaeus fimbriceps*, *Paradilepis scolecina*, *Valipora campylancristrota*, *Diplostomum spathaceum*, *Phillometroides cyprini*, *Argulus foleaceus*. It is observed that two species of Monogenea in different variations can be detected concurrent on the gills. More widely spread is *P. scolecina* and *V. campylancristrota* which can be explained by increased number of birds inhabiting territory around ponds that contribute spreading of invasion. In carp age of 2,5 years invasion range of 16 *Botriocephalus acheilognati* was registered intestinal wall ruptures. Still the problem is the nematode *Ph. cyprini*, which male was found between swimblader walls more often than females in scales pockets. The diversity of the parasites depends on technology of fish cultivation and as a consequence of environment. Investigation in 2008 was supported by LAD 120608/S263. This work has been supported by the European Social Fund within the Project "Support for the implementation of doctoral studies at Daugavpils University" Agreement Nr.2009/0140/1DP/1.1.2.1.2/09/IPIA/VIAA/015

Obligatory registration, the situation with fungi [Talk]

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Registration of names for fungi, or organisms treated as fungi, under the auspices of the ICN (previously the ICBN) became mandatory on the 1st January 2013. A brief history of the development of Index Fungorum, as the global fungal nomenclator, will be described. Following the rejection of registration, by the botanical community, in St Louis in 2001, and the likelyhood of no progress in Vienna in 2005, MycoBank was established as a voluntary registration system. The parallel development of Index Fungorum and MycoBank will be contrasted. Leading up to the Melbourne IBC in 2011, mycologist developed a forward thinking proposal to emend the then ICBN, and based on the success of the voluntary system, the proposal was accepted. At that time almost 90 % of nomenclatural novelties were entered in MycoBank and an identifier was published in the protologue. Recent decisions and discussions by the NCF will be examined; the mycological community is still learning but it was important to start.

Apomixis database at the University of Göttingen [Poster]

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Online databases are helpful tools for the collection of biological information by facilitating research and providing global access to the scientific community. The Department of Systematic Botany at the University of Göttingen (Germany) recently started with a new database on information about apomixis in angiosperm species. Apomixis is an alternative pathway to sexual reproduction limited to a low number of flowering plants, but widespread among most of angiosperm lineages. Apomixis is tightly linked to syndromes like self-fertility and polyploidy. Our easy to search and freely available collection of data on apomixis will help researchers to answer questions mainly related to reproductive strategies, contributing to the understanding of biogeographical patterns of cytotype distributions and origin and evolution of alternatives to sexual plant reproduction. The online database was created in cooperation with the Gesellschaft für wissenschaftliche Datenverarbeitung Göttingen (GWDG) using the programming environment Oracle Application Express (APEX). The Oracle database contains information on apomixis published since the first data recorded (1908). To date the database comprises more than 280 entries and will be continuously updated. Search terms like “family”, “genus”, and the type of apomixis *i.e.* “apospory”, “diplospory” or “adventitious embryony” can be used in the query. The respective bibliographical reference is given in the output table. A list of all currently available data can be displayed as well. The database is still in the testing phase. Ideas for improvement as well as the submission of further published data on apomixis are very welcome. The website form to search the database is available on the homepage of the Department of Systematic Botany under www.uni-goettingen.de/systbot. Contact: To submit new results to the database, please send an email to Simone.Klatt@biologie.uni-goettingen.de and attach your reference publication as pdf file.

New insights into the *Valeriana officinalis* agg in Austria [Talk]

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The *Valeriana officinalis* aggregate is a systematically complex taxon of Eurasian distribution. In Austria, the taxonomy and evolution of *Valeriana* is still unresolved. Since former surveys concentrated mostly on single accessions, a population-based approach was followed to better account for within-taxon variation. 80 populations of *Valeriana officinalis* agg, each consisting of 20 individuals, were collected throughout Austria, concentrating on North Tyrol and Vorarlberg. Karyological analyses comprised determination of DNA ploidy level using flow cytometry as well as absolute genome size measurement and chromosome counting of representative plants. Biometric morphological analysis was conducted using the characters proposed in the latest taxonomic revision of the aggregate in addition to leaf shape analysis using the software DetMorph. On a subset of plants, AFLP analysis and investigation of phytochemistry via HPLC and GC was carried out. We confirmed the three known ploidy levels for *Valeriana officinalis* agg (2x, 4x, 8x), but we also found unexpected genome size differences within individuals of tetraploid and octoploid populations, respectively, as well as plants with accessory chromosomes. The AFLP analysis showed good accordance with the three ploidy levels. The phytochemical analysis indicates that there are different chemotypes of valerian of the same ploidy level. Interestingly, the morphological data seemingly didn't support the differentiation seen from the karyological, phytochemical, and AFLP data.

Parasites of parasitoids: *Wolbachia* bacteria in Diplazon and their effect on DNA barcoding [Talk]

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Wolbachia are intracellular bacteria known for manipulating the reproductive systems of their invertebrate host species, thus distorting the diversity patterns found in mitochondrial DNA. *Wolbachia* infections have been suggested to potentially be detrimental for molecular species delimitation approaches such as DNA barcoding, especially if low levels of hybridization result in the transmission of a foreign mitochondrion along-side a *Wolbachia* infection between species. Although discussed for years, this phenomenon has been shown convincingly only in very few real cases, and its prevalence is unclear. In the hoverfly parasitoids of the genus *Diplazon*, barcoding recognizes at most twelve species, while morphology finds at least 16. Nuclear markers usually support the morphological species delimitations, and a failure of barcoding to delimit species in all cases coincides with the presence of *Wolbachia*, and vice versa. One species pair with identical barcodes turns out to be not even closely related in the nuclear markers, but shares the same *Wolbachia* infection. These results demonstrate the power of *Wolbachia* bacteria to distort the population biology of their insect hosts, and calls for caution when using mtDNA-based barcoding approaches to delimit and identify species. Further research is needed to evaluate how prevalent this phenomenon is in parasitoid wasps, which represent a large proportion of the unknown insect diversity on our planet.

Discovery and underestimated diversity of the amphibians and reptiles of Sulawesi and its offshore islands, Indonesia [Talk+Poster]

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Compared with the herpetofauna of the three Greater Sunda (shelf) Islands of Borneo, Sumatra, and Java, the diversity of amphibian and reptile genera on Sulawesi is impoverished. The oceanic character of the herpetofauna is the result of the million-year-long geographic isolation of Sulawesi which is separated from surrounding islands by deep ocean trenches. However, despite ambitious investigations by several industrious scientists during the past two centuries, recent fieldwork on Sulawesi and its smaller offshore islands has revealed that the diversity of amphibians and reptiles has been largely underestimated. Since the last herpetological synopsis was published in 1996, 36 new amphibian and reptile species plus five subspecies have been described or newly recorded for Sulawesi and its satellite islands. Seven species were redescribed or revalidated, nine have been overlooked, and 12 species, mainly snakes, were deleted from Sulawesi's species inventory because they had been erroneously recorded from the island.

In addition, more than 40 species, mainly skinks (family Scincidae), have been identified as new to science and await formal description. This represents an increase by 35%! In total, about 210+ different species of amphibians (ca. 50 spp.) and reptiles (ca. 160 spp.) are currently recognized from the Sulawesi region. They belong to six amphibian families (Bufonidae, Ceratobatrachidae, Microhylidae, Ranidae, Hylidae, and Rhacophoridae) and twenty reptile families (Agamidae, Dibamidae, Gekkonidae, Scincidae, Varanidae, Acrochordidae, Boidae, Colubridae, Cylindrophiidae, Elapidae, Homalopsidae, Pythonidae, Typhlopidae, Viperidae, Xenopeltidae, Emydidae, Geoemydidae, Testudinidae, Trionychidae, and Crocodylidae). Almost 60% of which are endemics. The degree of endemicity, however, probably represents a considerable underestimation due to lack of exact distribution data for many species.

Gigantic Diplura (Hexapoda): rediscovery of *Heterojapyx souliei* (Bouvier, 1905) in China and systematic implications [Poster]

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Extant representatives of the basal hexapod lineages rarely exceed body lengths of 20 mm. Some exceptional instances of ‘gigantism’ with body lengths of 35–58 mm, however, are known from two-pronged bristletails with pincer-shaped cerci (Diplura: Japygoidea). Species with such large body size belong to the Heterojapygidae and South American Dinjapygidae, which are assumed to globally form an alliance of species with a relictual Gondwanan distribution; apart from their body size, they are anatomically distinguished from other japygoids mainly by the high number of antennomeres equipped with trichobothria. The largest japygoids, however, were classified in the subfamily Gigasjapyginae Chou, 1984 within Japygidae. This subfamily currently comprises three Chinese species that are stated to share entire absence of trichobothria on the antennae. New samples of one of these three species, *Atlasjapyx atlas* Chou & Huang, 1984 from Sichuan Province, however, call for a revision of the systematic status of the Gigasjapyginae. We present evidence that *Atlasjapyx atlas* likely is synonymous with *Heterojapyx souliei*, the largest heterojapygid species known thus far. Originally described from Tibet, *H. souliei* has not been recorded again since its descripton by Bouvier in 1905. Unambiguous evidence for the synonymy of these taxa especially concerns proof of trichobothria on multiple antennomeres, the distinct shape of the pretarsal claws, and the distinct shape of the ultimate abdominal spiracles, all of which are characteristic for the genus *Heterojapyx*. Our findings corroborate the view that antennal trichobothria have likely been overlooked in all species of the Gigasjapyginae and that in the context of japygoid phylogeny a clade Gigasjapyginae is invalid.

Biogeography and niche evolution: a case study on *Cedrela* (Meliaceae) [Talk]

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Cedrela (Meliaceae) is a New World genus of deciduous trees in subtropical and tropical forests of seasonal or everwet conditions. This study unravels ancestral distribution patterns and ancient climatic niches of *Cedrela* by summarizing information from numerous fossil records and palaeosol studies. When compared to the current distribution and extant habitat diversity of the genus it becomes apparent that distribution patterns changed through time and that ecology and climatic tolerances of *Cedrela* were already diverse by the Miocene. In order to test for timing and the direction of evolution of climatic niches in *Cedrela* we combined distribution models of extant *Cedrela* with a dated molecular phylogeny based on nuclear (ITS) and three plastid markers (psbA-trnH, trnS-G and psbB-T-N). We calculated the relative disparity of climatic tolerances over time to test for niche evolution within subclades, or divergence among subclades and conservatism of climatic niches within closely related groups. Ancestral niche reconstructions unravelled that early evolutionary patterns were mainly driven by precipitation whereas temperature had an increasing impact on ecological diversification of the genus from the Miocene onwards. Molecular clock analyses dated most diversification events back to the Miocene, with divergences of living taxa from their closest living relatives being predominantly of late Miocene or early Pliocene age. Sister species pair comparisons revealed distinct scenarios of recent niche evolution.

High diversity and endemism of *Galium pusillum* polyploid complex in deglaciated Northern Europe [Poster]

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Galium pusillum agg. (Rubiaceae), an intricate polyploid complex harbouring 2x, 4x, 6x and 8x cytotypes, represents a unique example of rapid postglacial speciation in Europe. In northern half of Europe it splits into approximately ten morphologically, cytologically and ecologically distinct microspecies, including at least four diploid and low polyploid (4x) endemics of formerly glaciated areas of southern Scandinavia, Great Britain, and Iceland. Using cytological (flow cytometry) and molecular (AFLP, sequencing of low copy nuclear genes) methods together with ecological observations we aim at identifying major mechanisms involved in evolution of these postglacial endemics. Specifically, the main goal of our study is to distinguish between the *Galium* diversity originating via (i) independent postglacial immigration from different refugia and (ii) rapid postglacial in situ evolution (such as allopatric speciation, recurrent polyploidization and/or hybridization). Previous studies advocated a hypothesis of several independent immigration 'waves' of different *Galium pusillum* agg. lineages into the deglaciated area. In contrast, our flow cytometric data and preliminary molecular data distinguish two monoploid genome size groups of species, both at di- and tetraploid level, in formerly glaciated and unglaciated regions, suggesting possible independent evolutionary histories of these major lineages.

The first eleven years of post-pyrogenic succession in the Arctic pine forest [Poster]

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This work describes the post-pyrogenic succession pattern of the pine forest on the Oleniy Island, White Sea, during the first eleven years of its recovery. We analyzed two separate cases of post-pyrogenic succession differing in the degree of initial soil damage. Investigated factors included the total projective cover and abundance of individual plant species. Multivariate data analysis revealed that the rate of recovery was relatively stable at the better preserved site and changed from almost zero to higher values at the more damaged site. The difference in species composition at the two sites increased over time, which indicates diverging succession patterns. While Vaccinium genus contributed mostly to the similarities in the site development, *Ledum palustre* and *Equisetum sylvaticum* (from the better preserved site) and *Pinus sylvestris* and *Calluna vulgaris* (from the less preserved site) were responsible for the differences in succession flow.

Are there any cryptic species inside grass *Milium effusum* L. with a high molecular polymorphism? [Talk]

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Milium effusum L. (Poaceae, Poeae) is a perennial widespread woodland species distributed across Europa, Asia, in the northeastern parts of North America throughout much of the Holarctic ecozone with disjunction in the west of North America. Tetraploid ($2n=28$) chromosome number was constant in all the samples investigated. Plants from different parts of the range are morphologicaly uniform. Allozyme variation analyses found the species to be variable but no clear geographic patterns in the distribution of alleles were found among samples from Europe and the Altai Mountains (Tyler, 2002). The nuclear ribosomal DNA internal transcribed spacer region (ITS) was found to be informative in the phylogenetic studies at the species and intraspecies level. We investigated the region ITS1-5.8S-ITS2 in 4 species of *Milium*. *Milium effusum* was represented by samples from throughout most of its distribution range – from different regions of Europe, Caucasus, Siberia, Middle Asia, Eastern Asia, and Northern America. All sequences formed two distinct clades with the samples of *M. effusum* from Eastern Asia (Kamchatka, Kuril Islands, Primorsky krai, Japan, China) clustering into a separate clade than the rest of *M. effusum* samples which formed the second clade together with *M. transcaucasicum* and *M. schmidtianum* (all from the section *Milium*). The pairwise sequence divergence between two clades is 0,054. It is close to that between *M. effusum* and *M. vernale*, the species from the other section of the genus (0,060). Further research should be done to elucidate if plants from East Asia represent a separate taxon, subspecies or even cryptic species. The research was supported by DAAD, DFG and RFBR grants.

Publishing biodiversity: The interplay between Scratchpads and the new Biodiversity Data Journal [Talk]

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Data relevant to the study of taxonomy and biodiversity are being produced at an ever-increasing rate. Most of these data cannot be reused because the data are not publicly accessible, lack sufficient contextual metadata, or are published in a form that requires time-consuming manual extraction, *e.g.* PDF documents. A major impediment is the time it takes for researchers and publishers to structure and describe their data before publishing. The taxonomic community needs tools that accelerate this process, maximising the value of the time researchers invest in collecting describing their data. The taxonomic community also needs to embrace methods of publishing that support rapid dissemination and recombination of their work. The Scratchpad (www.scratchpads.eu) project is an example of initiative that has been working to address these issues. Scratchpads currently have over 7000 active users organised in more than 430 research communities. In March 2012 a second generation of the software, funded by the EU project ViBRANT (www.vbrant.eu), was launched. This system provides an infrastructure for creating, managing, linking and analysing data by embedding functions that permit the integration of research activities with a network of global biodiversity initiatives. Scratchpads help researchers structure their data and directly publish data papers on biodiversity-related subjects through a new, peer-reviewed, open access journal – the Biodiversity Data Journal (BDJ) (www.pensoft.net/journals/bdj). The BDJ is the first journal ever to complete the cycle from writing a manuscript, through submission, community peer-review and editing, to publication and dissemination within a single, fully XML-based, online collaborative platform. This next-generation journal aims at paving the way towards the Semantic Web and builds upon the success and technological advancements of its sister journals ZooKeys, PhytoKeys and MycoKeys. The journal will publish papers in biodiversity science containing taxonomic, floristic/faunistic, morphological, genomic, phylogenetic, ecological or environmental data. It is suggested that the interplay between Scratchpads and BDJ could lead to the formation of a solid virtual research support environment facilitating all phases of the biodiversity data workflow. In this talk we will present the main capabilities of Scratchpads and BDJ, to illustrate how researchers can gain greater exposure for their data.

Genomic consequences of *Wolbachia*-induced parthenogenesis [Talk]

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Wolbachia are endosymbiotic bacteria that are well-known for their ability to manipulate the reproductive system of their hosts. In some Hymenopteran insects, *Wolbachia* induce parthenogenesis by making unfertilized gametes develop as diploid females. When a new host becomes infected with a parthenogenesis-inducing *Wolbachia* and switches to asexual reproduction, purifying selection to maintain genome integrity is expected to become less efficient. As a result, *Wolbachia*-infected asexuals are expected to accumulate transposable elements and other mutations. We recently sequenced the genomes of both a *Wolbachia*-infected lineage and an uninfected sexual lineage of the parasitoid wasp *Leptopilina clavipes*. Sexual and asexual wasps are closely related and bear very similar loads of most transposable elements. However, the asexuals have undergone a burst of transposition of one gypsy-like element. Continued scrutiny of these genomes may clarify whether such transposon activity has caused the loss of sexual functionality in asexual males and females in this species.

On the use of stem- and crown group concepts and the definition of Elasmobranchii and Neoselachii [Talk]

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No generally accepted definition of Elasmobranchii (sharks, rays, skates) is currently available and any available definition strongly depends on the interpretation of which taxa form the Elasmobranchii. The same applies to the term Neoselachii. The definition, which is most commonly used is that Neoselachii consists of all living sharks, rays, and skates and those taxa that are placed phylogenetically well within modern groups alone (crown-group concept). The crown-group based definition naturally omits all extinct clades that cannot be included in any crown-group clade. Consequently, Neoselachii and Elasmobranchii is the same when only living sharks, rays and skates are considered. Members of the stem-lineage can be defined as taxa, which are more closely related to a particular crown group than to any other, but which are more basal than their most basal members. Consequently, stem-group members are all taxa, which precede the cladogenetic event shaping the crown-group. Stem-group representatives are often very difficult to recognize because they possess only few but not all synapomorphies found in the crown-group. A number of extinct sharks generally known from isolated teeth previously were identified as possible stem-group representatives. However, no unequivocal evidence for this ascertainment has been provided so far. One of the most important characters for identifying fossil elasmobranchs is their dental morphology since most fossil elasmobranchs, especially pre-Jurassic forms are known by isolated teeth only. However, the use of tooth morphologies alone as a taxonomic criterion might obscure phylogenetic patterns. Nevertheless, numerous studies in the past decades have convincingly demonstrated that the ultrastructure of the tooth enameloid differs among major elasmobranch clades probably providing a phylogenetic signal. A re-investigation of skeletal remains of Mesozoic hybodontiform and neoselachian sharks provided new information about character suits in extinct chondrichthyan clades. This allows specifying the terms and taxonomic contents of Elasmobranchii and Neoselachii by defining the total clade Neoselachii. Additionally, the identification of stem-group and basal crown group neoselachians gives deeper insights into character transformations and the systematic arrangement of crown group neoselachians.

Steppe plants in Central Europe: insights based on performance and genetic data [Talk]

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Based on a study transect towards the (north)western-most distribution limit of pannonian, submediterranean, pontic, and euro-siberian continental steppe plants in Central Europe, we investigate their biogeographical history, genetic structuring and diversity as well as their performance with special emphasis on the distributional periphery. Therefore, we analyse a set of steppe plants showing a similar, disjunct distribution pattern with more wide-spread continuous occurrences in the Pannonian Basin in Hungary compared to the western limit of the Pannonian area in Eastern Austria and to their (north) western-most outposts in western Germany (especially in Rhineland-Palatinate). For all steppe taxa four populations representing each of the three study regions are included. Species of our interest are *Adonis vernalis* (Ranunculaceae), *Carex supina* (Cyperaceae), *Inula germanica* (Asteraceae), *Linum flavum* (Linaceae), *Oxytropis pilosa* (Fabaceae), and *Poa badensis* (Poaceae). All six study species represent rare and endangered species with high nature conservation value in Central Europe. Along the study transect, we expect increasing isolation in a (north)westward direction, which might be associated with progressively reduced population genetic diversity and performance due to suboptimal conditions at the distribution range periphery. To uncover such patterns, genetic analyses are performed based on mainly nuclear Amplified Fragment Length Polymorphisms (AFLPs) as well as chloroplast DNA sequence data. Plant fitness is analysed based on fruit set, fruit mass, germination speed and rates. Here, we exemplarily report results from the performance part of our project and from the genetic part primarily represented by AFLP variation. In detail, we show fruit set and seed mass data as well as outcomes of germination tests for *Carex supina* (Cyperaceae), *Inula germanica* (Asteraceae), *Oxytropis pilosa* (Fabaceae), and *Poa badensis* (Poaceae) across the biogeographical study transect. The results of these four main study species clearly indicate significant differences in fruit set and germination success among species as well as when comparing study regions. AFLP data, for instance available for *Linum flavum* (Linaceae), provide first insights into biogeographical and genetic diversity patterns and the degree of isolation among populations and study regions.

QR-Codes to facilitate data capture and collection management for large-size (insect) collections [Talk]

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There may be as many as two to three billion specimens housed in natural history collections across the world. The largest taxonomic group is made up of insects, but only a very small amount of these specimens are already digitized and even less is available online, *e.g.* via the GBIF web portal (http://data.gbif.org). Hence, a large-scale effort is necessary to mobilize this valuable data for supporting studies in taxonomy, biogeography, and conservation, as well as questions of species diversity and invasive species, and for educational purposes. The major bottleneck to digitize and provide access to the information are the labour-intensive processes involved and the limited staff/work time available.

Here, we discuss the use of QR-Codes in digital collection management to facilitate the capture and handling of biodiversity data at individual specimen and metadata (collection unit) level.

We use QR-Codes at three different levels, 1) at specimen level, 2) at species level, and 3) at the level of larger collection units (drawers). For economic data capture, whole insect drawers are scanned and species contained are later separated into single digital objects. Via the QR-Code attached to each drawer or unit, every qualified user has direct access to relevant datasets from databases storing taxonomic information or multimedia objects. This way, more efficient search, handling and management of drawers and specimens may take place, directly in front of the insect cabinets, by using barcode scanners connected to tablet PCs.

For new material coming into the collection, every single specimen can be directly provided with a unique QR-Code on an individual label. These labels can be generated at the same time when printing the labels with standard locality information. QR-Codes at the specimen do not only facilitate access to relevant taxonomic information stored in a database, but also help collection managers in speeding up sorting specimens, and especially preparing loans and shipments. By scanning individual QR-Codes from pinned insect specimens of a sample or shipment, the curator or user can receive automatically not only a complete list of the respective specimens, but in addition also all available metadata connected to each specimen. This is easily achieved by collecting all scanned unique IDs in a digital shopping cart. The collected IDs are then used for data export from the database, and the generation of a csv-file, *e.g.*, for the taxonomic specialist. Therefore we see considerable potential in the use of QR-Codes to increase efficiency in collection management at several different levels, both for dealing with new as well as legacy material.

Divergent mitochondrial clades of snails with a *Trochulus hispidus* phenotype. How to confine a snail species? [Talk]

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For studying evolution it is compulsory to recognize species. However, for some taxa, this is not straightforward. An example is the *Trochulus hispidus* complex in which species delimitation was proven to be difficult. Hence we took a broad approach including individuals of *T. hispidus* from 129 locations covering a broad geographic distribution with a focus on the Eastern Alps and surrounding areas for morphological and genetic investigations. From 387 individuals a fragment of the mitochondrial COI gene was analyzed. We also included related taxa in our study: *T. oreinos*, *T. striolatus*, *T. coelomphala*, *T. clandestinus*, *T. biconicus*, *T. villosulus* and *T. villosus*. From 100 selected individuals representing different COI clades we analyzed a fragment of the mitochondrial 12S and 16S genes. Furthermore, nuclear sequences (appr. 1400 bp including parts of the 5.8S, ITS2 and 28S) from 49 individuals were analyzed. The mitochondrial variation of specimens determined as *T. hispidus* (on the basis of morphological and anatomical examination) was exceptional high (max. p distance 18 % in COI). The COI sequences of *T. hispidus* revealed nine distinct clades. Seven clades can be assigned to restricted, partly overlapping geographic regions, while two clades show a widespread distribution with no clear geographic patterns. In several cases quite divergent clades occur even at the same sampling locality. In the combined COI-16S-12S tree some related species, which are morphological well differentiated, are intermixed with *T. hispidus* clades. Hence *T. hispidus* is paraphyletic. The nuclear sequences do not differentiate between any of the mitochondrial clades, except *T. oreinos*. Thus, the nuclear data provide no argument for species status of any of the *T. hispidus* clades. For final conclusions on the existence of cryptic species and species delimitation it will be necessary to investigate possible gene flow between all syntopic clades in detail. This work has been funded by the Austrian Science Foundation (P19592-B17).

The when and where of Hymenodictyeae and Naucleeae, Rubiaceae [Poster]

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Rubiaceae is a large cosmopolitan plant family, most common in the tropics and subtropics. The family is commonly divided into three subfamilies; Cinchonoideae, Ixorideae and, Rubioideae. Ixorideae and, Rubioideae have their main distribution in the Paleotropics. Cinchonoideae on the other hand is predominantly Neotropical, this is also proposed to be the place of origin for the subfamily. The exception from the Neotropical distribution is the two sister tribes; Hymenodictyeae and Naucleeae. Hymenodictyeae consists of two genera; Paracorynanthe Capuron with two species, the genus is endemic to Madagascar, and Hymenodictyon Wall. with 24 species with a Paleotropical distribution. Naucleeae currently consists of 27 genera with a majority of its members in the Paleotropics. These two tribes are the earliest diverging lineages in the subfamily. Their biogeographical history will be discussed from the results of dating and biogeographical analyses based on both molecular and fossil data. The latest phylogenetic treatment of the tribes will be presented and give new insights to the complex generic limits within Naucleeae.

Introducing the FREDIE project with notes on the European mollusk diversity [Poster]

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FREDIE stands for 'Freshwater Diversity Identification for Europe' and is a nationally funded project aimed at bringing together DNA barcoding with taxonomic expertise for European freshwater organisms (www.fredie.eu). Included are freshwater fishes, mayflies and freshwater mollusks. The aim is to develop an online identification system for species diversity of these groups in Europe. Although DNA barcoding offers the possibility to accelerate detection and monitoring of biodiversity, its quality and significance is strictly bound to availability and quality of underlying reference data, especially reliable species determinations. Resources and expertise of three core institutes and a web of associated partners are combined to create a reliable and sustainable reference system. Representatives of nearly all species of the three groups occurring between Portugal and the Ural are currently collected, identified by experts and sequenced to become barcode references. In selected cases a refined identification system is planned including morphological characters and other genetic markers with better taxonomical resolution. We will provide the respective voucher specimens and a DNA collection as permanent references available to the scientific community. FREDIE generates molecular and morphological estimations of species numbers of the three organism groups for Europe, as well as deeper insights into their spatial structure on a large scale. For the mollusk work package we present the current status with actual species number estimations and highlight problematic areas in terms of taxonomic classification. The analysis of geographic variation in groups processed so far revealed both, previously known and also underappreciated phylogeographic breaks among different taxa. This has important conservation implications for those species and populations and further enhances our understanding of the biogeography and evolution of European freshwater mollusk diversity.

Open access to protist biodiversity information: from file cards to GBIF [Talk]

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Cataloguing protist biodiversity information started with card boxes and books giving access to algal names. After data basing in several databases, a substantial dataset of names information is now available and used by the Global Biodiversity Information Facility (GBIF) as a names backbone to classify biodiversity information. Protist data is part of currently more than 388 million records available via the data portals of GBIF (http://data.gbif.org/occurrences). GBIF is a global network of 58 countries and 47 international organizations providing standardised observation and specimen data via the Internet to give open access to our knowledge of biodiversity. A special interest portal for algae and protozoa data has been developed by GBIF Germany using the BioCASe technology (www.biocase.org). All taxa classified within the relevant higher taxa or published by data providers specialized on algae or protists were filtered for unified data output, including ambiregnal taxa. Diverse data relevant for taxonomy and monitoring are accessible through the AlgaTerra Information System for micro algal biodiversity (www.algaterra.org), a German GBIF provider. AlgaTerra comprises type information, specimen data as well as images, videos, morphological, literature and molecular data for micro algae. As a repository of primary biodiversity data AlgaTerra publishes voucher images of research projects, such as of diatom DNA barcoding. Advantages of publishing these images on the Internet are: (i) access to these data independently from the original publication, (ii) publication of images not limited by available space in a printed journal, (iii) addition of images after print publication possible, and (iv) images available for analyses in other contexts. Aim beyond the current GBIF scope is linking cell morphology information to molecular data of specific strains/taxa. These records are cross-referenced with research papers. Currently, AlgaTerra is subject to changes in its data architecture and layout. The database is migrating to the EDIT (European Distributed Institute of Taxonomy) Platform for Cybertaxonomy to achieve better integration of factual information related to taxonomic concepts. Portal development and extending quantity and quality of German providers by GBIF-D Plants, Algae and Protists (www.gbif.de) is funded by the Federal Ministry of Education and Research (BMBF, grant 01 LI 1001 A-F).

The EDIT platform for Cybertaxonomy: Building diverse biodiversity data portals for systematists [Software Bazar]

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The EDIT (European Distributed Institute of Taxonomy) Platform for Cybertaxonomy is a set of software tools and services that is being used for an increasing number of taxonomic information systems. The tools include fully-configurable taxonomic data portals and the EDIT taxonomic Editor software. Reliability and reusability of data are key requirements for each single tool and thus for the Platform as a whole. The portals are being adapted for specific interests of research groups, projects, and user communities. In addition to several Floras and specific taxonomic groups of higher plants and animals, the EDIT Platform is being used for the Information system and checklist of on-line database and information system for the vascular plants of Europe and the Mediterranean region Euro+Med PlantBase and the AlgaTerra information system for micro algae biodiversity. The user-friendly taxonomic Editor (EDITor) facilitates highly structured data entry, data integration, and presentation of taxonomic information such as classifications, synonyms, taxonomic concepts, types, literature references, geographic distributions, and images. The Federal Ministry of Education and Research (BMBF, grant 01 LI 1001 A-F) is funding a 3-year-project to extend the German GBIF community.

The loss of elements of seed reproduction and genetic diversity in populations of clonal plants [Poster]

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Most of herbaceous plants have the ability to combine sexual and vegetative reproduction. The ratio of these two types of reproduction for each species varies widely depending on the ecological and (or) genetic factors. In some populations of vegetatively mobile species there are processes leading to different disturbances of seed reproduction, and then complete sterility. Apparently, these processes are amplified at the boundary ranges of clonal species. The state of reproductive system, ploidy level and genetic diversity in populations of clonal plants from different families were studied. In all 7 populations of *Tulipa riparia* Knjasev, Kulikov et Philippov (Liliaceae) we observed o triploid ($2n=3x=36$) level. So we have marked abnormalities of the structure both female and male spheres. But in most populations there were more than 6 genotypes it seems that genotypic diversity is supported by the sporadic sexual reproduction. The genotypic diversity and status of male generative sphere in 14 populations of clonal *Cardamine trifida* (Lam. ex. Poiret) B.M.Jones (Brassicaceae) in the different parts of the area were investigated. We have found the different degree of sterility androecium including complete. In plants of Siberian and Central Russia populations retained the ability to seed reproduction and maintained a high level of genotypic variability. Ural populations differed in the degree of sterility androecium and the level of genotypic variability. We revealed the distribution of sterile clone in the valley of White River more than on 100 km. We investigated 3 populations of *Gladiolus tenuis* M.Bieb. (Iridaceae) in the main part of the area (Volgograd region) and 6 on the Urals. *G. tenuis* in the main part of the area is tetraploid ($2n=4x=60$) propagate by seeds and vegetative forming daughter bulbs. In these populations we have revealed high level of genotypic variation. On the Southern Urals we found sterile triploid clone ($2n=3x=45$) widely spread by vegetative propagation. Genetically identical individuals are detected from Bashkortostan to Guberlinskoy hills in Kazakhstan in the distant more than 500 km. The work was supported by The Russian Foundation for Basic Research (grant 10-04-00989-a) and by the Federal Program of Ministry of Education and Science of Russia (project 14.740.11.1032).

Identifying Norwegian Psychodidae using DNA barcodes (Insecta: Diptera) [Poster]

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40 species of Norwegian Psychodidae are known, however no comprehensive resource exist for their identification. The present study tests the utility of molecular methods to distinguish between the different species. Since 2011 a total of 81 cox1 sequences (DNA barcodes) of 18 different species have been compiled to form the basis of the first DNA barcode sequence library for Psychodine moth flies. The data set comprises nine genera in at least three different tribes. For 11 species, multiple specimens are sequenced; all of these are resolved as consistent clusters in neighbour-joining analyses. The morphotaxonomically problematic Psychoda albipennis complex, however, is very poorly supported and remains difficult also with the use of molecular methods. Overall, DNA barcoding is found to be a promising tool in the identification of Northern European Psychodidae.

Male genital homologies of the Psychodini and their phylogenetic significance (Insecta Dipt.: Psychodidae, Psychodinae) [Talk]

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Psychodini is the most species-rich and ecologically diverse subgroup of the Psychodinae, with more than 600 described species worldwide. The classification of Psychodini is disputed because of disagreements concerning character polarity. The main difference between classifications is the placement of the subtribe Trichopsychodina (= the *Threticus* group), which some consider to be basal Psychodini and some consider to be Paramormiini/Telmatoscopini. Detailed comparisons of the aedeagal apparatus of the Trichopsychodina and Psychodini s.str. finds a common ground-plan condition suggestive of an inclusive Psychodini concept including the Trichopsychodina. In the ground plan, this aedeagal complex consists of a symmetrical aedeagus of two phallomeres flanked by paired, symmetrical parameres. Two major modifications of this pattern exist: In *Threticus* and some other genera, the phallomeres and parameres have become asymmetrical through differentiation of the left and the right side. In most Psychoda, one paramere has been entirely reduced; and some Psychoda have no parameres at all. The genitalia of other Psychodinae and the phylogenetic significance of other character systems are briefly discussed.

Evolution, biogeographical history, and ecology of high alpine and arctic species of *Ranunculus* [Poster]

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The genus *Ranunculus* consists of more than 600 species, which are distributed predominantly in temperate and cold climates of almost all continents. Associated with this preference is the tendency of buttercups to colonize alpine habitats and thus it is no surprise that *Ranunculus* species occur in almost all major mountain systems of the world. Former molecular phylogenetic studies succeeded in assessing the relationships within and between the majority of clades comprising alpine *Ranunculus* species. However, one well supported clade including all North American and most Himalayan alpine species showed only weak resolution regarding the internal relationships. Our current study concentrates on refining the phylogenetic resolution of this arctic-alpine clade based on seven chloroplast markers and one nuclear marker (ITS of nrDNA). Maximum parsimony analysis reveals four well supported subclades corresponding to the four principal distribution areas that are represented in the clade: South Asia (Himalayas and Taiwan), North America/Arctic, Central Asia/Arctic and European lowland. The relationships between these subclades remain unresolved, but the branching patterns within the subclades and sister-species relationships could be elucidated in all groups except for the Himalayan one. The North American alpine species show a greater extent of ecological and geographical differentiation than the Himalayan species. Reticulate evolution, that appears to be negatively correlated with the extent of ecological differentiation, is supposed to be a major factor for unresolved relationships applying particularly to Himalayan rather than to North American alpine species.

Soil eukaryotic unicellular microorganisms facing crop fertilization [Talk]

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Soil organic and inorganic fertilizations have been commonly used since more than one century to increase yield of crop fields. Although their effect on plant growth through increase in nutrient availability is obvious, little is known about their impact on belowground microorganisms, particularly on a long term scale. Unicellular eukaryotes, which carry as diverse functions as primary production (*e.g.* microalgae), predation (*e.g.* protists) or decomposition (*e.g.* yeast), are key components in the soil food web and nutrient

cycles. As fertilization induces changes in natural nutrient cycles, important modifications in soil communities have to be expected in intensely fertilized soils. Soil DNA from different farmyard manure and mineral fertilization treatments (long term static fertilization experiment, Bad Lauchstädt, Germany) was extracted and served as template to amplifiy specific markers for fungi (ITS), protists (Kinetoplastida, Chrysophyceae and Cercozoa ribosomal 18S), photoautotrophs (plastid 23S), as well as a general marker for eukaryotes (18S). Subsequent high-throughput pyrosequencing rendered a total of 350 000 good quality sequences which were further clustered in operational taxonomic units (OTUs). First results indicated that manure fertilization induced significant changes in community composition of all screened groups, whereas mineral fertilization only played a minor role. Co-occurrence patterns of successfully identified abundant OTUs will be further analyzed to identify important links in the microbial food web.

Insect phylogenomics: new insights on the relationships of lower neopteran orders (Polyneoptera) [Talk]

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We investigated the relationships among insect orders with a main focus on Polyneoptera (lower Neoptera: roaches, mantids, earwigs, grasshoppers, stick insects, etc). The relationships between and within these groups of insects are difficult to resolve because only few informative molecular and morphological characters are available. Although phylogenomic and/or transcriptome data for polyneopteran representatives has slightly increased in recent years, continuing gaps in the order sampling prohibited extensive investigation on most key questions of polyneopteran relationships so far. The current transcriptome data set is the first one, which represents nearly all polyneopteran orders, and thus allows for the first time to test previous hypotheses on the relationships among polyneopteran orders, as well as the basal splits within Neoptera. In this context, we to focus especially on the following phylogenetic questions: 1) Are the lower neopterans a monophyletic group (= Polyneoptera). 2) Are Dermaptera and Plecoptera each other's closest relatives? 3) Are the Eukinolabia (Phasmatodea + Embioptera) monophyletic?

Evolutionary genomics and plant species diversification [Talk]

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Understanding the processes that facilitate the origin, functioning and maintenance of biological diversity is of great interest to the fundamental and applied life sciences. My group`s research interests revolve around the use of novel laboratory and computational tools for studying adaptive evolutionary responses, speciation, and species radiations in plants. To achieve these goals, we make use of Northern hemisphere 'model' taxa for which extensive genomic and biological resources are available, and we have initiated the transfer of knowledge gained from this work to other plant radiations in highly structured and species-rich environments in South America, Southern Africa and Southeast Asia. I will briefly highlight the basic concepts underlying our work and recent progress by my group.

Metastelma (Apocynaceae – Asclepiadoideae) – tracing convergent evolution and an unusual biogeographic pathway [Talk]

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Small, but complex flowers of high overall similiarity have so far encumbered understanding of the subtribe Metastelmatinae (tribe Asclepiadeae) in the Americas. Molecular analyses have helped to develop a conceptual framework for subtribe and genera delimitation, but morphological circumscription of the genera is still difficult. The genus *Metastelma* was hitherto understood to comprise small twining plants with whitish flowers, densely bearded corolla lobes and a corona of five simple, slender, staminal lobes. CpDNA analysis of 40 *Metastelma* species has revealed that three species conforming to the above description need to be transferred to different subtribes, two to the genus Tassadia and one to subtribe Gonolobinae. Of the species retrieved in Metastelmatinae, most South American ones are monophyletic with some South American species hitherto attributed to *Ditassa*, characterized by a corona of five double, slender corona lobes. This indicates that evolution and reduction of the inner corona lobes has occurred several times. The remaining species, including the type, *M. parviflorum*, are monophyletic (*Metastelma* s.str.). S-DIVA analysis supports the generally held view that the *Metastelma* s.str. is derived from South American stock, even though its centers of radiation are in the Caribbean and in central Mexico. The Caribbean has been settled at least three times: (1) by a widespread and speciose radiation, reaching Florida with *M. northropiae*; (2) by the *M. parviflorum* complex, which occurs in the Caribbean and along the north Coast of South America; and (3) by the ancestral of *M. anegadense* and *M. lineare*, endemics of Anegada and Puerto Rico, respectively. The Central American mainland species show a clear geographical structure with a center of diversity in central Mexico and two radiations along the Sierra Madre Occidental and one radiation along the Sierra Madre Oriental. Narrow species concepts are supported by molecular data, even though morphological differences are often vague. The genus possibly reached Central America via the Caribbean and the Yucatán peninsula, rather than via the Panamanian landbridge, although further studies are needed to bolster this hypothesis.

Origins, evolution and diversification of cleptoparasitic lineages in long-tongued bees [Talk]

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Cuckoo bees, or cleptoparasites, employ various strategies to deposit their eggs in the nests of other bees. In this study, we employ dating and diversification rate analyses, as well as ancestral state reconstructions, to trace the evolution of cleptoparasitism in long-tongued bees and explore the impact of cleptoparasitic strategy on diversification. Our results suggest that a strategy in which a closed host cell is parasitized and host offspring are killed by the adult parasite represents an obligate first step in the appearance of a cleptoparasitic lineage; this strategy is likely to evolve into a strategy in which a closed host cell is parasitized but in which host offspring are killed by the larval parasite, and finally into a strategy in which an open host cell is parasitized. These transitions are unidirectional, with no evidence of reversals. The transition to parasitizing open nest cells expanded the range of potential hosts for cleptoparasitic bees and played a fundamental role in the patterns of diversification seen in cleptoparasitic clades. We also discuss one of the long-standing mysteries surrounding the evolution of cleptoparasitism in bees: the prevalence of cleptoparasitic lineages in certain families and the conspicuous absence of such lineages in others.

Multiple transitions to parasitism in the Platyhelminthes

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The phylum Platyhelminthes is estimated to be comprised of over 100,000 species of flatworms, although only 30,000 are described. A propensity towards parasitism has undoubtedly contributed to their success and their ubiquity in all continents, oceans, freshwater and terrestrial environments. This life style is often complex and frequently involves the use of multiple hosts from many other animal phyla in order to find their way into vertebrates, by far the most common definitive host group. Molecular phylogenetic studies have provided the beginnings of a robust framework for understanding the evolutionary history of parasitism and major events can be pinpointed in the radiation of the group, such as the origins of obligate parasitism, endoparasitism and complex life cycles. A number of challenges remain, including understanding the role of parasitism in shaping the molecular composition of the genes used for phylogenetics, estimating the timing of major transitions from independent clock calibrations derived for example from host evolution or vicariance events, and the nature of ancestral host-parasite combinations that sparked additional radiations within major parasite lineages. Here we explore what we can safely infer, and what remains to be discovered in order to provide a more complete picture of the evolutionary history of parasitism amongst the flatworms. Finally, given their critical role in ecological interactions and the evolution of their hosts, platyhelminths serve as a reminder that what cannot be seen should not be ignored.

Phylogenetic analysis of the family Bostrichidae auct. at suprageneric levels (Coleoptera: Bostrichidae) [Poster]

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A phylogenetic analysis of the beetle family Bostrichidae auct. was conducted based on 122 adult morphological characters (96 multistate) of 31 genera and species, including at least one genus and speices from every currently accepted subfamily and tribe of Bostrichidae, and four outgroup taxa, two genera and species each of Anobiidae and Dermestidae. The most-parsimonius hypothesis suggests a distinctly different classification from those of previous workers on the family. The Lyctinae is divided into three tribes: Lyctini Billberg, 1820, Trogoxylini Lesne, 1921 sensu novo and Cephalotomini Liu, 2011 tribus novus. The Bostrichinae is divided further into four tribes: Bostrichini Laterille, 1802 sensu novo, Apatini Jacquelin du Val, 1861 sensu novo, Sinoxylini Lesne, 1899 sensu novo and Xyloperthini Lesne, 1921. This is the first phylogenetic study at suprageneric levels of Bostrichidae auct.. Because there are no previous phylogenetic studies for comparison, we discuss the most-parsimonius hypothesis in relation to morphological and biological information as well as the phylogenetic analysis.

Comparative floral structure in the sarracenioid clade (Ericales) [Poster]

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The sarracenioid clade is comprised of the families Actinidiaceae, Roridulaceae, and Sarraceniaceae. Monophyly, interfamilial relationships (Sarraceniaceae sister to the rest), and systematic position of the sarracenioid clade within the order have only relatively recently been established and are well-supported based on molecular phylogenetic analyses. In pre-molecular times, the three families have generally not been thought to be closely related and have therefore never been studied comparatively at the morphological level. This has led to the paradoxical situation that we now have clear phylogenetic hypotheses for the group, yet do not know any morphological features that characterize the clade. Actinidiaceae consist of three genera: *Actinidia* (~55 spp.), *Clematoclethra* (1 spp.), and *Saurauia* (~300 spp.), *Actinidia* and *Clematoclethra* are mainly native to Indochina, while *Saurauia* has a wider distribution of Indo-Malaya, Oceania, and the Neotropics. Roridulaceae are a monogeneric family with two species in the genus *Roridula* endemic to the Cape region of South Africa.The carnivorous family Sarraceniaceae consists of three genera: *Darlingtonia* (1 spp.), endemic to California and Oregon (USA), *Heliamphora* (?18 spp.), native to Brazil and Venezuela, and *Sarracenia* (11 spp.), found in temperate to subtropical USA. At a macroscopic scale, the vegetative morphology in these families is very diverse, ranging from small, herbaceous perennials in Sarraceniaceae with their conspicuous pitcher leaves to several meters tall lianas and trees in Actinidiaceae, and shrublets covered in glandular hairs in Roridulaceae. The flowers range in size from a few millimeters to several centimeters, the floral arrangement also varies, and they can be dioecious, subdioecious, or bisexual. We investigate and compare floral structure in the sarracenioid clade with the goal to characterize the clade at the morphological level and to identify potential structural synapomorphies for the clade as whole as well as for its subclades. Preliminary results indicate potential synapomorphies including a nucellar hypostase, a choripetalous corolla, cellular endosperm formation,

and unitegmic ovules. In the future, we will perform phylogenetic analyses, ancestral state reconstructions, placement analyses for fossil taxa, and biogeographic analyses to reconstruct the phylogenetic history and evolution of the clade.

Evolution of the plant green-island phenotype and *Wolbachia* infection in Gracillariidae leaf-mining micro-moths [Talk]

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Internally feeding herbivorous insects such as leaf-miners have developed the ability to manipulate the physiology of their host plants in order to improve their nutritional value. Indeed, certain leaf-miners can induce « green-islands » on yellow leaves in autumn. These green-islands are characterized by photosynthetically active green patches in otherwise senescing leaves, and correspond to regions with an increased concentration in cytokinins and an enriched nutritional environment. A recent study of the apple leaf-miner micromoth has suggested that endosymbiotic bacteria of the genus *Wolbachia* play an important role in green island induction but it is not known how widespread this tripartite interaction is. Here we study the *Wolbachia*/leaf-miner/green-island interaction by screening the presence of green-islands and *Wolbachia* in 133 specimens of 78 species of microlepidoptera including 64 leaf-mining Gracillariidae micromoths. We reconstructed a multiple gene molecular phylogeny for leaf-mining moths and used a comparative approach to show that there is intra and interspecific variability for the distribution of both the green-island phenotype and *Wolbachia* infection. Significant correlation was found between the evolution of both traits, so *Wolbachia* is likely to have played an important role in the evolution of the green-island phenotype, not only in the apple leaf-miner but also in Gracillariidae leaf-mining moths in general. However, some individuals are able to make green-islands without being infected by *Wolbachia*, which means that other other mechanisms, such as the presence of other endosymbionts have to be considered. We also reconstructed a multiple gene phylogeny for a complex of four closely related leaf-mining species feeding on apple. Several hundred specimens all producing green-islands were both sequenced and screened for *Wolbachia*. We found a strong correlation between the divergence of the four apple feeding species and the status of infection by *Wolbachia*. This suggests that *Wolbachia* may have played an important role in the diversification of their leaf-mining hosts. We also found two species that form green-islands but were not infected by *Wolbachia* and detected the presence of *Spiroplasma*. This

study opens new perspectives for the understanding of the mechanisms underlying host plant manipulation by endophagous insects. It raises questions about the ecology of the tripartite association between *Wolbachia*, leaf-miners, their host

Historical herbaria and archival DNA reveal the origin of an invasive insect [Poster]

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Determining the origin of alien invasive species is crucial to developing invasive species management strategies. However, the origin of many alien species remains uncertain because of the lack of historical data. For instance, the moth *Cameraria ohridella* (Gracillariidae) was described in 1986, as a genus new to Europe and had managed to invade almost all Europe since 1989. Its larvae are leaf miners on the white flowering horse-chestnut (*Aesculus hippocastanum*), causing significant damage to their summer foliage. The fact that the appearance of *C. ohridella* in much of Western Europe has been so recent and dramatic, without earlier detection by entomologists, has made its origin a subject of debate. Originally thought to be a relict species in the Balkans, a more recent hypothesis is that the moth is an example of a sudden host plant shift to horse-chestnut, probably from maple or sycamore (*Acer* spp.), maybe combined with long distance translocation. Examination of horse-chestnut samples in seven historic herbarium collections revealed that almost half of 71 sheets had leaf mines with larvae/pupae inside. This material came from natural populations in Albania and Greece and dated from 1981 back to 1879. We extracted DNA from 54 archival larvae and used five COI minibarcode primer pairs developed specifically for *C. ohridella*. We successfully amplified DNA minibarcode fragments from 10 larvae extracted from herbarium specimens from 1936 to 1981. These archival sequences confirm an identity and Balkan origin for *C. ohridella* and the herbarium data set its history back by over a century. The herbaria reveal three previously unknown mitochondrial haplotypes. We also detected local outbreaks back to 1961 and dynamic frequency changes, which may be associated with road development. In particular, comparison with a temporal series of herbarium samples (1936, 1974 and 1981) with a modern sample from Karitsa in E. Greece suggests the frequency of the invasive haplotype A has been increasing rapidly even within the Balkans. This case history demonstrates that herbaria are greatly underutilised in studies of invasive species origins, herbivore biodiversity and insect-plant interactions.

Detecting conflicts in large sets of phylogenetic trees [Talk]

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In many studies it is of interest to extract phylogenetic trees that describe common evolution from various datasets. We present a natural method to detect such trees. The method is based on an original algorithm to build evolutionary scenarios of genes and reconcile individual gene trees into a supertree [Lyubetsky, Gorbunov, Biology Direct, 2012; Molecular Biology (Mosk), 2009, 2012; Information Processes, 2010; Problems of Information Transmission, 2011]. The algorithm implements novel concepts of the gene evolutionary scenario and time slices imposed on the supertree to describe particular types of gene evolution events, such as gene duplications, losses and horizontal transfers. Unlike traditionally used approaches to the NP-hard reconciliation problem, the algorithm has a cubic complexity with respect to the size of input data and is mathematically proved to find the true supertree as a global minimum of the used functional, the total cost of individual tree reconciliations. The method is used to detect compatibility thresholds and extract trees suitable to provide correct reconciliations. We define a natural measure of compatibility between the current tree and the supertree in terms of the cost of individual gene evolution events inferred during reconciliation. It is the ratio of this cost to the number of edges in the current tree (the “conditional edge” cost). During the procedure trees with higher conditional edge costs are removed from the input set, and reconciliation is recomputed. Simulation experiments show that the quality of the current supertree reaches stationarity when the compatibility value enters a certain range. This range defines the set of trees that are compatible enough to describe common evolution, *i.e.*, the supertree. Analyses of biological trees support this observation in terms of inferring the known correct topology of the supertree only after a certain amount of trees is discarded according to this threshold. Given a very low time complexity and mathematical correctness of the algorithm, the method is applicable to large and very large sets of trees, which can be useful in many types of large-scale analyses of tree data.

To see the bigger picture – 3D Reconstruction and Character Evolution of Pallial Eyes in Pectinidae (Mollusca: Bivalvia) [Poster]

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Eyes in Pectinidae (Bivalvia, Pteriomorphia) have since long attracted scientists’ interest and were described for various species over the past two centuries. These eyes show a high level of complexity in morphological as well as functional aspects. Despite the fact that pallial eyes in Pectinidae demonstrate such complexity, studies so far mostly focused on functional aspects with only few examining the conjunction with different environmental or evolutionary traits. As Pectinidae is a large group of marine bivalves comprising more than 300 species worldwide they inhabit a diverse array of habitats, enabling an enormous radiation, and yielding many different life forms and adaptations. This apparent diversity led to the distinction of ecotypes based on morphology of the shell and life style. Here the evolution of the eyes within the Pectinidae has been examined using Masson Goldner Trichrom staining, 3D reconstructions of scanned slides and character tracing. To evaluate the impact of habitat and life style on the evolution of eyes we compared eyes within the major subgroups of Pectinidae representing the different life traits and habitats, as well as different depth ranges. Results clearly indicate a taxon clade/specific evolution in respect to characters such as cornea and lens while depth specific adaptations occur mainly in the light sensitive compartments as the retina. Successive reduction of eyes seems to occur from shallow to deep water species and leads to a total reduction in deep sea species.

The Irano-Turanian floristic region as a source for the Mediterranean floristic region: A case study from Rutaceae [Talk]

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The Irano-Tranian (I-T) floristic region is characterized by a high number of endemic genera and species. Despite its potential role as a source of xerophytic species for neighboring regions (*i.e.* Mediterranean region), the I-T region remains poorly studied within evolutionary frameworks. The aim of this study is to test various biogeographic scenarios, *i.e.* to investigate if the I-T region has been a potential source for the colonization of the Mediterranean region. We thus focused on *Haplophyllum* (citrus family), which is used to characterize the I-T region. Due to the fact that *Haplophyllum* contains species present in the Mediterranean region, it can be used to explore the biogeographic links between the two floristic regions. We performed molecular dating and ancestral range reconstructions analyses to investigate the extent to which past geological and climatic events of the regions explain the current distribution of the genus. Our results strongly suggest that *Haplophyllum* originated in the Central Asian part of the I-T region in the early Eocene and started to diversify within this region in the early Oligocene about concomitantly with vanishing the Tethys Ocean. *Haplophyllum* subsequently invaded the East Mediterranean basin in the middle to late Miocene during the Paratethys salinity crisis and rapid paleobiogeographic changes in the proto-Mediterranean. Finally, *Haplophyllum* stablished in the western Mediterranean part in the early Pliocene after the Messinian salinity crisis. Our study shows that the I-T floristic region can be a “donor” of xerophytic species to the “recipient” neighboring regions. The climatic conditions during the Miocene–Pliocene time caused for instance by the closure of the connections of the proto-Mediterranean Sea with neighboring Oceans and mountain chains uplifts added to a pronounced topographic heterogeneity caused significant range shifts promoting allopatric speciation in the I-T elements. The I-T floristic region thus requires serious conservation strategies by the governments of the countries that have the privilege to host its major evolutionary and biodiversity centers.

Insights into the hybridization occurring between the two molecular forms of the malaria mosquito *Anopheles gambiae* s.s [Talk]

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Anopheles gambiae s.s., the most important mosquito species transmitting malaria in sub-Saharan Africa, is experiencing an incipient speciation process triggered by human-made environmental changes, which is changing malaria epidemiology. The species is subdivided into two molecular forms, named 'M' and 'S', defined on rDNA-IGS mutations and distinguished for the M form-specific insertion of a SINE transposable element (~1 Mb upstream from IGS). M and S forms represent a model for the study of speciation at its early stage since they are diversifying in West and Central Africa despite some ongoing gene flow. In fact, M and S present some genome regions which are supposed to resist introgression – especially in the low-recombinant centromeric areas of chromosomes X and 2 ('speciation islands') – while the rest of the genome continuously homogenise. The observed pattern rises questions on whether divergence is essentially due to physical features of the genome that reduce recombination (*e.g.*, centromeres) despite gene flow, or to selection on adaptive genes clustered in the centromeric 'speciation islands' or elsewhere in the genome. Hybrids between M and S are rare in nature, but an unusually high degree of hybridization was found at the western extreme of their distribution range (*i.e.* The Gambia and Guinea Bissau). This secondary contact zone represents an opportunity to investigate how reduced reproductive isolation affects genetic differentiation in genomic regions known to be segregated between M and S forms elsewhere in Africa. While most studies focus on high-throughput SNPs assays on limited sampling, we genotyped a large number of *A. gambiae* s.s. specimens from Guinea Bissau (and from other African countries for comparison) focusing on two intronic regions known to segregate in sympatric M and S molecular forms out from the hybridization area: i) the intron-4 of a cytochrome P450, namely the Cyp4G16 gene, which maps in the low recombination region of the X-centromere, ~7 kb upstream from SINE locus, and ii) the intron-1 of the voltage-gated sodium channel (VGSC) gene mapping on chromosome 2, out from the centromere area. Our results indicate that in the secondary contact zone recombination occurs within the most divergent region of M and S genome (*i.e.* the X-centromere), as highlighted by the intron-4 of

Cyp4G16 data and support the hypothesis of asymmetric introgression from M to S, as shown by the analysis of intron-1 of VGSC gene.

Parasites – the hidden diversity [Talk]

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Although parasites are omnipresent and extremely diverse, they are usually invisible. Consequently parasitic taxa are mostly absent from biodiversity surveys and often not considered in ecological studies. Because of the high variety of parasites and their biological importance in ecosystems, this lack of attention creates a significant bias in our representation of the living world and researchers in these fields should be reminded of this hidden compartment of biodiversity. In this contribution, a review of the diversity of (zoo)parasites in both the better and lesser known taxonomic groups is offered, showing that parasitism evolved – sometimes at multiple occasions – in practically all animal lineages, including minor ones. The relative importance of parasites among the various animal phyla is reviewed and the number of parasitic species is estimated whenever possible. The importance of collecting data on parasites in biodiversity surveys is emphasised and suggestions to more efficiently reach this goal are proposed.

Integrative DNA taxonomy reveals cryptic diploid diversity in the common European Wall-rue fern [Poster]

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New taxonomic approaches promise to reveal cryptic diversity, even in well-studied fields as the European fern flora. The odds for the discovery of new cryptic fern species are high as sister taxa differentiate in their gross morphology slower than in some other flowering plants. We looked into the *Asplenium ruta-muraria* species complex within its European range, which is commonly known and recognised as the wall rue. In the taxonomy there are two taxa of different cytotypes accepted, however we followed evidences of more than one diploid taxon. In our study of 99 populations, where we estimated the DNA ploidy level applying flow cytometry to silica gel material, we found 41 diploid, 56 tetraploid and 2 mixed populations. For tree based species identification we sequenced up to three chloroplast DNA markers (trnLF, rps4, rbcL) for 105 specimens and up to two low copy nuclear DNA markers (pgiC, leafy) for 14 diploid specimens. We applied Bayesian population structure methods and F-statistics to an allozyme data from 31 diploid populations to test the hypothesis of putative diploid species. As a result we found diploids occurring in three distinct and restricted areas: the Maritime Alps, the South-eastern Alps and the Alpi Apuani in Italy. The tetraploids instead are widespread through Europe. The phylogenetic analyses unfold strong genetic distance between two maternal lineages, both comprising diploid and tetraploid specimens. The allelic allozyme diversity of the three diploid regions showed relatively low level of genetic differentiation but significant inter-regional differentiation over the entire data set. Further, the clustering results support two diploid entities with no unequivocal evidences for gene flow between them. Both approaches support the presence of a second diploid lineage within the *A. ruta-muraria* species complex, which is restricted to the Alpi Apuani and has been overseen so far because of the lack of morphological differentiation. Using various approaches we revealed cryptic diploid diversity in the common wall-rue fern. The two putative species occur in well-defined limestone regions, which pattern suggests regional isolation to promote genetic isolation. The low level of genetic differentiation in the nuclear genome could be explained by a recent separation. However, ferns are well-known for their high dispersal capacity and one needs to think about other enhancer for this case of cryptic speciation in such a restricted area.

DNA barcodes delineate cryptic species of the forest pest *Euproctis chrysorrhoea* (L.) (Lepidoptera: Lymantriidae) [Talk]

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Cryptic species diversity is common within insects but challenging in population genetic studies, particularly for implementing adequate integrated pest management programs and for managing insect resistance to insecticides (*e.g.* western flower thrips *Frankliniella occidentalis* (Pergande), whitefly *Bemisia tabaci* (Genn.), pine-feeding *Chionaspis* spp.). The brown tail moth (BTM), *Euproctis chrysorrhoea*, a forest pest, is widely distributed in Europe and also found in the coast of Maine (USA). Despite its broad host range (feeding on more than 26 different plants, from oak trees to wild roses), the BTM only demonstrates a shifted phenology when feeding on the evergreen strawberry tree *Arbutus unedo* (L.). If gene flow between populations from different hosts is systematically limited (*e.g.* due to insects mating exclusively on their hosts, or to differences in host plant phenology contributing to temporal isolation) host races or even cryptic species may develop. Yet, our analysis of sex pheromone gland extracts showed no differences in their chemical composition between females feeding on evergreen or deciduous hosts. Male individuals feeding on both host types also presented identical electroantennographic responses to gland extracts obtained from females feeding on both host types. We analysed the barcoding region of COI (658 bp) for 185 individuals collected from populations of deciduous and *A. unedo* hosts from several locations in Europe and the USA. Statistical parsimony and automated barcoding gap discovery methods provided unequivocal support for the existence of two cryptic species: one restricted to continental Spain, presenting two haplotypes, and another spread throughout the BTM's geographic distribution, comprising five haplotypes. A maximum-likelihood phylogenetic analysis of the seven BTM haplotypes also revealed the differentiation of a highly supported clade comprising the exclusively Spanish haplotypes. Furthermore, tests of species' delimitation applied to haplotype clades also pointed out the existence of cryptic species. Although the complex may include more species, as the sample size of some locations and hosts was low, none of the ones presently identified is exclusively associated with *A. unedo*. Host-insect chemical communication and/or epigenetic variability, with the expression of cryptic phenotypes without losing old phenotypes, might thus be the reason for the phenological change observed for populations feeding on this host.

Cryptic diversity in asexuals – the example of non-marine ostracods [Talk]

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Because of their excellent fossil record and wide variety in reproductive modes, non-marine ostracods are perfect model organisms for research on evolutionary biology and biodiversity. The ostracod morphospecies *Eucypris virens* is characterized by mixed reproduction and geographic parthenogenesis. It displays up to 40 cryptic species in Europe and Northern Africa, the highest number so far reported for a freshwater invertebrate. Cryptic diversity of *E. virens* follows neither patterns of geographic parthenogenesis and thus the reproductive mode nor geography. Its exceptionally high level of cryptic diversity explains the large genetic variability, which had been previously reported for this morphospecies. Such exceptionally high levels of cryptic diversity might not be typical for all non-marine ostracods with mixed reproduction as another ostracod genus from the same ostracod subfamily, *Bennelongia*, shows mainly regional species and few cryptic lineages in Australia. Darwinulid ostracods are one of the four remaining animal groups with putative ancient asexuality. We observed up to eight cryptic species in *Penthesilenula brasilienis* and three in *Darwinula stevensoni* at a global scale. Some of these follow continental distributions but also other factors must be responsible for speciation in this group. In putative ancient asexual oribatid mites, also vicariant processes seem to have led to cryptic diversity while ecological speciation might to some extent explain cryptic diversity in putative ancient asexual bdelloid rotifers.

Biases in phylogenetic reconstruction [Talk]

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Maximum likelihood (ML) and Bayesian tree reconstruction methods heavily rely on a specified model of sequence evolution. It is well known that violations of the model or of other assumptions made by the method can lead to the reconstruction of wrong phylogenetic trees. It is however widely believed that ML based methods are robust to modest violations of the model or its underlying assumptions. We present a set of very minor model violations, which on 4 taxon trees can have a strong effect on the reconstruction success of ML based methods. These model violations have not been analysed in the literature before and unfortunately are difficult to avoid when analysing real data sets with today's reconstruction methods.

An improved classification of Dipsacaceae based on morphological and molecular data [Talk]

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New data on fruit anatomy, floral characters, pollen morphology and DNA sequences make changes of the traditional classification of the family Dipsacaceae s.str. into three tribes (Dipsaceae, Knautieae and Scabioseae) inevitable. In the past, fruit characters (as development of membranaceous coronas, shape of diaphragmata, existence of foveoles, number, shape and indumentum of calyx elements) were widely used for the delimitation of genera. The present clarification of the phylogeny of Dipsacaceae clearly shows that these fruit characters often have originated in a parallel, convergent fashion and are homoplasious at the generic level. This makes it necessary to improve the classification of Dipsacaceae s.str. by the recognition of two subfamilies with eight tribes (Dipsacoideae with Bassecoieae, Pseudoscabioseae, Succiseae, Dipsaceae, Pterocephalidieae, Knautieae and Scabiosoideae with Lomelosioideae, Scabioseae) and a total of 15 genera. The phylogenetic position of these genera, especially of the relic E Asian genus *Bassecoia* and the new, poorly known E-African *Pterothamnus* is discussed. Furthermore, the family rank of Dipsacaceae s.str. and its affinities to Morinaceae, Valerianaceae and Triplostegiaceae are evaluated.

A transnational lichen inventory of the Alps: a long overdue task [Poster]

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The Alps are one of the largest continuous natural areas in Europe, stretching approximately 1,200 kilometres across eight countries, and including fourteen national parks. The Alpine Convention emphasizes the importance of this area and encourages transnational research and conservation projects. Lichens as unique models of fungal symbioses with macroscopically recognizable, light-exposed individuals are a predominant symbiotic life form of higher altitudes in the Alps. National checklists or catalogues exist for Austria, France, Germany, Italy, Slovenia and Switzerland. A comprehensive checklist of the lichens of the Alps is long overdue and will enable us to compare, for instance, the genera and species diversity of the Alps with those of other mountain systems of the world. The compilation of such a catalogue has been initiated as a multi-authored project more than ten years ago, which has unfortunately come to a standstill. We are now summarizing the abundant but scattered baseline information on lichen biodiversity in the Alps, which will lead to a transnational inventory of all lichen taxa present in the Alps, including data on their ecology. The information will be of use for experts, decision-makers, and amateur researchers.

Taking a look at model adequacy in phylogenetics: parametric bootstraps and pattern analysis [Talk]

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Although Maximum Likelihood methods are known to be principally consistent, they depend strongly on the quality of the multiple sequence alignment and the properties of the chosen substitution model to reflect the underlying historical processes which led to the observed data. Several methods have been established to evaluate relative model fit. However, in cases in which all applied substitution models are not adequate for the observed data, consistent and reliable results can not necessarily be expected. If a model fitted to a real dataset is correct, pattern spectra are expected to be similar to the ones obtained for data simulated with the same tree topology and the same model (parametric bootstrapping). For artificial datasets this not always true. We took a closer look at the evaluation of model fit based on pattern distribution.

Phylogeny and diversification of acoustically communicating European grasshoppers [Poster]

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The acridid grasshoppers (Acrididae) are an acoustically communicating and very species-rich group of insects that are suspected to have experienced different radiations during their cladogenesis. Nevertheless, crucial phylogentic relationships of European acridid grasshoppers still remain unresolved. Our projects aims at tracing the past and especially recent diversification of this group through time.

The *Hyles euphorbiae* complex (Lepidoptera, Sphingidae) – still a taxonomic problem? [Talk]

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The *Hyles euphorbiae* complex (HEC) is distributed across a large part of the Western Palaearctic reaching from Central Asia throughout Europe and Northern Africa to Macaronesia in the West and Yemen

in the South. It is characterized by a great larval and adult variability which has long been inspiring amateur and professional entomologists to describe new species, subspecies or (geographical) variants and to recurrently rearrange the taxonomy. The European species *H. euphorbiae* alone accumulated 102 synonyms until the year 2000. First molecular analyses indicated several mitochondrial lineages with numerous areas of introgression. Even well defined, distantly related species of the genus *Hyles* do not differ significantly in the morphology of their genitalia and readily hybridize, which further adds to the problem. We aim here to disentangle the taxonomy of the HEC by means of an integrative approach of total evidence. We interpret biogeographic structures by comparing larval and adult colour patterns, haplotypic data from mitochondrial markers (2284 bp of COI/II genes) and genotypic data from fast evolving nuclear markers (10 microsatellite loci) of more than 700 individuals from the entire distribution area. We discuss these in the light of the current knowledge about the ecological niche (host plants, climate niche modelling) and possible reproductive barriers (*e.g.* different female calling times).

Phylogeny of the holometabolous insect orders – new insights from transcriptomes and morphology [Talk]

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Holometabola is one of the most species-rich lineages of organisms. However, only for comparatively few species, mostly model organisms, extensive molecular data are available, and the evolution of this extremely successful lineage is still insufficiently understood. We provide for the first time a robust phylogenetic backbone tree based on large-scale EST data for representatives of all recognized holometabolan

orders. We carefully selected members of presumably basal groups, assuming that they are more conserved than more deeply nested representatives of the orders (*e.g.*, *Xyela* for Hymenoptera, *Nevrorthus* for Neuroptera, and *Micropterix* for Lepidoptera). We put special emphasis on an exhaustive validation of our data and applied new or improved methods in all steps of the analyses. Specifically, we used advanced approaches for orthology prediction and refinement of alignments, and we used selected data subsets for addressing specific relationships in a hypothesis-driven mapping approach to exclude biases caused by missing data. The addressed open questions include the internal relationships of Neuropterida, the internal relationships of Antliophora, and the position of Hymenoptera. Furthermore, we compiled a morphological data set considering several new character complexes as for instance the male postabdomen. In our analyses, we found overwhelming support for, *e.g.*, i) Raphidioptera as sister group to Neuroptera + monophyletic Megaloptera, ii) Hymenoptera as sister group to the remaining holometabolan orders, and iii) a sister group relationship of Siphonaptera and Mecoptera within Antliophora. Based on these results, we are able to describe and discuss the evolutionary histories of morphological character systems and life histories.

The power and challenges for stable and sensible scientific names for animals [Talk]

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As scientists, we all agree that the quality of our inferences relies on the quality of the data that goes in to them. Most information on the past and current living world is linked through the scientific names of organisms, so they are the key for information access about anything published or catalogued on biodiversity. The International Commission on Zoological Nomenclature (ICZN) is adviser and arbiter for the zoological community by generating and disseminating information on the correct use of scientific names. The ICZN is responsible for producing the International Code of Zoological Nomenclature – a set of rules for the naming of animals, and for the resolution of nomenclatural problems for both Recent and fossil taxa, permitting continuity of information retrieval through the history of life. By providing a kind of ‘high court’ and quasi-legal structure for problems in nomenclature, the ICZN is both the foundation for communication about this complicated body of information and an infrastructure for scientific information exchange. Animals make up the largest part of described biodiversity, with approximately 1.8 million living and 300,000 fossil species currently recognized, with about 2–4x more available names than recognised taxa. The ICZN has just launched its official updated registration site, ZooBank, for new publications and names: http://zoobank.org/ to provide an on-line definitive database for all zoological family, generic and species names – extinct and living. Development of this site has been in tandem with parallel work on a registration site for fungal names. This is part of an explicit strategy of cooperation among the different nomenclatural codes, with an aim to minimizing future differences among the Codes for names of plants, fungi, algae, animals and bacteria, as supported by the Int’l Committee on Bionomenclature (ICB): http://www.bionomenclature.net/. This, in turn, is part of a global effort to make all scientific names of organisms organised and machine-usable, the Global Names Architecture (GNA). Continued development of the ICZN’s authoritative names server and input from the user community will dramatically improve information access and ultimately the quality of all research that relies on stable scientific names of animals.

Biodiversity of *Klebsormidium* from highland soil crusts (Alps, Tyrol, Austria) [Poster]

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Klebsormidium Silva, Mattox et Blackwell is a widely distributed streptophycean algal genus in terrestrial ecosystems. The ability of *Klebsormidium* to survive and develop high biomass in extremely dry isolated, hot, or cold terrestrial conditions, is not completely understood and an interesting subject for investigation. Forty strains of *Klebsormidium* isolated from soil crusts collected in mountain region on different altitudes (Alps, Tyrol, Austria, between 600 and 3000 m altitude) were analysed using an integrative approach. The molecular phylogeny of ITS rDNA sequences showed that these strains belong to five clades (B, C, D, E and F) previously described by Rindi *et al.* (2011). Eight morphotypes have been observed among alpine *Klebsormidium* strains, four of which correspond with molecular clades: *Klebsormidium flaccidum* (East Europe; clade B), *K. flaccidum* (West Europe; clade C), *K. bilatum* (clade D) and *K. crenulatum* (clade F). Most of the strains belonged to the clade E, which represents four different morphotypes: *K. nitens* (corresponds partially clade E2 sensu Rindi), *K. pseudoflaccidum* (partially clade E2), *K. fluitans* (clade E3), and *K. dissectum* (clade E4). The data indicate a high diversity of Alpine *Klebsormidium* species that includes most of the known genetic and morphological diversity described for the genus. Only representatives of clade G (involves strains from arid desert environment) and some subclades of clade E (E1, E5 and E6, mostly containing freshwater strains) were absent among Alpine isolates. Most *Klebsormidium* strains from Alpine soil crusts (about 75 %) belonged to the E clade, which represents the most humid lineage among *Klebsormidium* species according to previous phylogenetic, morphological and ecophysiological data. The representatives of the most xerophytic lineages, clades G and F, are completely absent or are represented by only one strain in alpine soil crusts. The representatives of temperate lineages (clades B, C and D) are found in low numbers (1–6 strains). Despite of changing conditions during day and night in the higher Alps, most of the Alpine *Klebsormidium* strains belong to the humid group, which indicates that *Klebsormidium* has adaptation mechanism against desiccation and high light and UV irradiation. The distribution of the *Klebsormidium* strains showed no correlation to different altitudes in the Alps. All strains showed a high phenotypic plasticity, but a low genetic variability.

Diversity, speciation and co-evolution in fungal-parasitic fungi: the *Biatoropsis-Usnea* system as a model [Talk]

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Mycoparasitism – fungi parasitizing other fungi – is a common lifestyle that is particularly frequent within the Tremellomycetes (Basidiomycota). Relatively non-aggressive mycoparasitic fungi of this group are in general highly host specific, as it is usually the case in lichenicolous (lichen-inhabiting) taxa. It has been suggested that host-parasite co-evolution is a main speciation force in these associations. Species delimitation in lichenicolous Tremellales is often challenging since morphological characters are scant. Host-specificity is therefore a great aid to discriminate between species, although the actual diversity of certain groups is probably still underestimated. Here, we use the *Biatoropsis-Usnea* associations as a model to study factors inducing parasite diversification. *Biatoropis usnearum* (Tremellales) induces the formation of conspicuous galls or deformations on its hosts. These galls are remarkably variable in size, shape, and colour, and preliminary molecular data exist suggesting that *Biatoropsis usnearum* may in reality represent a species complex. *Biatoropsis* grows on *Usnea* and *Protousnea* (Parmeliaceae), two genera with an extremely high degree of phenotypic plasticity, which complicates the identification of species. We use morphological data and molecular methods – including the general mixed Yule-coalescent (GMYC) model – to assess the diversity of fungi currently assigned to *Biatoropsis usnearum*, and to determine the phylogenetic relationships among them. In parallel, we reconstruct molecular phylogenetic hypotheses of the *Usnea* and *Protousnea* hosts. We use recent co-phylogenetic analysis tools to detect possible events of host-parasite coevolution, and to assess the extent of cospeciation, duplication, host switching, loss, or divergence failure that could explain the patterns in this association.

Diverse Ty3-gypsy elements in sister *Anemone* and *Pulsatilla* genera: a structural and cytogenetic perspective [Poster]

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Eukaryotic transposable elements (TEs) are ubiquitous and widespread mobile genetic entities. Genome divergence through transposable elements activity and recombination are ongoing processes that occur within species. We have surveyed a set of TEs, amplified by PCR in the members of two sister genera *Anemone* and *Pulsatilla* using degenerative primer pairs matching Reverse Transcriptase (RT) and Integrase (Int) regions. The Blast search identified all TEs as Ty3-gypsy class of retrotransposons exhibiting homology to RT, RNAse H and Int. In *Anemone*, isolated elements showed great variations considering size, structure and chromosomal position. Despite their dispersed organisation on chromosomes, in some *Anemone* species, the elements were absent from the DAPI positive heterochromatin regions, while in other species, they showed significant clustering in the DAPI positive heterochromatin regions. In all investigated *Pulsatilla* species, FISH showed pericentromeric localization of elements on chromosomes. In the phylogenetic tree, the sequences showed clear separation into two clades suggesting that at least two subfamilies of Ty3-gypsy retrotransposons were isolated from the *Anemone* and *Pulsatilla* species. Diverse organization of Ty3-gypsy elements in *Anemone* and *Pulsatilla* genera suggest that they play an important role in plant genome evolution and speciation.

Parasitic life style and its consequences from an evolutionary morphology point of view: Examples from Crustacean groups [Talk]

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Parasitism is undoubtedly one of the strongest driving forces in the evolution morphological disparity, and the list of arthropod examples is extensive. Within the Crustacea, most (but not all) parasitic forms are derived from well-known free-living groups, but nonetheless, some of the most extreme examples of derived morphology can be found among them. As some of the groups are facing the same suite of extreme evolutionary challenges, the adaptations of morphology have followed convergent paths. In this talk I will present examples of both highly derived divergently and convergently developed morphology. By using examples from the fish parasitizing Branchiura and Copepoda, and the extremely specialized Rhizocephala, parasitizing other Crustacea, I aim to cover a wide range of morphology and how it can be interpreted into a better understanding of how parasitism drives evolution.

Genomic mosaicism confirms the complex hybrid origin of unisexuality in *Calligrapha* (Coleoptera: Chrysomelidae) [Talk]

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It is well established that unisexuality has a polyphyletic origin and that it may arise following different mechanisms, whereby interspecific hybridization is the most common in animals. *Calligrapha* (Coleoptera: Chrysomelidae) includes six known tetraploid unisexual species hypothesized to be the result of independent interspecific hybridization events between two bisexual species, based on the observed incongruence between nuclear and mitochondrial phylogenies. However, as this type of incongruence can arise due to other evolutionary processes, this mechanism must be confirmed. If unisexuality in *Calligrapha* is related to hybrid origins, the expectation is that these species will exhibit high nuclear heterozygosity due to genomic coexistence of alleles from their respective divergent parental species. Moreover, these alleles will be phylogenetically divergent among them and closer to their respective original genetic stock. To assert this point, we have studied genetic diversity for two single-copy nuclear genes (HtS and Wg) via cloning in 15 individuals of four unisexual (*C. apicalis, C. suturella, C. vicina and C. virginea*) and 22 individuals of six bisexual species of *Calligrapha*. For each individual an average of 16 clones were sequenced. As expected, the highest nuclear heterozygosities were found in unisexual species and phylogenetic analyses showed these divergent alleles to be related to different bisexual species, unambiguously identified as the parental species. These results confirmed the original hypothesis about hybridization associated to the origins of unisexuality in *Calligrapha*, but they also contributed an unexpected twist to this hypothesis. In most cases, the nuclear stocks for these divergent alleles are different from the one supplying with the mtDNA of every unisexual lineage, implying that at least three bisexual species were involved in the evolutionary path leading to *C. suturella* and *C. virginea* and possibly four in the case of *C. apicalis* (with three divergent sources of nuclear alleles, different from the donor of mtDNA). The origin of unisexuality in *Calligrapha* appears thus as a complex process where a series of successive hybridization events and involving different bisexual species may have taken place.

Evolution of soil preference in the Alpine and Balkan *Minuartia* series *Laricifoliae* (Caryophyllaceae) [Talk]

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Minuartia series *Laricifoliae* consists of 12 taxa that are largely native to the Alps and the Balkan Peninsula. All members of the series grow in open, rocky habitats and all but one taxon are endemic to particular substrates. However, although the individual taxa are substrate endemics, many different substrates are occupied by the series as a whole, with 3 taxa endemic to serpentine, 6 taxa endemic to limestone, 1 taxon endemic to siliceous rock, and one more of a generalist. We are using DNA sequence data and AFLPs to examine the evolution of soil preference within series *Laricifoliae*. Using AFLP and chloroplast haplotype data, we examined the evolution of *Minuartia laricifolia*, with the silicicolous subsp. *laricifolia* centered in the western Alps, and the serpentine subsp. *ophiolitica* from the northern Apennines. Subspecies *ophiolitica* appears to be most closely related to the Maritime Alps populations of subsp. *laricifolia*. Due to the high level of genetic diversity in the disjunct subsp. *ophiolitica*, it likely arose by vicariance instead of long-distance dispersal from subsp. *laricifolia*. This could have taken place during the glacial periods, when the species could have had a continuous distribution between the Maritime Alps through the Ligurian Alps to the Apennines. Using sequence data from the internal and external transcribed spacers of the nuclear ribosomal DNA as well as the trnQ-rps16 chloroplast spacer, we reconstructed the phylogeny of the entire *Minuartia* section *Spectabiles*, to which series *Laricifoliae* belongs. Series *Laricifoliae* appears to be ancestrally calcicole, and is composed of two major clades that differ in soil preference as well as a number of basal lineages. One of the two major clades is entirely calcicole, while the other is composed largely of plants that are confined to serpentine or siliceous rocks (including *M. laricifolia* discussed above). The change/shift in soil preference between these two major clades appears to have taken place on the Balkan Peninsula, with subsequent dispersal to the Alps and Carpathians. *Minuartia langii* (=) is a member of the large calcicole clade and thus does not appear to be closely related to the remaining two subspecies of *M. laricifolia*.

The evolution of sea anemone venom peptides [Talk]

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Peptide toxins from the venoms of animals such as snakes and cone snails evolve under positive selection as they are involved in a never-ending “arms-race” between prey and predator. We have shown that the same is true for voltage-gated sodium channel modifier toxins from sea anemones (Actiniaria), an order of sessile cnidarians that utilize their venom for catching prey and defending themselves from predators. However, these sea anemone neurotoxins exhibit an additional striking feature never described before for toxin genes, they evolve in a concerted manner, meaning that the toxin genes of one species are more similar to one another than to those of another species. This mode of evolution is extremely rare and we propose it is advantageous in this case as it allows the maintenance of many genes encoding a highly potent toxin, hence enabling its faster expression in large amounts. Moreover, we have shown that these neurotoxins are produced in ectodermal gland cells and are not restricted to nematocyst, the stinging organelles of sea anemones. The distribution of toxins between nematocysts and gland cells varies between species, possibly reflecting adaptations to different habitats, diets and predators. To extend our understanding of sea anemone toxins we analyzed for the first time via mass spectrometry approaches the protein mixture that is released from the nematocysts upon their discharge, uncovering a rich array of previously unknown toxins. Fourteen of these 20 proteins had no identified homologs in other animals, suggesting they are the products of taxonomically restricted genes, a finding which fits well their origin from a taxon-specific organelle. Interestingly, we localized one of the venom components, an astacin zinc metallopeptidase, not only to nematocytes (the cells containing the nematocyst) but also to pharyngeal gland cells, highlighting once again the existence of several venom delivery mechanisms and toxin-producing cell populations in sea anemones. In summary, our study in recent years has shed light on the evolution of sea anemone toxins and highlighted their unusual modes of evolution as well as their multiple cellular sources.

"It stings a bit but it cleans well": the antimicrobial potential of venoms from Hymenoptera [Talk]

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Venoms from Hymenoptera display a wide range of functions and biological roles. Recent works indicate that in many hymenopteran species, the venom also regulates microbial infections, both in stinging and stung animals. In addition, stinging Hymenoptera seem to constitute an under-exploited ecological niche for agents of vector-borne disease. Few parasitic or mutualistic microorganisms have been reported to be hosted by venom-producing organs or to use venom injection as a natural route of infection to enter stung animals. This may result from the presence of potent antimicrobial molecules in venoms, histological features of venom apparatuses and selective effects of venoms on immune defenses of targeted organisms. During this talk I will review for the first time the venom antimicrobial potential of solitary and social Hymenoptera in molecular, ecological, and evolutionary perspectives.

Phylogenetic species concept and biogeographic distribution of selected species of *Entoloma* (Agaricales, Basidiomycota) [Talk]

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Species of *Entoloma* section *Entoloma* are commonly recorded from both the Northern and Southern Hemispheres and, according to literature, most of them have at least Nearctic-Palearctic distribution. However, all these records are based on morphological species concepts and studies relating morphology, molecular data and species distribution have not been reported in this group. In this study, we employed phylogenetic species recognition criteria based on gene genealogical concordance (using phylogenies from nuclear ITS, LSU, rpb2 and mitochondrial SSU sequences) to answer specific questions considering

(1) the morphological species limits in *Entoloma* section *Entoloma* and (2) their geographic distribution in Europe, North America and Australia. For the four morphospecies addressed, *E. sinuatum*, *E. prunuloides*, *E. nitidum* and *E. bloxamii*, our results reveal strong phylogeographical partitions that were previously not known. For example, no collection from Australia proved to be conspecific with the Northern Hemisphere specimens. In addition, in most morphospecies, European and North American collections represent phylogenetically distinct sister taxa. Even within Europe, new lineages, representing newly discovered taxa, were uncovered for the red-listed *Entoloma bloxamii*. Our results clearly demonstrate the power of the phylogenetic species concept to reveal true evolutionary units, to redefine the morphological limits of the species addressed and to provide insights into the evolutionary history of key morphological characters for *Entoloma* systematics.

Inferring rates and patterns of killer whale diversification from mitogenomic and nuclear sequences [Talk]

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Historically, killer whales have been assumed to comprise a single, wide-ranging species with a diverse diet. Numerous studies have questioned this taxonomy because of groups of killer whales that display traits that are consistent with social and reproductive isolation, including differences in genetics, social structure, diet and behavior (acoustics and foraging). Prior to the advent of NGS technologies, genetic evidence was weak because traditional sequencing methods using only a small portion of mitochondrial DNA revealed extremely low worldwide genetic variation and little or no phylogeographic pattern. We initially sequenced the whole mitochondrial genome from 139 samples representing 8 ecologically distinct but regionally sympatric ecotypes in the North Pacific, Antarctic, and North Atlantic. All of the recognized ecotypes in the North Pacific and Antarctic contained reciprocally monophyletic clades with divergence times ranging from 150,000 to 700,000 years. Patterns between ecology and phylogeny in the North Atlantic were less well resolved, and suggested periodic connections between the North Atlantic and the North Pacific and Antarctic. Antarctic types were sister taxa to each other, though there is evidence that there are additional pelagic types in the Southern Oceans that may be closely related to or even part of wide-spread and poorly-studied populations at lower latitudes. In all cases, fluctuating sea levels and ice coverage at high latitudes could have resulted in repeated reduction and isolation of regional or oceanic populations, and ecological divergence may have occurred during allopatric periods through drift or selection, followed by secondary contact and diversifying selection due to highly constrained social structure and resource competition. Ongoing studies of mitogenomes and nuclear markers within two types in the North Pacific indicate very recent expansion of the "Resident" type, and no evidence of gene flow between the sympatric Resident and Transient types. All the evidence therefore suggests that the process of speciation is at a late stage and may have reached completion between these two ecotypes. We are currently expanding our sequencing of mitogenomes to include 300 additional samples to investigate population structure, demographic patterns and phylogenetic patterns when lower latitude samples are included, and to include SNP data from sequencing of 75 nuclear loci.

Biogeography and systematics: an introduction [Talk]

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Biogeography is the science that attempts to document and understand spatial patterns of biological diversity. Traditionally defined as the study of organismic distribution, both past and present, modern biogeography now includes studies of all patterns of geographic variation in life, from genes to entire communities and ecosystems. This talk will provide an introduction to the overall symposium theme and highlight some examples of biogeographic research topics investigated by the scientific community during the past decade. Topics covered will include i) the interplay between biogeography and systematics, ii) biogeography and niche evolution, and iii) the current state of knowledge about general biogeographic patterns in highly biodiverse regions of the world (like Southeast Asia and South America).

Biodiversity of spirurid nematodes [Talk]

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The spirurid nematodes (order Spirurida) is a group composed of diverse zooparasitic organisms. It includes more than 2800 species split into 12 superfamilies and 330 genera. Nowadays, morphologists and taxonomists generally accept the systematic proposed by Chabaud and initially published as part of the CIH Keys to the nematode parasites of vertebrates. The spirurids are gathered together as a result of the specific organisation of their head sensory organs, in association with their cephalic structures (development of lateral pseudolabia and loss of the triradiate symmetry), as well as by their life cycles involving arthropods as intermediate host and vertebrates as definitive hosts. Chabaud & Bain analysed the origin and evolutionary history of Spirurida using their adult morphology, host specificity and geographical distribution; they concluded that despite their morphological and biological homogeneity, spirurids most probably represent a polyphyletic group. The molecular phylogenies based on 18S rDNA also reveal spirurids and some of their family-group taxa as non-monophyletic. This presentation follows a recent review on Spirurida generalizing our knowledge of the biodiversity and the evolutionary history of the group based on larval and adult morphology, life cycles and molecular data.

Phylogenetic relationships in the buttercup family – Improvements brought by a multiple marker approach [Talk]

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The family Ranunculaceae (buttercup family) belongs to the first diverging order within eudicots, the most diversified clade of flowering plants. Understanding the evolution of floral traits in this family is therefore crucial in our understanding of floral evolution at the scale of eudicots. The first molecular phylogenies of the flowering plant family Ranunculaceae were published more than twenty years ago, and have led to changes in the classification of the family. However, the currently accepted classification is not yet well supported by molecular data, and relationships among subfamilies and tribes of Ranunculaceae remain an open question. In this study, we investigate these relationships using information from five new markers sampled from the three genomes, including two paralogs of the nuclear CYC-like gene. Phylogenetic analyses were performed on each marker separately, then on a combination of all new markers. The new markers were also combined with published sequences of additional markers previously used for phylogenetic inference in Ranunculaceae. Phylogenetic reconstruction was performed using Bayesian inference and maximum likelihood. The combination of multiple markers from the three genomes led to higher resolution and support of phylogenetic relationship among subfamilies of Ranunculaceae, and among tribes of subfamily Ranunculoideae. Our results suggest that tribe Adonideae is the sister group of Thalictroideae, challenging the monophyly of Ranunculoideae as currently circumscribed. The new phylogenetic background produced is used to make inferences about floral trait evolution in this family.

Biogeographic history of the Araceae [Talk]

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The Araceae family (3305 species, 118 genera) is one of the oldest lineages in the monocots and has a fossil record that includes Cretaceous flowers, fruits, pollen, and leaves. Araceae can be free-floating aquatics (lemnoids and *Pistia*), rainforest canopy epiphytes, or seasonal herbs adapted to arid and cold conditions. The family has a world-wide distribution, but the vast majority of species occur in the humid tropics. Six of the eight subfamilies and 16 genera occur disjunctly on two or more continents, separated by large ocean expanses. Fossil evidence shows that many groups once lived in regions they no longer occupy, indicating extinction. In my thesis, I inferred the biogeographic history of the Araceae family world-wide and for one clade also at a regional scale. I constructed an almost complete genus-level phylogeny based on chloroplast DNA (> 4300 basepairs) and performed divergence dating with different fossil constraints, clock models, uniformly and log-normally distributed fossil constraints, and complex or simple substitution models. A novelty is that my ancestral area reconstruction also takes into account past connectivity between landmasses as well as formerly occupied ranges (deduced from fossils). Effects of including fossils in the models were assessed by comparing runs with and without fossil occurrences. The results show that the Araceae clade diverged from the remaining Alismatales in the Early Cretaceous, during the final stages of the breakup of Pangea. Subfamilies began to diversify before the K/T boundary, and early lineages have persisted in Laurasia. A water-associated habit appears to be ancestral in the family. Several lineages reached South America in the Paleocene and Eocene, while most transitions to Africa, Southeast Asia, and Australia happened in the Oligocene and Miocene (often following trans-oceanic dispersal). Extinctions in the temperate region probably were caused by the climate cooling in the Oligocene. Past distributions inferred when models included fossil (no longer occupied) ranges differed in nontrivial ways from those without fossil ranges.

The role of body size in marine invasion through the Suez Canal and its implications for the Mediterranean species pool [Talk]

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The opening of the Suez Canal in 1869 re-established the link between the Mediterranean and Indo-Pacific realms, allowing hundreds of species to spread from the Red Sea (RS) to the Eastern Mediterranean (EM), with mollusks being one of the most prolific groups. This almost unidirectional interchange can be regarded as one of the largest human-mediated biogeographic experiments providing an excellent system for testing macroecological hypotheses. Body size correlates with many key life history traits and it has been long proposed to play an important role in mediating species invasions. Here we test this relationship using a taxonomically standardized database of body size and ecological characteristic of extant bivalves from the northern RS and the Levantine coast of the EM. Although our data suggest that successful RS invaders are a random sample of their source species pool with respect to body size, they are significantly larger than native EM species. Explanation of this pattern can be found in distinct shapes and modal values of the regional body-size frequency distributions (SFD) in the two areas. The Red Sea SFD is very similar to province-scale distributions documented for the Eastern Pacific bivalves and differs significantly from more log-normal Mediterranean SFD. The causes of this discrepancy are not clear and may be related to different biogeographic affinities of the two biotas or to the late Neogene extinctions and history of recolonization of the EM basin. Differences in body size may therefore translate into greater competitive abilities of the RS invaders, but other ecological or live history traits can be more important in determining which species from the donor region will spread into the novel areas. In spite of the apparent lack of size-selectivity among invaders, continued inflow of the RS species will progressively shift the EM SFD towards values typical for the Indo-Pacific realm, underscoring the importance of geographic barriers and species invasions in shaping body sizes in regional species pools.

Morphometrics as a tool in taxonomy [Talk]

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Whenever traditional taxonomy met high morphological variability, a great number of species, subspecies, and phenotypes was frequently distinguished, often based on minor morphologic deviations. To address such complicated taxonomical questions and gain a more objective view, new techniques of morphological analyses are required. This is particularly true for the paleontological record, where soft tissue is usually missing and DNA extraction impossible. In most cases a quantitative analysis of the hard-part morphology is the only way to resolve the taxonomy of closely related taxa. In this context the term 'morphometrics' was first used in the 1980s. It describes the quantitative study of biological shape variation,

combining a series of analytical methods from the fields of statistics, biomathematics, physics, and informatics. A broad variety of specific tools and methods is currently available and frequently used. Two of them will be outlined here. One approach addresses comparison of biological shape via homologous points termed landmarks. This is one of the most widely used techniques in morphometrics with applications in a variety of scientific (and commercial) fields, including evolutionary biology, ecology, medicine, and taxonomy. When homologous points are scarce or even lacking, however, the use of landmark analysis is highly problematic. In these cases it is more appropriate to analyze outlines or other curves which can be considered homologous in their entirety. Different tools are necessary for open vs. closed curves, respectively for simple vs. complex shapes. For closed complex curves Fourier analyses are most commonly used, which are based upon the decomposition of a complex function into a combination of simpler trigonometric functions. Using examples of recent and fossil gastropods from the literature and our own investigations, we will detail the advantages and disadvantages of both approaches, and discuss necessary prerequisites, common mistakes and precautions to avoid them.

Data acquisition of zoological and palaeontological fish collections for GBIF [Talk]

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The project IDES aims to set up a high performing information infrastructure which will be commonly used by four research collections belonging to the Staatliche Naturwissenschaftliche Sammlungen Bayerns (SNSB). The worldwide unique ichthyological collections are housed in separate buildings in Munich and Eichstätt and belong to four administrative independent institutions (Bayerische Staatssammlung für Paläontologie und Geologie, Jura-Museum Eichstätt, Staatssammlung für Anthropologie und Paläoanatomie München and Zoologische Staatssammlung München). IDES will mobilise and digitalise the data and metadata of Actinopterygii from Europe and adjacent seas, starting from the Mesozoic era (Trias) until collections of extant fishes. Mobile work stations with innovative imaging facilities will be established and adapted to the specific requirements of the various kinds of collection objects (dried collections of skeletons, wet collections, fossils, DNA and tissue collections) accompagnied by text information on paper documents with location data, descriptions *etc.* At the end of the project the data for more than 50.000 objects with 10.000 images will be accessible via the relational database system Diversity Workbench (DWB). This allows a sustainable and integrative data management and data flow starting with the imaging process, decentral data entry in the collection storage rooms until a central data archiving and data processing in close cooperation with the IT Center of the SNSB. The data flow includes the connection of the data sources to various web interfaces, wrapper installations and the data publication in international data networks like GBIF, FishBase and FishNet 2.

New data on the biodiversity of land flatworms of the genus *Microplana* Vejdovsky, 1890 from Germany (Platyhelminthes) [Poster]

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Land planarians are predatory and necrophagous flatworms inhabiting the forest floor that most likely colonized the land hundreds of millions of years ago. Currently there are about 850 nominal species worldwide, reaching the highest diversity in the tropics. In Europe there are approximately 19 native species of land planarian, belonging to the subfamilies Rhynchodeminae and Microplaninae. For Germany only 5 species of land flatworm have been reported, of which one is certainly an introduced species. We examined two small land planarians that were recently collected near Finsterwalde in Brandenburg and in addition we studied 3 animals from Schleswig-Holstein held in the collections of the Museum für Naturkunde, Berlin. Externally all specimens present a uniformly brown, almost cylindrical body, being only slightly flattened ventrally; the eyes are very difficult to observe in live or preserved specimens but can be observed in histological sections; body length about 25mm. The internal anatomy of the animals was examined on the basis of sagittal and transversal histological sections. The copulatory organs of the Finsterwalde specimens are orientated horizontally, with the prostatic vesicle placed in a muscular sack, together with the penis papilla. The sperm ducts and oviducts are placed between the fibers of the subintestinal transverse parenchymal muscle layer. In contrast, the copulatory organs of the Schleswig-Holstein specimens are orientated vertically, while the penis presents a large bulbar lumen and a prostatic vesicle is absent. The sperm ducts and oviducts of these specimens run under the subintestinal transverse parenchymal muscle layer. Our results suggest that the animals from Finsterwalde belong to a variety of *Microplana terrestris* (Müller, 1774), while the animals from Schleswig-Holstein may belong to a new species of *Microplana*. Our preliminary data point to a higher diversity of *Microplana* species for Germany than currently known.

Elucidating the genotype-phenotype map using *Arabidopsis* [Talk]

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Making sense of natural variation remains one of the greatest challenges in biology. Understanding how genetic variation translates into phenotypic variation, and how this translation depends on the environment is fundamental to our understanding of evolution, and has enormous practical implications for medicine, agriculture and energy production.We are attempting to tackle this problem using *Arabidopsis thaliana* as a model. Because it is highly self-fertilizing and naturally exists as inbred lines, *A. thaliana* can be brought into the laboratory and grown, in replicate, under different environmental conditions, in order to explore how the genotype-phenotype map works and has been molded by evolution. The presence of inbred lines, coupled with its compact, 120 Mb genome, also makes *A. thaliana* useful as a model for genomic approaches that will soon be possible in others organisms. As part of the 1,001 Genomes Project, we are sequencing well over 1,000 inbred lines, and are complementing these data with other kinds of "-omic" information, such as DNA methylation patterns and transcriptome measurements in large numbers of lines under multiple environmental conditions. For example, we are currently analyzing the data from a study that involved flowering time and multiple other phenotypes in a sample of 200 Swedish lines grown at two different temperatures. These data have been complemented with transcriptome (via mRNA-seq) and DNA methylation (via bisulfite sequencing) measurements of all lines under both temperatures. By supplementing the genome-wide associations between genotype and phenotype with the "in-between-ome", we hope to gain insight not only in which genetic polymorphisms are associated with phenotypic variation, but why.

By carrying out these kinds of studies in *A. thaliana*, which can be grown in replicate under controlled conditions, we also hope to gain insight into the limitations of these "brute force" genomic approaches, which are rapidly becoming economically feasible for a broad range of species, but may not be practicable from a biological point of view. In particular, we have learned much about the difficulties involved in identifying causal genetic polymorphisms through genome-wide association studies.

Modern palaeobiology stimulates "old fashioned" taxonomy – case studies from the aftermath of the Permian/Triassic mass [Talk]

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Modern quantitative palaeobiology and taxonomy are often seen as antagonisms but this is fundamentally misleading. First of all, large databases which are needed to study large scale diversity and ecological patterns are based on alpha taxonomy. It is clear that databases such as the Paleobiology Database do not only contain valuable but also misleading data such as outdated or wrong generic assignments or misidentifications (the latter is also a problem for GenBank). Statements that the errors are so severe and widespread that no real patterns can be found in such databases are probably too pessimistic ("garbage in – garbage out"). Statements that alpha taxonomy is not really science, intuitive, a "just so story" and basically not falsifiable are likewise polemic and not helpful. Taxonomic decisions are phylogenetic hypotheses based on character analyses and comparisons and are falsifiable by means of illustrations, descriptions and repository of type specimens. However, encompassing phylogenetic analyses are not very promising in many fossil invertebrate groups, *e.g.* within gastropods and bivalves, because the number of shell characters is small but the number of taxa is large. Interestingly modern paleobiology does not only rest on alpha taxonomy, it even stimulates new systematic studies. The great interest in the impact of mass extinctions leads to a closer look at taxa before and after mass extinctions in order to infer which taxa really survived or became extinct. Studies on early Triassic gastropods revealed that the generic assignments of many species were erroneous or outdated. Based on the restudy of types and on the study of newly collected well preserved material, many taxa have been re-assigned. Given the very low number of only *c.* 100 Early Triassic species, these re-assignments can change the entire picture of gastropod evolution at the Paleozoic/Mesozoic transition. The number of true survivors is restricted. However, there are surprisingly many genera originating in the Early Triassic and some of them are restricted to this time interval (singletons). Moreover, quantitative data about fossil assemblages are needed for sample standardization which is essential for diversity studies in deep time. This leads to a revival of encompassing monographic work including counts of all species present in collections or samples.

Recent immigrant rather than ancient tertiary element: diversification of *Callianthemum* (Ranunculaceae) in Europe [Talk]

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The European alpine flora is the product of a long history of immigration and local diversification of plant lineages of different provenance and timeframe. Comparative molecular phylogenetic studies that include age estimation analyses provide vital information to compile a more detailed account on the different floristic elements that are part of the alpine flora of Europe. The genus *Callianthemum* (Ranunculaceae) is a prominent representative of alpine plants that show a widely disjunct distribution range from the mountains of Japan to the Sierra Cantabrica in Spain. This genus of some 12 to 14 species is represented in Europe with three taxa: *C. coriandrifolium* is widely distributed in central European mountain ranges, while *C. anemonoides* and *C. kernerianum* represent two local endemics in the Eastern and Southern Alps. We use a dated phylogeny on the basis of cpDNA and nrDNA markers to reconstruct the spatio-temporal pattern of diversification of this genus and compare it to similar floristic elements from the genera *Leontopodium*, *Lomathogonium*, and *Saussurea*. Our investigations show that *Callianthemum* dates back some 45 to 50 mya, but that the diversification of extant species only started some 7 mya. Furthermore, the European species do not represent a monophyletic group but are the result of two independent immigration events during the Pleistocene. Hence, we do not find evidence that *Callianthemum* represents an ancient arcto-tertiary alpine element of the European mountain ranges, but rather is the result of migrations over huge distances on the Eurasian continent during the Pliocene and Pleistocene.

Infection and colony defense [Talk]

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The sessile nature of most colonial animals means they are sitting targets for attack by biotic enemies. Mechanisms of defense against competitors and predators are reasonably well known and include overgrowth, context-dependent inducible defenses such as spines and polymorphic zooids, and chemical warfare via the delivery of toxins. However, colonies also must contend with pathogens and parasites – an area that has received much less attention. Indeed colonies could be particularly prone to infection since they may provide a persistent, genetically homogenous resource and thereby offer unique opportu-

nities for exploitation by parasites over extensive spatial and temporal scales. Two key colony attributes contribute to the provision of this persistent resource: lack of allometric constraints (growth trajectories do not level off over time but extend indefinitely); the production of modules by totipotent cell lineages in meristematic tissues. Recent research provides novel insights into how these features of colonial animals may influence the nature of host-parasite interactions and parasite infection strategies. In particular, our demonstration of how endoparasites exploit colonial freshwater bryozoan hosts and how these hosts respond suggest the evolution of trait-mediated strategies based on colonial attributes that are employed by both the exploiters and the exploited.

Assessing the hidden biodiversity of Myxomycetes using molecular methods [Talk]

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Myxomycetes, or plasmodial slime molds, are a group of amoeboid organisms with a unique life cycle and a wide range of habitats. Some of them, like *Physarum polycephalum*, are used as model objects in cytology researches. However, modern biodiversity of Myxomycetes is clearly underestimated mainly because the current taxonomic system of Myxomycetes is based exclusively on morphological features. These tend to be rather variable, thus sometimes blurring the borders between species and creating morphotypes – groups of biological species combined together according to morphological traits. Resolving these artificial groups remains one of the main problems of modern systematics. In this study we shed light onto one of the largest morphocomplex – “*Physarum notabile*”, which includes more than 7 species from 2 genera. A molecular approach based on the 18S rDNA and elongation factor alpha (eF1a) sequences allows us to clarify the systematic position of these taxa and estimate the extent of genetic diversity (and thus possible cryptic species) inside the morphocoplexes. Using a combined morphological and molecular approach we described a new species, *P. pseudonotabile*, within the *Physarum notabile* morphocomplex. Moreover we disentangled the phylogenetic relations between different species and genera comprising this complex. Additionally, a phylogeographic analysis of the newly described species shows that it has a pronounced genetic structure that correlates with the geographical distribution of this taxon. Another case where genetical information helped to resolve a taxonomical ambiguity was the genus *Kelleromyxa*. Its taxonomical position was unclear since it possessed morphological traits typical for two distinct Myxomycete orders. Our analysis of the 18S rDNA gene places this taxon into the order Physarales. However, a new family can be proposed for this taxon, since it does not match exactly morphological descriptions of the two families inside the order, Physaraceae and Didymiaceae.

Unravelling character diversity in the peripatid velvet worms (Onychophora) [Talk]

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Low character diversity among peripatid velvet worms has long hampered taxonomic and systematic studies on this group. To find additional characters, we examined and compared four species of Peripatidae, two from the neotropics and two from South-East Asia, using morphological, molecular and karyotypic techniques. Scanning electron microscopy on embryos and specimens of varying ages revealed novel morphological characters and character states, including the distribution of different receptor types along the antennae, the arrangement and shape of papillae on the head, body and legs, the presence and shape of interpedal structures and fields of modified scales on the ventral body surface, the arrangement of lips surrounding the mouth, the structure of crural tubercles and genital and anal gland openings, and the presence and shape of embryonic foot projections. Karyotypic analyses revealed differences in the number and size of chromosomes among the species studied. The results of our phylogenetic analyses using mitochondrial COI and 12S rRNA gene sequences are in line with morphological and karyotype data. Taken together, these findings revealed a large number of unexplored, albeit useful, characters in Peripatidae. We suggest that analysing these characters in additional species would help clarify species diversity and phylogeny of Onychophora.

Biodiversity and phylogeny of venomous mollusks [Talk]

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The venomous snails (superfamily Conoidea) comprise one of the most biodiverse lineages of mollusks. Traditionally, the superfamily of venomous mollusks was divided into three major family groups, the cone snails (Conidae), the auger snails (Terebridae) and the turrids (Turridae). There are ca. 300–400 species in the family Terebridae, and 700–800 species in the family Conidae. However, the greatest biodiversity is in what used to be the family Turridae, (which has proven to be polyphyletic), with over 10,000 species. Many of these live at considerable depths, and are very small animals (<5 mm). Newer collection methods have made heretofore unavailable species much more accessible, but a significant fraction of all species are still unnamed.

The cone snails are the most intensely investigated lineage of venomous mollusks. They use their venom to catch prey, deter predators, and interact with competitors. The molecular components of cone snail venoms are relatively well understood; eachvenom has 50–200 different peptides, each acting on a different molecular target in the envenomated animal. The genes encoding these venom peptides undergo an unprecedented rate of accelerated evolution. As a result, the venom components are different in each species, with essentially no molecular overlap, even when venoms of closely-related species are compared. An overview of how the elucidation of venom components has helped to define phylogenetic relationships will be presented. A framework for understanding the venomics and overall phylogeny of the entire superfamily Conidaea will be presented.

Karyological variation of *Cyanus* perennials (Asteraceae) in Europe and its importance for speciation [Poster]

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Molecular systematic investigations of the genus *Cyanus* have provided conflicting information. Especially phylogenetic relationships of the perennial species of *Cyanus* sect. *Perennes* have remained unclear due to reticulate evolution. Extensive study of chromosome number/ploidy level and genome size variation of these taxonomically intricate taxa should help to elucidate their taxonomic affiliations and aspects of the evolution such as crossing barriers or historic and contemporary gene flow. To reveal cytogeographic pattern of *Cyanus* perennials in Europe, DNA ploidy level and/or chromosome numbers were examined for 268 populations (1013 plants) using flow cytometry and/or chromosome counting. Perennial taxa of the genus *Cyanus* have two base chromosome numbers, $x=10$ and 11, and diploid and tetraploid counts were confirmed based on them. New triploid level $x=30$ was discovered for *C. nyssanus*. The majority of taxa and populations consisted of a single cytotype. Cytotype variation is geographically structured: taxa with $x=11$ are widespread in northern latitudes and are ecologically diverse, taxa with $x=10$ are confined to Southern European mountains. Both diploid cytotypes ($2n=20$ and $2n=22$) have greater geographical ranges in Europe than their corresponding tetraploid cytotypes ($2n=40$ and $2n=44$). Sympatric occurrence is mainly observed for species differentiated in ploidy or in chromosome number, while equal cytotypes form parapatric contact zones. Experimental hybridizations showed that taxa of the *C. triumfetti* group ($2n=22$) hybridized easily and produced viable progeny. This argues for the importance of allopatry in speciation of taxa with the same chromosome number. The reproductive barrier between different cytotypes is assumed to be efficient for preventing hybridization. This barrier is broken only very rarely, *e.g.* by hybridization between *C. epirotus* ($2n=20$) and *C. graminifolius* ($2n=40$). Reproductive incompatibilities between the *C. triumfetti* ($2n=22$) and *C. montanus* ($2n=44$) groups were confirmed by hybridization experiments. An advantage of flow cytometry to study species delimitation and taxonomic relationships at the homoploid level was demonstrated. The results showed high (up to 21 %) and species-specific variation in the amount of nuclear DNA within particular cytotypes. Ecological differentiation of cytotypes and genome-size variants of *Cyanus* perennials was also studied.

Evolution of colonial animals: towards a “superorganism” [Talk]

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Unlike solitary animals, and similar to most plants, physiologically contiguous colonial animals are decentralized organisms. Their colonial body, however, is a single genetic individual producing “identical” gametes. The colony results from morphogenesis of reiterated units (modules and groups of modules) that are semiautonomous in their development, physiology, and structural architecture. The degree of autonomy of the modules (zooids) in a colony is directly correlated with the degree of colonial integration. In different animal phyla highly integrated colonies evolved a number of novelties illustrating a general trend towards a “superorganism” – common colonial parts (termed coenosarc); specific colonial growth and symmetry; different longevity of modules and the entire colony; structural and behavioural “co-operation” of modules; and even colonial locomotion. Also unlike solitary animals, this “superorganismic” level of organization yields a distinct component of phenotypic variation at the zooidal level. This morphological variability, termed polymorphism, is manifested in specific morpho-functional transformations of zooids and, sometimes, zooidal groups that work as colonial “organs”. The co-occurrence of alternate phenotypes within genetic individuals (colonies), and repeated evolution of distinct categories of these phenotypes in different animal groups, are of special interest for evolutionary biology.

Is the paddy rice system in Thailand a reproductive ground for semi-aquatic earthworms of the genus *Glyphidrilus*? [Talk]

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The semi-aquatic earthworms genus *Glyphidrilus* Horst, 1889 are unfamiliar earthworms that live on an ecotone between terrestrial and freshwater ecosystems of rivers, streams, canals, ponds, swamps and even in paddy rice system. The genus has been known since 1889. The distributions are interpreted with respect to geographical characteristics. They are highly endemic, and most are confined to a small region. The paddy rice system in Thailand may be an important system as a reproductive reservoir for the worms. *Glyphidrilus chiensis* is an example for this hypothesis. This species occupies the northeast of the Chi River system that drains into the Mekong River, covering all of the huge upper northeastern area that's mostly paddy systems, and has a range spanning almost 900 km. The soil preparation for rice seedlings in the rainy season (July to September) makes appropriate habitats for worms to reproduce and produce cocoons. Juveniles are gradually released later and drained to outer ditches for further growth and development. Adult worms will also emigrate to nearby canals when the rice cultivation is ready for harvesting (dry conditions). The immigration back into rice paddy fields when farmers start their new crops was always found suggesting a continuous cycle. Thus the paddy system may be an important reproductive ground for the worms' diversification. Field surveys and laboratory experiments are now in progress in order to test the above hypothesis.

Introducing the diversity of protozoa to the big data world [Keynote]

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An emerging vision of a future biology is of a discipline that is transformed into a 'big new biology' by its emphasis on sharing data. The change is motivated by the data management challenges created by the data deluge produced by new technologies, and by the opportunities to ask new classes of questions that could not be answered by access to limited data sets. Realization of this vision will require a number of technical and social challenges to be overcome. The technical challenge is to build the infrastructure to hold, manage, organize data and make the data available for re-use; the social challenge is to ensure that scientists participate in contributing data and in making this communal environment relevant. The problems that the students of the paraphyletic and polyphyletic protozoa will encounter exemplify the difficulties ahead. Initial challenges for biodiversity will be to compile a comprehensive system of organism names so that all data can be indexed against a standardized reference system. We have to overcome problems of mis-spellings, homonyms and synonyms of lower taxon names. Protistology is especially challenged with the instability and fluidity of meaning of higher taxon names, terms that offer an ontological framework for the species terms. The sources of the problems are discussed together with best practices that will minimize the current instability and will reduce ambiguity.

Hybridisation in the genus *Potentilla* – the case study *P. alpicola* La Soie [Talk]

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Hybridisation is presumed to be an important mechanism in speciation and evolutionary adaptation of plants, often accompanied by polyploidisation, and linked to apomixis. All three phenomena are considered major drivers of speciation in the highly polymorphic genus *Potentilla*. Morphologically variable, polyploid and apomictic *Potentilla alpicola* was chosen as a model to study the origin and the evolution of hybrid forms. Combined analysis of AFLPs, cpDNA haplotypes and ploidy levels revealed that *P. alpicola* populations in South Tyrol originated from crosses between *P. pusilla* and two cytotypes of *P. argentea*. Three identified lineages comprising two ploidy levels differed in parentage and the complexity of the evolutionary process. A geographically wide-spread lineage contrasted with locally distributed lineages. Populations of *P. collina* studied in addition were regarded recent derivatives of the hexaploid *P. argentea*. The observation of clones within both *P. alpicola* and *P. collina* suggested an apomictic mode of reproduction. The case study of *P. alpicola* support that hybridisation, polyploidisation and apomixis play a significant role in the creation of polymorphism in the genus *Potentilla*. However, multiple origin of hybrids and backcrossing are considered to produce a variety of evolutionary insignificant forms, which exist aside of stabilized, established lineages.

Divergent adaptation from beyong genetics in *Dactylorhiza* allopolyploids (Orchdaceae) [Talk]

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Without being encoded in the underlying DNA-sequence, epigenetic information influences the identity of cells and their response to the external and internal environment by modulating gene expression and regulating the activity of transposable elements. However, epigenetic variations can be both under direct environmental disruption and selection, and they may be generated at a much higher rate than genetic diversity, especially in rapidly changing environmental conditions. Several spontaneous or induced epigenetic variants were shown to be (meta)stably inherited across multiple generations. We are testing if divergent epialleles can be responsible for distinct adaptations and therefore have evolutionary implications in a non-model system in *Dactylorhiza*. We have studied natural epigenetic variation in three allotetraploid sibling orchid species (*D. majalis* s. str., *D. traunsteineri* s. l., and *D. ebudensis*) that differ radically in geography/ecology. The epigenetic variation released by genome doubling has been tuned by divergent selection in species-specific patterns that have an impact on the ecology and evolution of the three sibling allopolyploids, hundreds of generations after their formation. Genome-wide genetic investigations, including high-throuput RAD-sequencing results, consistently fail to uncover relevant genetic differentiation that could relate to the phenotypic differentiation between the allopolyploids. We conclude that stable epigenetic divergence in this group is largely responsible for persistent ecological differences, which then set the stage for species-specific genetic patterns to accumulate in response to further selection and/or drift. In order to improve the general understanding of natural phenotypic variation and organismic adaptive strategies, we need to complement the gene- and genome-centered view, currently dominating our evolutionary perspective about variation, heritability and adaptation, with a substantial consideration of epigenetic factors.

Evolutionary relationships and cryptic diversity in claroteid catfish from Lake Tanganyika [Talk]

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Lake Tanganyika (LT) is the oldest and deepest of the East African great lakes and is amongst the most diverse freshwater habitats in the world. It is home to a broad array of endemic radiations including at least three independent catfish radiations. The number of catfish species described from LT has increased in recent years but to date only the genus *Synodontis*, which includes cryptic species, has been studied in some detail. This work uses a multi-gene approach to address the evolutionary relationships within the sub-family Claroteinae, which has also diversified within LT. The novel phylogeny reveals a large-scale LT radiation including cryptic diversity within the endemic genera *Phyllonemus* and *Lophiobagrus*. Mitochondrial data strongly supported the cryptic species and, using *Phyllonemus* as a focal genus, the support of nuclear data was evaluated using Bayesian species delimitation with results sensitive to population size. These results suggest that catfish diversity within LT may be underestimated due to the presence of cryptic species. Many of these cryptic species appear to be locally restricted and highlight the need for fine-scale sampling. Diversification scenarios will be discussed for this radiation including the relative roles of allopatric speciation and isolation by distance in contrast to convergent evolution in driving this pattern of cryptic speciation. In addition, this system provides an opportunity to investigate the relative roles of intrinsic and extrinsic factors in driving diversification leading to cryptic species in ancient lakes.

Three roles evolutionary theory has been assigned in cladistics [Talk]

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The relationships between cladistics and evolutionary theory are complex since cladistics' very beginning. This complexity is exemplified by cladistics' most extreme positions: first, Hennig's (1950, 1966) process cladistics, which is based on a rich set of evolutionary hypotheses, notably on speciation processes; second, Nelson and Platnick's (1981) pattern cladistics, for whom "evolution is an explanatory theory for systematic patterns that are observed on independent theoretical premises" (Brower 2000: 145), which prevents us from basing cladistics on any kind of evolutionary claim. Most cladists find their way between the two, depending on their own aims, methods and scientific background. In order to criticize one or the other position, one must first know what s/he is talking about. While the debate between process and pattern cladistics is very lively, it is almost never based on an accurate description of what kind of evolutionary hypotheses are effectively used in cladistics, at which step of the investigation, and for which purpose. Now, a quick review of cladistic literature since the 50s shows that the ways cladists refer to evolutionary hypotheses are as diverse as they are numerous. My aim is to provide a typology of the roles that evolutionary theory can play in cladistics, based on an analysis of which roles systematists had it actually play in cladistics' history. While evaluating the relevance of each of these roles is my ultimate goal, this particular talk is only a first step, and hence only descriptive. I shall describe and discuss three possible roles evolutionary theory can play in cladistics: First, evolutionary theory can be a founding theory for cladistics. In this case, evolutionary biology provides hypotheses which allow to found and therefore to justify the main principles of the cladistic method. Second, evolutionary theory can be an auxiliary theory for cladistics. In that case, evolutionary biology provides a certain amount of evolutionary hypotheses which can help formulate such or such assumption about cladistic relationships, in a more or less explicit and crucial way. Third, evolutionary theory can be a background theory for cladistics, *i.e.* a theory which is not directly used by it, but which nonetheless justifies its general aim and therefore its use. There are at least three ways in which evolutionary theory can be said to be a background theory for cladistics, which I shall detail.

Data papers as incentives for opening biodiversity data: One year of experience and perspectives for the future [Poster]

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A Data Paper is a scholarly journal publication whose primary purpose is to describe a dataset or a group of datasets, rather than to report a research investigation. As such, it contains facts about data, not hypotheses and arguments in support of those hypotheses based upon data, as found in a conventional research article. Its purposes are three-fold: * to provide a citable journal publication that brings scholarly credit to data publishers; * to describe the data in a structured human-readable form; * to bring the existence of the data to the attention of the scholarly community. The description should include several important elements (usually called metadata, or “description of data”) that document, for example, how the dataset was collected, which taxa it covers, the spatial and temporal ranges and regional coverage of the data records, provenance information concerning who collected and who owns the data, details of which software was used to create the data, or could be used to view the data, and so on. The metadata can be used to form a data paper manuscript. An important feature of Data Papers is that they should always be linked to the published datasets they describe, and that link (a URL, ideally resolving a DOI) should be published within the paper itself. Conversely, the metadata describing the dataset held within data archives should include the bibliographic details of the Data Paper once that is published, including a resolvable DOI. At the time of submission of the Data Paper manuscript, the data described should be freely available online in a public repository under a suitable data license, so that they can be retrieved for reuse, resampling and redistribution by anyone for any purpose, subject to one condition at most – that of proper attribution using scholarly norms. GBIF and Pensoft pioneered a workflow between the GBIF’s Integrated Publishing Toolkit (IPT) and the journals ZooKeys, PhytoKeys and MycoKeys to automatically export metadata into the form of a data paper manuscript, based on the Ecological Metadata Language (EML). In 2012, Pensoft launched a new Biodiversity Data Journal that developed an article authoring platform called Pensoft Writing Tool (PWT). PWT offers several flexible data paper templates to link to major biodiversity platforms, such as GBIF, Scratchpads, BIOCASE, CDM and others. The present talk describes the basic principles of these workflows piloted within the EU-funded projects ViBRANT and EU BON.

Automated registration model for eukaryotic organisms: The opportunities for and responsibilities of publishers [Talk]

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With the appearance of the opportunity to publish taxonomic novelties online, the process of post-publication recording brought into focus the concept of pre-publication registration. Electronic registration of taxonomic and nomenclatural acts in online registries is a dynamic process and, despite the current progress, four major questions remain to be answered: (1) When registration of a nomenclatural act should take place – before or after manuscript acceptance, or after publication? (2) Who should be responsible for the registration – authors, registries or publishers? (3) Who validates the record at the registry? (4) Who validates the accuracy of the finally published bibliographic metadata? The talk describes a general XML communication model for publishers and registries in streamlining the registration and making it cost efficient through automated, server-to-server messaging. The workflow was developed by Pensoft's journal PhytoKeys and the International Plant Name Index (IPNI) and currently is being piloted within the EU-funded project pro-iBiosphere for ZooBank, Index Fungorum and MycoBank. The starting phase of the model was supported in part by the ViBRANT project. In our view, the automated registration of nomenclatural acts and the quality control of the bibliographic metadata in the registries should be a primary responsibility of publishers and registry curators, and to a lesser extent of authors. The model follows three-step process: Step 1. Upon acceptance of the manuscript, a publisher-based tool sends an XML message to the registry containing the type of act, the taxon names, and preliminary bibliographic metadata of the article (title, authors, and journal). Step. 2. The registry server sends back an XML response containing the unique identifier (*e.g.*, LSID, PURL) of the act; the LSIDs are included and appear in the final publication. Step 3. On the day of publication, the journal sends an automated XML message to the registry that contains the exact bibliographic details of the published article (*e.g.*, authors, title, journal, issue no, date of publication, pagination, *etc.*) to be completed for the specific act. In addition, we also believe that registration of nomenclatural acts and inclusion of their identifiers in the publication should be set as mandatory for all groups of organisms, no matter whether they are published on paper or in a digital format.

1KITE Hymenoptera – On the phylogeny and evolution of sawflies, wasps, bees, and ants [Talk]

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1KITE (1K Insect Transcriptome Evolution) is an international research initiative started in 2011 that aims to study the transcriptomes of 1,000 insect species encompassing all recognized insect orders (www.1kite.org). One of the largest taxonomic subprojects of 1KITE focuses on the phylogeny and evolution of Hymenoptera (sawflies, bees, wasps, and ants). Transcriptomes of more than 200 Hymenoptera species will be sequenced, representing all major lineages. Preliminary analyses of the already available nucleotide sequences show that the obtained data are of unparalleled size and quality. We aim to generate a 4,000-gene data set with virtually no missing data. Phylogenetic tree inference based on these data will allow us to answer some of the most intriguing questions in Hymenoptera phylogeny, such as: which group diverged first in Apocrita (wasp-waisted wasps)? What is the sistergroup of Aculeata (stinging wasps)? From which group did the bees (Anthophila) evolve within Apoidea? Additionally, we hope to confirm or reject phylogenetic hypotheses that are supported by other markers (molecular or morphological) but that are still controversially discussed. These relationships include, for example, the monophyly of Proctotrupomorpha and Vespoidea, and the sistergroup relation of Chrysidoidea to all remaining Aculeata. The expected results from this project will promote our understanding of key features in Hymenoptera evolution, such as xylophagy, ecto- and endoparasitoidism, secondary phytophagy, origin of stinger, and eusociality. 1KITE also fosters the development of new or improved methods and software for data quality assessment, phylogenetic reconstruction, and molecular dating that will allow for advanced analyses of large data sets. By doing so, the project paves the way for an in-depth understanding of the phylogeny and evolution of Hymenoptera in the era of phylogenomics.

Orthology prediction in the large-scale transcriptome project 1KITE [Talk]

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Identification of orthology among amino acid or nucleotide sequences is a substantial prerequisite when using them to infer phylogenetic relationships of the organisms from which these sequences have been sampled. However, orthology prediction is not a trivial task when working with transcriptome data because of their inherent incompleteness. The large amount of data in transcriptome libraries can be an additional challenge for assessing orthology of sequences. Within the 1KITE project (1,000 Insect Transcriptome Evolution [1kite.org]), we will assess orthology using a newly developed bioinformatic pipeline that builds on and extends an approach proposed by Ebersberger *et al.* (2009). Thus, translated transcript sequences are mapped to pre-selected orthologous amino acid sequences. The pipeline uses profile hidden Markov models (pHMMs) to rapidly and specifically detect candidate orthologs, and then tests the proposed orthology of the hits by a reciprocal search against the complete proteomes of reference species (*i.e.*, species with a completely sequenced proteome). We employ a relational database system with a versatile structure for flexible analyses. This talk outlines the mapping and reporting algorithm and its integration in the transcriptome data analysis pipeline of the 1KITE project.

Access to the planktonic biodiversity of the northern Adriatic [Poster]

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The northern Adriatic is the northernmost, shallow and enclosed part of the Adriatic (Mediterranean). It is characterized by complicated set of steep ecological gradients thus providing a large variety of ecological conditions. Due to its characteristics the northern Adriatic is a natural experimental basin for marine research under different perspectives (from climate change to the ecology of evolution). However, access to and detailed information about its biodiversity is still not organized at a desirable level. In a cooperation between the BGBM Berlin (Germany) and the CIM Rovinj (Croatia) we undertake first steps to institutionalize the access to data about the planktonic biodiversity as well as to the respective biodiversity resources. Efforts include the connection of local databases to the Global Biodiversity Information Infrastructure (GBIF), the connection of the phytoplankton cell culture at the CIM as well as the DNA-sample collection at the CIM to the DNA Bank Network. A formal investigation of the so far collected information about the northern Adriatics planktonic biodiversity aims at a taxonomically and systematically correct set of data. Tests of barcoding markers prepare for biodiversity analyses with next generation methods. This bilateral cooperation is supported by the German academic exchange service (DAAD) and the Croatian ministry for science, education and sports.

Parallel evolution in *Crenicichla* [Cichlidae]: Analogous diversification process in two unrelated species flocks [Poster]

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Crenicichla is the most species rich genus within the Neotropical Cichlidae with a widespread distribution in cis-Andean South America. In the La Plata basin at least two species complexes, *C. missioneira* and *C. mandelburgeri*, from the Uruguay and Paraná/Iguazú River drainages, respectively, are known. Despite that these complexes are separated from each other for several millions of years (13–15 % divergence in cyt b), are not closely related, and have been evolving in biogeographically separate areas, they both have developed a striking resemblance between their species in: 1. coloration patterns (lateral band, bars, blotches); 2. similar head/mouth morphologies (length of jaws, mouth size, dentition). Both complexes also include at least one “thick-lipped” form. These morphologically distinct species within each complex live often sympatrically and even syntopically and form mixed species flocks. The astonishing resemblance between forms of both species complexes suggests that the mouth morphologies may develop repeatedly in geographically isolated habitats of a similar type. Such situation is well-known from African lake cichlids and the common explanation is that closely related morphological forms likely evolve by disruptive evolution of trophic traits connected with exploitation of different food resources. Within the *C. mandelburgeri* flock, molecular phylogenetic analyses support the hypothesis of a close relationship of the syntopic forms differing in mouth arrangement. In the *C. missioneira* complex, we can find similar ecomorphological variation among syntopic forms with the same coloration pattern as well; in this case we, however, lack compelling molecular evidence about the species' relationships (very low divergence in mitochondrial sequences). The *Crenicichla* species complexes apparently represent an early stage of evolution. Reconstructing the recent history of these radiations is complicated by the fact that many species still share the ancestral genetic polymorphisms, with possible influence of hybridization. Sequencing of commonly used genomic markers hence does not provide sufficient resolution to unravel the multi-layer and possibly reticulated phylogenetic network among the nascent species. Therefore, other additional methods (*e.g.* SSR, AFLP, NGS-RADseq) must be applied, hand-in-hand with thorough morphological analyses of the used samples, to uncover the details of diversification within these highly interesting species complexes.

A national inventory of biosdiversity: The German Barcode of Life Project (GBOL) [Talk]

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on behalf of the GBOL consortium
www.bolgermany.de/team/gbol-institutionen

The GBOL (German Barcode of Life) project is a large-scale DNA barcoding campaign to capture the genetic diversity of animals, fungi and plants in Germany. GBOL has been granted a funding of approximately 5 million Euros by the German Federal Ministry of Education and Research (BMBF) for an initial period of 3 years. Launching the GBOL project is a step towards collecting, processing, data sharing and deposition of samples in conventional and molecular collections in order to facilitate the compilation of an open, validated DNA barcode library of biodiversity. GBOL is a national network of natural history museums and other research institutions which will provide their professional taxonomic expertise and existing infrastructure (collections / biobanks, databases, bioinformatics platforms and laboratories) to comprehensively collect, catalog, describe, and sequence the eukaryotic species in Germany. Involved institutions: ZFMK, Zoologisches Forschungsmuseum Alexander Koenig, Bonn ZSM, Zoologische Staatssammlung München SMNS, Staatliches Museum für Naturkunde Stuttgart SMNK, Staatliches Museum für Naturkunde Karlsruhe Senckenberg am Meer, Abt. DZMB, AG Molekulare Taxonomie mariner Organismen, Wilhelmshaven (associated institute) BGBM, Botanischer Garten und Botanisches Museum Berlin, Freie Universität Berlin Nees-Institut, Universität Bonn AvHI, Universität Göttingen IEB, Universität Münster Universität Tübingen BSM, Botanische Staatssammlung München (associated institute) JKI, Julius Kühn-Institut, Braunschweig (associated institute) SMNG, Senckenberg Museum für Naturkunde Görlitz University Bielefeld

Comparing plant-insect interactions across continents [Talk]

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Given the high diversity of plants and insects their interactions are the ideal measure to determining diversity and evolutionary trends. Herbivores have been widely used to estimate global patterns, diversity numbers and study evolutionary processes. However, it remains open whether there is a similar pattern across continents, regions or even in the same type of forest? Seed feeding insects are amongst the most diverse and specific groups within the herbivores. They play a major role in forest dynamics, though their difficulty to identify by morphological means have neglected them from many studies. Using phylogenetics and the numerous species-delimiting techniques recently developed, have allowed identification of cryptic species and reliable determination of their host trends. Seed feeding insects reared from several forests in the Americas, South-East Asia and Australia provide insights in the complex patterns in this guild. Our data provides clear evidence that the degree of host-specificity in seed-feeding insects is correlated to diversity, thus providing a better understanding of diversity patterns. But can this inference be extrapolated to all insect guilds?

Genetic Variation and Hybridization in the Genus *Bolboschoenus* in Central Europe [Poster]

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Four closely related taxa (*B. laticarpus*, *B. maritimus*, *B. planiculmis*, *B. yagara*) of the genus *Bolboschoenus* (Cyperaceae) are distributed in Central Europe. Due to weak morphological differentiation they were formerly classified within one widely conceived species *Bolboschoenus maritimus*. However, these species differ markedly in ecology and area of distribution. We examined the genetic diversity using amplified fragment length polymorphism (AFLP) and sequences of the rDNA internal transcribed spacer (ITS) as markers to find out whether the genetic diversity among species will correspond to their classification based on morphology, and to confirm or refute the supposed hybrid origin of *B. laticarpus*. Samples were collected from 35 native populations. Four AFLP selective primer pair combinations were employed to analyze 350 samples. The obtained AFLP data supported a delimitation of separate taxa corresponding to morphological differentiation. Additionally, results of Bayesian model-based clustering analyses indicated a hybrid origin of *B. laticarpus*, with *B. planiculmis* and *B. yagara* as parental taxa. The ITS rDNA sequence differentiated only a cluster with *B. yagara* accessions, whereas *B. maritimus*, *B. planiculmis* and *B. laticarpus* clustered in the same group. Keywords: AFLP, hybridization, ITS, model-based clustering.

Fitness data of steppe plants in Central Europe: a comparative analysis based on fruit set, mass, and germination rates [Poster]

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We study a transect towards the (north)western-most distribution limit of pannonian, submediterranean, pontic, and euro-siberian continental steppe plants in Central Europe. Generally, we are interested in the genetic structuring, genetic diversity patterns, and the performance of those steppe plants at their actually absolute distributional limit. Therefore, we are analysing a comparative set of steppe plants showing a similar, disjunct distribution pattern with more wide-spread occurrences in the Pannonian Basin in Hungary compared to the western limit of the continuous Pannonian area in Eastern Austria to the (north)western-most outposts in western Germany (namely in Rhineland-Palatinate). Along this transect we expect increasing isolation in a westward direction which might be accompanied by progessively reduced population genetic diversity and fitness. In general, genetic analyses are performed using mainly nuclear Amplified Fragment Length Polymorphisms (AFLPs) and chloroplast DNA sequence data. Plant fitness is analysed based on fruit set, fruit mass, germination speed and rates. Here, we report results from the performance part of our project. We present fruit set and mass data as well as outcomes of germination tests performed in climatic chambers. The plant taxa analysed comparatively in this respect are *Carex supina* (Cyperaceae), *Inula germanica* (Asteraceae), *Oxytropis pilosa* (Fabaceae), and *Poa badensis* (Poaceae). For all four species four populations representing each of the three study regions were analysed. Our data indicate significant differences in fruit set, the weight of fruits, germination, and the relationships between these parameters when comparing the four study species.

Estimating floral biodiversity in the past: Examples from Upper Triassic floras [Talk]

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The major challenge in estimating biodiversity in the past is the incompleteness of the fossil record. In fossil plants, taxonomic uncertainty associated with a lack of characters and disarticulation contributes to this challenge. During a plants' life cycle, several organs or units (leaves, flowers, fruits, seeds, pollen) are regularly shed or released for different purposes (preventing desiccation, reproduction, dispersal, *etc*.). In the fossil record, these units are usually found isolated and very rarely in organic connection. While these isolated organs have earlier been usually described as disconnected artificial morphotaxa, the ambition and purpose of modern studies of fossil floras is to re-connect them to reconstruct so-called whole-plant-taxa. These do not only serve for a better understanding of biodiversity in the past and ecology of the respective flora/ecosystem, they are also of particular importance for phylogenetic studies of *e.g.* seed plant evolution, as they provide as natural species much more information than a morphotaxon. This talk will give a number of examples from Upper Triassic floras of Lower Austria, southern Sweden and eastern China, where modern cuticular analysis was used as a key method to identify isolated plant organs that ought to derive from the same plant species and consequently to restore whole plants as natu-

ral taxa. By this, the distribution of individual plant 'species' in the past can be better estimated. Hence, estimates about the taxon richness of fossil plant assemblages become more comparable.

Phylogenetic relationships of the operculate land snails of the genus *Pollicaria* Gould, 1856 (Prosobranchia: Pupinidae) [Talk]

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Phylogenetic relationships the operculate land snails of the genus *Pollicaria* Gould, 1856 were investigated by analyzing mtDNA sequences and allozyme electrophoresis data. The results presented monophyletic by Maximum likelihood and Bayesian Inference. A clade of *P. rochebruni* and *P. mouhoti* shows sister relationships with *P. elephas* and *P. crossei* but it's still not robust. Allozyme data also revealed a high divergence among species. Within *P. mouhoti*, the monophyly was well supported on both mtDNA and allozyme data. However, allozyme data revealed low level of gene flow and a very high value of Nei's genetic distances among populations suggesting that these may actually represent or else be evolving into separate species. Biogeographical and taxonomic implications of this species will be discussed based on mtDNA analyses.

Molecular and morphological systematics of the dauber bees (*Megachile* subgenus *Chalicodoma*) in the western Palaearctic [Talk]

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The dauber bees (Hymenoptera, Megachilidae, *Megachile* subgenus *Chalicodoma*) have long fascinated entomologists. Réaumur was the first to describe their conspicuous, exposed nests of hardened mud on the southern wall of his house in Paris and Fabre used them extensively in his notorious experiments on nest recognition and orientation. However, this subgenus is currently in taxonomic disarray in the Western Palaearctic. Thirty eight species are recognized in this biogeographic zone, but the status of several species remains unclear, and males are unknown for nearly half of the species. The females bear few morphological characters and their identification has largely relied on pilosity, which is highly variable. To clarify the systematics of this subgenus, a detailed morphological study (male hidden sterna, punctation of the females) was combined with a molecular approach. One mitochondrial gene as well as four nuclear markers were sequenced for 48 terminals representing the majority of the species and subspecies. Sequencing of the mitochondrial gene was challenging because of the particular abundance of nuclear pseudogenes (Numts) in most species. Several techniques (mitochondrial isolation, template dilution and nested PCR) were necessary to obtain clean mitochondrial sequences. Twenty six species are recognized as valid, of which three are new to science. No clear barcoding gap exists in the mitochondrial dataset, mainly due to the presence of very deep (up to 12 %) divergences within "species", as defined by morphology and nuclear markers. For some species, widely different mitochondrial haplotypes coexist in Europe, although mostly not in sympatry. Our results, in conjunction with molecular dating, suggest that the

mitochondrial marker reflects the complex pattern of post-glacial recolonization of Europe, rather than the presence of cryptic species. The implications of our results on barcoding and on our understanding of species delimitation are discussed.

Hidden diversity of terrestrial green algae (Viridiplantae) discovered by ITS-2 DNA barcode [Talk]

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Traditionally terrestrial green algae have been classified according to the morphological species concept. However, phylogenetic analyses of SSU rDNA sequences have revealed that most of the traditional genera and species are polyphyletic and need taxonomic revisions. Many terrestrial green algae show a phenotypic plasticity demonstrated by experiments of cultured material. This makes the unique species identification very difficult. In addition, many microalgae show only few diacritical morphological characters. Unfortunately most of the terrestrial green algae reproduce only asexually and the biological species concept cannot be used for identification. The newly developed ITS-2 DNA barcode correlated with the biological species concept and has been now extrapolated to asexual species and genera. Using this barcode terrestrial green algae could be clearly identified at species level and new lineages could be discovered. The new species have been confirmed using an integrative approach, which includes phylogenetic analyses of SSU and ITS rDNA sequences with morphology and life cycle of these species as well as physiological and biochemical characters (*i.e.* polyol production). Based on these results traditional terrestrial genera such as *Chlorella*, *Coccomyxa*, and *Chlamydomonas* have been revised and new genera and species have been described. Unexpectedly many lineages contain several isolates, which either morphologically develop a high degree of phenotypic plasticity, but showed a low genetic diversity like in *Chloroidium* and *Coccomyxa*, or, strains with morphological unity have a high genetic variability like in *Jaagichlorella*. Summarizing, the ITS-2 barcode can be used to identify species and discovered hidden genetic diversity.

Large scale species delimitation method for hyperdiverse groups [Talk]

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Speciation is rarely an instantaneous event, but rather a process during which the characters (DNA, morphology, ecology...) will accumulate differences at various rhythms. Consequently, species delimitation methods should rely on several lines of evidence, and species should be considered as hypotheses that will

be modified with additional characters. Furthermore, traditional approaches are sometimes not adapted, especially in hyperdiverse groups such as the Turridae (Gastropoda, Conoidea), where most of the species remain unknown and where homoplasy and plasticity makes morphological characters weakly reliable. We propose to overcome these difficulties by using first COI barcodes, analysed with a new method we developed, called ABGD (Automatic Barcode Gap Discovery), which automatically identifies in the pairwise distribution of genetic distances the limit between intra and interspecific distances. We use a range of prior intraspecific divergence to infer from the data a model-based limit for intraspecific divergence. The method then detects the barcode gap as the first significant gap beyond this limit and uses it to partition the data. Inference of the limit and gap detection are then recursively applied to previously obtained groups to get finer partitions until there is no further partitioning. Species hypotheses obtained with ABGD were also compared with results from GMYC, and then modified and validated using other available evidences (an unlinked gene – 28S, geographic and bathymetrical distributions and morphological characters) in an integrative context. Following this methodology, we delimited 94 species of Turridae, of which more than 50 are likely new to science.

Do mate-searching males foster cryptic speciation in the orchid genus *Ophrys*? [Poster]

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Following the biological species concept, based on reproductive isolation through pollinator specificity the sexually-deceptive orchid genus *Ophrys* was split into several complexes, comprising morphologically highly similar species. However, low genetic differentiation in phylogenetic analyses suggested that pollinator sharing is more common than previously expected. The high species diversity of this genus may thus be an overestimate, species delimitations being disrupted by gene flow and introgression. Alternatively, low genetic and morphological differentiation may be a consequence of radiation mediated by pollinator shifts coupled with low selection pressures on morphological characters. By integrating pollination experiments, chemical and morphological analysis we aim at answering the question whether the pollinator delimited taxa of the *Ophrys tenthredinifera* complex are indeed cryptic species differentiated by floral chemical compounds and pollinator biology. *Ophrys tenthredinifera* is one of the most diverse species groups of the genus, having a diversity hotspot on the Aegean Islands. The high morphological variability, close relatedness of its species and complex distribution patterns, make it an ideal model system for studying the evolution of cryptic diversity. Pollinator experiments have been used to identify the taxa occurring in Tunis and on the South Aegean Islands (Crete, Rhodes and Samos) according to their attractivity to a specific pollinator. The amount of morphological changes was assessed by reconstructing 3D flower models from μCT scans. Additionally, chemical analyses of the floral scent from the Cretan taxa were performed. In order to understand the direction of pollinator switches, we also analysed the distribution patterns of the species and their pollinators. Pollinator choice experiments have confirmed the specific relationship between the studied taxa and their pollinators, results which are corroborated by the differences found in the chemical compounds implicated in pollinator attraction. Morphological differences were however week between most species. Low selection pressures on morphological characters coupled with short divergence times, would explain this low level of morphologic divergence. Our results further indicate that while most speciation events were allopatric, sympatric speciation may have taken place in Crete.

Mitochondrial and nuclear markers show complex history of Chiffchaff (*Phylloscopus collybita*) in Eurasia [Talk]

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The glacial refugia hypothesis indicates that during the height of the Pleistocene glaciations the temperate species that are today widespread in Paleartic survived in small and climatically favourable areas located on the southern limits of ice sheets. Refugial populations that evolved in allopatry are expected to have accumulated independent genetic differences that may be used as genetic markers to trace expansion routes. In the periods of interglaciations, recolonization of northern parts of the Eurasia from southern refugia went in several directions depends of organism mobility and suitable habitat presence on the north. After expanding their ranges from separate glacial refugia these diverged genomes meet and form “suture” zones. They seem to be narrow, genomically diverse and dissected and the source of most northward postglacial expansions. The Chiffchaff (*Phylloscopus collybita*) is one of the commonest forest bird species across Eurasia. The range of this species includes whole Europe except most of the Iberian Peninsula, and majority of the temperate Asian subcontinent east till Pechora basin. Previous phylogenetic study of Chiffchaff revealed several independent lineages and narrow suture zones located in Urals and Sweden. However to the date most of the data on hybrid zones between different lineages and locations of these zones are lacking. In this presentation we report phylogenetic study of mitochondrial DNA (ND2) and nuclear DNA (AC01) variation in *Ph. collybita* based on samples collected in most of the species range. Our data point to the existence of wide admixture zone predominately in the Balkans where 3 different mitochondrial lineages of *Ph. collybita* meet and hybridize. Additionally one basal lineage have been discovered in southern area of the Lesser Caucasus and included in analyses. Together, these results provide new insight into the molecular evolution of Chiffchaff and indicate significance of the hybridization for delimiting species level.

Different niche occupation by phylogeographic clades of *Pelagia noctiluca* revealed by ecological niche modelling [Talk]

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Phylogeographic clades were found in widespread holoplanktonic cnidarian species *Pelagia noctiluca* over the Pacific and Atlantic Ocean and Mediterranean Sea based on mitochondrial COI haplotypes. Due to its pelagic life cycle is difficult to characterize subtle differences among suitable niches and information about suitable niche among different phylogeographic clades can be valuable source of information as well connected with unique history of their lineages. The suitable niche occupied by different clades were identified by ecological niche modelling. Georeferenced haplotypes of *P. noctiluca* were used and models were run with marine environmental datasets Bio-ORACLE and Aquamaps, resampled using ArcView 3.2 to the highest resolution in order not to lose any environmental information. The models were inferred using the maximum entropy algorithm available in Maxent version 3.3.3a with default settings for maximum number of iterations (500), maximum number of background points (10000) and convergence threshold (0.00001), the most important variables for species distribution were determined. Suitable niches were confirmed at northern coast of Mediterranean and Red Sea, east and west coastal shelf of Atlantic Ocean, as well coastal sea of Asia and Australia are suitable for Atl-Med clade. Different scenarions of niche modelling were perfomed, either with all existant clades or exclusion of Pacific clade from model. Exclusion of Pacific clade from model revealed that Pacific coasts of Central America are not suitable niches for *P. noctiluca*. Findings about niche preferences raises questions whether different life stages of *P. noctiluca* required different niche or this indicate incipient speciation.

Community phylogeny and biogeography of figs and wasps [Talk]

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Fig wasps are a polyphyletic assemblage of Chalcidoidea (and few braconids) that develop in the inflorescences of fig trees (Moraceae, *Ficus*). They are subdivided into pollinating fig wasps that belong to the family Agaonidae and non-pollinating fig wasps (NPFW) that comprise, among others, five unrelated subfamilies strictly associated with *Ficus*: Otitesellinae, Sycoecinae, Sycoryctinae, Epichrysomallinae and Sycophaginae. Figs and their enclosed communities of fig wasps constitute an ideal model to compare radiation patterns between co-associated lineages of gall-makers and parasitoids. Fig wasps form rich communities of interacting species (up to 36) that differ among regions of the world and among groups of *Ficus*. We present the molecular estimates of global phylogenies of figs and four fig-pollinating wasp subfamilies, investigate the biogeographical histories of the main fig wasp subfamilies and finally compare the timing of radiation and dispersion of major clades with available data on *Ficus*. Our dating analyses indicate that the current pantropical distribution of figs and their associated pollinators arose simultaneously in Eurasia during the Late Cretaceous ?75 Ma. Our data suggest a post-Gondwanan origin for the NPFW, at most 50 Ma. Most NPFW originate in Eurasia, but Sycophaginae dispersed out of Australia

and subsequently colonised both paleo- and neotropics. Most NPFW radiated together with their host fig and associated pollinator through the tropics. They probably colonized the New World via the North Atlantic land bridges. Reconstructing the history of host colonization and association over space and time is central to understanding how fig wasp communities were assembled. Our study highlights the potential for combining molecular phylogenetics with multiple methods of dating of interacting groups (plants/gall-makers/parasitoids) to reconstruct the historical biogeography of plant–herbivore associations.

Genetic basis of postzygotic hybridization barriers in *Capsella* [Talk]

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Reproductive isolation among most plant species is established by different mechanisms that can act either pre- or postzygotically. One important postzygotic barrier is caused by malfunction of the endosperm. The endosperm is a terminal nutritive tissue supporting embryo growth that is consumed by the embryo during seed development or after germination. The endosperm is essential for viable seed formation and therefore, mechanisms disrupting endosperm development play a major role in reproductive isolation. Similar reciprocal effects on endosperm development have been reported in response to interploidy crosses, suggesting that unbalanced parent-of-origin specific genes are the underlying cause for endosperm failure in response to interspecies hybridizations. A well-known phenomenon observed in interspecies hybridization is that the degree of seed failure due to endosperm breakdown is depending on the direction of the cross. We show that in the genus *Capsella* reciprocal crosses between outcrossing *C. grandiflora* and selfing *C. rubella* result in clearly different seed abortion rates. We characterized seed development in the hybrid crosses and aim for mapping the locus/loci that causes hybrid seed failure in *Capsella*.

Epigenetic alterations and flower morph determination in *Linaria pelisseriana* (Plantaginaceae) [Talk]

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Cleistogamy, self-pollination within permanently closed flowers, results from arrested flower development. Since it drastically lowers energy costs for flower production and shortens generation times, it can have considerable fitness advantages, especially when plant growth is resource-limited, availability of pollinators is scarce or habitat instability selects for accelerated seed production. Several mechanisms have been proposed for cleistogamous flower development involving either ecological factors or genetic

determinism. *Linaria pelisseriana* (L.) Mill. (Plantaginaceae) is a Mediterranean therophyte, exhibiting an extraordinarily rigorous form of dimorphic cleistogamy, with larger, potentially insect-pollinated chasmogamous flowers and smaller, reduced cleistogamous flowers on different individuals. This phenomenon was first observed on the Ionian Islands (Greece), and in all populations investigated so far individuals of both flower morphs have been found in close spatial proximity. Although chasmo- and cleistogamous individuals differ significantly in morphological traits/ size parameters, and despite the expected genetic isolation of cleistogamous individuals, genome-wide genetic fingerprints (AFLPs) did not supply any evidence for a genetic differentiation of individuals based on their flower morphs. Neither was it possible to detect any differences in accompanying vegetation or surrounding microhabitat. Mendelian inheritance in a one-allelic system seems unlikely, since offspring in glasshouse experiments exhibited parental or complementary flower morph stochastically, with a likelihood of around 50 %, respectively. Considering this evidence we test hypotheses of alterations in short- to midterm gene regulation, which possibly are mediated via epigenetic mechanisms, such as DNA methylation, to result in flower morph switches between generations. Therefore, we scan the *L. pelisseriana* methylome using methylation sensitive amplified polymorphism (MSAP) for differences correlated with the two flower morphs, analysing cleisto-and chasmogamous individuals of 4 populations from the Ionian Islands and one population from the Greek mainland (NW Peloponnesus). We discuss the involvement of epigenetics in development and trait determinism by adding a different perspective on the links between genotype, epigenotype and environment to result in phenotypic variation.

Trans-adriatic disjunctions – insights from *Gentianella crispata* (Gentianaceae) [Poster]

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Amphi-adriatic distributions are a biogeographic pattern repeatedly observed in plants common in the Central and Eastern Mediterranean floristic province. Frequently, this distribution type is characterised by a large distribution area on the Balkans and regional to local, isolated occurrences in Southern Italy. *Gentianella crispata* (Gentianaceae), a monocarpic, biennial mountain plant producing diaspores with low dispersal capabilities, has its centre of distribution in the South Dinarids and is also found in one small, isolated population in Calabria (Italy).This study investigates the Pleistocene and postglacial biogeographic dynamics of the species, including the relationship of the Italian population to its source area on the Balkan Peninsula, using AFLP fingerprint and cpDNA sequence data obtained from 17 accessions covering the whole distribution area. To test for possible admixture, which is regularly reported for other species of *G.* section *Gentianella*, one accession each of *G. anisodonta* and *G. bulgarica*, co-occurring with *G. crispata* at the NW and SE edge of its distribution range, respectively, were included. Central and marginal populations on the Balkan Peninsula are compared to the isolated Italian population with respect to population genetic parameters such as genetic diversity, rarity and allele frequencies. Molecular data are complemented with morphometric analyses to assess the phenotypic variation of populations with regard to their degree of isolation and geographic position in the range. We discuss the origin of the Italian population, possible dispersal routes and reasons for the limited distribution even though suitable habitats are available in the Apennines. Furthermore, possible Pleistocene range shifts and postglacial recolonisation of mountain ranges on the Balkan Peninsula are inferred. Patterns in *G. crispata* are confronted with similar cases to hypothesize about more general trends in amphi-adriatic disjunctions, as well as refugia and migration routes on the Balkans.

Bars that bear out bristles: DNA barcoding and NDE in Protura – a rewarding task in a tricky group [Talk]

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Protura are tiny entognathous hexapods living in the soil. Due to the lack of conspicuous morphological characters, species determination is extremely challenging and only a handful of scientists are able to accomplish this task. The present study was triggered by the close spatial vicinity of our university to the worlds´ biodiversity hotspot of Protura where 23 syntopic species could be found (Christian and Szeptycki 2004). To test the species diversity recorded by traditional morphological determination, the molecular range of 171 specimen of Protura occurring in Austria was examined with two markers, the DNA barcoding region of the mitochondrial CO1 gene and a fragment of the nuclear 28S rDNA. Aim of this pilot project was the establishment of DNA barcoding in Protura applying a non-destructive DNA-extraction method. The commonly used CO1 Folmer primer-set for invertebrate taxa produced no useful results even under various PCR conditions. Therefore primer design and testing became an essential part to establish DNA barcoding in Protura. Due to high intergeneric variation at both ends of the DNA barcoding fragment, the newly designed PCR-primers worked in certain genera only, but performed poorly when applied across our complete taxon sampling. A small set of 28S rDNA primers turned out to work efficiently and almost universally across the investigated proturan genera, but length variation in divergent domains and problems in sequencing argue against the use of 28S rDNA as an alternative DNA barcode, at least for Protura. We successfully generated 88 CO1 barcodes (mean length 750 bp) and 90 28S rDNA sequences (approx. 1000 bp). Both markers separate the investigated proturans into 5 major clades and 13 well supported sub-clades. The recorded molecular clusters are exactly corroborated by the morphological determination at both genus and species level. Additionally we discovered a new species to science and the first record of a species for Austria. Our study demonstrated the great value of DNA barcoding for taxonomically challenging groups. It certainly will help to facilitate species determination in Protura for a broader scientific community. This will be of special importance for many studies in soil ecology where this hexapod group presently remains undetermined in almost all cases.

Single origin of subterranean adaptations in a lineage of Pyrenean beetles (Coleoptera: Leiodidae) [Talk]

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The evolution of the adaptations to the subterranean environment has attracted continuous attention from evolutionary biologists, but despite the detailed knowledge of the molecular and physiological basis of some of these adaptations, their origin and evolution remains poorly understood. This is specially the case for large radiations of exclusively subterranean species, commonly assumed to be the remnant survivors of several independent colonisations of the underground environment, with the subsequent extinction of all epigean relatives. Here we study the evolution of the subterranean adaptations in a diverse clade of Leptodirini beetles from the Pyrenees, including more than 220 species. We use ca. 5 Kb of combined mitochondrial and nuclear markers to reconstruct a robust phylogeny of the group, and map the evolution of the habitat of the species (epigean or shallow endogean, superficial subterranean environment, caves), their life cycle (three, two or one larval instars) and general body shape and size. Our results show the single origin of the adaptations to the deep subterranean medium in a large clade of strictly Pyrenean species (*i.e.* excluding some areas in the Basque Country), including a range expansion to the Catalonian coastal mountains in the Late Miocene of a lineage fully adapted to the underground (genus *Troglocharinus*). These results challenge the assumption that the highly specialised cave beetles are unable to disperse and diversify other than at very limited geographic and temporal scales.

Evolution of α-glycerotoxin, an unusual neurotoxin produced by venomous annelids [Poster]

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Glyceridae (bloodworms) are annelids that possess a pharynx bearing four teeth, which are connected to venom glands. Until now, only a few studies are available regarding the venom composition of these worms. In a study (Meunier *et al.*, 2002, EMBO Journal 21: 6733–6743) a neurotoxin named α-glycerotoxin (Gltx), which was produced by *Glycera tridactyla*, was examined more precisely. This glycoprotein is characterized by its specific effect on the nervous system. It causes the specific activation of presynaptic Cav2.2 channels and its effects seem to be completely reversible. Furthermore, this unusual toxin is found, so far, only in members of the glycerid polychaetes. We established transcriptome libraries of venom gland tissue from *Glycera tridactyla* using Illumina sequencing technology. By using amino acid data from protein sequencing of short fragments of purified α-glycerotoxin for BLAST analyses and by using different molecular methods in the laboratory, we were able to identify a ~4150 bp coding sequence. This mRNA-seq is determined by a poly-A tail at the 3'-end and enables the verification of an N-terminal signal peptide. Moreover, domain searches revealed the presence of different domains, like a calcium-binding EGF domain or WSC domains. The Illumina data were also used for expression studies, indicating that this protein is not exclusively expressed in the venom glands, but also in surrounding pharynx tissue. PCR experiments with conserved and degenerated primers were performed and other α-glycerotoxin-bearing species could be identified. Interestingly, phylogenetic analysis reveals a nested position of this clade within Glyceridae and coupled with results of domain searches we hypothesize an ancient horizontal gene transfer explaining this pattern.

Fitting in the phylogenetic cracks of deep-sea isopods [Talk]

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Janiroidea is the most speciose taxon amongst isopods and gave rise to the oldest isopod lineages in the deep-sea. The “munnopsoid radiation” for example is thought to have colonized the abyss as early as the Permian. Janiroidea currently comprises 24 families plus seven genera with uncertain affinities. Most deep-sea families have a wide or cosmopolitan distribution, and are commonly encountered in abyssal soft sediments. Their relationships however within this asellote superfamily are still a matter of debate. Phylogenetic studies have often been contradictory. Results have been found to depend on the method of inference and the dataset applied. Despite their relative popularity amongst isopod researchers, the positions of ubiquitous families such as Munnopsidae, Desmosomatidae and Macrostylidae are still unknown. This is probably caused by the old age of their last common ancestor and hence an erosion of phylogenetic signal in genes and morphology. Furthermore, unavailability of some taxa in previous phylogenetic studies may have enforced such uncertainties. In order to “fit the cracks” in the janiroidean tree and improve its resolution, a new morphological dataset was compiled and analyzed. It includes representatives for all janiroidean families. Several oddities, such as currently undescribed and unusual macrostylid-like isopods and genera incertae sedis have been included to break long branches. The results shed new light on the evolution of deep-sea isopods. Traditional views on the phylogeny of Janiroidea are discussed in the light of the new data.

Impediment be resource: sexual dimorphisms in Macrostylidae (Crustacea: Isopoda) [Poster]

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Sexual dimorphisms impose difficulties for allocating conspecifics in many animals, such as in asellote isopods. Adult males are often characterized by pronounced morphological differences after final moult compared to females and juvenile males. These are potentially related to pre-copulatory dispersal and/or search for mating partners. In several families, females tend to show great morphological similarity, while the males bear aberrant character states. In the deep-sea isopod family Macrostylidae Hansen, 1916, for example, sexual dimorphism is regarded to be amongst the relevant explanations for why of 50 % of the described species only one sex is known. Thanks to molecular evidence, such problems can be avoided. Above that the rising awareness of sexual dimorphisms and DNA-based allocation provides the possibility to apply dimorphism-related characters in taxonomy, systematics and phylogeny. This poster presents a preliminary approach to identify, characterize and apply sexual-dimorphism based morphological information in the understudied Macrostylidae. Using “DNA barcodes” amongst other markers, extremely dimorphic sexes could be allocated. The morphological information obtained will be valuable to infer a phylogeny of the Macrostylidae.

Not only better sampling but also better modelling [Talk]

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Most, if not all, of the sites in a sequence do not evolve according to the same pattern; this is because each residue is characterised by specific biophysical environments and different evolutionary constraints. Homogenous models of sequence evolution fail to account for this assumption and may, for example, misinterpret the non-phylogenetic signal embedded in highly saturated positions; indeed, the deeper the nodes in the phylogeny, the higher the risk of falling in such type of systematic error. An effecting way of overcoming this problem is the employment of among-site heterogeneous models of sequence evolution. Here we outline various examples of how these models, most of which belongs to the “CAT-family”, have helped producing phylogenies that significantly differs to those obtained using homogenous models. Examples span from arthropods to rodents, and from large phylogenomic to mitogenomic and classical rRNA datasets. Not only heterogeneous models are clear improvement in term of fit to the datasets, but notably recover phylogenies more congruent with morphology and other sources of evidence. We also show that the use of among-site heterogeneous models also affects molecular clock estimates, which are typically older when using homogeneous models in nodes describing radiations of fast evolving species. Although both an adequate taxon and gene sampling are needed to address many phylogenetic problems, we advocate that more importance should be given to the accurate modelling of sequences rather than to massive harvesting of data, except if this allows to break long branches.

High throughput species identification of moths using NGS along a gradient of deforestation in Amazonia [Talk]

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In the fields of ecology and conservation biology, when information requiring species-level identification is needed, many groups of living organisms are generally excluded de facto from the studies, merely because of the lack of access to the scarce specific taxonomic expertise and because of the largely unexplored and overwhelming diversity of some taxa, in particular in the species-rich inter-tropical regions. Molecular diversity, using for instance species-specific DNA barcodes as proxies to characterize species, can alleviate this impediment. When a reference library exists, DNA sequences can lead to actual species names and thus open access to all past information such as conservation status, known distribution and ecological attributes. Our work, building on the existing framework of an ecological study in Amazonia, tests the applicability and potential of high throughput molecular identification using next generation sequencing (NGS) in two moderately diverse families of moths (Saturniidae and Sphingidae) for which a comprehensive reference library is available. We report and compare the results of three distinct approaches: (1) species identification using morphology; (2) sequencing of DNA barcodes for a few specimens in each species as distinguished by approach (1), followed by species identification through sequence comparison against an existing reference library; (3) NGS approach to retrieve DNA barcode information after pooling tissues of all collected specimens for each of the 54 study sites. The results and conclusiveness of this study, which was designed to investigate how the diversity of various animal and vegetal groups varied along a gradient of deforestation and land-use intensity, are compared and discussed. Molecular identification performs remarkably; NGS, in particular, expedites the process of species identification for large numbers of specimens. Studies employing molecular methods for species identification will permit more taxonomically inclusive ecological studies and will be more easily combined and compared in the future through the assembly and release of large databases of genomic biodiversity data.

Integration beyond total evidence – examples from the Gnetales [Talk]

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Utilization of molecular data resulted in nothing less than a revolution for systematic biology some twenty years ago and today we are assembling the tree of life with an incredible speed, resolving deep divergences as well as relationships among closely related taxa. Some phylogenetic questions have however proven more difficult to answer than others and one of the most well-known examples is the evolutionary relationships among the six major clades of seed plants. Although studies based on DNA data largely overturn what we thought we knew (based on morphology), there are strong conflicts among and within loci. Unresolved phylogenies matter because understanding relationships are the key to answering, even addressing, practically all other ecological and evolutionary questions on a group. But how can we discriminate between seemingly well-supported, yet incompatible, hypotheses? Are there limits to which questions can be answered using "only" molecular data? One important reason for the struggle with seed plant phylogeny is conceivably the fact that most seed plants that have been present on Earth are extinct. Fossils constitute the bridge between the sparse remnants of the historical diversity, however, productive studies of fossils require comprehensive comparative work and extensive knowledge of the study system. Integrative studies, in which several kinds of data are analyzed, and living and fossil diversity is covered, goes beyond total evidence. Therefore, and because the problems with seed plant phylogeny are so complex, it is likely beneficial to focus on sub-clades and resolve the puzzle piece by piece. I will try to exemplify the power of integrative studies, using our work with evolution in *Ephedra* of the Gnetales, a small group of seed plants that has attracted much attention because of its "enigmatic" morphology and possible affinity with either conifers or angiosperms. Our projects are interdisciplinary; neobotanical systematics meets ecology and entomology, palynology, biochemistry, palaeobotany and climatology. I hope to demonstrate that integration between traditional fields and collaboration between specialists offer opportunities for progress in a field where studies based on only DNA data from living species have failed to answer our questions, as is the case with major events in seed plant evolution.

Species: natural facts or scientific hypotheses? [Talk]

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During the last three decades it was discovered that a large part of biodiversity remains un-described. During the same period of time the technologic developments (such as manipulation of bigger datasets using information technologies but also access to new biological characters such as DNA and other molecular data), have brought many new data about organisms. Thus, both the magnitude of biodiversity and the multiplication of the tools available to analyse biodiversity, have opened new challenges for the systematists. Either for estimating the magnitude or the structure of biodiversity, systematists use the species category as a fundamental unit. In this context, new and more efficient strategies need to be develop for species delimitations . These strategies have to fully take advantage of all sources of data. Firstly, an agreement on a definition of the species category should be found. As emphasized by de Quieroz, the distinction between the defining properties of the category "species" from the practical criteria allowing species delimitation, is a way to solve the apparently endless debate of the 'species problem'. This reformulation of the problem puts forward that, when a taxonomist describes a new species, he formulates a scientific hypothesis rather than he discovers a new fact. This reformulation revivifies the meaning of taxonomic revisions. Indeed the taxonomic revisions consist on re-evaluating old hypotheses in the light of new data (new characters or, new specimens, but also new analysis tools). The new practices have to feed and expand the taxonomic revision scheme. These new practices are based either on new sources of biological data (like molecular characters), or on new analysis methods (like those based on the coalescence theory). Based on a robust concept of the category "species ", these practices can be easily integrated to other, more classical taxonomic practices.

Characterization of the microbial consortium associated to *Varroa destructur* and its host, *Apis mellifera* [Poster]

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Varroa destructor is a parasite mite that accomplishes its reproductive cycle exclusively in honey bee colonies. *Varroa destructor* was originally a symbiont of the Asian bee *Apis cerana*. After the first contact with colonies of *Apis mellifera*, at the beginning of the sixties, it spread all over the word except from Australia and Madagascar. *Varroa destructor* is a parasitic mite feeding on old bee larvae, pupae in sealed cells and adult bees. It is well known that this mite can act as a vector of several pathogenic agents, both bacterial and viral, which altogether cause a syndrome called varroasis. It has been estimated that the affect families die within two year after the last treatment. The aim of this work is to characterize the microbial consortium associated to *Varroa destructor* and to its host, *A. mellifera*. In fact, scientific bibliography lacks a broad-spectrum analysis of the mite microbiome. On the other hand, the bacterial consortium of *A. mellifera* was studied mostly in the adult insect, while data about larvae are scarce. Microbiome samples were collected from nine beehives in North of Italy. Samples were subjected to 16S ribosomalRNAgene pyrosequencing (454 Life Sciences). 16S data processing and diversity estimates were performed using QIIME (Quantitative Insights Into Microbial Ecology) toolkit.

The link between names and taxa in rank-based taxonomic systems: synonymy and homonymy in higher taxa of birds [Talk]

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A vigorous debate in systematics centres on whether traditional, rank-based nomenclature or phylogenetic nomenclature is better able to maintain nomenclatural stability. Despite two decades of debate, there have been no quantitative studies that assess the causes and magnitude of nomenclatural instability in practice. I present a quantitative analysis of nomenclatural instability in birds. The dataset included 826 name-taxon associations in seven major classifications of birds published between 1934 and 2007. High levels of synonymy (38 % of taxa, affecting 68 % of names) and homonymy (18 % of names, affecting 46 % of taxa) were found. On average, supra-generic taxa accepted in all seven classifications are known by 3.3 different names, and very few (2 %) of these taxa are known by a single name. A significant inverse relationship between taxonomic stability and nomenclatural stability was found. Furthermore, each new classification introduced additional names for previously recognized taxa and re-applied previous names to other taxa. Overall, 94% of synonyms and 69% of homonyms were caused by differences in opinion among taxonomists about the rank of taxa. In addition, variation in the taxonomic contents of names did not become less with increased recognition of names. These findings argue against recent claims that taxonomists using rank-based nomenclature spontaneously settle on a consensus about the choice of taxon names. These results further indicate that rank-based nomenclature so far has failed to accomplish a reasonably stable association of taxonomic names and clades.

Two-step tree building approach for generating mega-phylogenies: an alternative to traditional super matrix methods [Poster]

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Alexander Antonelli *et al.* are currently working on a bioinformatics pipeline called “SUPERSMART” (Self-Updating Platform for Estimating Rates of Speciation and Migration, Ages and Relationships of Taxa). The method will download sequences from GenBank (through PhyLoTa), build a genus-level chronogram based on a few slow evolving genes and a set of fossils (one for plants, one for animals, and one for fungi), then breaks this tree down into many species-level, multi-gene datasets that are analyzed under a multi-species coalescent method and secondarily dated. This method of tree-building has several advantages compared to traditional super matrix methods. (i) The alignment will face less problems with saturation and missing data in the species level datasets (ii) The smaller species level datasets make the use of more thorough methods for phylogeny inference and the incorporation of the multispecies coalescent computationally feasible. There are however, several uncertainties regarding the two step tree building method that can be potentially disadvantageous. These are regarding (i) The effect on the topology and support of nodes (ii) The effect of the secondary calibrations on age estimates and the width of their trust intervals. To test the viability of the tree-building method employed by “SUPERSMART” species level mega chronograms of the plant order Gentianales will be reconstructed using both a traditional super-matrix and a “SUPERSMART” approach. Future studies: Using the obtained Gentianales species level chronogram in a bio-geographical context focusing on the disjunction between the South American and African tropics.

Reproductive differentiation into sexual and apomictic polyploid races in *Potentilla puberula* (Potentilleae, Rosaceae) [Talk]

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Potentilla puberula exhibits extensive intraspecific variation in ploidy. Embryological evidence for sexual reproduction and high frequencies of odd ploids indicated spatial co-existence of sexuality and apomixis raising questions about mechanisms governing the co-occurrence of reproductive modes within populations. In order to answer these questions, we explored (i) the association of ploidy with cytological pathways of seed formation, the mating system, and pollen viability and (ii) reproductive interrelationships among cytotypes on the population level. The study is based on 22 populations representing five cytotypes (tetraploid–octoploid) from East Tyrol. Embryo ploidy and the endosperm/embryo ploidy ratio (*i.e.* the peak index) inferred by a flow cytometric seed screen were used to calculate the male and female genomic contributions to the embryo and endosperm. As a new indirect approach to test for the occurrence of intercytoype crossings, we related the cytotypic diversity of populations to variation in the male genomic contribution. The mating system was determined conducting manual self- and cross-pollination and estimating seed set and pollen: ovule ratios. The study revealed a rare example of intraspecific differentiation into sexual and apomictic cytotypes at the polyploid level. Tetraploids thus formed seeds almost exclusively via sexuality whereas penta- to octoploids were overwhelmingly apomictic. The tetraploid cytotype exhibited a xenogamous mating system. In higher ploids we observed a breakdown of the (gametophytic) self-incompatibility-system, although cross-pollination yielded higher seed set than selfing. The proposed allopolyploid origin of P. puberula together with functionality of the self-incompatibility-system in the tetraploid cytotype suggested that the tetraploids may be functional diploids. Pollen quality varied within wide ranges but was loosely associated with reproductive mode. The variation can be explained by the hybrid origin of the species and opposing effects of meiotic irregularities and increased numbers of genomes. No significant association between cytotypic diversity of populations and variation in the male genomic contribution to sexually-derived seeds was observed, indicating that tetraploids are reproductively isolated from the apomicts, presumably by prezygotic barriers.

Ancient asexual scandals in soil: Oribatid mites [Talk]

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There is a remarkable abundance of parthenogenetic animal taxa in soil. Among the most interesting of these groups are oribatid mites (Oribatida, Acari). In oribatids several ancient old parthenogenetic lineages exist but there are also recent parthenogenetic offshoots. In addition, there is evidence that at least once sexual reproduction re-evolved from parthenogenetic ancestors. The talk will provide an overview on the evolution of parthenogenesis in oribatid mites and will provide a general ecological theory on the evolution of sex, *i.e.* the 'Structured resource theory of sexual reproduction' (SRTS), explaining conditions favoring sexual vs. parthenogenetic reproduction and also geographic parthenogenesis. Oribatid mites are presented as ideal model group for testing predictions of the proposed SRTS.

Census of tardigrades in the nature reserves Parc national du Mercantour and Parco Naturale delle Alpi Marittime [Poster]

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The "European Distributed Institute of Taxonomy" (EDIT) stimulates "All Taxa Biodiversity Inventories+Monitoring" (ATBI+M) in the Parc national du Mercantour and Parco Naturale delle Alpi Marittime as the first European pilot sites to apply the science of taxonomy to the conservation of biodiversity. ATBI include intensive community efforts to identify and record all living species that exist within a given area. Together with the parks' management boards, EDIT coordinates activities from scientists from over 27 mainly EU-based, scientific institutions that thus cooperate to work together on a baseline biodiversity assessment of the two parks. We collected more than 300 moss cushions from the two nature reserve sampling sites. In 79 samples we found eutardigrades and heterotardigrades of the species *Milnesium tardigradum tardigradum* Doyère, 1840, *Hypsibius* cf. *convergens* (Urbanowicz, 1925), *Hypsibius* cf. *dujardini* (Doyère, 1840), *Diphascon* (*Diphascon*) *pingue* (Marcus, 1936), *Diphascon* (*Diphascon*) cf. *pingue* (Marcus, 1936), *Diphascon* (*Adropion*) *prorsirostre* Thulin, 1928, *Diphascon* (Adropion) cf. *mauccii* Dastych & McInnes, 1996, *Macrobiotus harmsworthi* group, *Macrobiotus hufelandi* group s.l., *Paramacrobiotus areolatus* group, *Paramacrobiotus richtersi* group, *Minibiotus* sp., *Echiniscus canadensis* Murray, 1910, *Echiniscus granulatus* (Doyère, 1840), *Echiniscus* cf. *granulatus* (Doyère, 1840), *Echiniscus merokensis merokensis* Richters, 1904, *Echiniscus* cf. *merokensis merokensis* Richters, 1904, *Echiniscus quadrispinosus cribrosus* Murray, 1907, *Echiniscus trisetosus* Cuénot, 1932, *Testechiniscus spitsbergensis* (Scourfield, 1897) and a new species of *Echnisicus*. This first results of the Tardigrada inventory in the first European site reflects the high biodiversity due to the geographic positions of the territory and the alpine, mediterranean and ligurian climatic influences. This study was partly supported by the Slovak Scientific Grant Agency (VEGA) as a Project No. 1/0294/09 to P. Degma, and partly supported by the German Federal Ministry of Education and Research, BMBF (0313838) as project FUNCRYPTA to R.O. Schill.

Measurement of temporal changes of ethanol concentration and DNA degradation in the invertebrate wet collection of the Natural History Museum in Vienna [Talk]

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Ethanol is a widely used fixative and preservative for zoological objects in scientific collections. Usually 70 % to 80 % ethanol is used, which is often denatured by various substances. The beginnings of the invertebrate collections of the NHMV date back more than 200 years. They also comprise type specimens for hundreds of species, uniquely and often irreplaceably defining their respective species. Over years the content of jars has been refilled regularly with 75 % ethanol. In this mixture increased evaporation of ethanol compared to evaporation of water is expected to dilute the initial concentration over time. This dilution might result in concentrations insufficient for preservation and subsequently to degradation of DNA in the specimens. Therefore, ethanol concentration from more than 500 jars of several size categories and with different locking systems has been measured. The jars were selected from the collections of Evertebrata varia, Molluscs, Millipedes, Centipedes, Crustaceans and Arachnids. Selected samples of selected species were tested for the evidence of DNA and the DNA quality. Ethanol concentrations have disclosed alarming ranges of variation, particularly in smaller jars.

Naming of organisms in an era of molecular-based discovery [Talk]

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The first decade of DNA barcoding has been a period of transition in which taxonomic and genomic research practices have come into contact. Some foundational concepts and work processes in taxonomy are being re-thought as a result. Previously, the formation of species concepts and their publication with formal names has been the fundamental taxonomic practice. Taxonomists distil character data from preserved specimens and either associate or differentiate them from species with similar characteristics. Barcoding, like traditional taxonomy, relies on characters extracted from preserved voucher specimens, but the greatest volume of data are DNA sequences in digital form, like genomics. Sequencing technologies allow us to extract large volumes of data from an organism and quickly generate clusters of similarity and dissimilarity with other individuals. As more and more sequence data are published without associated species names, the importance of taxonomic names and the return on investment made in taxonomic products are being opened to examination. To what degree do these resulting clusters and the labels we place on them suitable proxies for Code-compliant names? Next Generation Sequencing (NGS) and other approaches allow us to extract enormous amounts of DNA sequences from mixtures of organisms, and the resulting data characterize genetic variability without reference to variation among individuals or species contained in the mixture. How good a proxy for species diversity can NGS provide? The biodiversity crisis has generated calls for faster description of species and a range of responses have been proposed. Hire more taxonomists? Support 'cybertaxonomy' to increase efficiency? Replace traditional nomenclature with DNA sequencing and automated clustering? Bodies such as nomenclatural commissions and the IUBS International Committee of Biological Nomenclature can propose additional solutions that involve modernizing the standards around which taxonomic practices are designed. Some examples from DNA barcoding illuminate the obstacles and benefits.

High-performance imaging of entomological collections [Poster]

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A high-performance imaging system for creating high-resolution images of whole insect drawers is presented. DScan is a prototype scanning machine that allows fast and efficient digitisation of entomological drawers. The resulting images allow the inspection of insect specimens at a high resolution. The level of detail can be adjusted as required, for instance in relation to the size of the insect specimens. The image quality is in most cases sufficient for specialists to recognize the taxon at genus level. The primary aim of this system is the on-demand-digitisation. Because the contents of and arrangement of specimens within drawers is changing if they are part of an active research collection, re-scanning of drawers needs to be quick and easy. All components of the system are industrial standard and can be adapted to meet the specific needs of entomological collections. A controlling unit allows the setting of imaging area (drawer size), step distance between individual images, number of images, image resolution, and shooting sequence order through a set of parameters. The system is highly configurable and can be used with a wide range of different optical hardware and image processing software.

Evolving towards the top: phylogeny and evolution of the European endemic *Phyteuma* (Campanulaceae) [Talk]

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Phyteuma, phylogenetically nested within *Campanula*, comprises 24 species mainly distributed in Europe (only a single species also in northern Morocco) and is morphologically characterized by flowers with a deeply (4)5-lobed corolla and a peculiar opening mechanism. Due the lack of a comprehensive molecular-phylogenetic study of *Phyteuma*, both its circumscription and relationship to other genera, such as *Physoplexis* or *Asyneuma*, and evolutionary processes concerning, for instance, chromosome number (dysploid series from $x=10$ to $x=14$) or habitat evolution (lowland and alpine species), are insufficiently understood. Here, we test previous hypotheses on the phylogenetic relationships of and within *Phyteuma* using phylogenetic analyses of plastid and nuclear DNA sequence data from usually multiple accessions of nearly all currently recognized *Phyteuma* species and from putatively closely related genera. Specifically, we answer the following questions: (1) Is *Phyteuma* a monophyletic group distinct from *Physoplexis*, as suggested by morphological and karyological differences? What is the closest relative of *Phyteuma* and *Physoplexis*? (2) What are the phylogenetic relationships within *Phyteuma* and do inferences from molecular data agree with the intuitive phylogenetic hypothesis suggested by the latest monographer of

the genus? Using the thus established phylogenetic framework, we (3) investigate chromosome number evolution (including newly obtained chromosome data) to test whether different chromosome numbers correlate with phylogenetic lineages in *Phyteuma*; (4) reconstruct the biogeographic history of this genus to identify patterns of range formation with particular emphasis on the relationships between lowland areas and high mountain ranges as well as among different high mountain ranges; and (5) reconstruct habitat evolution with special emphasis on alpine habitats.

Biotic control of local biodiversity – Jurassic rudist bivalve reefs from the Alpine-Carpathian transition [Talk]

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The Hippuritida, commonly known as rudist bivalves, evolved at around the Middle to Late Jurassic transition and persisted until the end of the Cretaceous. As soon as by the Late Jurassic, representatives of one of their two basal families, the Epidiceratidae, formed densely grown patch reefs in shallow lagoonal settings. The Tithonian-Berriasian carbonate platforms of the northern Tethys margin are well-known for their remarkable species richness, which was promoted by a complex environmental patchwork of fringing ooid bars, scleractinian patch reefs, and lagoonal habitats. Identified as the cradle of the modern crab fauna, these environments, in particular the Ernstbrunn-Pavlov Platform of NE Austria and SE Czech Republic and the Štramberk Platform of NE Czech Republic, also hosted an extraordinary high diversity of gastropods, bivalves, scleractinians, and other benthic invertebrates. This is, however, not true for the immediate surrounding of the Epidiceratidae. In favourable settings, these bivalves, which are frequently also found as associates in coral build-ups, grew to patch reefs of several decimetres in height and extent. Unlike coral reefs, however, these build-ups are characterised by a remarkably low biodiversity both of constructors and reef dwellers. We investigated three-dimensionally preserved frameworks from carstic fissures as well as 10 subsequent sections through a 0.2 m^3 epidiceratid reef preserved in massive limestone (more than four square metres in total) in order to obtain statistically significant data sets. Data confirm the mere absence of encrusters or bio-eroders from living epidiceratid bivalves, as well as the total absence of additional frame-builders from the bivalve reef. Moreover, the richness and abundance of reef dwellers is significantly depleted with regard to the surrounding high-diversity habitats. We suggest that biochemical repellents produced by the rudists may have caused this remarkable drop of local biodiversity. During the latest Jurassic, rudist bivalves formed only locally dense populations – during their bloom in the Late Cretaceous, however, the Hippuritida dominated most of the tropical–subtropical shallow marine carbonate settings. As a result, biodiversity in these extensive areas was effectively down-levelled by biotic interaction. Consequently, the Hippuritida, which constitute a major group of reef-forming biota in earth history, did not promote but suppress diversification.

Comparative floral structure and systematics in the balsaminoid clade (Ericales) [Talk]

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During the past two decades, our understanding of the phylogenetic history of many groups of organisms has been revolutionized by the use of molecular methods and new analytical tools. In the angiosperms, the asterid order Ericales is a prominent example. Previous concepts about taxonomic composition as well as general systematic affinity differ dramatically from current hypotheses. Not only in the Ericales but also in many other groups of organisms, we are now in the unsatisfying situation to have well-supported phylogenetic hypotheses, yet the structural and functional traits that characterize these groups are unknown due to the lack of appropriate comparative studies. However, such studies are clearly very important not only for a better general understanding of the evolution and the biology of organisms, but also in connection with modern genomic, metabolomics or developmental genetic (evo-devo) approaches. In order to understand biological function comprehensively, both higher levels of organismal organization and the broader phylogenetic context need to be taken into account. In addition, structural knowledge is essential for the analysis of fossil taxa and their incorporation into phylogenetic analysis. The balsaminoid clade has been identified as the first-diverging lineage of the Ericales and its monophyly is strongly supported in molecular phylogenetic studies. While a closer relationship of Marcgraviaceae and Tetrameristaceae had been recognized for a long time, the systematic position of Balsaminaceae was much debated in the past. It is therefore not surprising that non-molecular synapomorphies for the clade have largely been lacking. In order to search for potential synapomorphies for the clade as a whole as well as for its major subclades, we have comparatively studied floral structure in representatives of all three families using a combination of serial microtome sectioning, scanning electron microscopy (SEM) and Micro X-ray computer tomography (MicroCT). We find that the entire clade is strongly supported by the shared presence of several floral characters including thread-like structures on anthers, punctiform stigmas, strongly developed commissural areas in the style, mucilage in the ovary, as well as a series of histological features. In addition, a sister-group relationship between Tetrameristaceae and Balsaminaceae is supported by the partial postgenital fusion of filaments and ovary and a distinctly star-shaped stylar canal.

The potential contribution of the endosymbiont *Wolbachia* to speciation-with-gene-flow in *Rhagoletis* fruit flies [Talk]

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The question how one species evolves into two or more species is a critical question concerning the great diversity of life on the Earth. Different pre- and postzygotic isolation mechanisms are considered to be a first step in the split of one species in two. In this context factors contributing to the evolution of reproductive isolation include geographic isolation and ecological isolation. However, oft-forgotten players in speciation process of insects, one of the most species-rich groups of life on Earth, are endosymbiontic bacteria. The frugivorous genus *Rhagoletis* (Diptera: Tephritidae) contains about 60 different species with a broad geographic distribution and a complex pattern of host plant associations. Genetically and taxonomically similar species form different species groups. Members of these groups have different evolutionary histories: Species of the *R. pomonella* species group infests a broad range of different hosts that range from hawthorn, snowberries and blueberries to apples. These species were formed due to the adaptation to different hosts. Host choice is positively related to mate choice and resulted in prezygotic isolation and subsequent in ecological speciation. In contrast, the *R. cingulata* species group infests cherries and contain two geographically separated species, *R. cingulata* in the Eastern United States and R. indifferens in Western United states that likely speciated by classic allopatric mode of geographic separation. Wolbachia is a widespread endosymbiontic bacteria, that can influence the reproduction of its host. These effects range from male-killing, parthenogenesis, and feminization to cytoplasmic incompatibility. Different *Wolbachia* strains among a population can form pre- and postzygotic isolation and can lead to speciation. A few cases that have demonstrated that *Wolbachia* has contributed towards speciation suggest that this endosymbiont should not be ignored in speciation studies of insects. Here we reopen the well-studied speciation history of different *Rhagoletis* species and add *Wolbachia* as additional third layer. We show a phylogenetically similar *Wolbachia* community in different host races of *R. pomonella* and its distribution over space and time, and an extensive variety of *Wolbachia* strains within the *R. cingulata* species complex. We discuss potential impacts on the evolutionary history and speciation of its host and the evolution of the *Wolbachia* communities within.

How to cope with megadiverse groups? An integrative approach towards reconciling taxonomic concepts in Dendrobiinae [Talk]

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The Dendrobiinae are a morphologically highly diverse subtribe within the largest and taxonomically most challenging orchid subfamily, the Epidendroideae. In its traditional circumscription the majority of species within the subtribe belong to the genus *Dendrobium* s.l. (1200+ species), one of the three orchid

mega genera, with a distribution across the Indo-Asian, Australasian and Pacific regions. In the past, highly divergent taxonomic concepts have been proposed, yet the monophyly of many of the discerned taxonomic entities remains to be tested. To this end we present a broad scale molecular phylogeny of Dendrobiinae based on plastid and nuclear markers (matK, ycf1, ITS, xdh) and assess the taxonomic value of morphological characters to delineate natural groups within the subtribe. The study is an important step towards providing a phylogenetic framework as a basis for reconciling the disparate taxonomy of Dendrobiinae.

The potential of μCT technique in taxonomy – a case study on insects [Talk]

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During the last decade, non-invasive techniques, such as micro-computer-tomography (μCT), have become increasingly important for morphological analyses. However, μCT data are rarely found in studies focusing on taxonomy. The internal morphology of insect genitalia has been shown to be of greatest value for taxonomic studies. Their investigation by means of non-invasive techniques would be very useful not only to study their structure in situ, but also to keep valuable type material safe and undamaged. We used praying mantids (Insecta: Mantodea) in order to elucidate the potential value of μCT data for taxonomic studies and performed scans of the male genitalia using a Xradia MicroXCT 200 imaging system at different magnifications. The results are compared to traditional taxonomic data (*i.e.*, morphological drawings) and the advantages and disadvantages of μCT as a routine method for taxonomic work are discussed.

Septal compass and septal formula – a new method for phylogenetic investigations of the ear region in sciuromorphs [Talk]

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In previous studies, morphological investigations of the ear region in rodents were focussed on the three auditory ossicles or the bony labyrinth. Bony septa in the middle ear region, more precisely in the epitympanic recess and the tympanic cavity were described, but their phylogenetic value was not realized. For a better comparability of morphological and phylogenetical differences, a new method for investigating the ear region is developed. With the 'septal compass', the characteristic internal anatomy of the middle ear is gathered. In doing so, 'primary' and 'secondary septa' can be distinguished, depending on their spatial direction and position in the epitympanic recess and the tympanic cavity. Supplementary to the compass, the 'septal formula' allows a numeric description of this anatomy and is used similiar to the 'dental formula'. Applying the compass and the formula on the ear region of sciuromorphs in which phylogenetic relationships based on morphological data are not consistent, remarkable anatomical differences are observed. In sciurids, ventrally and dorsally laying 'primary' and 'secondary septa' are formed. Glirids do not possess any septa in the epitympanic recess, but show additionally sinus in posteromedial direction. In *Aplodontia rufa*, the anatomy of the ear region is quite different, whereby a network of bony septa is observed. This is also seen in one of the oldest known rodents, *Ischyromys typus*, and can not be gathered with the 'septal compass'. Therefore, a bony network can be postulated as a ground plan character of sciuromorphs, which has been reduced in different ways in glirids and sciurids. For further investigations of the internal anatomy of the ear region in rodents, the 'septal compass' and the 'septal formula' are particularly suitable for illustrating and investigating phylogenetic issues.

Hydra and its symbionts – A transcriptomic screening for ecologically important loci [Poster]

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In case ecological conditions change for an organism, selection can favour previously neutral or deleterious variations of a gene. These conditions can be external (*e.g.* habitat shifts) or internal (*e.g.* symbiont shifts). Present day advanced sequencing technologies enable the fast and reliable identification of novel genes of ecological importance which are under positive selection. In our study we used the symbiotic model species *Hydra viridissima* (Hydrozoa, Cnidaria) to identify possible candidate loci of ecological importance. We compared transcriptome data from two laboratory *Hydra* strains with native origins in Madagascar and Germany. They are characterised by different endosymbiotic green algae species. The transcriptomes were scanned for open reading frames with significant patterns of positive selection using Ka/Ks-ratios. Selected candidate loci were amplified from *Hydra* specimens collected in *e.g.* Europe, Australia and America. The candidate loci were analysed in the context of climate data as well as using co-phylogenies of *H. viridissima* (based on CO1) and their symbiontic algae (based on ITS). Our study design enabled us to test the identified candidate loci for their influence on adaptation to different climates and/or symbionts.

Hybridization as a source of intraspecific cichlid color pattern diversity [Poster]

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Novel phenotypes can originate from hybridization between phenotypically differentiated populations, *e.g.* in secondary contact, in particular when transgressive segregation gives rise to offspring much different from the parental phenotype. This makes hybridization a potent candidate mechanism in the evolution of phenotypic diversity in closely related taxa. In the East African rift Lake Tanganyika, the endemic fish genus *Tropheus* exhibits an extremely high level of geographic color pattern variation. In the history of the genus, the allopatric distribution of the stenotopic, littoral rock dweller has repeatedly been disturbed by lake level fluctuations and associated shoreline changes, causing secondary contact between previously isolated color morphs. Genetic data suggest that several of the extant populations experienced massive amounts of gene flow from other populations, which may, at least in some cases, have influenced their color phenotype. One of the candidate hybrid color morphs was analyzed in more detail, and indeed showed clear signals of genetic admixture between two putative parental morphs. The geographic distribution of the three morphs is consistent with a scenario of hybridization in secondary contact. Moreover, the F1 of an experimental cross between the putative parent morphs display a color pattern very similar to that of the putative hybrid morph. Given that along the shores of Lake Tanganyika numerous populations have been subjected to cycles of allopatric divergence and secondary contact, hybridization may have contributed significantly to the evolution of color pattern diversity in this genus.

Phylogenetic relationships and dysploidy in *Capsicum*: Evidence from DNA sequences and other multidisciplinary data [Talk]

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DNA sequences of two plastid markers (trnH-psbA, matK) and of the single copy nuclear gene waxy from two outgroup genera and 23 taxa of *Capsicum* (Solanaceae) are quite congruent. They support earlier reports on *Lycianthes* as the only other member of tribe Capsiceae in the New World and as link to other Solanoideae genera. *Capsicum* is clearly monophyletic, entirely diploid and includes four clades (or grades) with two different chromosome base numbers, $x=12$ and 13. The strict consensus tree from the ML analysis of the combined plastid markers and the only ML phyogram from the nuclear gene waxy clearly place the clade of *C. rhomboideum* (1), centred in the NW of S-America with $x=13$ in a most basal position within *Capsicum* and closest to the wide-spread *Lycianthes* ($x=12$). Both share the plesiomorphic characters of small and undifferentiated innermost mesocarp cells and the complete absence of pungent capsacinoids, otherwise common in *Capsicum*. This suggests that the origin of the genus was coupled with a dysploid change from $x=12$–13. Clearly related to (1) is the clade of *C. villosum* (2a) which also includes the somewhat aberrant *C. campylopodium* (2b). This clade is centred in SE-Brazil, also has $x=13$, but already exhibits the apomorphic giant innermost mesocarp cells and capsacinoids typical for the genus.

The closely following grade (3) with x = 12, signals a phylogenetic return from x = 13 to x = 12 within the genus, as supported by karyological and other data. This basal x = 12 grade (3) includes the species groups of *C. flexuosum* (3a) in central, *C. parvifolium* (3b) in northern S-America, and *C. coccineum* (3c) + *C. minuti-florum* (3d) mainly in Bolivia. Grade (3) marks the phylogenetic transition towards the speciose x = 12 crown clade (4) of the genus which consists of the closely linked species groups of *C. pubescens* (4a), *C. baccatum* (4b), *C. galapa-goense* (4c) and *C. annuum* (4d). These groups are not yet fully separated by crossing barriers and include all cultivated members of the genus. In retrospect: The morphological, anatomical, karyological, phytochem

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Comparison of dark septate endophytic fungi communities among arctic tundra vegetation types [Talk]

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Dark septate endophytes (DSE) are a group of root-inhabiting fungi that are distinguished by the formation of special morphological structures called microsclerotia. DSE colonization is particularly widespread in extreme environments and these fungi are ubiquitous in the roots of arctic and alpine plants. Nonetheless, relatively little is known about the diversity and ecological roles of these fungi in tundra habitats. Our research focuses on the biodiversity of DSE and their community composition in various tundra vegetation types. Here, we present the first DNA-based diversity assessment of DSE fungi in arctic soils based on high-throughput DNA sequencing of soil samples collected along the North American Arctic Transect that spans all five bioclimatic zones of the arctic tundra biome. Multiple species in several genera of DSE fungi were detected and their diversity will be presented in a phylogenetic context. Furthermore, we apply multivariate ordination methods to compare the distributions of these species across various bioclimatic zones and soil types and discuss their correlations with climate, vegetation, and edaphic factors.

Phylogeographic structure of Siberian larch *Larix sibirica* revealed with cytoplasmic DNA markers [Talk]

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Contemporary genetic diversity of a species contains information about past climatic and geological events shaped its populations. We investigated genetic variability of Siberian larch – one of the most tolerant to the cold and drought conifer tree, distributed from the Polar tree line to the steppes of Mongolia. Population samples collected range-wide were surveyed with four mitochondrial (mt) DNA loci and five microsatellite loci of chloroplast (cp) DNA. Spatial genetic structure was much stronger in mtDNA (Gst= 0.564, Nst=0.617) than in cpDNA (Gst=0.041, Rst=0.047). Nst significantly exceeded Gst in mtDNA indicating phylogeographic structure. Spatial Analysis of Molecular Variation (SAMOVA) of the geographic distribution of mitotypes revealed eight distinct population groups supposedly corresponding to the Pleistocene refugia. At least three population groups are located in South Siberia and Central Asia. We suggest the refugia corresponding to these groups were located in Altai Mts., south Sajan Mts and the coast of Baikal Lake. We also investigated historical demography of western and eastern subspecies of *L. sibirica* and other larch species of the North Asia (*L. gmelinii* and *L. cajanderi*) using approximate Bayesian computation (ABC) analyses of cpSSR data with a special reference to the Pleistocene population dynamics. All larches demonstrate posterior distributions of the age of the population expansion with a mode in a range of 22,0000–1,340,000 years BP suggesting the post bottleneck population recovery following some mid-Pleistocene glaciation well before the LGM. This study was supported by the Russian Foundation for Basic Research, grant no. 10-04-96000.

Phylogeny and biogeography of the genus *Abies* Mill. (Pinaceae) based on the cytoplasmic DNA sequence data [Talk]

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The genus *Abies* (fir) is one of the largest and most complex conifer genera. It includes about 50 species, widely distributed across the Northern Hemisphere. A phylogenetic analysis based on five chloroplast DNA fragments (total length 5550 b.p.) and two mtDNA loci (total length 4330 b.p.) was performed on 35 Abies species and Keteleeria davidiana. The resulting cpDNA phylogeny supports six major fir lineages and describes the relationships among them. The mtDNA data produces a reticulate network instead of a tree suggesting inter-lineage recombination. Nine observed groups of mtDNA haplotypes are associated in general to the particular cpDNA clades. The mtDNA lineages are strongly than the cpDNA associated with geography, for instance the North American firs belonging to several distantly related cpDNA clades, share single mtDNA clade that could be interpreted as a consequence of the hybrid speciation. We discuss the biogeographic implications following from the joint analysis of cpDNA and mtDNA together with paleontological data. This study was supported by the Russian Foundation for Basic Research, grant no. 11-04-00709.

Morphological and ecological evolution of a Gesneriaceae lineage in Neotropical rainforests [Talk]

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The Neotropics include seven out of 34 global biodiversity hotspots and their extraordinary species richness has challenged the evolutionary biologist to investigate the factors driving diversification processes. Patterns of species diversity have been attributed to a complex history of geological, climatic and ecological changes, as well as, adaptations and morphological evolution. Recent studies used phylogeny based approaches to identify how phenotypic differences among species emerged and have been maintained. In this study, we generate a molecular phylogeny of the *Codonantopsis-Codonanthe-Nematanthus* (CNC) plant group, and investigate the dynamics of its phenotypic evolution, in the light of their historical biogeography. This clade (46 spp.) belongs to the new world lineages of the Gesneriaceae family (tribe Episcieae), encompassing a highly differentiated floral morphology, related with pollinator interactions. CNC group displays a disjunct geographic distribution between Neotropical rainforests. Our phylogeny reveals the presence of a basal monophyletic clade distributed in Central and northern South America (*Codonanthopsis*), and two clades endemic to the Brazilian Atlantic Forest (*Nematanthus* and *Codonanthe*). Floral morphology and climatic preferences were compared across clades. Additionally, we infer clade-specific rates of trait evolution and ecological differentiation, and analyze their temporal variation. Our results suggest that within the *Nematanthus* clade a sustained increase in the rates of morphological divergence took place, whereas, no significant differences could be attributed to the geographic distribution. This pattern correlates to the evolution of the flower resupination, suggesting a key innovation effect of this trait. Shifts in rates of morphological evolution may be decoupled from changes in ecological differentiation, on a temporal and clade specific basis. We conclude that complex interactions between morphology, climatic niche and biogeography contributed to shape the diversification of CNC clade.

The Pandora's box of *Neopetrosia exigua* (Bearing the wrong identity: all about the Indo–Pacific *Neopetrosia exigua*) [Talk]

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Sponges are ecologically important elements of tropical benthic communities, such as coral reefs. Some of them are of considerable commercial interest due to their production of bioactive compounds. However, the difficulty of sponge taxonomy, as well as species identification of promising species, often remains problematic. *Neopetrosia exigua* (Kirkpatrick, 1901), a haplosclereid sponge species that inhabits Indo-Pacific coral reefs, presents such difficult case to be resolved. This species has extensively been mentioned in the scientific literature for its bioactive metabolites, but it probably represents a species complex nevertheless. Currently, two species names are accepted as junior synonyms of *N. exigua*, namely *Neopetrosia*

pandora de Laubenfels, 1954 and *Xestospongia pacifica* Kelly-Borges & Berquist, 1988. We here carried out an assessment of the main morphological characters (spicule dimensions) of those holotypes, which have been the base of sponge taxonomy for centuries. Additionally, we examined the holotype of *Petrosia chaliniformis* Thiele, 1899 because our freshly collected "*N. exigua*" from Indonesia appeared morphologically most similar to this species. To test hypotheses about species identity based on morphological characters, we successfully sequenced a fragment of the 28S rDNA of both holotypes of *N. pandora* and *X. pacifica*. Furthermore, we were able to obtain a partial sequence of the mitochondrial cox2 gene from both holotypes. Attempts to obtain sequences from the century-old holotypes of *N. exigua* and *P. chaliniformis* unfortunately were unsuccessful. Based on our molecular and morphological assessment, *N. pandora* appears different from our freshly collected *N. exigua*. As a result, we suggest that *N. pandora* should be a valid species and not being synonymised to *N. exigua* anymore. We propose, based on the priority rule, that *Neopetrosia exigua* (Kirkpatrick, 1901) and *Xestospongia pacifica* Kelly-Borges & Berquist, 1988 should be transferred to the junior synonym of *Neopetrosia chaliniformis* (Thiele, 1899). After solving this species complex, future studies, *e.g.*, on the ecology, biogeography and bioactive compounds of *N. exigua* will rest on a much safer taxonomic foundation. Keywords: Porifera, *Neopetrosia exigua*, *Xestospongia pacifica*, *Neopetrosia pandora*, *Neopetrosia chaliniformis*, junior synonym, morphological character, 28S rDNA, mitochondrial cox2

Blank spaces in understanding of biodiversity as a whole panarchy across scales and levels [Talk]

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Biodiversity is system sustaining functioning of Biosphere under geological and climatic changes. The crucial point on way to understanding of biodiversity – an integrated versatile system is a lack of adequate developed theoretical concept. We may take the principle of panarchy – an antithesis to the word hierarchy – as a start point for development of the needed concept. L. Gunderson & C. Holling wrote: "The cross-scale, interdisciplinary, and dynamic nature of the theory has led us to coin the term panarchy for it. Its essential focus is to rationalize the interplay between change and persistence, between the predictable and unpredictable." This means there is no main level of biodiversity system with multiple interrelated elements of different levels and scales in continual adaptive cycles. Can we adequately identify and quantitatively assess the integrated value of biodiversity system? How can we integrate values of diversity on different levels/scales to quantitatively assess a total diversity of life? There are multiple spots in theory and practice of biodiversity studies which don't give us such possibility. Some of them: 1) There is a complementarity of diversity on different levels; but as example we can't assess how species diversity in genus taxocene influences on intrapopulation diversity. There are cases when increasing of mollusk or crustacean species diversity are associated with decreasing of intrapopulation diversity. 2) Every biological/ecological system can exist in several alternative steady states. We don't evaluate diversity of steady states on different levels – genotype, individual, population, ecosystem. We do not know how to "write in" a multiplicity of stable states of biological systems in an integrated value of total biodiversity. 4) Evolution and dynamics of biota is characterized by two stages – the coherent and incoherent. During coherent stage a system realizes a smooth adaptation to the changing environment within the existing norms of reaction; during incoherent stage – there are destabilization of system and its transformation in new state. How may we compare biodiversity of these two stages? 3) Many species can be in ecosystem in two states – active and sleeping (resting stages). It generates several unanswered questions. It's not full list of the black spaces. Only remember about the Principle of Complementarity we will be able to overcome difficulties; a polylogical mentality goes to replace monological one.

Speciation of hyperdiverse taxa across the highly complex New Guinean terrane system: diving beetle genus *Exocelina* Broun [Talk]

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New Guinea is attractive for scientific research ever since Wallace not only because it is one of only three remaining major tropical wilderness areas with a very rich biodiversity, but also because of the complexity of its geological origin and colonization history in combination with the scarcity of information on them. Which factors have promoted the incredibly diverse radiations in New Guinea? Understanding speciation mechanisms here remains in its infancy, despite some earlier landmark contributions. In our study, we use diving beetles of the genus *Exocelina* Broun, 1886 as a proxy for hyperdiverse New Guinean fauna. This genus is a recently discovered water beetle group with high levels of diversification and endemism throughout the Oriental and Australian Regions. At present, it includes 94 valid species. With 41 species described from the island, New Guinea is the core of the biodiversity of the genus. Our recent taxonomic revision updates the number of described species to 63, with an approximation of total fauna of up to > 130 species. Phylogenetic analyses, based on molecular data, substantiate New Guinean *Exocelina* as a monophyletic group, which emerged from a single colonization event by an Australian species that led to a radiation of very high number of New Guinean species. We use molecular phylogenetic inference to provide a robust tree for ca. 100 species of New Guinean *Exocelina*, revealing large scale patterns of diversity across the region, as well as a temporal framework to reconstruct the evolution of the group in space and time. We relate rates of diversification to global climate change and to geological change connected to the terrane accretion history of New Guinea.

Bayesian inference of macroevolutionary processes using the fossil record [Talk]

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Analytical advances in molecular phylogenetics and palaeobiology have provided us with tools to estimate the tempo and mode of biotic evolution. However, most studies have relied on a single source of data: either molecular phylogenies or fossil occurrences. Few attempts have yet been made to compare results based on evidence from both, despite large discrepancies in the patterns recovered for almost all organism groups. This situation might derive from limited interaction between molecular systematists and

palaeobiologists, but also from widely different methods and assumptions employed, making comparisons statistically difficult. Here we present a new hierarchical Bayesian framework to jointly estimate times of origin and disappearance of taxa and rates of speciation and extinction based on the fossil record. Speciation and extinction rates can vary through time and their temporal dynamics can be decoupled. A data set of mammal fossils spanning from the Miocene to the present is used to investigate diversification processes through time and across clades. Our method represents a step toward an integrated approach that combines phylogenetic and fossil information to infer macroevolutionary processes.

Exploring the quality of phylogenomic datasets to infer insect evolution [Talk]

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The resolution of the Insect Tree of Life has recently improved using phylogenomic data; *e.g.* the sister-group relationship of Hymenoptera to remaining Holometabola or the intra-ordinal relationships within some holometabolan orders; *e.g.* in Hymenoptera or in Coleoptera. Despite this increase in resolution, several ambiguities within the Insect Tree exist. Recent discussions center around (i) the basal pterygote divergence ("Palaeoptera Problem"), (ii) the polyneopteran relationships (unresolved polytomy) and (iii) the monophyly of Paraneoptera and their position within Neoptera. However, it remains unclear if these ambiguities within the Insect Tree arise due to the lack and/or overlap of genomic and/or transcriptomic data or due to the incongruence in the phylogenetic inference. In addition to addressing phylogenetic questions with new genomic information (derived from 454 expressed sequence tag (EST) data) for three representatives of hitherto unsampled polyneopteran orders: Zoraptera (*Zorotypus gurneyi* ?), Plecoptera (*Nemurella pitetii*) and Dermaptera (*Forficula auricularia*)), we further addressed several mechanistic problems relevant to phylogenetic reconstruction. These problems include missing data, phylogenetic resolution, and taxon and gene sampling, all of which contribute to the underlying data quality and consequently the resolution of a certain phylogenetic question. The difficulty inherent in insect systematics and the existence of competing phylogenetic hypotheses offers a great opportunity to explore the source of incongruence in phylogenomic studies more generally. Here, we test several phylogenetic hypotheses within the Insect Tree and explore how support for these hypotheses might be influenced by missing data, matrix selection, gene and taxa number/choice and the biological function of the genes. We further characterized the strength of support for the concatenated phylogenetic hypotheses using a newly developed approach, RADICAL, which allows us to identify the problematic nodes within the Insect Tree and quantify their relative weakness. In sum, this study (i) provides new insights into the evolution of three ambiguous insect orders, (ii) highlights the problems in insect systematics despite the use of numerous characters even in the context of this phylogenomic dataset and (iii) demonstrates which factors might influence the phylogenetic inference.

Australia's King Orchid – one species or many? A phylogeographic approach to resolving taxonomic limits [Talk]

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The King Orchid (*Dendrobium speciosum* s.l.; sect. Dendrocoryne) is a mainly lithophytic species complex occurring within the mesic biome of Australia's east coast with an impressive north-south distribution spanning more than 2500 km. Species delimitation within the *D. speciosum* complex is contentious, with competing taxonomic concepts discerning from one to eleven distinct species, and different infraspecific entities. To provide a robust basis for taxonomic delimitation, the phylogeography of the *Dendrobium speciosum* complex was investigated using DNA fingerprinting (AFLPs). Neighbor Joining, NeighbourNet and Bayesian clustering analyses revealed phylogeographic structure within the complex and identified strongly supported northern and southern groups separated geographically by a lowland dry corridor. The phylogeographic structure was consistent with a contracted distribution modeled for past drier periods such as at the last glacial maximum. Due to evidence of recent gene flow between northern and southern groups and relatively shallow divergence between them, the *D. speciosum* complex should be treated as a single species with two infraspecific groups.

When frequent intercytotype gene flow hampers polyploid speciation in primary contact zones [Poster]

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Polyploidy, a possession of more than two chromosome sets in somatic cells is considered a major mechanism of vascular plants evolution. Theory predicts that genome duplication may enhance ecological tolerance of polyploids in comparison to diploid relatives due to increased genetic variability and thus altered biochemistry, morpholgy and/or life-history traits. *Pilosella rhodopea* (syn.: *Hieracium rhodopeum*) (Asteraceae), species confined to the alpine belt of the Balkan mountains, represents a unique diploid-polyploid complex with up to five ploidy levels (2x-6x) occurring almost exclusively in mixed-ploidy populations and triploids being the most frequent cytotype. Previous cytogeographical, morphological and molecular data (ITS, allozymes) suggested an autopolyploid nature of polyploids in *P. rhodopea*. In

present study, we aim to answer the questions whether these autopolyploids have a single or multiple origin and whether the autopolyploidization has induced a shift in microhabitat preferences of cytotypes. Using the more discriminant fingerprinting markers (AFLPs) we found that the plants of different ploidy levels within single population were genetically closer than the plants of the same cytotype from different populations. This finding indicates a multiple independent origin of polyploids and frequent gene flow in rarely documented primary diploid-polyploid contact zones. Intercytotype gene flow involving reduced and unreduced gametes underlies the formation and coexistence of different ploidy levels. Based on detailed transect study performed at two localities, there was no evidence for microhabitat differentiation among cytotypes. Our results suggest that sympatric polyploid speciation currently does not take place in *P. rhodopea*, likely due to unrestricted gene flow preventing genetic differentiation and thus speciation processes.

Assessing cryptic diversity of Amazon lowland amphibians in Peru using mtDNA [Poster]

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The Amazon lowlands are known to host the highest local diversity of amphibians in the world. Several molecular studies in the last decade, suggest that species richness of amphibians in the Neotropics may be still grossly underestimated. The present study was focused on six widespread species of hylid frogs (two of *Scinax*, and four *Hypsiboas*). We sampled eight localities across the Peruvian Amazon which spanned the north, centre and south east of Peru, covering a geographic distance of 1000 km approx. from north to centre and 790 km approx. from centre to south. As part of a larger DNA barcoding effort, we estimated genetic diversity and divergence by sequencing the mitochondrial genes 16S and CO1 and combined these data with previous published studies. Multiple sequence alignments were made for each dataset and phylogenetic analyses were carried out with a Maximum likelihood approach. Based on the criteria for candidate species, we found five confirmed candidate species of *Hypsiboas*), and seven unconfirmed candidate species (three from *Hypsiboas* and four from *Scinax*). The results of this study provide new and important data that will be helpful in the study of diversity of amphibians in Peru.

Taxonomic placement of *Ericabatrachus baleensis* (Amphibia, Anura) and assessing data to include in phylogenetic analyses [Talk]

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The Bale Mountains Frog, *Ericabatrachus baleensis* (Largen, 1991), is the only species in its genus and is endangered and endemic to Ethiopia. During a recent field expedition, the species was rediscovered after 25 years. There is great uncertainty regarding its phylogenetic placement in Ranoidea. Previous proposals have tentatively assigned this taxon to the families Petropedetidae, Phrynobatrachidae, Pyxicephalidae, based on morphological evidence. The objective of our study is to resolve the phylogenetic position of this taxon within Ranoidea. We sequenced five molecular markers (12S, 16S, 28S, RAG1 and H3A) to carry out this analysis and combined them with data from previously published works. To account for problems associated with combining genes with such different evolutionary mechanisms we assessed the effect of using different partitioning schemes based on saturation of the different gene partitions and codon positions. Here, we shall present the results of the phylogenetic relationships of *Ericabatrachus baleensis* within Ranoidea following the proposed approach.

Investigating the origin of incongruence between gene trees of the mushroom-forming fungi [Talk]

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The Agaricomycetes – mushroom forming fungi – are currently divided into 12 major well established lineages, whose relationships relative to one another are still unresolved. Using multi labeled trees of genefamilies from 45 Basidiomycete genomes we aim to map the processes leading to the different phylogenetic signals for different genes. This includes hybridization, genome duplication, rapid radiations, heterotachy, positive selection and paralogy. The main goal is not to get a fully resolved tree, but to understand to what extent different processes have been involved in the evolution of the Agaricomycetes.

A new framework for quantifying lineage-specific patterns of trait covariation [Talk]

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Phylogenetically controlled allometric studies have become the principal approache to study the co-evolution of traits across particular comparative samples. Allometric residuals are, however, limited in that they do not provide any information on the process that underlies their deviation from allometry. Consider, for example, traits Y and X for extant species S. A positive residual of Y over X may be the results of either of 3 fundamentally different evolutionary processes occurring on the evolutionary lineage of S: Y increased relatively more than X, Y increased while X decreased, Y decreased relatively less than X (vice versa for a negative residual of Y over X). Positive and negative residuals may thus reflect processes that include each trait to both outpace and underpace the other trait. I present a novel framework to study trait covariation in comparative samples that considers all possible evolutionary scenarios of trait increase/decrease between two traits. This approach is based on an adaptive peak-based method that allows inferring variable rates of evolution for individual lineages of a phylogenetic tree without a priori parameterization, estimating realistic trait values of extinct species, and incorporating fossil values for model validation/calibration. I will demonstrate the empirical applications of this framework by providing new insights into a long-standing debate in evolutionary biology: the validity of relative brain size. Smaers J.B., Dechmann D., Goswami A., Soligo C., Safi K. 2012 Comparative analyses of evolutionary rates reveal different pathways to encephalization in bats, carnivorans, and primates. Proceedings of the National Academy of Sciences USA. (doi:10.1073/pnas.1212181109).

Open up the treasure chest of prokaryotic metadata for comparative biodiversity analyses [Talk]

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Within the Global Biodiversity Information Facility (GBIF) the Leibniz-Institute DSMZ constitutes the German node GBIF-D Bacteria & Archaea. The focus of the node is to mobilize prokaryotic organism related data, so called metadata. This data is currently not present in any of the publicly available databases. Although relevant information is already available in primary descriptions for new taxa or recorded descriptions of living bacterial collections, these sources of knowledge are often neither centrally located nor structured searchable and accessible via the Internet. Microbial diversity has many aspects *e.g.* taxonomy, habitats, physiology, morphology, substrate spectra and genomic characteristics. In the meantime more than 400 data fields have been defined covering the different facets of microbial diversity information in order to organize the mobilized data into searchable database content. A new integrative mobilization concept includes the extraction of the source information as well as the structuring and evaluation of primary data. The content is generated by making use of information retrieval and text mining methods. These taxon-related prokaryotic metadata is set into relation with aspects of the molecular biology *e.g.* the 16S rRNA sequence or metagenome data of related bacterial communities. This enriched data background will offer possibilities of completely new biodiversity analyses. Those also comprise amongst others the comparison of microbial distributions, the alignment of physiological with Omics-data, the conformity of degradation patterns and the synthesis of natural products. All mobilized data is made publicly available via the GBIF data portal (http://data.gbif.org) and also under the newly launched DSMZ webportal “BacDive – The Bacterial Diversity Metadatabase” (http://bacdive.dsmz.de). In order to obtain more detailed information about this project, feel to visit the corresponding poster.

Open up the treasure chest of prokaryotic metadata for comparative biodiversity analyses – Ongoing projects [Poster]

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Bacteria and Archaea are usually invisible to the human eye but omnipresent in soils, water and even our bodies. In order recognize their individual functions and interactions with higher organisms as well as their importance ecological systems more data describing microbial species is highly needed. This data is referred to as metadata. Apart from recording information about taxonomic classification, geographic origin and their availability in culture collections, metadata of prokaryotes will dramatically increase the interaction with scientific key issues. Centralized and freely available information enables advanced analysis and research regarding issues like biological interactions of bacterial species or bacteria with higher taxa, geographical coincidence or potential metabolic properties taking genomic and metagenomic data into account. Digitization and mobilization case example: Myxobacteria The largest collection of Myxobacteria, the “Reichenbach Collection of Myxobacteria” originated in Braunschweig is now part of the DSMZ microorganism strain catalogue. Besides the cultures themselves, a comprehensive archive of index cards additionally contains descriptions on growth habits, appearance of fruiting bodies, details of geographic origin and data regarding the habitat of the strains. Included in the collection is also a comprehensive archive of images of the cultures, showing their growth on media and formation of their fruiting bodies. In order to preserve this rich source of taxon associated information all images and index cards have been digitized. Corresponding information is available via the DSMZ portal “BacDive – The Bacterial Metadatabase” (http://bacdive.dsmz.de) as well as the GBIF data portal (http://data.gbif.org). However, to enable data analyses and comparative studies on this source of information the digitization is just the first step of processing. The data in text format has to be structured and made evaluable by text and data mining methods which are integrated into individual data mobilization concepts. This subsequent data processing provides the basis to gain insights about cross-species relationships, distinct roles in the ecological patterns, potential sources of drugs or even pathological threats.

Planktonic ciliates in alpine and subalpine lakes: diversity, biogeography and the role of ultraviolet radiation [Talk]

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Subalpine lakes that are surrounded by vegetation bear a great variety of around 50 to 150 planktonic ciliate morpho-species detectable throughout the year. Their species-specific seasonal occurrence is strongly coupled to environmental conditions such as food availability or oxygen gradients. In contrast, in oligotrophic alpine lakes above the treeline only a handful of species are found in the ice-free season with less than five predominant morpho-types. Beside low temperatures, low nutrient availability and low coloured dissolved organic matter such remote lakes are characterized by their shallowness allowing the ultraviolet radiation (UVR, 290–400 nm) to penetrate the whole water column. Solar UVR is a stress environmental factor amongst others that drives, for instance, the species-specific distribution of planktonic ciliates. For example, the common *Balanion planctonicum* is frequently found near the surface in subalpine lakes which is in contrast to alpine lakes where the species prefers to remain in the greatest depths. Assessing avoidance to minimize UV stress we found that UVR was one factor driving the distribution patterns of *B. planctonicum*. Another photoprotective mechanism in ciliates is the accumulation of specific sunscreen compounds, the mycosporine-like amino acids (MAAs). We investigated the sunscreens in several populations of a yet undescribed *Bursaridium* species in a set of lakes in the Austrian Central Alps and found that the same suite of the MAAs was also detected in the ciliates food algae. Further, we identified intraspecific variations in these populations from molecular analyses of the cytochrome c oxidase showing that at least one population differed by 24.6 %. As the latter population lives in the highest situated lake at 2,830 m a.s.l. we assume that UVR might be one factor causing this genetic variation as even cultivated specimens react different to food and light conditions in comparison to the other populations. Supported by the Austrian Science Fund FWF (P21013-B03) and the Austrian Academy of Sciences (project 'DEcadal deTECTion of biodIVErsity in alpine lakes').

Environmental differences supporting taxonomic distinction between African Bush Mangoes (*Irvingia* spp.) [Talk]

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African Bush Mangoes (*Irvingia* spp., Irvingiaceae) are priority food trees in West and Central Africa. The sweet mesocarp of the fruit is edible while a sauce prepared from the seeds forms an important aspect of the local diet in the region. However, apart from sweet fruited trees there are bitter and inedible ones, but which contain seeds of superior quality. These entities are morphologically difficult to distinguish. This has led to different opinions about the taxonomic level at which the difference should be recognized. Some prefer to recognize the two entities as different species, while others opt for the variety level. Clarity about their status is important for in- and ex-situ conservation strategies and also for future breeding and domestication programs. Furthermore, sweet African Bush Mangoes are widely cultivated in the

Dahomey Gap, the dry savannah corridor between the two West African forest blocks, but there is doubt about their natural occurrence in this region. This study evaluates the environmental differences between bitter and sweet trees as an additional and novel source of information to support a taxonomic decision. It also uses this approach to investigate the possibility that the Dahomey Gap is part of the natural distribution range of sweet trees. Data from wild occurrences were combined with climatic and soil data in Maxent to produce environmental niche models for bitter and sweet trees. Environmental niche identity tests were carried out using ENM-Tools. Wild sweet trees are predicted in the Guinean-Congolian phytogeographical region, while the predicted occurrence of bitter trees extends to the dryer Guineo-Congolia/Sudania and Lake Victoria regions. The niche difference is highly significant, supporting the idea that sweet and bitter trees belong to two different species: *Irvingia gabonensis* (Aubry-Lecomte ex O'Rorke) Baill. and *Irvingia wombolu* Vermoesen, respectively. This conclusion is also supported by a phenological study, but a molecular study using AFLPs and cpSSRs did not reveal any clear distinction. We also conclude that bitter trees occur naturally only in a small part of the Dahomey Gap: the Volta forest region, while the environmental envelope of sweet trees excludes the Dahomey Gap. This supports the idea that no truly wild sweet fruited populations are present there. Sweet trees were most likely introduced to this ecoregion by the Ibo and Yoruba tribes coming from Nigeria and migrating in a western direction.

Biogeographical and molecular phylogeny of Turkish and Iranian *Artemisia* with ITS and ETS [Talk]

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Artemisia belongs to Asteraceae, the largest family of the Eudicotyledones and is one of its largest genera with about 500 taxa. Diversity centers of *Artemisia* are mainly in Northern hemisphere in the temperate and cold temperate regions of Eurasia, North America and Asia and a limited number occur in Southern hemisphere. The genus is divided into different Subgenera or Sections depending on authors *Absinthium*, *Artemisia*, *Dracunculus*, *Seriphidium*, *Tridentatae*. To better understanding the evolutionary history of this genus, in this study we have sampled all the taxa of Turkey (26 taxa) and Iran (22 taxa) and we have sequenced them with ITS and ETS. We have included them in a large phylogeny based on published sequences from genbank with those regions. The Iranian and Turkish species of *Artemisia* belong to four subgenera: *Absinthium*, *Artemisia*, *Dracunculus* and *Seriphidium*, but the majority of them are in subgenus: *Artemisia* and *Seriphidium*. The evolutionary history of these two subgenera is different, Iranian and Turkish species in subgenus *Artemisia* have a long history with accumulation of mutation where

Iranian and Turkish *Artemisia* subgenus *Seriphidium* have known a very rapid radiation and are hardly distinguished from each other with ITS and ETS data. This study contributes to a better understanding of the phylogeny and classification of *Artemisia* and to the biogeography of this genus in the Irano-turanian region.

Understanding variation patterns and evolutionary processes in the *Alyssum montanum – A. repens* complex (Brassicaceae) [Poster]

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Alyssum montanum-A. repens complex is a group of perennial herbs with the centre of diversity in the Mediterranean. They grow in dry, exposed sites from the sea level up to the alpine belt in most of C and S Europe and adjacent regions. Their wide distribution range is joined with a considerable morphological and ploidy level variaton and numerous infraspecific taxa are traditionally recognized. The primary focus of our studies is to describe variation patterns of these taxa, to identify their evolutionary history in the context of Mediterranean refugia, as well as to propose a sound taxonomic concept of this group. Recently, we revised the circumscription of subspecies of A. montanum in C Europe and revealed their different evolutionary histories: recent expansion in widespread diploid-tetraploid subsp. *gmelinii*, increased interpopulation diversity in geographically restricted diploid subsp. *montanum*, and an allohexaploid origin of stenoendemic subsp. *pluscanescens*. One of the progenitors of subsp. *pluscanescens* is *A. repens*, confirmed to be a distinct species and comprising slightly differentiated diploids and tetraploids. We also recognized an Apennine species *A. diffusum* with three subspecies occupying distinct geographic regions: diploid subsp. *garganicum*, tetraploid subsp. *calabricum* and diploid to hexaploid subsp. *diffusum*. In our ongoing studies we focus on the populations from the Balkan and Iberian Peninsulas and from Morocco, employing flow cytometry, morphometric analyses, AFLP analyses and cpDNA sequences. Several local endemics from the Balkan Peninsula: *A. wierzbickii*, *A. reiseri*, *A. moellendorfianum*, *A. handelii* and *A. cuneifolium* subsp. *pirinicum* are confirmed to be distinct. We found a lot of variation, but no clear structure in major part of the Balkans (Bulgaria, Greece, Serbia), suggesting very complex evolutionary history in this area. Populations from the western Balkans (NE Italy, S Slovenia, Croatia, W BiH) emerged as a clearly differentiated lineage which is further structured. It is composed of two genetically and geographically separated diploids (northern and southern group) and a group of genetically admixed tetraploids (presumably allopolyploids). We provide also an insight into the cytogeography and phylogenetic relationships of populations of *A. atlanticum*, *A. cuneifolium*, *A. gadorense*, *A. loiseleurii*, *A. montanum* and *A. nevadense* in France, Spain and Morocco.

Barcoding Fauna Bavarica: Myriapoda (Chilopoda, Diplopoda) [Poster]

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An account of ongoing DNA barcoding of Bavarian myriapods (Chilopoda and Diplopoda) in the framework of the "Barcoding Fauna Bavarica" project, GBOL (German Barcode of Life) and IBOL (International Barcode of Life) is given. Our "Barcode library" currently includes over 120 species group taxa representing all chilopod and diplopod main lineages occurring in Bavaria (and Germany), often in between four and ten specimens sampled from different areas. The species stock thus comprises at the moment over 80 % of the Diplopoda and 65 % of the Chilopoda recorded for Bavaria. The current dataset of partial COI sequences leads to well supported DNA lineages in NJ and other analyses well corresponding with traditional morphological species delineations. Most of the Bavarian species in our dataset can thus be correctly identified using the DNA barcodes. Moreover our data include examples for both high and low interspecific sequence variability among closely related species, and high and low intraspecific variation as well, suggesting, *e.g.*, existence of species previously undetected by morphological analyses alone. Apart from species identification, our data seem useful for analyses of glacial and/or ongoing alpine speciation processes, species delimitation and taxonomic revisions, especially needed for the huge legacy left by, *e.g.* C.W. Verhoeff, K. Strasser, Z. Matic and C. Attems that is of peculiar importance for the whole southern German and alpine region.

Innovative digitalisation techniques for GBIF: Workstations at the Munich nodes, diplopod gonopods as a case study [Talk]

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Within the framework of GBIF-D project “Competence Centres for innovative Data Mobilization”, funded by the Federal Ministry of Education and Research (BMBF)), the GBIF-D participant nodes Fungi & Lichens [http://www.gbif-mykologie.de/], and Invertebrates II [http://www.gbif.de/evertebrata2], established several imaging workstations optimized for various types of collection objects, viz. workstations with high-performance cameras for digitalization of zoological macro and micro objects, flat and three dimensional fungal and lichen samples (herbarium sheets and three dimensional mycological/lichenological objects), and units for imaging entomological collection drawers [http://zsm-entomology.de/wiki/DScan]. Furthermore, two mobile digialisation units with integrated cameras (tablet PC, smartphone are in use. [http://wiki.gbif.de/web/Digitalisierung_an_den_SNSB]. The specification of the digitalisation units includes a short description of the workflow starting with data acquisition, management of (meta-) data with Diversity Workbench applications until the publication of image data together with quality-assured textual (meta-) data in the GBIF portal. We use the gonopod preparations of Diplopoda housed at ZSM to show how internet accessible, high resolution extended field of depth photographs, in combination with primary information on type material and old taxonomic descriptions, will enable taxonomists to reanalyse and revise the huge work left by C.-W. Verhoeff, one of the most important myriapodologists of the past who left about 10,000 specimens at the ZSM, and many more in other collections. Photo stacks of the gonopods are generated with a microscope unit configured for high resolution and depth of field. They are mounted to highest quality images by using computer programs such as Helicon Focus. These mediafiles are linked to the data records provided to GBIF via the SNSB data publisher and – in parallel – present another element of the Global Myriapod Information System (GloMyrIS; http://www.gbifev2.mwn.de/GloMyrIS/searchh_myr.htm).

Evolution of tepal morphology and pollination in Calycanthaceae [Talk]

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In Calycanthaceae, as in many early diverging angiosperm groups, tepals do not only play a role in pollinator attraction, but also in pollinator reward. Despite its very small species number (10 sp.), Calycanthaceae display two very different pollination syndromes: (1) beetle-pollination including some complex trap flowers containing well-differentiated food bodies, and (2) fly-pollination with more open flowers secreting nectar via nectarioles (small groups of cells around a nectary stomata). Beetle pollination is present in Idiospermum australiense the earliest diverging lineage, and thus appears to be ancestral within the family. In Idiospermum, non-differentiated tissues from the tepal surface are consumed by the beetles. Floral organs in Calycanthaceae exhibit conspicuous movements during anthesis that differ between species, even between species with similar pollinators. Differences in pollination are also accompanied by striking differences in phenology in temperate species: beetle pollinated species flower in late spring-early summer, whereas fly-pollinated species flower in mid autumn or mid-late winter. How did food bodies and nectarioles evolve? Are they homologous? How can floral organ movements be best interpreted functionally? How did the change in phenology evolve? Were there features exapted from one syndrome to the other? To address these questions we used a broad range of methods. Serial sectioning and scanning electron microscopy allowed us to gain detailed understanding of the histology and morphology of the tepals differentiations, and allowed us to hypothesize origins for nectarioles and food bodies. High resolution X-Ray computed tomography (HRXCT) allowed to model three-dimensional changes accompanying pollination syndrome transition and to understand the intricate interplay of the different floral organ in the complex trap flowers in an unprecedented fashion (presence of a “pollinator torus” in male stage

Calycanthus flowers, just below the anthers). Finally, ancestral character state reconstruction allowed us to understand the evolutionary history of these complex characters sets (histology, morphology, floral movements, 3d floral arrangement, and phenology), and diversification rate analysis allowed us to understand their relative species richness, thus emphasizing the power and necessity of integrated research approaches.

X-ray tomography of plant tissue: novel staining methods allow high resolution imaging [Poster]

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Study of plant morphology, development, function, and ultimately evolution, requires detailed three-dimensional visualization and modelling. X-ray microtomography (micro-CT) allows straightforward visualization and modelling of complex plant and animal objects. However, the low absorbance of most plant tissues has earlier been an obstacle for the use of this method in plant sciences (with the notable exception of wood and permineralized, or charcoalified fossils). Here we present several staining methods allowing obtention of high contrast and high resolution reconstructions of any plant tissue/organ using a commercial MicroCT system. Stains were selected from the transmission electron microscopy literature. Fixed material of *Arabidopsis thaliana* flowers were infiltrated for 12h to a week. We quantified: (1) contrast improvement, (2) homogeneity of the stain, (3) penetration of the tissue, and (4) selectivity of stain. The studied samples proved unequal in their performance. If (1) all stains allowed for improvement in contrast, improvement was however especially noticeable with KMnO4, PbCit, BiTart, OsO4, and PTA. (2) Homogeneous staining was allowed by: I3, BiTart, OsO4 (small objects), PbCit (although often with precipitates), PTA, and UAc. (3) Penetration of the tissue was best with I3, PbCit, BiTart, PTA, and UAc (the latter improved by two times dilution of the solution in methanol). (4) Highly selective staining as such was not obtained. However, noticeable staining for pollen was obtained with I3, OsO4, PTA, UAc; for stigmata with: I3, OsO4, PbCit; for ovules with: I3, BiTart, PbCit, PTA, UAc; for vasculature with I3, OsO4, BiTart, PbCit, PTA, UAc; for cell walls with: OsO4, BiTart, PbCit, PTA, UAc; for cell nuclei with: UAc, PTA. Staining methods, by allowing straightforward imaging of fixed floral material, open a broad field of possibilities. For instance, this method can be applied to the study of quantitative traits that can be regressed against gene expression or sequence polymorphism data. Micro-CT can also be applied to samples that are difficult to study via serial sectioning or electron microscopy. Moreover it can also be applied to the study of pollination, where precise 3d matches between pollinator and flower morphologies can be quantified.

Software bugs and identification of mislabeled sequences [Talk]

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Because of the molecular data avalanche that is generated by next generation sequencing technologies, input datasets are growing at a rapid pace, analysis pipelines are becoming ever more complex (and error-prone), and whole-genome phylogenetic analyses require the use of supercomputers. In other words, phylogenetic inference is rapidly transforming into a computational science such as, for instance computational astrophysics or fluid dynamics. Therefore, our field is now facing similar challenges with respect to reproducibility of results, exchange of data, and code verification. In this talk I will address the difficulties and challenges inherent to this paradigm shift and provide examples for spectacular bugs in phylogenetic inference and tree visualization programs that are typically and unfortunately used as black boxes. Morever, I will outline how using parallel computing for computing the likelihood on large, whole-genome, alignments, makes reproducing results almost impossible. Finally, I will briefly outline some preliminary work on identifying mislabled GenBenk sequences using phylogenetic methods.

Utilization of shell morphometrics in North Atlantic Scaphopoda (Mollusca) [Poster]

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Scaphopod molluscs live burrowing in marine sediments, from the intertidal to the deep-sea. Less than 600 recent species are recognized and separated mainly by characters of their tubular shell. In addition to the texture, number of and changes in the longitudinal sculpture, shell shape is an important species delineator. Shell measurements are of particular interest in species of the Gadilidae with shells also tapering towards the anterior end implying finite growth. The North Atlantic gadilid fauna is incompletely known and explored with morphometric tools. This preliminary study demonstrated the potential and the pitfalls of shell morphometrics in gadilid scaphopods. Emerging systematic questions of reliable taxon delineation and identification in the genera *Cadulus* and *Siphonodentalium* are being discussed.

Evolutionary dynamics in disjunct populations of the peat moss *Sphagnum subsecundum* [Talk]

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Genetic and morphological similarity between populations separated by large distances may be caused by frequent long-distance dispersal or retained ancestral polymorphism. It has recently been shown that gene flow has occurred several times throughout history among populations of various peat mosses (*Sphagnum*) separated by the Atlantic ocean. In the present study we explore evolutionary patterns and dynamics in disjunct populations constituing the “Pacific Rim” clade of *Sphagnum subsecundum*. It has been suggested that morphological variation within this clade may reflect the existence of more than one species. Extent of long-distance dispersal, likely glacial refugia, patterns of taxon divergence and processes causing such divergence in Pacific Rim plants are analysed using molecular markers, and the results from these analyses will be presented.

Skeletal morphology and growth of freshwater stingray *Potamotrygon falkneri* (Chondrichthyes, Myliobatiformes) [Poster]

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The South American freshwater stingray family Potamotrygonidae (Neoselachii; Chondrichthyes) consists of four well-established genera: *Heliotrygon*, *Plesiotrygon*, *Potamotrygon* and *Paratrygon* which are represented by numerous species of uncertain taxonomic status. The *Potamotrygon falkneri-castexi-menchacai* complex recently has been re-analysed and has been considered a single species, *Potamotrygon falkneri*. Here, we present a morphological study of juvenile and adult specimens representing three different growth stages. The neurocranium, the synarcuale and total length of specimens were measured to obtain more information about growth trajectories of this species. Data were transformed into percentage of disc width (%DW) to allow direct comparisons with other stingrays in previous but also forthcoming studies. Fin rays and vertebrae counts were conducted based on radiographs. Skeletal structures are analysed in detail and comparatively described for the first time. Additionally, dermal denticles of three different regions of juveniles and adults were examined. Main results of this comparison are: 1) proportions of the neurocranium differ with age; 2) dermal denticles in different body regions but also different growth stages differ; 3) identification of characters with phylogenetic importance (*e.g.*, fusion pattern of the first ceratobranchials, connection between pro-, and mesopterygium, lateral expansion of radials, dermal denticles); 4) significant morphological changes of the clasper organ and posteriormost pelvic radial during growth, and 5) increase in tooth row number during growth. Examination of different growth stages of a single species thus has high potential for estimating ontogenetic similarities and providing information about the phylogenetic signal of characters.

Platyzoa – a monophyletic group or a long-branch artifact? [Talk]

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Lophotrochozoa, one of the three major bilaterian taxa, comprises several worm-like taxa. The relationship of these taxa to each other is still unresolved. One taxon within Lophotrochozoa, which has been proposed based on morphological data, is Platyzoa comprising Platyhelminthes, Gastrotricha, Syndermata and Gnathostumulida. Platyzoan taxa are generally direct developers, lack a vascular system and their worm-shaped body is usually ciliated, flat and non-segmented. However, unique morphological autapomorphies supporting the monophyly of Platyzoa are lacking. Recent phylogenomic results showed some progress and generally placed monophyletic Platyzoa as sister to the other lophotrochozoans. However, the inclusiveness and monophyly of Platyzoa as well as the relationships of the platyzoan taxa is still controversial. Moreover, substantial support for platyzoan relationships is still lacking even in these recent phylogenomic studies. This is, among other reasons, due to the facts that all taxa exhibit long branches and that several taxa such as Gnathostomulida and Gastrotricha are only poorly covered with respect to taxa and number of analyzed genes. To address these issues we generated large EST databases using next generation sequencing technologies for four gastrotrichs, one gnathostomulid, three syndermatans and two platyhelminths. We will present the results of our phylogenomic analyses based on a better taxon sampling of platyzoans as well as substantially increased data coverage.

Hyles euphorbiae (Lepid.: Sphingidae) cold adaptation: Proteomic and transcriptomic candidate biomarker identification [Poster]

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Hyles euphorbiae inhabits large parts of the Palaearctic ranging from the Iberian Peninsula to Southwestern Siberia. Overwintering diapause pupae are exposed to extremely different temperature regimes across their large distribution area, ranging from mild average 11°C during winter in the Mediterranean climate to an average of −23°C or below in Siberia. In order to understand to what extent processes such as phenotypic plasticity of freeze protection mechanisms or local adaptation to freezing winter temperatures may explain the current geographic distribution of *Hyles euphorbiae*, we are interested in molecular mechanisms underlying cold adaptation. Embedded in an evolutionary/ecological context, this research aims at identifying molecules that are differentially expressed after gradual cooling of diapause pupae from 20°C to below 0°C (cold treatment). These represent candidate biomarkers to study diversification and speciation processes in the *Hyles euphorbiae* species complex (HEC). Cold treated and untreated reference specimens were compared using a proteomic approach based on two-dimensional electrophoresis of protein extracts from whole pupae. Differentially expressed protein spots were analysed by tandem mass spectrometry and this allowed identifying 13 distinct proteins involved in biological processes such as lipid transport, cytoskeleton and muscle assembly, chitin and cuticle assembly, metabolism, protein translation, and response to oxidative stress. We further investigated whether the activation of these biological processes is also reflected by gene expression profiles based on the transcriptome by performing SuperSAGE for the same specimens as used for proteomics. The main goal of this analysis was to estimate the amount of differentially expressed genes that are annotated by the same gene ontology terms (GO-Terms) as the 13 differentially expressed proteins. This approach revealed that related GO-Terms were also found to be significantly enriched among differentially expressed genes, *i.e.* activation of the same processes is also detectable in gene expression profiles at the RNA level.

Interpretation of patterns of genetic variation within endemic plant species of oceanic islands [Talk]

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Oceanic islands offer many opportunities for understanding patterns and processes of evolution. The availability of molecular markers in recent decades has opened up avenues for using population genetics as a means of revealing aspects of divergence and speciation. With such powerful tools, the challenge becomes now to explain more effectively the causes for the observed genetic patterns. A common pattern seen in taxa of oceanic islands is lowered levels of genetic variation within and among populations. The often invoked explanation for this observation is the founder effect, whereby the successful colonizer contains a restricted range of genetic variation in comparison with that in populations of the continental progenitor. Through time, however, *i.e.*, over millions of years, the original signature from the founder effect will normally be erased, due to mutation, recombination, drift, and selection. The types and degrees of genetic modifications that occur, therefore, must be due to other factors, all of which should be considered at least initially in attempting to explain patterns of genetic variation. The age of the island is extremely important, because oceanic islands subside as the submarine plates subduct under adjacent continental plates. With this subsidence also comes erosion due to wind, rain, and wave action, which grind down the relatively soft volcanic substrates (excepting basalts that usually remain as resistant ridges). The mode of speciation is also of significance. With anagenesis, genetic variation continues to accumulate through time, whereas with cladogenesis the gene pool is continually split into populations of adaptively radiating species. Biological characteristics of the island taxa also will impact levels of genetic variation, with breeding system, population size, and habit (relating to generation time) being especially important. Hybridization between closely related taxa is another factor that can affect levels of genetic variation within and among populations. Finally, human disturbance has been considerable in oceanic islands, resulting in harvesting of forests and species of economic value, introduction of domestic animals, and inadvertent introduction of invasive plants. Explanation of observed levels of genetic variation within introduced, native, and endemic species of oceanic islands, therefore, requires consideration of many interconnected physical, biological, and anthropomorphic factors.

Novel insights into the Mesozoic paleobiogeography of extant birds [Talk]

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The historical biogeography of extant birds during early avian evolution is poorly understood. This is largely due to the fact that the long-lasting uncertainty in avian systematics has so far hampered the reconstruction of the historical geographical ranges of ancestral bird species. The very recently established robust consensus between nuclear sequence-based and retroposon-based phylogenomics finally provides the unique opportunity to infer the paleobiogeographic events that occurred throughout certain parts of early bird evolution. Here I show that, using parsimony and Bayesian methods for ancestral area reconstruction, it is possible to congruently reconstruct vicariance or dispersal events that have led to extant birds' distributions and date back to the Mesozoic part of their evolution. My results show that most extant bird taxa originated in certain parts of the former supercontinent Gondwana. Furthermore, the paleobiogeographic reconstructions suggest that during the Upper Cretaceous, several vicariance or dispersal events between different continents occurred. This includes a potential migration from South America to Africa and a subsequent potential migration from Africa to South America.

On input and output in phylogenetic inference [Talk]

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Phylogenetic reconstruction uses Darwins "descent with modification" as background knowledge. Both model based approaches and parsimony make use of a character concept to reconstruct hierarchical, phylogenetic relationships among taxa. In both approaches each single phylogenetic character constitutes a transformation series. The two approaches, however, deviate from each other in underlying assumptions. Parsimony analyses use the differential distribution of states of characters as evidence. They thus encompass homology hypotheses for each single character state. To fit the demands of phylogenetic inference, Szucsich and Wirkner proposed a restriction of the homology concept to hypotheses that explain certain correspondence by maintenance along diverging lineages, thus representing hypotheses of "descent without modification". The proposed phylogenetic character concept now combines such homology hypotheses with hypotheses of evolutionary transformations. The latter serve as explanations for the observed variation among states of a phylogenetic character. They thus incorporate "modification" into the background knowledge of phylogenetic reconstruction. Such transformations now can be used as evolutionary events, which can be assigned as unambiguously as possible to concrete periods of a genealogical tree. A transformation, unambiguously assigned to an internal branch then represents a synapomorphy, which supports monophyly of groups of organisms. To allow an assignment to a concrete lineage characters in parsimony have to meet some basic demands. The use of parsimony as an optimality criterion for phylogenetic reconstruction is sufficiently justified since it represents the synthesis among all homology and transformation hypotheses of the data matrix. Model based analyses do not necessitate homology hypotheses for corresponding patterns within a single character, but assume that evolution can be approximated by a model of evolution. Maintenance and transformations are modeled with a likelihood function. This demands for a limited set of possible transformations. The character concept in model based methods and in parsimony encompasses many common assumptions and hypotheses. Only in parsimony approaches, the reconstruction of a matrix encompasses character specific hypotheses of character state homology. In contrast model based analyses demand for an assumption of a model of evolution, generalized over the entire set of jointly analysed characters.

Patterns of gene flow between *Dactylorhiza allopolyploids* with focus on alpine hybrid swarms (Orchidaceae) [Talk]

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Hybridization and genome doubling regularly stimulate evolution in flowering plants, most probably starting with their origin. Multiple origins are the rule for most allopolyploids and iterative allopolyploidy often results in substantially different lineages. It is interesting how such species can maintain distinctiveness while sharing the same genetic heritage and ploidy level. Allopolyploids *Dactylorhiza majalis* s.s., *D. traunsteineri* s.l. and *D. ebudensis* have been independently formed through unidirectional hybridization between the widespread diploids *D. fuchsii* and *D. incarnata*. Differing considerably in morphology and ecological tolerance, the two allopolyploids *D. majalis* s.s., and *D. traunsteineri* s.l. are distributed across Europe, covering areas in which they are sympatric (Alps), parapatric (Scandinavia) and allopatric (*e.g.*, Pyrenees with *D. majalis* only and Britain with *D. traunsteineri* only), whereas *D. ebudensis* is found only on the Scottish island of North Uist. In the context of their similar genomic background, our previous studies have consistently found their patterns of gene expression and DNA methylation to have been shaped by divergent selection in response to environmental pressures. By using nuclear microsatellites we investigated the patterns of gene flow between those sibling allopolyploids at different localities in Europe. Our first results show no genetic differentiation despite the visible phenotypic divergence between the allopolyploid lineages. The results indicate that populations in the Alps and Scandinavia function as hybrid swarms with potential implications for the genetic patterns of these species across their entire distribution. The weak genetic differentiation and the presence of gene flow between the allopolyploids point toward a very strong divergent selection required in order to maintain the observed phenotypic divergence. Additional indirect conclusions can be formulated regarding the apparently limited homoeologs repatterning that affected the allopolyploids, a mechanisms that can result in reproductive isolation between recurrently formed allopolyploids.

ForBio – The Research School in Biosystematics [Poster]

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ForBio is a network-based research school to advance PhD education in biosystematics in Scandinavia. The research school was initiated by the four Norwegian university museums and it is open for membership to Norwegian, Swedish and Danish PhD students and postdocs. Our ambition is to train a new generation of biosystematists to meet the society's needs for biodiversity expertise and at the same time to strengthen the research in biosystematics in Scandinavia. To achieve that, we offer a wide range of both practical and theoretical courses in biosystematics and provide a platform for facilitating teaching and research collaboration between Scandinavian research institutes. Our courses can also be attended by professionals working in relevant fields (nature management, governmental offices, independent research institutions) and students at non-Scandinavian universities. ForBio to date has about 120 members and 50 associates.

Of hot spots and white spots – Species diversity in aplacophoran mollusks [Talk]

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The aplacophoran molluscs (Solenogastres and Caudofoveata) are two of the so-called minor mollusk taxa, pointing to their relatively low species diversity (about 350 and 250 species, respectively). A current project investigates the diversity and distribution of aplacophoran species in Norwegian waters. The first year focused on the Western Norwegian coast, the North Sea and the Norwegian Sea. About 600 lots of specimens were sorted and identified. Within the 37 species encountered, there were two species of Solenogastres new to Norway and 17 species new to science. The new species come from both the relatively well known coastal areas as well as the deep Norwegian Sea. Including the new findings, the Norwegian solenogaster fauna thus contributes almost 10 % to the total global diversity. Other "hot spots" of diversity are Antarctica, the Mediterranean Sea, and the coast off Galicia (Spain). For Australian waters, in contrast, there are less than ten species of aplacophoran mollusks described. But does our current knowledge reflect in any way real patterns in diversity and distribution? Results of the current Norwegian project are presented and aspects of global species distribution are discussed.

Molecular systematics and phylogeography of the snorkel snails genus *Rhiostoma* (Cyclophoridae) from Thailand [Talk]

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The snorgel snails genus *Rhiostoma* Benson, 1860 are endemic to Southeast Asia with the peculiar characters and the extensive geographic variations. However, the shell morphology identification caused taxonomic problematic. To establish the robust phylogenetic relationships among *Rhiostoma* species, we interpreted molecular and morphological analyses of snails sampled from Thailand and nearby countries. Analyses of the mitochondrial cytochrome oxidase subunit 1 and 16S rRNA gene sequences are investigated to reconstruct the evolutionary history of the genus using neighbour-joining (NJ), maximum likelihood (ML), and Bayesian inference (BI) methods. The results suggested to the monophyly, and confirmed shell morphology and the geographic isolation which supported the sister relationships such as *R. housei*, a wide ranges distribution species, *R. chupingensis*, the southern Thailand species and Malaysia, and *R. hainesi* is an endemic species only in the short range distributed areas in Thailand. In addition, the results also demonstrated the importance of geographical barriers and climatological events to species diversification and the overall geographical structure of the extant snorkel snail diversity.

Unique patterns of decapentaplegic expression in embryos of the onychophoran *Euperipatoides rowelli* (Peripatopsidae) [Poster]

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Like in other protostomes, the gene decapentaplegic (dpp) specifies the dorsal body region in various arthropods. However, the specific expression patterns of this gene vary among different arthropod groups. To clarify the conserved versus derived states and to identify potentially unique roles of this gene, the corresponding data from Onychophora (velvet worms), one of the closest arthropod relatives, are required. We therefore analysed the expression patterns of a dpp ortholog in embryos of the onychophoran *Euperipatoides rowelli*. Our data revealed no detectable levels of dpp expression in the early developing embryo prior to the formation of the germ band. However, different dynamic patterns of dpp expression occur during further development. An initial transitory domain appears in the mesoderm anlagen of the antennal segment. After this domain has disappeared, a distinct signal occurs in the dorsal and ventral extra-embryonic tissue, in the dorsal mesoderm of each developing limb, and on each side of the embryonic head above the developing lips. These findings suggest different roles of dpp in onychophoran development. While the expression in the anlagen of the first body segment might be unique to Onychophora, the involvement of dpp in limb development resembles that in arthropods, despite its occurrence in different germ layers. The expression in the dorsal and ventral extra-embryonic tissue might be also unique to Onychophora and this peculiar pattern contrasts with the assumption of a generally conserved function of dpp in dorsal patterning in protostomes. Our ongoing expression studies of the dpp antagonist short gastrulation (sog) will show whether the Dpp/Sog signalling specifies the dorsal and ventral body regions in the onychophoran embryo.

The refugial theory [Talk]

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A refugium is a geographical area where a population, species, or community has survived environmental instabilities over long periods of time. The theory suggests that existing genetic and species diversity is shaped by historical environmental changes and predicts that the long-term persistence of biodiversity is dependent on refugia. I will summarize several attempts in defining refugia, compare different approaches and point out how hypotheses of refugia can be tested with empirical biodiversity data in biogeographical research. I will also highlight how future studies might contribute to substante the general biological significance of refugia, to identify climate change refugia, and to study the evolutionary potential of and processes in refugial and non-refugial populations

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Diversity workbench – Mobilisation of high quality species occurrence data for GBIF [Talk]

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The modularised data repository platform ‘Diversity Workbench’ (= DWB) represents a highly scalable virtual research environment for bioscience and geoscience data with regard to the storage and management and elementary analysis of data. The platform includes a number of user interfaces for data curation and transfer between the individual components and for import and export of data. Data maintenance processes and data transfer between the single database components within the DWB, are exemplified by a workflow scenario in the GBIF-D context. Further, examples for data import and export of object-related and taxon-related data and terminologies are shown: • Flexible data import of observation and collection data from text files is achieved by use of a configurable data import wizard. • A data replication tool for synchronizing observational and collection data supports the maintenance of data which are stored in distributed DWB installations. • A specific user interface supports checking, validating and importing lists of taxonomic names in taxon databases. • Each component within the DWB includes functionality to search and update linked datasets from other DWB components. • Tools for georeferencing data exist. • Online name thesauri, nomenclators, species databases and Catalogue of Life data are accessible as web services. • An open access DWB installation is currently set up to provide terminologies and gazetteers (data access under common creative license) for DWB users and others. • Data may be exported in various standard markup formats. • Interfaces for user-driven export of standard data for third party wrappers exist, *e.g.* to deliver DWB content data (collection and observation data) to GBIF. DWB installations may be set up in virtualized server environments. Several are preliminarily hosted at the SNSB IT Center but administrated by GBIF-D node institutions. The service is considered a starting point for long-term cooperations between science infrastructure institutions like Natural History Collections with regard to technical and conceptual know-how transfer.

AnnoSys – A generic annotation system for biodiversity data [Talk]

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Traditionally, natural history collection objects are annotated in written form and the annotations are added directly to the specimen. Specimen annotations, *e.g.* concerning their taxonomic identity, are a quality control mechanism that improves the scientific value of herbarium specimens. However, with data increasingly becoming accessible via the Internet, the traditional flow of annotation information is currently interrupted, because on-line users of data are not able to add annotations to the digital record of the specimen and reporting them back to the original source. Currently missing is a general online annotation system that ensures the continuation of the traditional data sharing and documentation of specimen data. AnnoSys therefore develops an annotation data repository for networked and highly complex biodiversity data available via the internet. It is based on a prototype developed in the context of SYNTHESYS, but uses the W3C Open Annotation Core Data Model and Extension Specification, based on the RDF data model to store annotation information. While AnnoSys principally is open to support any kind of biodiversity data, the focus of the prototype is on collection data in the botanic domain provided by the GBIF/BioCASe system. The Annotation System combines a desktop-like user application interface with the following components: A Repository that persistently saves all annotations together with the original XML-document the annotation refers to. This allows users to compare the original record with the annotated data at the point in time the annotation was created. The repository will also provide efficient query functions to search annotations using specific criteria like specific taxonomic groups or locations. The exchange component provides an interface for downloading the original XML documents from BioCASe data providers or other sources into the repository. It is also intended to provide services allowing external systems to search and access any data stored within that repository. A message system installs information flows to notify annotators, data providers and interested users about the ongoing state of annotation workflow processes. A security component is responsible for the administration of user accounts, including secure user authentication, authorization and access rights management.

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anymals+plants – building a mobile biodiversity observation community [Talk+Software Bazar]

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anymals+plants is a social network dedicated to map the worlds biodiversity on a local level. Based on an App for android smartphones every user is informed about his local biodiversity, and given opportunity to log and share observations. Information about local biodiversity is gathered from GBIF and presented alongside with pictures, facts and its local name of every species. This information shall teach the user and thereby increase his observational capabilities. After one and a half year of operation we surpassed 70.000 downloads and 8000 contributed observations of over 1500 different species. We will present current results of the data collected so far, discuss limitations and future goals of the project.

Areas of endemism under the semantic conception paradigm [Talk]

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Historical biogeography is seeking for relationships between areas of endemism. Since its inception, many authors have debated upon their “nature”. What are areas of endemism? How to define them? According to Axelius (1991), an area of endemism is a specific combination of at least two (or more) endemic species which is the most common definition in use nowadays by biogeographers. Many others also defined areas this way (*e.g.* Humphries and Parenti, 1986; Harold and Moï, 1994). Others like Rieppel (2007) or Crother and Murray (2011) defend the theory that areas are individuals simply because species are indivuals. Here we would like to give, through an ontological reasoning, a different point of view. The philosophical semantic conception of scientific theories claims that theories are models (*i.e.* sets of objects and relations with logical constraints). We present an alternative evolutionary model accounting for areas. We demonstrate the consistency of this model according to the ontology it provides, the interdisciplinary it accounts for (*i.e.* reduction of historical biogeography and temporal dimension to the same model) and towards the faithfulness of the “adequacy to reality” protocol.

Xper3: Introducing social taxonomy [Poster & Software Bazar]

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The deep social and scientific impact of web 2.0 stimulates sharing of digital data and proposals of ‘cybertaxonomy’ projects to study global biodiversity and climate changes. The generalization and the integration of knowledge-base management systems into current taxonomic work may be the next revolution in taxonomy. International projects are already opening the way for this new, delocalized taxonomy. As a web 2.0 counterpart of Xper2, Xper3 comes with all of Xper2s’ features and is inherently collaborative: users can edit, analyze and share their descriptive data online Furthermore, Xper3 introduces several new features such as the possibility to create calculated descriptors, a more efficient data storage solution (SQL-compliant Relational databases) and the interactive identification (*i.e.* multiple-access keys) through a web-service. The Xper3 data model is closely based on the SDD (Structured Descriptive Data) format, which makes it compatible with any other application using this standard format. Xper3 is still in its early development states, we will demo the descriptive data edition interface this week, and a full-featured demo version will be released in 2013.

Speciation under gene flow? The case of *Mauremys caspica* and *M. rivulata* [Talk]

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The stripe-necked terrapins *Mauremys caspica* and *M. rivulata* are a sister species occupying a similar ecological niches and occurring in more or less mutually exclusive parapatric distribution ranges. The ranges of the two species are forming a narrow contact zone over hundreds of kilometres. We used 13 quickly evolving microsatellite loci and five nuclear genes for gaining insights in gene flow and hybridization of 13 populations of *M. caspica* and 18 populations of *M. rivulata* from the contact zone and compared these to randomly chosen individuals from the whole distribution range of each species.

The undiscovered world of tropical ichneumonid parasitoid wasps (Hymenoptera) [Talk]

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The megadiverse parasitoid wasp family Ichneumonidae has been thought to have an anomalous latitudinal species richness gradient. Especially the koinobiont (specialist) groups have been found to be more species rich in temperate than tropical latitudes. However, recent studies have questioned this classic assumption. Here, I demonstrate which koinobiont subfamilies may have a regular species richness gradient in the Western Hemisphere based on relative abundance data from the southern US, Central America, and western Amazonia. I also show that additional sampling in tropical forests can reveal reservoirs of very high unknown ichneumonid diversity. As an example, I present a study which found over 170 undescribed Neotropical orthocentrine species. This is over three times the number of all currently described tropical orthocentrine species. I conclude that the difficulty in establishing species richness patterns of Ichneumonidae probably follows from the relative lack of taxonomic expertise and the low density of ichneumonid species throughout the landscape.

Heritable responses of plants to stress exposure [Talk]

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When faced with a rapidly changing environment, epigenetic inheritance and heritability of stress-induced phenotypes may be relevant responses at a scale that is intermediate between within-individual phenotypic plasticity (short-term and dynamic) and genetic population adaptation (long-term and more stable). Epigenetic mechanisms such as DNA methylation are often proposed as candidate mechanism for transgenerational effects, either as a cause of shifted offspring trait means or increased trait variation after stress exposure in previous generations. However, current evidence for methylation-mediated and multi-generation persistence of transgenerational effects is limited. I will present our work on heritable effects of stress exposure in plant lineages that lack genetic variation, apomictic dandelions and inbred Arabidopsis. Lacking genetic variation, such model systems are suitable for exposing the effects and determining the ecological relevance of epigenetic inheritance. In the dandelion system we explore heritable effects of stress exposure on DNA methylation, transcriptome, metabolome and trait levels. In Arabidopsis we used a four-generation experimental design to assess transgenerational effects of parental salt stress on offspring performance under field conditions, with explicit tests of multigenerational persistence of induced effects and also of the effect of multiple subsequent generations of stress exposure on subsequent expression of transgenerational effects.

Colour polymorphism in common primrose (*Primula vulgaris* Huds.): many colours – many species? [Talk]

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Primula vulgaris exhibits flower colour polymorphism in the eastern part of its range, especially pronounced on the NE coast of the Black Sea. This polymorphism in the Caucasian populations has been taxonomically described and some segregated species are listed as rare and endangered. We used sequence variation in two chloroplast noncoding regions (trnL-trnF and rpl32-trnL) and the complete nuclear internal transcribed spacer (ITS) of ribosomal DNA region to investigate correspondence between flower colour and geographical distribution of both nuclear and chloroplast haplotypes. It appears that variability in these DNA regions does not correlate with flower colour, being, however, clearly structured geographically. We used nested clade analysis (NCA) to explore this geographical structure. It seems that the territory of the *Colchis refugium* on the E coast of the Black Sea contains both the highest flower colour and haplotype diversities. The results suggest that common primroses colonized the NE coast of the Black Sea from this refugium, spreading along the coast westward. At the same time, the analysis of ITS haplotypes indicates that P. vulgaris colonized the Crimea from NW Anatolia. This makes it clear that no segregated species can be recognized within flower colour polymorphic *P. vulgaris* in the Caucasus region. However, its phylogeography needs further detailed study on a broader scale.

Diversity of wood-inhabiting Basidiomycetes in deciduous forests of the Orel region (the Central Russian Upland) [Talk]

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Wood-inhabiting fungi, primarily polypores and corticioid Basidiomycetes, represent one of the key heterotrophic components which provide the process of plant destruction, dead organics utilization and matter and energy cycling in forest ecosystems. The Centre of European Russia has a long history of economic developing lands (incl. deforestation and urbanization), being the territory with deciduous forest type of vegetation initially. The diversity of lignicolous fungi has been investigated within the Orel region as a model area where this group was unstudied until recently. Fruit bodies of Basidiomycetes were collected by route approach and identified according to macro- and microscopic features. Sampling was taken in natural and artificial forests (52°39' – 53°25' N, 35°13' – 37°15' E) principally with *Quercus robur*, *Tilia cordata* and *Betula pendula* domination. To date a total of 304 species from 106 genera, 39 families and 20 orders are known for this territory. The most frequent species belong to genera *Antrodiella*, *Bjerkandera*, *Byssomerulius*, *Cerrena*, *Cylindrobasidium*, *Daedeleopsis*, *Fomes*, *Fomitopsis*, *Ganoderma*, *Hymenochaete*, *Oxyporus*, *Peniophora*, *Phellinus*, *Phlebia*, *Piptoporus*, *Polyporus*, *Radulomyces*, *Schizopora*, *Steccherinum*, *Stereum*, *Trametes*, *Xylodon et al.* Among detected fungal diversity a number of species, *e.g. Crustomyces expallens*, *Perenniporia narymica*, *Protomerulius caryae*, *Pseudocraterellus undulatus*, *Tomentella pilosa*, are recorded as rare and occasional for Europe. More than 70% of species revealed were found on fallen trunks, logs and twigs of deciduous trees and shrubs. Species richness of wood-inhabiting Basidiomycetes at all of localities observed depended on mainly a quantity of coarse woody debris (CWB), an ecosystem disturbance level and a presence of azonal or introduced wood flora elements that can have distinctive fungal consors. Ecological conditions which influence species richness of lignicolous fungi, their distribution and occupation of diverse substrate types are taken into account. The study was supported by The Ministry of education and science of Russia, project 14.132.21.1328, and by the Russian Foundation for Basic Research, project 12-04-31867.

Lineus viridis (Nemertea) comprises two cyptic species with a global distribution along the northwestern European coast [Talk]

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Until the 1960s *Lineus ruber* and *Lineus viridis* were regarded as color variants of a single species by most nemertean researchers. Further studies conducted at the French coast (Roscoff and Dinard) revealed differences in some biological aspects in these variants including spawning and development. They were subsequently considered as separate species. Although the color differences were assumed to be reliable species identifiers, with *L. viridis* having greenish and *L. ruber* having reddish body colorations, all kinds of green-brown and red-brown intermediates can be found in the sampling areas along the central-European Atlantic coast. A comparative survey of the population structure of both putative species on French and the German coasts was conducted using mitochondrial (COI) as well nuclear (ITS) markers to avoid data misinterpretation due to mitochondrial introgression. The sequence data show that while all *L. ruber* specimens analyzed belong to a single species, L. viridis is a complex of two cryptic species. The data also show that *L. ruber* is not present in the North Sea and further elucidated the population structure of both species of L. viridis. Members of both *L. viridis* species were found at every sampling site along the continental western European coast including Brittany (France) and Sylt Island (Germany). Their coloration always exhibits a similar range of variation. The study shows that (1) mitochondrial and nuclear marker sequences successfully allow species delimitation and identification, (2) color patterns are not reliable for species identification, and (3) sequence data reveal two cryptic species in these lineid heteronemerteans.

Robustness of phylogenetic inference [Talk]

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Among the criteria to evaluate the performance of a phylogenetic method, robustness to model violation is of particular practical importance as complete a priori knowledge of evolutionary processes is typically unavailable. For studies of robustness in phylogenetic inference, a utility to add well-defined model violations to the simulated data would be helpful. We therefore introduce ImOSM, a tool to imbed intermittent evolution as model violation into an alignment. Intermittent evolution refers to extra substitutions occurring randomly on branches of a tree, thus changing alignment site patterns. This means that the extra substitutions are placed on the tree after the typical process of sequence evolution is completed. We then study the ro- bustness of widely used phylogenetic methods: maximum likelihood (ML), maximum parsimony (MP), and a distance-based method (BIONJ) to various scenarios of model violation. Violation of rates across sites (RaS) heterogeneity and simultaneous violation of RaS and the transition/transversion ratio on two nonadjacent external branches hinder all the methods recovery of the true topology for a four-taxon tree. For an eight-taxon balanced tree, the violations cause each of the three methods to infer a different topology. Both ML and MP fail, whereas BIONJ, which calculates the distances based on the ML estimated parameters, reconstructs the true tree. Finally, we report that a test of model homogeneity and goodness of fit tests have enough power to detect such model violations. The outcome of the tests can help to actually gain confidence in the inferred trees. Therefore, we recommend using these tests in practical phylogenetic analyses.

First venomous crustaceans: transcriptome profiling and 3D reconstruction of the venom glands of cave dwelling Remipedia [Talk]

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Venomous animals are ubiquitous in aquatic and terrestrial habitats across the world. However, our understanding of fundamental issues about the biology and evolution of venoms and venomous organisms is incomplete because the main empirical pillars of venomics – the scientific study of venoms – are currently limited to a few well-studied taxa such as spiders, scorpions, reptiles and cone snails. In order to broaden and strengthen the foundation of venomics, a renewed focus on neglected putatively venomous taxa is needed, especially on taxa that are distantly related to known venomous species. In this respect aquatic cave dwelling remipede crustaceans are an extraordinarily promising group, as Crustacea is the only major traditional arthropod lineage that lacks known venomous species. We present here the first 3D morphological reconstruction of the venom apparatus of remipedes, as well as a transcriptomic profile of genes expressed in their putative venom glands based on next generation sequencing. The results shed new light on the convergent recruitment of venom toxins in the animal kingdom.

Sea cows through time and space – a new classification concept for the order with biogeographic implications [Talk]

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Sirenia, or sea cows, are a group of mammals, which have a long and rich fossil record dating back into the early Eocene and reflect the transition to fully aquatic life-styles as one of the best-documented examples in vertebrate evolution. Sirenians were and still are a common part of tropical and subtropical shallow-water environments and are well-known from Africa, North America and Europe. They were most divers during the Oligocene and Miocene often characterised by short sympatric offshoots of particular taxa. While the monophyly of sirenians is well supported by morphological and molecular data, the systematic relationships of different groups within the Sirenia are still obscure. There have been made very few changes to the traditional classification concept of Sirenia in the past, which considers four families: the "Prorastomidae" and "Protosirenidae" that are extinct and restricted to the Eocene, and the "Dugongidae" and Trichechidae that have extant representatives. Of these families, the "Dugongidae" are the most diverse and successful sirenian group, but conspicuously paraphyletic including the exclusively extinct subfamily "Halitheriine" that comprises a number of genera that are invariably paraphyletic, too. This study presents the morphology based results of the taxonomic revision of the genus *Halitherium*, which forms the basis for the establishment of the subfamily "Halitheriinae". For this purpose, abundant skeletal material originally assigned to this taxon was reinvestigated or initially examined. Additionally, as many taxa for comparison as possible were investigated to produce a revised, supplemented and extended character-taxon matrix resulting in the largest data set on Sirenia so far. The subsequent phylogenetic analysis using robust cladistic principles reveals that the main nodes of the resulting phylogeny are well supported by synapomorphies. However, the terminal taxa are mainly defined on the basis of homoplasies, which reflect the common adaptation of these mammals to a life in water. Moreover, the revision of the genus *Halitherium* combined with biogeographic data provides new implications for the taxonomy and systematics of Sirenia on a larger scale. The necessity of an expansion of the taxonomic concept of Sirenia to abandon the traditional suprageneric classification is underlined here.

Floral cups in Rubiaceae. A developmental model [Talk]

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According to a developmental model worked out by Leins and Erbar (2010), different kinds of floral cups such as perianth tubes, hypanthia, and also phenomena such as gynophores or androgynophores can be explained by the activity of annular or disc-shaped intercalary meristems in the floral axis, just below the respective whorl of floral primordia. In Rubiaceae, floral cups are present in the form of calyx and corolla tubes. In the past, based on ontogenetic investigation of the corolla tube, three developmental character states were defined: early and late sympetaly, and the transition between both. Moreover, it became clear that in some Rubiaceae, the corolla tube actually is a stamen-corolla tube. Despite these observations, it remained difficult to understand the varying superposition of the stamens on the corolla tube or at its base, or other corolla phenomena such as corolla splits. As for the calyx tube, few developmental data are available. Therefore, we studied the development of calyx, corolla and androecium in strategical species of Rubiaceae in order to test the developmental model for floral cups of Leins and Erbar. Our observations make us conclude that a rubiaceous tubular corolla essentially consists of a combination of a corolla tube sensu strictu and a stamen-corolla tube, each formed from a proper annular intercalary meristem, and with, in some species, on top of these also a postgenitally formed corolla tube (by fusion of corolla lobes). Depending on the proportions of each, the stamens can be attached at the base of the tubular corolla or higher up. In species with corolla splits, the ontogeny of the tubular corolla affects the formation and position of the splits. Early sympetaly and the ‘transition’ between early and late sympetaly can also be explained by the activity of an underlying intercalary meristem.

Secondary Metabolites versus Kleptocnides in Cladobranchia (Nudibranchia, Gastropoda) [Talk]

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The lack of a physical defence in soft bodied animals usually leads to the evolution of diverse alternative defensive strategies. We investigated the strategies in the nudibranch taxon Cladobranchia and could detect following: secondary metabolites are sequestered from the food, or a de novo synthesis occurs. Another strategy is the incorporation of functional cnidocysts. Cladobranchia feed on a high variety of cnidarian species, which commonly exhibit a functional cnidom for capturing prey organisms or for defence. However, this is not the case for many soft corals (Octocorallia), which seem to produce defensive natural products instead. In contrast, Hydrozoa are usually considered to exhibit a functional cnidom, but nearly nothing is known about their ability to produce natural products. In this contribution, results on these specific defence mechanisms are shown for several cladobranch species in relation to their food organisms. According to our knowledge on cladobranch phylogeny and food organisms, a preliminary evolutionary scenario of defensive strategies will be outlined.

Disentangling complex biogeographic patterns in *Hoya* (Apocynaceae): when taxon sampling obscures phylogenetic signals [Talk]

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Hoya is a species-rich, mostly epiphytic genus within tribe Marsdenieae (Apocynaceae) that occurs in tropical and subtropical forests of the Indomalayan and Australasian realms, including the Indo-Australian Archipelago (IAA). Earlier studies have reconstructed a general phylogenetic structure within the genus, but also reported incongruences between nuclear and plastid DNA markers. Here I show how the use of a necessary large taxon sampling in combination with genetic incongruence can influence even more negatively the reconstruction of phylogenetic inference. These problems can be overcome by the exclusion of rogue taxa from the data set and the subsequent analysis of general molecular differentiation patterns. I present a hypothesis on how *Hoya* has evolved and diversified in the tropical forests of the IAA region and I propose possible ecological and morphological parameters forming the base of biogeographic patterns.

The larvae of *Drusus franzressli* Malicky and *D. spelaeus* (Ulmer) – newbies in the Drusinae grazer clade [Poster]

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The poster gives a description of the hitherto unknown larvae of *Drusus franzressli* (Malicky 1974) and *Drusus spelaeus* (Ulmer 1920) which belong to the grazer clade of subfamiliy Drusinae (Trichoptera: Limnephilidae). Information on the morphology of the larvae is given and the most important diagnostic features are illustrated. In the context of already available keys, the larvae of *D. franzressli* and *D. spelaeus* key together with *Metanoea flavipennis* (Pictet 1834), *M. rhaetica* Schmid 1955, *D. improvisus* McLachlan 1884, *D. nigrescens* Meyer-Dür 1875 and *Ecclisopteryx malickyi* Moretti 1991. The species of this group may be easily separated by differences in dorsal outline and sculpturing of pronotum, presence/absence of lateral gills at 2nd and 3rd abdominal segments, start of lateral fringe and distribution. With respect to distribution, *D. franzressli* is a large-scale endemic species of the Hellenic western Balkan, whereas *D. spelaeus* is an endemic of the western Alps (Grenoble area).

DiversityMobile – Recording and Processing Data in the Field via Smartphone [Software Bazar]

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DiversityMobile is a smartphone application, designed for monitoring ecological and biodiversity data in the field. It is a component of the modularised Diversity Workbench (DWB) framework for the management of biodiversity and environmental research data. DiversityMobile is implemented for the Windows Phone versions 7.5 to 8 and uses GPS functionality as well as digital imagery, audio and video recording options. A sophisticated user interface design facilitates the gathering and storage of monitoring and ecological data in the field, independent of a given internet connection. The user interface is highly configurable and accesses a range of web services provided by the SNSB IT Center (Bavarian Natural History Collections), which include taxonomic name lists, digitized topographic maps and various terminologies as well as data from previous gatherings. Gathered data and assigned multimedia objects may be submitted to a data repository via WebServices. DiversityMobile users are encouraged to subsequently process their field data in the laboratory using DWB managing components to a) optimize them for subsequent analysis using specific software and b) forward them to information platforms for data publishing. The application is freely available at the Windows Phone Marketplace.

Exploring the methylome: A new DNA methylation-enrichment-bisulfite-sequencing method (MEBS) [Talk]

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DNA methylation plays a key role in epigenetic regulation, increasing the demand of technologies for its research. Studying the methylome of many samples is costly. We propose a newly designed method by linking three generally used methods: DNA methylation-enrichment-bisulfite-sequencing (MEBS). MEBS is specifically enriching methylated genomic regions by MBD protein capture, with subsequent nucleotide-specific methylation analysis by bisulfite next generation sequencing of the entire methylome. Using this method we generated high quality sequence data. Methylation occurs mainly in CpG islands, but also in transposable sequences as well as gene regions. Most methylated cytosines are found in CpG dinucleotides. Those results are expected, but show that the method works.

Responses of butterfly & dragonfly assemblages to climatic fluctuations in Germany [Talk]

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The Community Temperature Index (CTI), *i.e.*, the average thermal conditions of the ranges of species in a community or assemblage, was introduced to measure the impact of climate change on species assemblages. We applied this index to a long-term dataset of butterflies and dragonflies from the German Free State of Saxony covering 35 and 20 years, respectively, and compared it with data of the German butterfly monitoring scheme TMD from this and other German states. The results indicate that butterfly and dragonfly assemblages respond to oscillations in annual mean temperature within the next generation. Due to different generation times, this results in a time lag of up to one year in butterflies, but up to five years in dragonflies. The results also confirm that climate warming has affected butterfly and dragonfly assemblages during the last 2–3 decades by changing their composition towards species adapted to higher ambient temperatures. However, adaptation of butterfly assemblages to climate warming in Saxony is apparently insufficient to keep pace with the rate of climate warming during the past 35 years. The decrease of cold-tolerant species (*e.g.* from peat-bogs or montane habitats), which are severely affected by higher temperatures, is only partly counterbalanced by an increase of thermophilic generalists, whereas xerothermophilic habitat specialists appear unable to profit from increasing temperatures.

The origin and loss of global biodiversity [Keynote]

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Systematics plays a pivotal role in understanding biodiversity, since it involves discovering and describing new species (alpha taxonomy) and uncovering the evolutionary relationships among them (phylogenetics). In this talk, I will emphasize the role that phylogeny can play in understanding the origins of biodiversity patterns. I will discuss examples showing how phylogeny can contribute to understanding the origins of biodiversity patterns, from those at the largest scale (*i.e.* why are there more species in the tropics than in temperate regions? why are there more species on land than in the ocean?) to more local-scale patterns (*i.e.* why do some habitats within a region have more species than others? why do some regions have higher local-scale richness than others?). Finally, I will describe how phylogeny can contribute to understanding major threats to biodiversity.

A survey of alpine lepidopteran biodiversity and genetic diversity in the Dachstein massif [Poster]

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Invertebrates of the European Alps are characterized by a high level of population fragmentation and endemism. The large extension of alpine habitat in Austria boosts the nation's scores of endemic taxa. According to Rabitsch and Essl (2009; Endemiten – Kostbarkeiten in Österreichs Pflanzen- und Tierwelt, Naturwissenschaftlicher Verein für Kärnten und Umweltbundesamt Gmbh, Klagenfurt und Wien), the highest number of endemic taxa in Austria is found among beetles (174 taxa), followed by snails (80 taxa) and spiders (46 taxa). Similarly, butterflies contain many endemics (33 species), most of them with alpine or subalpine distribution. Reasons for restricted distributions of lepidopteran species are the dependency on the larval host plant, which may have a fragmented distribution itself, and loss of flight, which occurred particularly frequently in species occurring at high elevations. Population fragmentation, lack of gene flow from outside and small population sizes contribute to a pattern of reduced genetic diversity, and may put populations at risk of extinction, especially in a changing environment. In my thesis work, I address the association between dispersal capacity and genetic diversity in several species of diurnal butterflies and nocturnal moths in an alpine meadow on the Dachstein mountain. Lepidopteran biodiversity in an area of 5000 m^2 at an elevation of 2000 m will be recorded (with a special focus on endemics), and focus species representing different mobility classes will be selected and monitored for cytochrome c oxidase I (COI) sequence diversity. The data will show whether dispersal capacity is indeed a predominant determinant of population genetic diversity, or whether additional factors (*e.g.* host plant, diurnal vs nocturnal life style, fragmentation vs endemism) play a major role as well.

Pluralism in phylogenetics and the poverty of Popperianism [Talk]

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The rise of phenetics and, especially of cladistics spurred interest in the philosophy of science as it applied to systematics. Seemingly the most commonly articulated view among early cladists was that systematics is an essentially Popperian science that is based on the falsification of testable hypotheses. In turn, early debates employed interpretations of Popperian philosophy of science as tools to argue for or against particular preferred or disparaged methodologies. Some more recent discussions have focused on the meaning of corroboration. Whereas philosophy is obviously relevant to ontology and epistemology aspects of phylogenetics, and logical analyses is widely applicable to the tasks of assessing the coherence of theories of systematics, I will argue that, aside from some very general prescriptions regarding good scientific practice that barely merit the label “philosophy”, explicit philosophies of science, none of which have provided adequate descriptive accounts of the progress of science, have very little to tell us about the methodology of phylogenetic inference. Indeed, over-zealous philosophising by phylogeneticists might just be an unhelpful distraction. I question to what extent a single, well-formulated philosophy of systematics or of phylogenetics is desirable in principle or achievable in practice. I argue that some methodological pluralism is both inevitable and desirable.

Contrasting niche occupation and crossing patterns in polyploid contact zones [Talk]

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Background: The interplay of ecological niche differentiation and hybridization dynamics in contact zones is only poorly understood, especially in polyploids. Methods: In diploid-tetraploid and tetraploid-hexaploid contact zones of the alpine plant species *Jacobaea carniolica* (syn. *Senecio carniolicus*), all individuals were mapped and cytotyped. Based on AFLP fingerprints individuals were categorized as parental, F1, F2 or backcrosses. Niche overlap based on Landolt indicator values for accompanying species was calculated. Results: Whereas in the diploid-tetraploid contact zone almost no hybridization occurred, pentaploid hybrids were common (ca. 15% of the individuals) in the tetraploid-hexaploid contact zone. Pentaploids interacted more strongly with hexaploids than with tetraploids. Almost all tetraploids but only about half of the hexaploids were categorized as parental genotypes, and backcrosses occurred mainly with hexaploids. The occurrence of F2 individuals indicates that pentaploid hybrids are not sterile. Niches of tetra- and hexaploids were differentiated along a complex gradient including temperature, light, nutrients and soil reaction. Pentaploids had a much larger niche overlap with tetraploids than with hexaploids. The niches of diploids and tetraploids showed a broad overlap. Conclusions: The strength of crossing barriers between cytotypes seems to be inversely related to the magnitude of ecological differentiation. Thus, pre- and postzygotic barriers complement each other enabling the co-occurrence of cytoypes in *J. carniolica*. Hybridization with hexaploids leads to loss of gametes in tetraploids which may contribute to their restricted distribution. The fertility of pentaploids gives evidence that they may not necessarily be dead ends of evolution.

Deep non-bilaterian phylogenomics: different genes do tell different stories [Talk]

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Deep-level metazoan relationships have long been a controversial issue. A well-resolved phylogeny of non-bilaterian animals is needed to provide a robust framework for understanding early animal evolution. Recent attempts to resolve this difficult question using phylogenetic analyses of large-size molecular (phylogenomic) datasets failed to find an agreement on the relative position of major metazoan lineages. For example, one of these studies found ctenophores to be the sister-group to the remaining Metazoa and favored a sister-group relationship between sponges and cnidarians, while other analyses suggest that the Placozoa are the sister-group to the remaining Metazoa or that sponges are a paraphyletic assemblage that share a grade of construction rather than common ancestry. From these hypotheses, many claims have been made with far reaching implications for the early evolution of animals. To address the causes for the observed inconsistencies of non-bilaterian relationships, we constructed a novel supermatrix containing 122 genes with increased non-bilaterian taxon sampling. Phylogenetic analyses of the complete dataset and its two non-overlapping multi-gene partitions produced conflicting trees. This result demonstrates the effect of gene sampling on phylogenetic inference. The observed discrepancies resulted from different levels of saturation and different degrees of Long Branch Attraction artifacts in the two partitions. Additional systematic errors were derived from significant variation in amino acid substitution patterns in different lineages that violate the stationary assumption of models frequently used to reconstruct phylogenies. Our results suggest that the accuracy of phylogenetic inference may be improved substantially by selecting genes that evolve slowly across metazoan lineages and applying more realistic substitution models. However, additional sequence-independent data might be required to unequivocally resolve the branching order of all non-bilaterian groups.

Reproductive morphotypes of *Cytheridella ilosvayi* Daday, 1905 (Ostracoda, Crustacea) revealed by morphological analyses [Talk]

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Ostracods are well-known for their variety of reproductive modes. Nonetheless, there is only limited knowledge about morphological variability of soft and hard parts in relation to the reproduction mode. In particular, intraspecific morphological variation of coexisting parthenogenetic and sexual females lacks a sound documentation. We have investigated the intraspecific limb and shell variability of the neotropical freshwater ostracod species *Cytheridella ilosvayi* which has been known so far to reproduce only sexually. Limb variability of adult and juvenile individuals (down to A-3) is generally low. Though, highest variation is shown by podomere proportions of the antennas, while thoracopods and setae provide minor influence on the variability. Based on discrimination analyses shell parameters (*i.e.*, shell length, position of the transversal sulcus) emerge to be more important for differentiation of groups than limb ratios. Adult females exhibit a large size range in which two clearly separated morphotypes exist. The presence of two morphologically similar females and only one type of males indicates a mixed reproduction population in which parthenogenetic and sexual reproduction coexists. According to correspondence in limb ratios between smaller females and males these are interpreted as being sexual. Consequently, the large females are assumed to be parthenogenetic.

ARB & SILVA: A software environment and databases for ribosomal RNA sequence data [Software Bazar]

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Sequencing ribosomal RNA (rRNA) genes is currently the method of choice for phylogenetic reconstruction, nucleic acid based detection and quantification of microbial diversity. The phylogenetic software package ARB has been developed for more than 20 years at the Technical University Munich to cope with rRNA analysis. It has primarily been implemented to handle rRNA gene data, but can be easily used for any kind of sequence data. Besides import/export, data management and alignment functions, a powerful sequence editor is implemented which can be used for nucleic acid as well as amino acid sequences. A unique maximum parsimony approach allows the reconstruction and evaluation of large trees which is a prerequisite for accurate phylogenetic classification. In 2007 the interactive software tool ARB was supplemented by the SILVA project to provide a central, comprehensive web resource for up to date, quality controlled databases of aligned small- and large subunit rRNA sequences from the Bacteria, Archaea and Eukarya domains. The latest publicly available full database release 111 contains 3,194,778 small subunit and 288,717 large subunit rRNAs. Beside reference datasets in ARB and FASTA format, the SILVA website now offers a set of tools for the evaluation of primer and probes as well as alignment and classifications services. ARB and SILVA are freely available at www.arb-home.de and www.arb-silva.de, respectively.

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The phylogenetic species concept and artificial taxonomic inflation – a critical comment on mammalian classification [Talk]

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Recently, many new mammal species have been named, sometimes more than doubling the number of species of a given taxon. This was done mostly by raising subspecies to species rank as a consequence of applying the phylogenetic species concept (PSC) that has become popular among taxonomists over the past 20 or so years. Much of this taxonomic inflation is artificial due to shortcomings of the PSC and unjustified reliance on insufficient morphological and/or genetic data. Species splitting is often particularly spurious if it is based on gene trees inferred from mitochondrial DNA only and/or phenetic analyses aimed at diagnosability. Uncritical acceptance of new species also creates an unnecessary burden on the conservation of biodiversity.

The evolution of metazoan chitin synthases reveals new insights into the ground pattern of Lophotrochozoa [Talk]

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Chitin synthases are involved in the production of one of the world's most prominent biopolymers, namely chitin. Chitin appears to be widespread among various metazoan groups, but in contrast to insects, nematodes and fungi, little is known about the evolution of these powerful enzymes in other eukaryotes. Our study unravels CS evolution, showing that CSs are common in all major metazoan groups. Our comprehensive evolutionary analysis reveals that lophotrochozoans exhibit an unexpected high diversity of CSs, most of them with an N-terminal myosin motor domain (MMD). Finally, we show that four CSs have already been present in the ground pattern of Lophotrochozoa, three of them linked to an MMD. The lophotrochozoan CS diversity suggests a role not only in the formation of mollusc shells, but also of annelid and brachiopod chaetae. Furthermore, our gene expression studies show remarkable tissue specificity for chitin synthase expression in some metazoan representatives. This spatio-temporal characterization of chitin synthases promises to be the first step towards unraveling the exact functions of chitin synthases.

Testing a Bayesian approach for comparison of biogeographical and climatic hypotheses [Talk]

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Inferring the impact of biogeographical and paleoclimatic events on diversification has been a central question in evolutionary biology. Here a Bayesian approach for hypothesis comparison that takes advantage of prior information and that serves as an alternative to the traditional null-hypothesis testing method is proposed. The aim of this study is to explore if assigning constrained-age priors to nodes of interest in a time calibrated phylogeny would serve as a means for hypothesis comparison. These priors would be equivalent to scenarios leading to lineage diversification under competing hypotheses (*e.g.* diversification triggered by a geographic or climatic event or not). Ranking and comparing the likelihood of the competing hypotheses, modelled under different priors, would allow the user to select the hypothesis that explains best the data and thus assign a level of confidence to evolutionary inferences. Simulations were executed to evaluate the influence of the dataset size and the temporal location and span of the competing hypotheses on the performance of the proposed method. Competing hypotheses were ranked using four techniques: Akaike Information Criterion (AIC); Bayes Factors (BF) estimated using marginal likelihoods calculated with Harmonic Mean (HM), Path Sampling (PS) and Stepping Stone (SS) approaches. The selection power of these techniques was also evaluated. The correct hypothesis is ranked as the best hypothesis at least 85% times. For a best performance, data sets with 3,500–10,000 bp sequences are required. The proposed method is most reliable when competing hypothesis are not temporally too close. Calculating marginal likelihoods with PS and SS led to stronger inferences than when using HM. When applying AIC, the correct hypothesis was the best ranked with moderate to strong support if large datasets and temporally distant hypotheses were compared. The proposed method was applied to selected published phylogenies to demonstrate its performance on real datasets.

Underestanding the reticulate evolution of polyploid genus *Curcuma*: controversial signals from nuclear low-copy genes [Poster]

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The genus *Curcuma* L. (Zingiberaceae) is a diverse polyploid complex containing several taxa of economic importance, but its systematics is still poorly understood. Recent phylogenetic insights from ITS and cpDNA sequence data uncovered basic structure of four main lineages within the genus, while the relationships among these lineages remains unresolved. We used four potentially unlinked nuclear DNA regions of the genes LEAFY, GLOBOSA, G3pdh, and diketide CoA synthase (DCS) and three regions of cpDNA to evaluate the relationships within *Curcuma*. Gene trees reconstructions resolved four highly supported main lineages within each dataset, same as previously suggested by ITS and cpDNA. The topologies of particular gene trees were hardly incongruent. Species tree as well as relative dates of divergence times between lineages have been inferred to discriminate between hybridization and lineage sorting that are alternative explanations for topological conflicts between gene trees. At least one event of whole genome duplication before diversification of the genus *Curcuma* followed by gene-specific loss of gene copies might explain mosaic pattern of incongruent gene tree topologies. The role of hybridization is also suggested, manifested by chloroplast capture revealed by comparison of relative ages of the main lineages in nDNA and cpDNA gene trees.

Patterns of endemism of the Southern Atlantic forest of Brazil: Relicts of a rich past or a contemporary diversification [Talk]

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The south-Brazilian Atlantic coastal forests are known for their high plant diversity. We looked into an unstudied facet of that diversity: endemism patterns. Our study took place in the region of the Babitonga Bay, Santa Catarina, Brazil, covering an area of roughly 350 km^2. We studied the distribution of endemic plants, their life history traits, mating patterns and distribution of related species, in order to elucidate the historical and natural processes that lead to the phenomenon of local endemism in an apparently contiguous biome. We propose two main mechanisms that explain endemism in the coastal forests of south Brazil: firstly, current diversification occurs mainly in taxa that tend to hybridize, thus, hybridization produces a great mass of new and local forms; and secondly, relicts of a colder and/or dryer climate flora that disappeared elsewhere still persist locally in that region, probably due to its unique climate found at the limit between moist tropical and temperate.

Does the head anatomy of Evanioidea clarify the phylogenetic placement of aculeate wasps? [Poster]

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Major advances in hymenopteran phylogeny have recently been made through highly coordinated efforts in the Tree of Life project (HymAToL), funded by the American NSF. These efforts resulted in the most comprehensive analysis to date on the phylogenetic relationships of Hymenoptera, using a combined approach. The resulting phylogeny is well resolved and many clades well supported, but some problem areas remain. One of the latter is the position of the aculeate wasps, including such well known insects as hornets, bees and ants. Traditionally, they have been regarded as the sister group of the Ichneumonoidea, one of the largest parasitic wasp taxa. In the new hypothesis, the Aculeata are placed as the sister group of the Evanioidea, a comparatively small and heterogenous assemblage comprising parasitoids of woodliving insects (Aulacidae), bee nest 'cuckoos' (Gasteruptiidae), and cockroach egg capsule predators (Evaniidae). The Aculeata-Evanioidea relationship is moderately supported by molecular data, but not by any known morphological characters. The aim of the project is to address this newly suggested phylogenetic hypothesis by exploring the internal head anatomy. As a first step, the heads of each one representative of the three evanioid families are studied. Interesting features are visualized by 3D reconstruction and characters that might be phylogenetically informative are discussed.

Barcoding diatoms with the 18S V4 region: setting an example for protists? [Talk]

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DNA barcoding is a tool that uses a short, standard portion of DNA to identify organisms based on a shared database of DNA sequences. In diatoms, a consensus on an appropriate DNA barcode has not yet been reached, and several markers are still in discussion (*e.g.* nuclear 18S rRNA, 28S rRNA, 5.8S rRNA + ITS2, mitochondrial cox1, plastid rbcL). Recently the CBOL Protist Working Group (ProWG) decided on the V4 region on the 18S rRNA gene as a pro-barcode for biodiversity assessments. The ProWG agreed on the 18S V4 region as a pro-barcode because a) of the possibility to design universal primers in all studied protist groups, b) of its discriminatory power and c) the current DNA data bases are most extensive for

18S. DNA barcoding is especially interesting in regard to high throughput methods (*e.g.* NGS) used in the analysis of environmental samples. Therefore we have established a standard procedure for DNA barcoding in diatoms to develop a standardised identification tool to serve routine water quality assessments using the 18S V4 region (Zimmermann *et al.* 2011; http://www.gbif.de/botany/barcoding_3). Here we demonstrate the feasibility of using the V4 barcode in a 454-pyrosequencing approach for species-level analysis of benthic freshwater diatoms commonly used for biomonitoring. Although considerable effort is still needed until NGS tools will be commonly applied to identify species from environmental samples, our results indicate the potential of an environmental barcoding approach for biomonitoring programs. To optimise environmental barcoding with the V4 marker for water quality assessment, we chose the river system Neisse/Oder (Czech Republic/Germany) as study area. The diatom flora of the Neisse/Oder is well known and is representative for a typical central European river system. This enables us to compare the results from the NGS with the morphological analysis of the same samples in order to evaluate the accuracy of the DNA barcoding approach. This applied approach needs a reliable taxonomic reference database, which is being established at the BGBM, and which will provide the basis for a DNA based identification system. To build the reference database DNA barcodes generated via Sanger sequencing of specific diatom taxa are linked to light-/scanning electron microscope-photographed vouchers. This database contains up to now sequences of 550 diatom strains. It will be freely accessible through AlgaTerra (www.algaterra.org).

Phylogenetics and biogeography of the Neotropical Quiinaceae (Malpighiales) [Talk]

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The neotropical Quiinaceae, the pantropical Ochnaceae s.str., and the Seychelles-endemic Medusagynaceae (=Ochnaceae s.l.) form a well-supported clade within Malpighiales and were merged into a single expanded Ochnaceae s.l. in the most recent APG classification. Infrafamilial relationships are, however, still poorly understood due to the lack of comprehensive molecular studies and insufficient taxon sampling. Here, we present a dated, phylogenetic framework for Quiinaceae based on five gene regions to unravel relationships within the family and to elucidate its position in the Ochnaceae s.l. There is support for a clade of Quiinaceae and Medusagynaceae, both being sister to Ochnaceae s.str. *Froesia*, the morphologically most distant genus, is sister to the rest of Quiinaceae. Contrary to former hypotheses, *Lacunaria* and *Touroulia* form a clade that is sister to *Quiina*, *i.e.* the simple-leaved genera (*Quiina*, *Lacunaria*) do not form a monophylum. *Quiina glaziovii*, an endemic of the Brazilian Mata Atlantica rainforests, comes out as sister of the rest of *Quiina*. Further intrageneric relationships and biogeographic aspects are discussed.

Molecular identification of earthworms using multiplex PCR [Talk]

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For many ecological studies a reliable species identification is an indispensable prerequisite. In studies on earthworms the limited external morphological characteristics often hamper identification. Moreover, most of the morphological characteristics are only visible in adult individuals and thus assigning juvenile earthworms to a species is usually not possible. Like in many other ecological studies on earthworms, our field research resulted in a high number of juveniles. Only 14.5% of the collected specimens are identifiable adults. Excluding the juveniles from the research would be a great loss of information. To overcome this problem we developed a molecular identification assay, based on three mitochondrial genes, cytochrome c oxidase I (COI), 12SrDNA, and 16SrDNA. Primers specific for genera, species or subspecies were designed and combined in a multiplex PCR assay. Species identification was possible via the length of the PCR-product. The assay was optimized to be fast and cheap to ensure high throughput without losing specificity and sensitivity. To underline the importance of a good taxonomic delimitation of species and a reliable identification tool, we also show how the identification of juvenile earthworms changes the accuracy of our research on an earthworm community in the Great Smoky Mountain National Park, Tennessee, USA.

Multiple allopolyploid formation in *Cardamine* (Brassicaceae): insights from microsatellite markers [Talk]

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Recently formed allopolyploid species represent excellent model systems to study early stages of polyploid evolution. *Cardamine schulzii* (Urnerboden, Switzerland) was regarded as one of the few nascent

allopolyploid species that were formed within the past 200 years. This polyploid, suggested to be an autoallohexaploid originating from the triploid hybrid C. ×insueta, was intensively studied at the time of its discovery and in the following two decades (1970s-1990s), but neglected later on. In our project, we took an integrative, multi-method approach to reveal more details of the polyploid origins and evolutionary processes in the hybridogenous population at Urnerboden. Results from microsatellite markers are presented here. We targeted progenitor-specific loci and alleles, to track their presence in the hybrids, reveal fine-scale genetic structure of the hybridizing progenitors and polyploids, and address the question of single vs recurrent polyploid origins. We confirmed hybridization between the sympatric diploids *C. amara* and *C. rivularis* auct. giving rise to the triploid *C. ×insueta*, and inferred its multiple origins (at least four origins assumed). On the other hand, we rejected the postulated origin and genome constitution of *C. schulzii*. Instead of the autopolyploid origin from *C. ×insueta*, we provide evidence that *C. schulzii* (represented in fact by two cytotypes, hypohexaploid and hypopentaploid) originated by hybridization between *C. ×insueta* and locally co-occurring hypotetraploid *C. pratensis* s.str. Each of the two cytotypes of *C. schulzii* was genetically uniform, suggesting a single origin. Long-term persistence of *C. schulzii* is presumably achieved by its perennial growth and clonal reproduction, and only negligible evolutionary potential can be as yet assumed. This contrasts with *C. ×insueta*, which appears as an established allopolyploid harbouring moderate genetic variation, partly fertile albeit triploid, and capable of vegetative reproduction. Even with reduced fertility, multiple origins coupled with occasional sexual reproduction, intra- or even interspecific gene flow (mating with *C. pratensis* s.str.), can increase genetic variation, generate unique genotypes, and, thus, may have profound evolutionary consequences. In conclusion, our studies highlight the immense complexity and dynamics of the studied *Cardamine* populations, and call for further studies from various perspectives.

Sorbus aucuparia fruit crop infestation by specialised *Argyresthia conjugella* at individual and population level [Poster]

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The predator satiation hypothesis was proponed to explain masting in plants. High interannual variation in seeding is suggested to be an adaptive strategy reducing the pressure of seed predators. The predator satiation hypothesis assumes that in years of heavy crops the predator population is satiated by providing the overabundance of food or oviposition sites (functional response of predators) and in years of low seed production the predator population is reduced by starvation or lack of oviposition sites (numerical response of predators). We used the long-term data to test relationship between *Sorbus aucuparia* (Rosaceae; Maloideae) fruit production and infestation of its fruits by a specialised pre-dispersal seed predator, *Argyresthia conjugella* (Lepidoptera, Yponomeutidae) at individual and population level. *S. aucuparia* is in Europe one of the most common trees bearing fleshy fruits. The study was done in subalpine old-growth spruce forest on the Babia Góra massif (1725 m a.s.l.) in the Western Carpathians (Poland). Fruit production was studied on a 27-ha plot; all rowan trees were searched for fruits in 2004–2012. To study pre-dispersal seed predation 30 individuals were randomly chosen and over 2005–2012. In years 2004–2012 mean individual seed production varied considerably from 0.4 to 5212 fruits per tree. In years 2005–2012 the mean intensity of fruit infestation was high (on average 73%; range 19–100%). At population level, functional and numerical responses of predators to the variation of fruit production were proved. The highest was annual fruit production the lowest was the percentage of infested fruits in the population ($R=-0.82$; $p=0.01$). And the highest was the ratio of the current to previous-year fruit crops the lowest was the percentage of infested fruits in the population ($R=-0.85$; $p=0.01$). At individual level, the percentage of infested fruits per individual was not correlated with the individual fruit production and with the ratio of the current to previous-year fruit crops. The percentage of infested fruits per individual was not correlated with distance to the nearest tree, except in year of heaviest fruit crop (2009) when it was positively correlated with the distance to the nearest tree. The percentage of infested fruits per individual was also not correlated with the tree diameter. To conclude, our results showed that the predator satiation process in Sorbus aucuparia works at the population level and not at the individual level.

List of Posters

Poster titles are sorted by 1) poster session, 2) symposium, and 3) alphabetical order by first author. Student posters are indicated by an asterisk before the poster number and will be evaluated for the GfBS Student poster prize.

Poster Session A – Tuesday/Wednesday (19 to 20 Feb. 2013)

Symposium 2

A1 – Kirjusina *et al.*: Parasitofauna of carps in fish farms of Latvia

*A2 – Sandionigi *et al.*: Characterization of the microbial consortium associated to *Varroa destructur* and its host, *Apis mellifera*

Symposium 5

*A3 – Richter *et al.*: Evolution of α-glycerotoxin, an unusual neurotoxin produced by venomous annelids

Symposium 6

A4 – Geiger: Introducing the FREDIE project with notes on the freshwater fish diversity of the Mediterranean hot-spot

*A5 – Gholipour *et al.*: Diversity of lichens on the tomb of Cyrus the Great, Pasargadae, Iran

*A6 – Kebbab *et al.*: Key habitats of large grey mongoose, *Herpestes ichneumon*, in Djurdjura national park, North Algeria

A7 – Koch & Arida: Discovery and underestimated diversity of the amphibians and reptiles of Sulawesi and its offshore islands, Indonesia

*A8 – Neumann *et al.*: New data on the biodiversity of land flatworms of the genus *Microplana* Vejdovsky, 1890 from Germany (Platyhelminthes)

Symposium 10

*A9 – Buresi *et al.*: Nervous system evolution: how to integrate novel data from an unconventional species, *Sepia officinalis*?

*A10 – Treffkorn & Mayer: Unique patterns of decapentaplegic expression in embryos of the onychophoran *Euperipatoides rowelli* (Peripatopsidae)

Symposium 11

A11 – Böttinger *et al.*: OpenUp! introduces a new system for data quality control and semantic enrichment of scientific biological multimedia data

Symposium 11

A12 – Gleisberg *et al.*: Free access to biodiversity data? How to contribute to GBIF – and why

A13 – Hoffmann *et al.*: The BioCASe Monitor Service v1.2

*A14 – Kurzrock & Geiger: Introducing the FREDIE project with notes on the European mollusk diversity

A15 – Penev *et al.*: Data papers as incentives for opening biodiversity data: One year of experience and perspectives for the future

A16 – Schmidt *et al.*: High-performance imaging of entomological collections

A17 – Söhngen *et al.*: Open up the treasure chest of prokaryotic metadata for comparative biodiversity analyses – Ongoing projects

A18 – Todt & Willassen: ForBio – The Research School in Biosystematics

Symposium 13

*A19 – Malkowsky *et al.*: To see the bigger picture – 3D reconstruction and character evolution of pallial eyes in Pectinidae (Mollusca: Bivalvia)

A20 – Staedler & Schönenberger: X-ray tomography of plant tissue: novel staining methods allow high resolution imaging

*A21 – Ung *et al.*: Xper3: Introducing social taxonomy

Symposium 14

*A22 – De la Cadena *et al.*: Phylogenetic assessment of taxonomic and ecological biodiversity of herbivore beetles in the dry tropical forest

A23 – Lopez-Vaamonde *et al.*: Historical herbaria and archival DNA reveal the origin of an invasive insect

A24 – Żywiec *et al.*: *Sorbus aucuparia* fruit crop infestation by specialised *Argyresthia conjugella* at individual and population level

Symposium 19

*A25 – Bagherian-Yazdi *et al.*: First demonstration of interspecific hybridisation in *Myrmica* ants by geometric morphometrics (Hymenoptera: Formicidae)

*A26 – Eriksson *et al.*: Possible ancient hybridization in *Medicago*

A27 – Grant *et al.*: Genome size in *Botrychium* species and their evolution in the monilophyte basal group

*A28 – Hanzl *et al.*: What drives the coexistence of di- and tetraploids in the primary contact zone of relict serpentine *Knautia arvensis*?

*A29 – Zaveska *et al.*: Understanding the reticulate evolution of polyploid genus *Curcuma*: controversial signals from nuclear low-copy genes

Symposium 21

*A30 – Almeida *et al.*: Molecular phylogeny and biogeography of the fern genus *Microgramma* C. Presl (Polypodiaceae – Polypodiopsida)

A31 – Cadahia-Lorenzo *et al.*: Phylogenetic position of the helicid species *Cylindrus obtusus* based on nuclear and mitochondrial DNA marker sequences

*A32 – Franz *et al.*: The biogeography and phylogeny of Lymnaeidae (Gastropoda: Pulmonata) in Southeast Asia – Insights from new data

*A33 – Hauenschild *et al.*: The role of biogeographic barriers on the evolution and current distribution of *Dysoxylum* (Meliaceae) in South East Asia

A35 – Jörger *et al.*: Back to the sea? First ontogenetic data of limnic slugs (Acochlidia, Heterobranchia)

*A36 – Plenk *et al.*: Fitness data of steppe plants in Central Europe: a comparative analysis based on fruit set, mass, and germination rates

*A37 – Reich *et al.*: Trans-Adriatic disjunctions – insights from *Gentianella crispata* (Gentianaceae)

A38 – Steiner: Utilization of shell morphometrics in North Atlantic Scaphopoda (Mollusca)

Symposium 28

A39 – Flot & Van Doninck: Genomic signatures of ameiotic evolution in the bdelloid rotifer *Adineta vaga*

A40 – Klatt *et al.*: Apomixis database at the University of Göttingen

A41 – Kutlunina: The loss of elements of seed reproduction and genetic diversity in populations of clonal plant

Open Session

*A34 – Hering *et al.*: Transcriptome analyses in representatives of Tardigrada and Onychophora suggest that colour vision evolved in arthropods

A42 – Arnault *et al.*: Enrolling high-tech farmers in functional biodiversity assessment: A practical experience of technology development and transfer between researchers and agricultural sector players in France

*A43 – Bär & Mayer: Anatomy of slime glands and biochemical composition of glue secretion among velvet worms (Onychophora)

A44 – Bleidorn *et al.*: Immunocytochemical investigations of anterior muscle regeneration in *Eurythoe complanata* (Amphinomidae, Annelida)

*A45 – Coryell *et al.*: Uncharted waters: Characterizing sodium channel diversity in spiders (Araneae)

A46 – Koch *et al.*: Gigantic Diplura (Hexapoda): rediscovery of *Heterojapyx souliei* (Bouvier, 1905) in China and systematic implications

*A47 – Riehl & Brandt: Impediment be resource: sexual dimorphisms in Macrostylidae (Crustacea: Isopoda)

*A48 – Stepanek & Kriwet: Skeletal morphology and growth of freshwater stingray *Potamotrygon falkneri* (Chondrichthyes, Myliobatiformes)

A49 – Zimmermann *et al.*: Does the head anatomy of Evanioidea clarify the phylogenetic placement of aculeate wasps?

Poster Session B – Thursday/Friday (21 to 22 Feb. 2013)

Symposium 1

B1 – Berger: Nomenclator *Ciliophorum* and Monograph of the Hypotricha, two works documenting the biodiversity of ciliates (Ciliophora)

B2 – Demchenko *et al.*: ITS-2 Barcode supports the systematics in *Microglena* (Chlorophyceae), a genus investigated by an integrative approach

B3 – Mikhailyuk *et al.*: Biodiversity of *Klebsormidium* from highland soil crusts (Alps, Tyrol, Austria)

B4 – Pfannkuchen *et al.*: Access to the planktonic biodiversity of the northern Adriatic

Symposium 3

*B5 – Dillenberger & Kadereit: Maximum polyphyly: A new delimitation of *Minuartia* (Caryophyllaceae)

B6 – Giere: The orbital mosaic in mammals: characters and implications

B7 – Liu & Schönitzer: Phylogenetic analysis of the family Bostrichidae auct. at suprageneric levels (Coleoptera: Bostrichidae)

*B8 – Scharn & Antonelli: Two-step tree building approach for generating mega-phylogenies: an alternative to traditional super matrix methods

Symposium 4

B9 – Davolos & De Matthaeis: A cryptic species of *Orchestia mediterranea* Costa, 1853 (Amphipoda) revealed by DNA sequence-based phylogenetic analysis

B10 – Gereben-Krenn *et al.*: Molecular differentiation and ecology in cryptic bumblebee species of the *Bombus lucorum* complex

*B11 – Marquardt: Integrative DNA taxonomy reveals cryptic diploid diversity in the common European Wall-rue fern

B12 – Martin *et al.*: Evidences for several species within the cosmopolitan eurybathic deep-sea lysianassoid amphipod *Eurythenes gryllus* s.l.

*B13 – Rakosy *et al.*: Do mate-searching males foster cryptic speciation in the orchid genus *Ophrys*?

*B14 – Siu-Ting *et al.*: Assessing cryptic diversity of Amazon lowland amphibians in Peru using mtDNA

Symposium 7

B15 – Degma & Schill: Study of Tardigrada biodiversity in Maritime Alps – A new *Echiniscus* species from Italy

*B16 – Dingová Košuthová & Westberg: Arctic-alpine lichens of the Tatry Mountains, their ecological indicator values and life history traits

*B17 – Duda *et al.*: New assessment for an old species: the Austrian endemic *Trochulus oreinos* (Gastropoda: Pulmonata: Hygromiidae)

B18 – Durak & Żywiec: The expansion of woody species on the abandoned subalpine grasslands of the Western Bieszczady Mts.

B19 – Graf *et al.*: Three new species of *Drusus*: Adult genital and larval characterisation

*B20 – Lebmann *et al.*: Evolution, biogeographical history, and ecology of high alpine and arctic species of *Ranunculus*

B21 – Mayrhofer *et al.*: A transnational lichen inventory of the Alps: a long overdue task

B22 – Schill & Degma: Census of tardigrades in the nature reserves Parc national du Mercantour and Parco Naturale delle Alpi Marittime

B23 – Waringer *et al.*: The larvae of *Drusus franzressli* Malicky and *D. spelaeus* (Ulmer) – newbies in the Drusinae grazer clade

*B24 – Wiesmair: A survey of alpine lepidopteran biodiversity and genetic diversity in the Dachstein massif

Symposium 9

*B25 – Grand *et al.*: LisBeth: a new cladistic tool for phylogenetics and biogeography

Symposium 12

*B26 – Bog *et al.*: Population genomic analyses along elevational transects through a hybrid zone of two *Senecio* species (Compositae)

*B27 – Flemming & Klussmann-Kolb: Testing molecular markers for phylogenetic signal – A case study in opisthobranch Gastropoda

B28 – Stuckas *et al.*: *Hyles euphorbiae* (Lepid.: Sphingidae) cold adaptation: Proteomic and transcriptomic candidate biomarker identification

*B29 – Meinecke & Mayer: Phylogeny and diversification of acoustically communicating European grasshoppers

B30 – Mlinarec & Besendorfer: Diverse Ty3-gypsy elements in sister *Anemone* and *Pulsatilla* genera: a structural and cytogenetic perspective

B31 – Olšavská: Karyological variation of *Cyanus perennials* (Asteraceae) in Europe and its importance for speciation

*B32 – Piálek *et al.*: Parallel evolution in *Crenicichla* (Cichlidae): Analogous diversification process in two unrelated species flocks

*B33 – Schweyen *et al.*: *Hydra* and its symbionts – A transcriptomic screening for ecologically important loci

B34 – Šingliarová *et al.*: When frequent intercytotype gene flow hampers polyploid speciation in primary contact zones

B35 – Španiel *et al.*: Understanding variation patterns and evolutionary processes in the *Alyssum montanum – A. repens* complex (Brassicaceae)

Symposium 15

*B36 – Baccei *et al.*: DNA methylation pattern analysis in the symbiosis between *Apis mellifera* and its parasitic mite *Varroa destructor*

Symposium 17

B37 – Jahn: The International Committee on Bionomenclature: its mandate, achievements and future

Symposium 29

B38 – Decaens *et al.*: DNA barcoding reveals unexpected biodiversity patterns in earthworm communities at the Nouragues Research Station (FG)

*B39 – Gaub *et al.*: Molecular determination of larval Digenea as basis for epidemiology, biodiversity and medical data

B40 – Huemer *et al.*: Lessons from a nearly complete barcode library for European Gracillariidae leafminers

*B41 – Kvifte & Andersen: Identifying Norwegian Psychodidae using DNA barcodes (Insecta: Diptera)

*B42 – Pisova *et al.*: Genetic variation and hybridization in the Genus *Bolboschoenus* in Central Europe

B43 – Spelda *et al.*: Barcoding Fauna Bavarica: Myriapoda (Chilopoda, Diplopoda)

Open Session

B44 – Evarte-Bundere *et al.*: Using the morphometric values for identification of most common cultivated infraspecific taxa of *Tilia platyphyllos*

B45 – Ghobad-Nejhad *et al.*: Taxonomic revision and phylogeny of *Corticium* s.l. (Corticiales, Basidiomycota) in Europe

B46 – Gunta *et al.*: Using the morphometric values for identification of most common cultivated infraspecific taxa of *Tilia platyphyllos*

*B47 – Kolář *et al.*: High diversity and endemism of *Galium pusillum* polyploid complex in deglaciated Northern Europe

*B48 – Kopylova-Guskova *et al.*: The first eleven years of post-pyrogenic succession in the Arctic pine forest

*B49 – Krüger *et al.*: The when and where of Hymenodictyeae and Naucleeae, Rubiaceae

*B50 – Löfstrand & Schönenberger: Comparative floral structure in the sarracenioid clade (Ericales)

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Author Index

The index includes the family names of all first and co-authors in the Abstracts section. (Page numbers point to the start page of the respective abstract (co-)authored by the person listed, which is not necessarily identical to to the page where the person is actually mentioned.)

Addendum (late abstracts)

This section is present in the online version only and includes abstracts received after printing of the abstract volume. Abstracts listed in alphabethical order by first author.

Bayesian Species delimitation in the *Silene cryptoneura* group [Talk]

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Species level relationships in Silene cryptoneura group including *S. cryptoneura*, *S. salamandra*, *S. insularis* were investigated with data from one chloroplast locus and five potentially unlinked nuclear loci. We applied the multispecies coalescent model under a Bayesian framework to compare alternative species delimitations in the group. Four minimal groups were defined from the data. The classification model with four species, in which the SW Anatolian *Silene cryptoneura* is split into two geographically vicariant species and the SE Aegaean island endemics *S. insularis* and *S. salamandra* are two seperate species got the highest support by both considering all 15 possible guide trees using BP&P and by comparing Bayes Factors from *BEAST analyses.

EDAPHOBASE – a new generation data warehouse for soil animals and beyond [Talk+Software Bazar]

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EDAPHOBASE (www.edaphobase.org) is a database within the Global Biodiversity Information Facility (GBIF) network, which collects most comprehensive information for some highly relevant soil animals (Nematoda, Enchytraeidae, Lumbricidae, Gamasina, Oribatida, Chilopoda, Diplopoda, and Collembola). The database combines data on the species, their collecting locality and ecological parameters. At present, we focus on Germany and neighbouring countries, but it is intended to incorporate data from other European countries in the future. Data were derived from publications and collections from German museums and research institutions but also from unpublished results of field studies (theses, reports).

The data comprise up-to-date taxonomic thesauri, geographical references, soil composition, vegetation, meteorological data, sampling and extraction methods, quantities of collected organisms, identification methods, preparation techniques, and behavioural data. The data quality in EDAPHOBASE is guaranteed by critical evaluation of the data by ecological and taxonomic experts prior to data input.

EDAPHOBASE offers a wide range of tools for data inclusion (client, GIS-tool, semi-automatic literature analysis; presented on the software bazaar) and data exploration. Simple queries are possible as well as more sophisticated analyses of different data groups concerning, e.g., geographical distribution or preferences and tolerances with regard to specific niche parameters or effects of anthropogenic perturbation. Since EDAPHOBASE covers the long history of investigation on soil organisms it will be possible to reveal major ecological alterations as a reaction to modifications in land-use techniques or effects of climate change.

Reproduction of freshwater bryozoans [Talk]

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Despite their common occurrence and worldwide distribution in ponds, lakes, streams and rivers, freshwater bryozoans comprise a relatively small group of about 100 species. They are sedentary, filter-feeding, colonial animals with complex life cycles. Freshwater bryozoans propagate both sexually and asexually. They are hermaphroditic and viviparous, but one of the most striking characteristics is their extraordinary variety of modes of asexual reproduction. Asexual propagation can take place by fragmentation and fission and, most importantly, by the formation of resting stages. These dormant bodies consist of chitinised shells protecting the germinal mass and yolk cells. They are developed as colony occurrence of the freshwater bryozoans is usually restricted to a limited time of the year.

In the case of the class of phylactolaemates these resting stages are categorised as statoblasts while in the class of gymnolaemates so-called hibernaculae are formed. Statoblasts are polymorphic and are divided in floating (floatoblasts) and sessile (sessoblasts and piptoblasts) forms. Floatoblasts drift on the water surface with the help of a gas-filled annulus that facilitates dispersal and colonisation of new substrates. They show a high variability and special forms can be developed such as the spinoblasts which possess hooks and the leptoblasts which are characterized by a thin translucent shell and immediate germination after being released from the colony. Sessoblasts as well as hibernaculae are cemented firmly to the substrate and thus promote the local persistence of the bryozoan colony. Piptoblasts are simply bean-shaped and remain in the colony until it decays. This variety of buoyant / sessile, short / long-living and asexual /sexual propagules is unique among freshwater invertebrates.