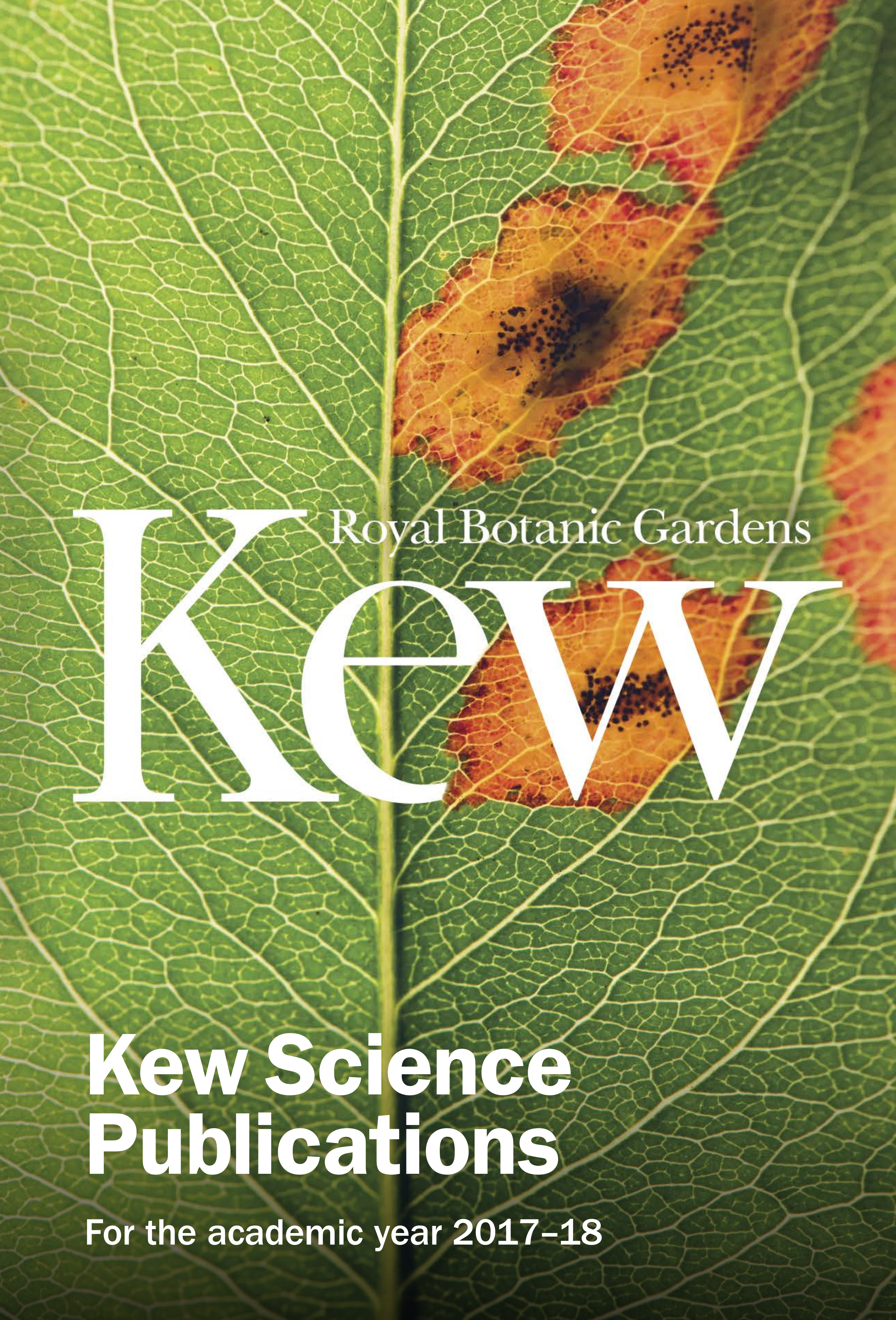


Royal Botanic Gardens
Kew

Kew Science Publications

For the academic year 2017–18

Foreword

Kew's mission is to be a global resource in plant and fungal knowledge. Kew currently has over 300 scientists undertaking collection-based research and collaborating with more than 400 organisations in over 100 countries to deliver this mission. The knowledge obtained from this research is disseminated in a number of different ways from annual reports (e.g. stateoftheworldsplants.org) and web-based portals (e.g. plantsoftheworldonline.org) to academic papers.

In the academic year 2017-2018, Kew scientists, in collaboration with numerous national and international research partners, published 358 papers in international peer reviewed journals and books. Here we bring together the abstracts of some of these papers. Due to space constraints we have included only those which are led by a Kew scientist; a full list of publications, however, can be found at kew.org/publications

* Indicates Kew staff or research associate authors.

Please find out more about Kew's scientific activities through the Kew Science webpages at **www.kew.org/science**

We present these publications under the four key questions set out in Kew's Science Strategy 2015–2020:

Dr Paul Wilkin (Acting Director of Science)
& Dr James Wearn (Strategic Operations Manager)

1

What plants and fungi occur on Earth and how is this diversity distributed?

Big Blue Pinkgills, formerly known as *Entoloma bloxamii* occur in Britain: *E. bloxamii* s. str., *E. madidum*, *E. ochreoprunuloides* forma *hyacinthinum* and *E. atromadidum* sp. nov.

Ainsworth*, M., Douglas*, B. & Suz*, L. M. (2018). *Field Mycology* 19 (1): 5–14. DOI: 10.1016/j.fldmyc.2018.01.004.

This study began as a small component of a Natural England Species Recovery Project (SRP) focused on generating DNA barcode (ITS region, Schoch *et al*., 2012) sequences from non-lichenised fungi officially regarded as conservation priority species in England, i.e. those named on Section 41 of the NERC Act 2006. In a few cases, the sequencing results indicated that two or more distinct species were hiding under a single name (cryptic species); a finding with clear implications for our understanding of their distribution, ecology and conservation status. For example, we found that the name Marram Oyster *Hohenbuehelia culmicola* had been historically applied to two British dune-inhabiting species with clearly distinct barcode sequences and fruit-body morphology. We distinguished the true *H. culmicola* from the newly-described *H. bonii* and then revised and, where necessary, redetermined many of the available British collections (Ainsworth *et al*., 2016).

Seed dispersal syndromes in the Madagascan flora: the unusual importance of primates.

Albert-Daviaud*, A., Perillo, S. & Stuppy*, W. (2018). *Oryx* 52 (3): 418–426. DOI: 10.1017/S0030605317001600.

Madagascar is one of the most threatened biodiversity hotspots, and protection of its biodiversity is becoming increasingly urgent as deforestation of the island continues. For the long-term success of conservation efforts it is essential that key ecological processes, such as seed dispersal, are protected and restored. Therefore, the identification of ecological gaps is a vital task. For Madagascar, only little is known about plant–animal interactions, and traditional methods of ecological research are too time-consuming to provide crucial information about breakdowns in these interactions. To identify likely dispersal gaps we therefore used a theoretical approach to analyse plant–disperser interactions in Madagascar. We used data science tools to impute missing data on relevant plant traits to subsequently predict the most likely dispersal agents for each of Madagascar's endemic plant species. We found that 38% of the endemic species (N = 8,784) are endozoochorous, and among these 26–41% display a primate syndrome and 17–19% a bird syndrome (depending on the definition of syndromes). This lower percentage of endozoochorous species and higher percentage of species with a primate syndrome in Madagascar compared to other tropical areas reflects the unusual disperser guild on the island. Only five bird species but 20 lemur species are frugivorous, and 16 of those lemur species are currently threatened with extinction. The disappearance of frugivorous lemurs would significantly change the vegetation dynamics of Madagascar's ecosystems, and a high proportion of Madagascar's endemic plants would enter an extinction vortex.

Pseudoclitocybaceae fam. nov. (Agaricales, Tricholomatoid clade), a new arrangement at family, genus and species level.

Alvardo, P. *et. al.* (including Liimatainen*, K., Niskanen*, T. (2018). *Fungal Diversity* 90 (1): 109–133. DOI: 10.1007/s13225-018-0400-1.

A new classification of several clitocyboid taxa is here proposed to accommodate results from multigenic phylogenetic inference. The analysis of ITS rDNA as well as a combined dataset including 18S and 28S rDNA, tef1 and rpb2 data, support significantly a shared monophyletic origin of the genera *Pseudoclitocybe*, *Musumecia* and *Pogonoloma*, and the species *Clitocybe alexandri* and *C. harperi*. The new family Pseudoclitocybaceae is here proposed to name this clade, characterized by the presence of loop-like clamp connections in most species, absence of cystidia, and parallel hymenophoral trama with broad, cylindrical hyphae with intracellular granulations. The new genera *Clitopaxillus* and *Harmajaea* are proposed to accommodate the type species *C. alexandri* and *H. harperi*, as well as the combination *H. wellsiae*. In addition, two new species are described: *C. fibulatus* has a differential distribution of clamp connections in the basidiome, while *H. guldeniae* is, by now, an exclusively European taxon with brownish pileus, somewhat decurrent gills, ovoid spores and basidia longer than those of *H. harperi*. Finally, the species concept within *Pseudoclitocybe* and *Pogonoloma* is discussed and descriptions of the most representative species are provided.

New finds in New Guinea *Hydriastele*.

Baker*, W. J., Heatubun*, C. D. & Petoe*, P. (2018). *Palms* 62 (3): 145–154.

Four newly described species of *Hydriastele* from New Guinea are illustrated in this photo feature.

× *Dactylodenia lacerta* (Orchidaceae): a morphologically cryptic hybrid orchid new to science from the Lizard Peninsula, Cornwall.

Bateman*, R. M., Murphy, A. R. M. & Tattersall, B. G. (2017). *New Journal of Botany* 7: 64–77. DOI: 10.1080/20423489.2017.1408189.

We describe the first reported hybrid to occur in nature between *Dactylorhiza praetermissa* and *Gymnadenia borealis* as × *Dactylodenia lacerta* R.M. Bateman & Tattersall. This vigorous plant was found and digitally imaged on a roadside verge of Crousa Downs on the Lizard Peninsula of Cornwall by Barry Tattersall in June 2016, and tentatively identified as a hybrid new to science. However, detailed morphometric analysis using 40 characters and based partly on the initial images failed to confirm its hybrid origin, suggesting instead that it was a slightly deviant plant of D. praetermissa. Comparison of the hybrid with its putative parents by DNA sequencing of nuclear (ITS) and plastid (trnL-F) regions later confirmed the F1 hybrid nature of the plant, as well as identifying *D. praetermissa* as the hybrid's ovule-parent and *G. borealis* as its pollen-parent. This result contrasted with prevailing theory that pollinators (in this case, most likely bumblebees) should preferentially transfer pollinaria from the shorter-spurred plant to the longer-spurred plant. The Crousa Downs plant is thus best described as a cryptic hybrid that shows strong maternal dominance in inheritance patterns, perhaps reflecting the fact that its ovule-parent is allotetraploid but its pollen-parent is diploid. A brief review of × *Dactylodenia* hybrids in the British Isles concludes that opportunities for the origin of this particular hybrid are severely limited by the contrasting habitat preferences and geographic distributions of its parents. An ongoing future for this apparently unique plant is unlikely due to local authorities' inappropriately-timed mowing regimes.

Clarified relationship between *Dactylorhiza viridis* and *Dactylorhiza iberica* renders obsolete the former genus *Coeloglossum* (Orchidaceae: Orchidinae).

Bateman*, R. M. & Rudall*, P. J. (2018). *Kew Bulletin* 73 (4): DOI: 10.1007/S12225-017-9728-Z.

Two decades have passed since DNA evidence first demonstrated an intimate relationship between the circumboreal species *'Coeloglossum' viride* and the temperate Eurasian genus *Dactylorhiza* s.s. Most subsequent molecular phylogenies showed *'C.' viride* to diverge after the *D. incarnata* group. The law of monophyly therefore dictated inclusion in *Dactylorhiza* of *'C.' viride*, irrespective of its undeniably distinctive morphology. Those orchid enthusiasts still determinedly seeking reasons for retaining the genus *Coeloglossum* have often used as a justification the one published molecular study that suggested that *D. viridis* diverged earlier than *D. incarnata*. Interestingly, these respective phylogenetic positions are supported by recent data-rich studies based on next-generation sequencing. However, recent DNA phylogenies also show that *D. iberica* — long regarded as morphologically distinct but nonetheless universally accepted as belonging within the genus — diverged penecontemporaneously with *D. viridis*. Thus, in order to justify maintaining *'Coeloglossum'* as a separate monotypic genus it would also be necessary to transfer *D. iberica* to a new monotypic genus, thus recognising two genera that are not only monotypic but also show only modest molecular divergence from the remaining dactylorchids. Examining in greater detail the morphology and micromorphology of *D. viridis* and *D. iberica*, we show that both species possess multiple morphological character states that are unique within the genus *Dactylorhiza*, but argue that greater phenotypic disparity is commonly the case in early-divergent lineages per se. Review of previous publications discussing *D. iberica* revealed little knowledge of its autecology, and contradictory

DNA-based inferences that can be traced back to just two original specimens. We also suggest that morphological and molecular variation within both species has been under-estimated and under-explored.

Morphometric comparison of British *Pseudorchis albida* with Icelandic *P. straminea* (Orchidaceae: Orchidinae).

Bateman*, R. M., Rudall*, P. J. & Denholm, I. (2017). *New Journal of Botany* 7: 78–93. DOI: 10.1080/20423489.2017.1408191.

Although the majority of taxonomic studies of European orchids treat *Pseudorchis* as a monotypic genus, some observers have argued that the apparently circumboreal segregate *P. straminea* should also be treated as a full species. Here, we compare detailed in vivo measurements of 55 plants from nine populations of *P. albida* in Britain with ten plants from three populations of *P. straminea* in Iceland. We apply morphometric statistics to data for 31 morphometric characters, culled from an original set of 36. We also review current (limited) DNA-based evidence of their evolutionary divergence. Of the 31 variable morphometric characters, 14 help to distinguish the two species, including labellum dimensions, spur length, flower colour, bract and leaf lengths, leaf colour and apical hooding. Molecular divergence (notably in ITS) approximates the lowest level needed for acceptance of species-level distinction, but thus far, the molecular information is typological and does not encompass seemingly intermediate populations of ‘*P. tricuspis’* occurring in the mountains of central Europe. *Pseudorchis* has the potential to become a valuable model system for the study of speciation and subsequent inter-/post-glacial migration. Despite persistent rumours, we found no evidence that P. straminea (or ‘*P. tricuspis*’) occurs in the British Isles; nonetheless, this species should continue to be sought in suitable habitats in northern Scotland. Morphological variation within *P. albida* is comparatively low, though the most exposed of our study populations exhibits (presumably ecophenotypic) dwarfing.

Molecular phylogenetic study of *Scleria* subgenus *Hypoporum* (Sclerieae, Cyperoideae, Cyperaceae) reveals several species new to science.

Bauters, K., Goetghebeur, P., Asselman, P., Meganck, K. & Larridon*, I. (2018). *PLoS One* 13 (9): e0203478. DOI: 10.1080/14772000.2018.1473898.

Populations of the columnar cactus genus *Eulychnia* (Cactaceae) are an iconic sight in the Chilean Atacama Desert. The most recent taxonomic treatment of the genus suggested to accept up to seven taxa at species level based on morphological data. To date, species boundaries and infrageneric relationships in *Eulychnia* have not been investigated using a molecular approach. In this study, sequence data were generated for six chloroplast markers (rpl32-trnL, trnH-psbA, trnL-trnF, trnQ-rps16, trnS-trnG, and ycf1) for the seven species. Where possible, samples were collected from the south and north of the distribution range of widely distributed species, as well as plants from two morphologically distinct populations in the Atacama and Coquimbo Regions. Evolutionary trends of morphological characters were investigated using ancestral state reconstruction, and the habitat of the Chilean taxa was taken into account based on latitudinal and altitudinal distribution, precipitation regime, and vegetation zones. Two major clades were retrieved in the molecular phylogenetic hypotheses, a northern clade and a southern clade, which can easily be distinguished morphologically by differences in rib shape and type of the indumentum of the pericarpel and the hypanthium. The only *Eulychnia* taxon found outside Chile is most commonly accepted as *Eulychnia iquiquensis* subsp. *ritteri*. However, its isolated geographic distribution and the fact that this taxon is not most closely related to E. iquiquensis but was retrieved as sister to the rest of the northern clade in our molecular phylogenetic results support the recognition of *E. ritteri* at species level. Our results also provide some support for the two recently published species, *E. chorosensis* (previously placed in *E. acida* s.l.) and *E. taltalensis* (previously considered to be part of *E. breviflora* s.l.). The relationships in the southern clade need further study.

Scleria cheekii, a new species of *Scleria* subgenus *Hypoporum* (Cyperaceae, Cyperoideae, Sclerieae) from Cameroon.

Bauters, K., Goetghebeur, P. & Larridon*, I. (2018). *Kew Bulletin* 73 (27): DOI: 10.1007/S12225-018-9752-7.

An endemic species of *Scleria* (Cyperaceae) from Cameroon, *Scleria cheekii* Bauters, is described as new to science. Scleria cheekii is an annual known from basalt pavements in the Bamenda Highlands in Cameroon. It can be distinguished from related species by the presence of tuberculated yellow-orange translucent tissue covering the trigonous stipe. This species is described, illustrated and compared with morphologically closely allied species.

The application of scientific names to plants in cultivation: *Salix vitellina* L. and related taxa (Salicaceae).

Belyaeva*, I. V., Epantchintseva, O. V., Govaerts*, R. H. A., McGinn, K., Hunnex, J. & Kuzovkina, Y. A. (2018). *Skvortsovia* 4 (2): 42–70.

The nomenclature and taxonomy of the taxa related to *S. vitellina* L. are clarified. Two new combinations, *Salix* × *fragilis* L. f. *vitellina* (L.) I.V.Belyaeva and *S.* × *pendulina* f. *salamonii* (Carrière) I.V.Belyaeva, are made and one new form, *S.* × *pendulina* f. *erythroflexuosa* I.V.Belyaeva, is described. Twenty-seven names are synonymised to the three accepted names including seven as new synonyms. Eleven new typifications are made. Fifty-one existing cultivars are assigned to the three taxa accepted by the authors and brief descriptions of them are provided.

Strobilanthes jomyi (Acanthaceae), a remarkable new species from South India.

Biju, P., Josekutty, E. J., D., R. & Wood*, J. R. I. (2017). *Phytotaxa* 332 (1): 75–80.

A new species, *Strobilanthes jomyi*, is described and illustrated from Kerala, India. The new species is similar to *S. ixiocephala* in its spheroidal, echinulate pollen, but differs in its pendulous inflorescence, thinly hispid style, exserted stamens and 4-seeded capsule with entirely pubescent seeds. It is also similar to *S. ciliata* in the form of its inflorescence and exserted stamens and style, but differs in its ovate-elliptic leaves with crenate margin, hairy bracts and bracteoles, glandular-pubescent ovary and gland-tipped capsule, pubescent seeds and spheroidal, echinulate pollen. Its possible relationships are discussed based on its pollen and floral morphology.

Iris tibetica, a new combination in *I.* ser. Lacteae (Iridaceae) from China: evidence from morphological and chloroplast DNA analyses.

Boltenkov, E. V., Artyukova, E. V., Kozyrenko, M. M. & Trias-Blasi*, A. (2018). *Phytotaxa* 338 (3): 223–240. DOI: 10.11646/phytotaxa.338.3.1.

Historically, the species composition of *Iris* ser. Lacteae has been controversial. Morphological and molecular analyses have been conducted here including specimens covering most of their distribution range. The results suggest *I.* ser. Lacteae includes three species: the well-known *I. lactea* and *I. oxypetala*, plus a newly defined taxon which is endemic to the Gansu and Qinghai provinces, China. We here propose it as a new combination at the species rank, *I. tibetica*. Morphologically, this species is close to *I. lactea* but

differs by its horizontal, creeping rhizome, scapes with no more than two flowers, its bracts reach the middle of the first flower, its broader inner perianth segments, its obovate with obtuse apex outer perianth segments, and its fruit apex always abruptly narrowed to a very short beak. The most useful qualitative and quantitative morphological characters used to distinguish this species are highlighted. Additionally, all three names are here typified, and a neotype for the name *I. lactea* and a lectotype for the name *I. tibetica* are designated. Notes on distribution and habitat are provided for all the accepted species.

Legume morphology.

Borges, L. M., Marazzi, B., Lewis*, G. P. & Fay*, M. F. (2018). *Botanical Journal of the Linnean Society* 187 (1): 158.

No abstract available.

Genetic diversity maintained among fragmented populations of a tree undergoing range contraction.

Borrell*, J. S., Wang, N., Nichols, R. A. & Buggs*, R. J. A. (2018). *Heredity*: DOI: 10.1038/s41437-018-0132-8. 121: 304–318

Dwarf birch (*Betula nana*) has a widespread boreal distribution but has declined significantly in Britain where populations are now highly fragmented. We analyzed the genetic diversity of these fragmented populations using markers that differ in mutation rate: conventional microsatellites markers (PCR-SSRs), RADseq generated transition and transversion SNPs (RAD-SNPs), and microsatellite markers mined from RADseq reads (RAD-SSRs). We estimated the current population sizes by census and indirectly, from the linkage-disequilibrium found in the genetic surveys. The two types of estimate were highly correlated. Overall, we found genetic diversity to be only slightly lower in Britain than across a comparable area in Scandinavia where populations are large and continuous. While the ensemble of British fragments maintain diversity levels close to Scandinavian populations, individually they have drifted apart and lost diversity; particularly the smaller populations. An ABC analysis, based on coalescent models, favors demographic scenarios in which Britain maintained high levels of genetic diversity through post-glacial re-colonization. This diversity has subsequently been partitioned into population fragments that have recently lost diversity at a rate corresponding to the current population-size estimates. We conclude that the British population fragments retain sufficient genetic resources to be the basis of conservation and re-planting programmes. Use of markers with different mutation rates gives us greater confidence and insight than one marker set could have alone, and we suggest that RAD-SSRs are particularly useful as high mutation-rate marker set with a well-specified ascertainment bias, which are widely available yet often neglected in existing RAD datasets.

A synopsis of the genus *Smythea* (Rhamnaceae).

Cahen*, D. & Utteridge*, T. M. A. (2018). *Kew Bulletin* 73 (2): DOI: 10.1007/S12225-017-9724-3.

A synoptic revision of the genus *Smythea* Seem. (Rhamnaceae) based on morphological evidence is presented. A total of 11 species are recognised; five new species are described: *Smythea batanensis*, *S. beccarii*, *S. hirtella*, *S. poilanei* and *S. poomae*, six new synonyms are established and a new combination is made: *S. oblongifolia*. Several new distribution records are reported, including *S. macrocarpa* for Borneo and Sumatra and *S. oblongifolia* for India. Generic delimitation between *Smythea* and the closely related genus Ventilago is clarified, and useful characters to identify the genera are discussed and illustrated. Distribution maps are given for each species, as well as a preliminary conservation assessment based on IUCN guidelines.

Definition and diversity.

Cannon*, P. F., Aguirre-Hudson*, B., Aime, M. C., Ainsworth*, A. M., Bidartondo*, M. I., Gaya*, E., Hawksworth*, D. L., Kirk*, P. M., Leitch*, I. J. & Lücking, R. (2018). *In:* Willis*, K. J. (ed.) *State of the World's Fungi*. Richmond: Royal Botanic Gardens, Kew, pp. 4–11.

What are fungi and why are they important? How many species, families and phyla are currently known to science and why is it so difficult to work these numbers out?

A linear sequence to facilitate curation of herbarium specimens of Annonaceae.

Chatrou, L. W., Turner*, I. M., Klitgaard*, B. B., Maas, P. J. M. & Utteridge*, T. M. A. (2018). *Kew Bulletin* 73 (39): 1–10. DOI: 10.1007/S12225-018-9764-3.

This paper provides a linear sequence of four subfamilies, 15 tribes and 106 genera of the magnoliid family Annonaceae, based on state-of-the-art and stable phylogenetic relationships. The linear sequence facilitates the organisation of Annonaceae herbarium specimens.

Kupeantha (Coffeeae, Rubiaceae), a new genus from Cameroon and Equatorial Guinea.

Cheek*, M., Alvarez-Aguirre*, M. G., Grall*, A., Sonké, B., Howes*, M. J. R. & Larridon*, I. (2018). *PLoS One* 13 (6): e0199324. DOI: 10.1371/journal.pone.0199324.

Two new coffee relatives (tribe Coffeeae, Rubiaceae), discovered during botanical expeditions to Cameroon, are examined for generic placement, and the placement of three previously known species (*Argocoffeopsis fosimondi*, *A. spathulata* and *Calycosiphonia pentamera*) is reinvestigated using plastid sequence (accD-psa1, rpl16, trnL-F) and morphological data. Seed biochemistry of the new species and pollen micromorphology (only one of the two species) are also studied. Based on the plastid sequence data, the new taxa are nested in a well-supported monophyletic group that includes *Argocoffeopsis* and *Calycosiphonia*. Within this clade, three well-supported subclades are recovered that are morphologically easy to diagnose: (1) Calycosiphonia (excluding *C. pentamera*), (2) *Argocoffeopsis* (excluding *A. fosimondi* and *A. spathulata*), and (3) a clade including the above excluded species, in addition to the new species. Based on the results, *Kupeantha*, a new genus of five species, is described, including two new Critically Endangered taxa from the Highlands of Cameroon: *Kupeantha ebo* and *K. kupensis*. Phytochemical analysis of *Kupeantha* seeds reveals compounds assigned as hydroxycinnamic acid derivatives, amino acids and ent-kaurane diterpenoids; caffeine was not detected. *Kupeantha* is the first new genus described in tribe Coffeeae in 40 years.

Kindia (Pavetteae, Rubiaceae), a new cliff-dwelling genus with chemically profiled colleter exudate from Mt Gangan, Republic of Guinea.

Cheek*, M., Magassouba, S., Howes*, M. J. R., Doré, T., Doumbouya, S., Molmou, D., Grall*, A., Couch*, C. & Larridon*, A. (2018). *PeerJ* 6: DOI: 10.7717/peerj.4666.

A new genus *Kindia* (Pavetteae, Rubiaceae) is described with a single species, *Kindia gangan*, based on collections made in 2016 during botanical exploration of Mt Gangan, Kindia, Republic of Guinea in West Africa. The Mt Gangan area is known for its many endemic species including the only native non-neotropical Bromeliaceae *Pitcairnia feliciana*. *Kindia* is the fourth endemic vascular plant genus to be described from Guinea. Based on chloroplast sequence data, the genus is part of Clade II of tribe Pavetteae. In this clade, it is sister to *Leptactina sensu lato* (including *Coleactina* and *Dictyandra*). *K. gangan* is distinguished from *Leptactina s.l.* by the combination of the following characters: its epilithic habit; several-flowered axillary inflorescences; distinct calyx tube as long as the lobes; a infundibular-campanulate corolla tube with narrow proximal section widening abruptly to the broad distal section; presence of a dense hair band near base of the corolla tube; anthers and style deeply included, reaching about mid-height of the corolla tube; anthers lacking connective appendages and with sub-basal insertion; pollen type 1; pollen presenter (style head) winged and glabrous (smooth and usually hairy in *Leptactina*); orange colleters producing a vivid red exudate, which encircle the hypanthium, and occur inside the calyx and stipules. *Kindia* is a subshrub that appears restricted to bare, vertical rock faces of sandstone. Fruit dispersal and pollination by bats is postulated. Here, it is assessed as Endangered EN D1 using the 2012 IUCN standard. High resolution LC-MS/MS analysis revealed over 40 triterpenoid compounds in the colleter exudate, including those assigned to the cycloartane class. Triterpenoids are of interest for their diverse chemical structures, varied biological activities, and potential therapeutic value.

Taxonomic monograph of *Oxygyne* (Thismiaceae), rare achlorophyllous mycoheterotrophs with strongly disjunct distribution.

Cheek*, M., Tsukaya, H., Rudall*, P. J. & Suetsugu, K. (2018). *PeerJ* 6: e4828 DOI: 10.7717/peerj.4828.

Oxygyne Schltr. (Thismiaceae) is a rare and little-known genus of achlorophyllous mycoheterotrophic perennial herbs with one of the most remarkable distributions of all angiosperm plant genera globally, being disjunct between Japan and West–Central Africa. Each species is known only from a single location, and in most cases from a single specimen. This monographic study names, describes and maps two new species, *Oxygyne duncanii* Cheek from cloud forest in SW Region Cameroon and *O. frankei* Cheek from gallery forest in the Central African Republic, representing the first new *Oxygyne* species described from Africa in 112 years, and raising the number of described Oxygyne species from four to six. *Oxygyne duncanii* is remarkable for sharing more morphological characters with two of the three Japanese species (*O. hyodoi* C.Abe & Akasawa, *O. shinzatoi* (H. Ohashi) Tsukaya) than with the geographically much closer type species of the genus, O. triandra from Mt Cameroon. Based mainly on herbarium specimens and field observations made in Cameroon and Japan during a series of botanical surveys, we provide descriptions, synonymy, mapping and extinction risk assessments for each species of *Oxygyne*, together with keys to the genera of Thismiaceae and the species of *Oxygyne*. The subterranean structures of African *Oxygyne* are described for the first time, and found to be consistent with those of the Japanese species. We review and reject an earlier proposal that the Japanese species should be segregated from the African species as a separate genus, Saionia Hatus. The only character that separates the two disjunct species groups is now flower colour: blue or partly-blue in the Japanese species compared with orange-brown in the African species. Studies of the pollination biology and mycorrhizal partners of *Oxygyne* are still lacking. Two of the six species, *O. triandra* Schltr. and *O. hyodoi*, appear to be extinct, and the remaining four are assessed as Critically Endangered using the IUCN 2012 criteria. To avoid further extinction, an urgent requirement is for conservation management of the surviving species in the wild. Since few achlorophyllous mycoheterotrophs have been successfully cultivated from seed to maturity, ex situ conservation will not be viable for these species and protection in the wild is the only viable option. While natural habitat survives, further botanical surveys could yet reveal additional new species between Central Africa and Japan.

An annotated checklist of the genus *Pseuderanthemum* Radlk. (Acanthaceae) in Thailand.

Choopan, T., Grote, P. J., Chayamarit, K. & Simpson*, D. A. (2018). *Thai Forest Bulletin (Botany)* 46 (1): 90–111. DOI: 10.20531/tfb.2018.46.1.13.

A checklist of the genus *Pseuderanthemum* in Thailand is presented, including ecological data, distributional information and specimen citations. Sixteen taxa are recognized, of which 11 taxa are native and five are introduced, including two new species; *Pseuderanthemum thailandicum* T.Choopan & P.J.Grote and *P. lanceophyllum* T.Choopan. A key to the species is also given. Lectotypes for 5 names are also designated.

Pollen morphology of subfamily Nelsonioideae (Acanthaceae) in Thailand.

Choopan, T., Grote, P. J., Chayamarit, K. & Simpson*, D. A. (2018). *Asia-Pacific Journal of Science and Technology* 23 (2): 1–9.

The pollen morphology of Thai Acanthaceae Subfamily Nelsonioideae was investigated. The pollen type was tricolpate. Their apertures were longitudinal narrow colpi with acute ends. The polar axis length (P) was 16.3-42.5 μm and equatorial axis length (E) was 17.5-37.5 μm. The largest size was represented in *Staurogyne dispar*, while the smallest showed in *Nelsonia canescens*, *Staurogyne glauca*, and *S. parvicaulis*. The shape varied from suboblate to prolate. Micro-foveolate, foveolate, and rugulate tecta were found in 6, 11, and 7 taxa of *Nelsonia* and *Staurogyne*, respectively. Psilate was only revealed in *Staurogyne macrobotrya*. The wall thickness varied from 1.25-2.5 μm depending on species.

A new species *Danaea* (Marattiaceae) from the Atlantic Forests of Brazil.

Christenhusz*, M. J. M., Almeida, E. M. & Felix, L. P. (2018). *Phytotaxa* 356 (3): 226–232. DOI: 10.11646/phytotaxa.356.3.

With a long fossil history (Taylor, Taylor & Krings 2009), Marattiaceae are among the earliest lineages of vascular land plants and are an important link to understanding land plant evolution. The family currently has a pantropical distribution, but was more widely distributed in the past. In the neotropics the family is represented by the genera *Marattia* Swartz (1788: 128), *Eupodium* Smith (1841: 190) and *Danaea* Smith (1793: 420). An additional three genera are found in the paleotropics and in total the family has an estimated 135 known species (Christenhusz & Byng 2016).

Plants of the World. An illustrated encyclopedia of vascular plants.

Christenhusz*, M. J. M., Fay*, M. F. & Chase*, M. W. (2017). Richmond: Kew Publishing.

No abstract available.

Cheniella gen. nov. (Leguminosae: Cercidoideae) from southern China, Indochina and Malesia.

Clark*, R., Mackinder*, B. A. & Banks*, H. (2017). *European Journal of Taxonomy* 360: 1–37. DOI: 10.5852/ejt.2017.360.

For much of the last thirty years, the caesalpinioid genus *Bauhinia* has been recognised by numerous authors as a broadly circumscribed, ecologically, morphologically and palynologically diverse pantropical taxon, comprising several subgenera. One of these, *Bauhinia* subg. *Phanera* has recently been reinstated at generic rank based on a synthesis of morphological and molecular data. Nevertheless, there remains considerable diversity within Phanera. Following a review of palynological and molecular studies of *Phanera* in conjunction with a careful re-examination of the morphological heterogeneity within the genus, we have found strong evidence that the species of *Phanera* subsect. *Corymbosae* are a natural group that warrant generic status. We describe here the genus *Cheniella* R.Clark & Mackinder gen. nov. to accommodate them. It comprises 10 species and 3 subspecies, one newly described here. Generic characters include leaves that are simple and emarginate or bilobed; flowers with elongate hypanthia which are as long as or much longer than the sepals; pods that are glabrous, compressed, oblong,

indehiscent or tardily dehiscent; and with numerous seeds, the seeds bearing an unusually long funicle extending most of the way around their circumference. A further distinctive floral character was found to be a fleshy disc on which the staminodes are mounted. An analysis carried out for this study reveals *Cheniella* to be characterised by a pollen type that is unique to the genus and previously unknown in the Leguminosae. Species diversity is richest in southern China, the full distribution extending westward to India and south- and eastward through Indochina into Malesia.

A synopsis of *Rhinacanthus* (Acanthaceae) in Angola and Namibia.

Darbyshire*, I., Nanyeni, L., Chase, F. M. & Gonçalves, F. M. P. (2018). *Kew Bulletin* 73: 21. DOI: 10.1007/s12225-018-9746-5.

The three species of the genus *Rhinacanthus* Nees occurring in Angola and Namibia are documented, including a full description of the new species *R. angolensis* I. Darbysh. and an expanded description of the scarce species *R. kaokoensis* K. Balkwill & S. D. Will. A key to their identification is provided, together with notes on their conservation status and species affinities.

A review of issues of nomenclature and taxonomy of *Hypericum perforatum* L. and Kew's Medicinal Plant Names Services.

Dauncey*, E. A., Irving*, J. T. W. & Allkin*, R. (2017). *Journal of Pharmacy and Pharmacology*. DOI:10.1111/jphp.12831.

Ambiguous and alternative plant names can lead to ineffective regulation, misinterpretation of literature, substitution of raw material or the failure to locate all published research. Kew's Medicinal Plant Names Services (MPNS) maps all names used for each plant in medicinal plant references onto current taxonomy, thereby providing for disambiguation and comprehensive access to the regulations and references that cite that plant, regardless of the name used. MPNS also supplies the controlled vocabulary for plant names now required for compliance with a new standard (Identification of Medicinal Products, IDMP) adopted by medicines regulators worldwide.

Morphological variation in pollen grains of *Mucuna* (Leguminosae): new biogeographic and evolutionary patterns.

de Moura, T. M., Bogler, D., Miranda, J. M. D., Gaglioti, A. L. & Lewis*, G. P. (2018). *Plant Systematics and Evolution* 304 (7): 861–869. DOI: 10.1007/s00606-018-1516-1.

Mucuna comprises 105 species with an overall pantropical distribution and is divided into three subgenera: *M*. subg. *Mucuna*, *M.* subg. *Stizolobium* and M. subg. *Macrocarpa*. Although phylogenetic studies have supported the occurrence of three main clades, evolutionary relationships among them are not fully resolved. The objective of this study was to examine pollen grain morphology from representatives of all three subgenera and map these onto the phylogenetic trees generated by analysis of other characters. Pollen grain surface, form, size, and aperture number were compared. A Bayesian inference tree using matK sequences was constructed. The results indicate that the representatives of *M*. subg. *Macrocarpa* have the smallest pollen grains in the genus (a synapomorphic character here identified for this subgenus) and that species of subgenus Mucuna (those with umbelliform inflorescences) have the largest pollen grains. Additional morphological diversity of the pollen grain surface was noted: reticulate and/or micro-reticulate (in all three subgenera), perforate, gemmate or verrucose (only in *M*. subg. *Mucuna*). For all studied taxa, the pollen grains are triaperturate, except for two species of *M*. subg. *Mucuna*, which have tetraperturate pollen. The phylogenetic tree obtained using the matK marker resolved *M*. subg. *Stizolobium* as the earliest diverging lineage in *Mucuna*. Based on this phylogeny, a reticulate ornamentation pattern of the pollen surface may represent the ancestral state for the genus, while the larger pollen size and the foraminate, gemmate, and verrucose ornamentations are derived characteristics within the genus. These putative derived ornamentations have been observed only in neotropical species.

Sub-Saharan botanical collections: taxonomic research and impediments.

Demissiew*, S., Beentje*, H., Cheek*, M. & Friis*, I. (2017). In: Friis, I. & Balslev, H. (eds.) *Tropical Plant Collections: Legacies from the Past? Essential Tools for the Future? Scientia Danica, series B, Biologica* 6, pp. 97–115.

Many historical specimens from sub-Saharan Africa are only found in European herbaria, but a higher number of newer specimens than widely assumed are kept in African herbaria, with a concentration in eastern and southern parts of the continent. Many of these herbaria were initiated in connection with independence of former European colonies in Africa, fewer were built on well-established herbaria from the colonial period. There are many gaps in collecting coverage, not least with regard to areas of high plant diversity; this is often caused by poor access or political instability. High species diversity exists in both humid and arid parts of Africa. Lack of collections from and knowledge about areas of high species diversity makes it difficult to prioritise conservation efforts. Gaps in taxonomic knowledge exist in certain large families, such as Rubiaceae, or in large genera, such as *Cyphostemma* (Vitaceae), *Euphorbia* (Euphorbiaceae), *Ipomoea* (Convolvulaceae), *Polystachya* (Orchidaceae), and *Barleria* (Acanthaceae). Newly collected specimens are now mainly kept in African herbaria, but lack of training and resources in tropical African herbaria are important challenges to prevent African botanists from continuing a somewhat declining European activity, partly caused by the downgrading in priority given to herbaria in European universities and research institutions. Encouraging examples of progress are the many regional African floras that have now been finished or nearly finished in collaboration between African and European herbaria, and the increasing digitization of herbaria and the general development of relevant services on the Internet, which provides new possibilities for botanical studies in Africa.

Flowering in darkness: a new species of subterranean orchid *Rhizanthella* (Orchidaceae; Orchidoideae; Diurideae) from Western Australia.

Dixon, K. W. & Christenhusz*, M. J. M. (2018). *Phytotaxa* 334: 75–79. DOI: 10.11646/phytotaxa.334.1.12.

Few plants are so cryptic as the underground orchids, *Rhizanthella* Rogers (1928: 1), of Australia. Unlike the species on the eastern seaboard of Australia, the Western Australian species spend their entire life cycle, including flowering, below the soil surface (only rarely with the tips of the bracts showing), making them unique among orchids and indeed, among flowering plants generally (Brown et al. 2013). Discovery in 1928 of the first underground orchid in Western Australia was an international sensation where the plant was described as ‘a remarkable subterranean orchid’ (Wilson 1929). The new taxon described in this paper resolves the enigmatic, disjunct distribution of *Rhizanthella* in Western Australia, where there was thought to be a central and southern node of a single species, *R. gardneri* Rogers (1928: 1).

Coleus namuliensis and *Coleus caudatus* (Lamiaceae): a new species and a new combination in the Afromontane flora of Mozambique and Zimbabwe.

Downes*, E. & Darbyshire*, I. (2017). *Blumea* 62: 168–173. DOI: 10.3767/blumea.2017.62.03.02.

The new species *Coleus namuliensis* (Lamiaceae) is described from the granite outcrops and grasslands of Mt Namuli in Zambezia Province of Mozambique. It has previously been confused with *Plectranthus caudatus*, a species that is restricted to the quartzite outcrops of the Chimanimani Mountains on the Mozambique-Zimbabwe border for which the new combination in *Coleus* is formalised in this paper. Other potential confusion species are discussed and a rationale for applying the generic name *Coleus* rather than *Plectranthus* is provided. Despite their highly restricted ranges, *C. namuliensis* and *C. caudatus* are both considered to have a conservation status of Least Concern at present, although climate change may pose a longer-term threat to their survival.

Lemurophoenix laevis.

Dransfield*, J. & Marcus, J. (2018). *Palms* 62 (2): 70–76.

No abstract available.

878. *LUPINUS MUTABILIS*.

Eastwood*, R. J. & Hughes, C. E. (2018). *Curtis’s Botanical Magazine* 35 (2): 134–148. DOI: 10.1111/curt.12233.

Lupinus mutabilis Sweet is illustrated. The history of its cultivation and domestication is described, nomenclature and typification are discussed, and a full description, two paintings, an illustration and a distribution map are presented.

Charles Deering (c. 1690–1749): author of an early flora of Nottingham.

Edmondson*, J. (2018). *Archives of Natural History* 45 (2): 283–291. DOI: 10.3366/anh.2018.0520.

George Charles Deering, born Georg Karl Dering (or perhaps Döring) in Dresden about 1690, practised as a physician in Nottingham from 1735 until his death in 1749. He was the author of an early flora covering the environs of Nottingham (1738) utilizing John Ray’s nomenclature, and a posthumously published historical account of Nottingham (1751). He studied in Leiden under Herman Boerhaave and in Paris with the Jussieu brothers, and had close connections with Johann Jacob Dillenius and John Martyn the elder. Notable features of his flora are discussed, including the people with whom he worked, his first records of plants in England, and his early mention of phenology.

Distribution and new variability of *Aegilops cylindrica* Host in Azerbaijan.

Eldarov, M., Aminov, N. & van Slageren*, M. (2018). *Genetic Resources and Crop Evolution* 65 (4): 1307–1316. DOI: 10.1007/s10722-018-0615-8.

This paper presents results of surveys carried out during 2009–2016 in different regions of Azerbaijan to study the distribution of *Aegilops cylindrica*. Two new varieties and four new formae have been identified within this species, based on spike morphology. Eco-geographical data result from both herbarium specimens and from monitoring in the wild. Ecological information results from climate data (altitude, rainfall, temperature) from within the areas of collection. We also present information on the description, systematics and bioecological features of *Ae. cylindrica*, as well as essential nomenclature, distribution, and habitats in Azerbaijan and beyond.

The Kew Review: Conifers of the World.

Farjon*, A. (2018). *Kew Bulletin* 73: 8. DOI: 10.1007/s12225.

When a natural group of plants has over many years been comprehensively and intensively studied, a large body of data, analysis and evaluation has accumulated. It is in the nature of such work on the taxonomy of such a group that this information is to be found scattered in various publications, such as research papers, checklists, monographs, Floras and other compilations. As time and research progress, some of this information will become outdated and superseded by new publications, but other information remains current and valuable. To give a review of this can provide us not only with a guide to this resource, but also with an introduction to the group in question. It may stimulate new research, as inevitably we will find that all has not been said and done, even about a group so well studied as the conifers. I hope that this paper will meet these aims.

Functional diversity and ecological requirements of alpine vegetation types in a biogeographical transition zone.

García-Gutiérrez, T., Jiménez-Alfaro, B., Fernández-Pascual, E. & Müller*, J. V. (2018). *Phytocoenologia* 48: 77–89. DOI: 10.1127/phyto/2017/0224.

The first vegetation type, characterized by Eurosiberian-like mesophilous grasslands (Armerion cantabricae), was dominated by hemicryptophytes, having taller plants with larger leaves and bigger seeds, and higher requirements for soil moisture and nitrogen. The second vegetation type, representing Mediterranean-like communities (Festucion burnartii), was mainly dominated by chamaephytes and showed higher requirements for continentality, light and pH. The Eurosiberian type was more diverse than the Mediterranean type in leaf area and pH requirements, but less diverse in life forms. Our results demonstrate how two vegetation types that to co-occur in the same alpine landscape have distinct species characteristics with specific functional traits and ecological requirements. This is likely driven by environmental filtering along meso-topographical gradients, favouring species with Mediterranean distribution in stressed habitats, and species with Eurosiberian distribution in microhabitats that retain soil water and nutrients. The distribution of functional diversity along these gradients may explain the resilience of alpine plant species in biogeographical transition zones of southern Europe.

The plants around us. A guide to some familiar Botswana plants.

Heath*, A. M. & Heath*, R. A. F. (2018). Lütetsburg: Knyphausen Stiftung.

No abstract available.

A monograph of the *Nengella* group of *Hydriastele* (Arecaceae).

Heatubun*, C. D., Petoe*, P. & Baker*, W. J. (2018). *Kew Bulletin* 73: 18. DOI: 10.1007/s12225-018-9743-8.

A taxonomic revision is presented of the *Nengella* group of the palm genus *Hydriastele* (Arecaceae: Arecoideae) in New Guinea, which comprises slender understorey or midstorey palms with small, protandrous inflorescences. Seven species are accepted: *Hydriastele aprica*, *H. divaricata* sp. nov., *H. flabellata*, *H. montana*, *H. pinangoides*, *H. simbiakii* sp. nov., and *H. splendida* sp. nov. All species are illustrated and their distributions are mapped. In addition, a key to species and preliminary IUCN Red List Assessments are provided.

Plate 872. *Cochemiea pondii* subsp. *maritima*. (Cactaceae).

Hind*, D. J. N. (2018). *Curtis's Botanical Magazine* 35 (1): 49–62. DOI: 10.1111/curt.12224.

Cochemiea pondii subsp. *maritima* is illustrated, the species and all three subspecies described, each provided with a full synonymy, statements on distribution, habitat and ecology, etymology, phenology, and conservation status. A commentary is given on the re-acceptance of *Cochemiea*, separated from *Mammillaria*. Cultivation notes are provided; the species, and in particular subspecies *maritima*, is far from common in cultivation and not widely available. The discussion covers aspects of recognition of the subspecies, type collections, related taxa, and comments on the addition of several more species to the genus by Doweld.

The taxonomy and morphology of *Schizomeria* (Cunoniaceae) in New Guinea, the Moluccas and the Solomon Islands, with notes on seed dispersal and uses throughout the genus.

Hopkins*, H. C. F. (2018). *Kew Bulletin* 73 (11): 1–41. DOI: 10.1007/S12225-017-9726-1.

Schizomeria is a genus of forest trees or occasionally understorey shrubs represented by some seven species in New Guinea, one of which extends west to the Moluccas and two eastwards to the Solomon Islands; an additional two or three species occur in eastern Australia. In New Guinea, *Schizomeria* grows from lowland to subalpine forest, with most species occurring in the montane zone. This revision presents a key to the species, plus synonymy, descriptions, distribution maps, provisional conservation assessments and an index to collections for the taxa in New Guinea, the Moluccas and the Solomon Islands; local names are given in an Appendix. Species delimitation in New Guinea is not always straightforward and several taxa are quite variable, or have blurred boundaries, or both. Morphological characters that are useful in distinguishing among species include the type and distribution of the indumentum, the structure and position of the inflorescence (whether terminal, falseterminal or axillary) and the presence or absence of subspherical glands on the leaves. The flowers are polysymmetric, green, white or pale yellow, with small, 3-toothed petals; some species are andromonoecious. The subspherical or ellipsoidal drupes have a brown, orange, yellowish or whitish epicarp; they are dispersed by vertebrates, including cassowaries, fruit-bats and other arboreal frugivores including pigeons. The timber has some commercial value plus a number of local uses. Data for the Australian taxa are included in the discussions of dispersal and uses.

Names and types relating to the South American genus *Lamanonia* (Cunoniaceae) and its synonyms, the identity of *L. speciosa*, and an account of the little-known *L. ulei*.

Hopkins*, H. C. F. (2018). *Kew Bulletin* 73 (10): 1-21. DOI: 10.1007/S12225-017-9731-4.

Publication details for names that refer to the South American genus *Lamanonia* and its synonyms, *Belangera* and *Polystemon*, are reviewed, including names published by Vellozo, Cambessèdes, David Don, Pampanini and Engler, amongst others. The types of these names, collected by Saint-Hilaire, Glaziou, Sellow and others, are also reviewed and lectotypes designated where appropriate. A specimen of the handwriting of David Don is provided. The types of *L. grandistipularis* and *L. speciosa* are clearly conspecific and so *L. speciosa* is removed from the synonymy of *L. ternata* and now takes priority over the name *L. grandistipularis* for a shrub or small tree from campo rupestre in Minas Gerais and Bahia in Brazil; this species has sharply toothed, coriaceous leaves and large stipules that are usually persistent on fertile stems. A description, illustration and distribution map are provided for *L. ulei*, which has largely been overlooked as an accepted species, but which is distinguished from all other species in the genus by a distinctive layer of dense greyish or fawn indumentum formed of small hairs on the abaxial surface of the leaflets.

Palmeras útiles en tres comunidades indígenas de La Pedrera, Amazonia colombiana.

Jaimes, M., Betancur, J. & Cámara-Leret*, R. (2018). *Caldasia* 40 (1): 183–199. DOI: 10.15446/caldasia.v40n1.68851.

We studied the knowledge and use of palms in three indigenous communities (Angostura, Curare and Yukuna) near the corregimiento of La Pedrera, Colombian Amazonia. Between June and July of 2010 ethnobotanical data was recorded through structured interviews with 53 informants. The data was analyzed using three indices: relative importance of use category (IR (c)), relative cultural importance (IC (s)) and relative species importance (IR (s)). We found 34 useful palms species, used in nine different use categories. According to the IR (c) the most important use categories were Human Food, Construction and Utensils and tools. Notable among these were the direct consumption of fruits, preparation of beverages, the use of the entire palm and the leaves for housing, and the manufacture of weapons for hunting and utensils for daily use. According to the IR (s) and IC (s) the most important species were chontaduro (*Bactris gasipaes*), canangucho (*Mauritia flexuosa*), milpesos (*Oenocarpus bataua*), and asaí (*Euterpe precatoria*). Palms play an important role in all three communities, but there is a notable decrease in knowledge about uses associated with culture and ritual ceremonies. According to the indices or relative cultural and relative species importance, the species that were important in this study resembled those found in other Colombian Amazon communities.

Six new species of *Barleria* L. (Acanthaceae) from Northeast Tropical Africa.

Kelbessa, E. & Darbyshire*, I. (2018). *Kew Bulletin* 73: 1. DOI: 10.1007/S12225-017-9725-2.

Six new species of *Barleria* L. (Acanthaceae) are described from northeast tropical Africa: *B. gidoleensis* Ensermu & I. Darbysh., *B. baluganii* Ensermu, *B. ferox* Ensermu & I. Darbysh. and *B. negeleensis* Ensermu & I. Darbysh. from Ethiopia and *B. ensermui* I. Darbysh. and B. shebelleensis Ensermu & I. Darbysh. from Somalia. All the species are illustrated and their affinities and conservation status are discussed. A note on the presence of *B. parviflora* R. Br. ex T. Anderson in northern Somalia is also included. In addition, a foreword is presented on the great contribution to Acanthaceae taxonomy and African botany made by Professor Ensermu Kelbessa, who sadly passed away in August 2016.

Two new names and five lectotypified taxa for the genus *Smilax* (Smilacaceae), and the transfer of *Smilax petiolatumidus* to the genus *Dioscorea* (Dioscoreaceae).

Kladwong, P., Chantaranothai*, P. & Simpson*, D. A. (2018). *Thai Forest Bulletin (Botany)* 46 (1): 44–57. DOI: 10.20531/tfb.2018.46.1.07.

Smilax asiatica Kladwong, Chantar. & D.A.Simpson and *S. goeringii* Kladwong, Chantar. & D.A.Simpson are proposed as new names for two later homonyms, *S. laevis* A.DC. and *S. japonica* (Kunth) P.Li & C.X.Fu, respectively. Two taxa are reduced to synonymy: *S. petiolatumidus* B.R.Moore, Narkkong, Th.Moore & Lutat is placed into the synonymy of *Dioscorea cirrhosa* Lour. and S. zeylanica var. *penangensis* A.DC. is a new synonym of *S. asiatica*. *Smilax ferox* Wall. ex Kunth and *S. polyacantha* Wall. ex Kunth are newly recorded for Thailand. *Smilax asiatica*, *S. ferox*, *S. lanceifolia* var. *opaca* A.DC., *S. polyacantha* and *S. zeylanica* var. *penangensis* are lectotypified.

Nomenclatural notes on the family Smilacaceae in Thailand.

Kladwong, P., Chantaranothai*, P. & Simpson*, D. A. (2018). *Kew Bulletin* 73: 18. DOI: 10.1007/s12225-018-9751-8.

A nomenclatural synopsis of 11 of the 28 *Smilax* species recorded in Thailand (*S. bracteata*, *S. calophylla*, *S. corbularia*, *S. davidiana*, *S. extensa*, *S. hemsleyana*, *S. luzonensis*, *S. myosotiflora*, *S. myrtillus*, *S. perfoliata* and *S. prolifera*) is presented. Three names, *S. helferi* var. *maingayana*, *S. microchina* and *S. ocreata* are placed into synonymy of *S. luzonensis*, *S. davidiana*, and *S. perfoliata*, respectively. *Smilax prolifera* is reinstated. Ten taxa, *S. calophylla*, *S. extensa*, *S. helferi*, *S. helferi* var. *maingayana*, *S. hemsleyana*, *S. myosotiflora*, *S. myrtillus*, *S. ocreata*, *S. stenopetala* and *S. woodii* are lectotypified.

Pollen morphology of selected species of the genera *Chrysodracon* and *Dracaena* (Asparagaceae, subfamily Nolinoideae) and its systematic implications.

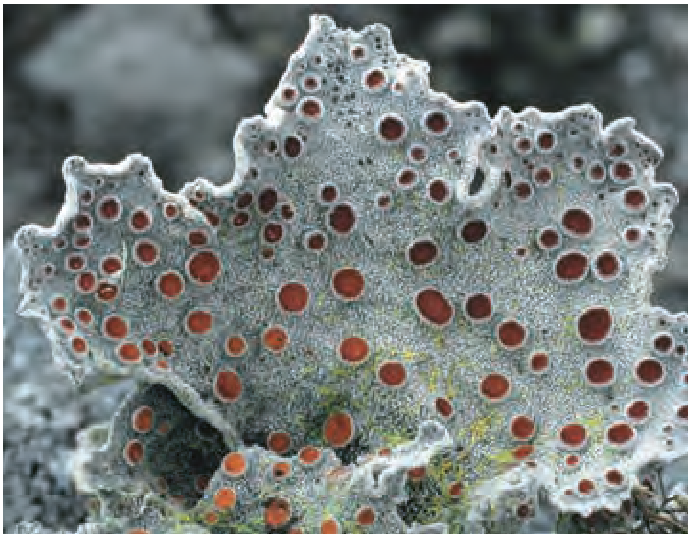
Klimko, M., Nowińska, R., Jura Morawiec, J., Wiland Szymańska, J. & Wilkin*, P. (2018). *Plant Systematics and Evolution* 304: 431–443. DOI: 10.1007/s00606-017-1486-8.

Pollen grains of 3 species from the genus *Chrysodracon* and 20 species from the genus *Dracaena* were examined by light, scanning electron and fluorescence microscopy. The basic shape of the pollen grains is subprolate and prolate, but prolate-spheroidal pollen grains may also be found. Pollen of *Chrysodracon* and *Dracaeana* is dispersed as monads, rarely as dyads. In terms of size, the pollen grains studied were classified as medium-sized and large. There are two different types of apertures: monosulcate and monoulcerate in *Dracaena* and monoulcerate in *Chrysodracon*. The surface of the non-apertural areas is psilate-perforate, irregularly folded, microreticulate and fossulate. Ornamentation of the apertural region is microreticulate, microreticulate-baculate, baculate, psilate-perforate, psilate-perforate-verrucate, granulate and irregularly folded. Irregular perforations are present, and the wall structure is tectate-columellate. Our results suggest that some species of *Chrysodracon* and *Dracaena* may be separated based on their pollen grain micromorphology on the distal region.

Nova pesquisa sobre as coleções de Richard Spruce na Amazônia: uma colaboração Brasil-Reino Unido.

Kruel, V. F., Martins, I., Nesbitt*, M. & Milliken*, W. (2018). *Ethnoscientia: Revista Brasileira de Etnobiologia e Etnoecologia* 3 (2): 1–6.

The Northwest Amazon comprises a large region of equatorial forest on the border of Brazil, Colombia and Venezuela, which has been inhabited by indigenous peoples since the pre-colonial period. Today they occupy 80% of its area. Travellers such as Richard Spruce, who visited the region in the 1850s-1860s, described the vitality and dynamics of these populations, demonstrated by the size of their longhouses, their extensive inter-communal ceremonies, and their rich material culture. The biocultural objects and associated information collected by Richard Spruce constitute a unique point of reference for the useful plants, ethnobotany, anthropology and environmental history of the region. Housed at the Royal Botanic Gardens,



Kew and the British Museum, both in London, this under-researched collection incorporates indigenous plant-based artefacts, samples of useful plant products, detailed archival notes on the use of plants by inhabitants of the Amazon, and accompanying herbarium voucher collections. This paper focusses on an ongoing research programme aimed at building capacity in Brazil to research, cataloguing and mobilising data from these biocultural collections, and developing these important resources for improved understanding of the useful and cultural properties of plants. It aims to build collaborative relationships, making biocultural collections and associated data freely accessible online, and above all to strengthen capacity of indigenous communities on the Rio Negro for autonomous research into material culture and plant use. We present the activities we have developed in the first two years of the programme. Workshops at Kew, Rio de Janeiro and São Gabriel da Cachoeira have enabled the Spruce collections to be fully digitised and artefacts made available through the Reflora portal (reflora.jbrj.gov. br). Training has been given in collection and study of biocultural objects, both to museum staff and representatives of indigenous communities, and a research agenda developed that focuses on better understanding of the shifting relationships between people and natural resources over the last 200 years. We discuss how a broad collaboration has led to constructive, culturally appropriate engagement with local communities, providing a portal into the world of scientific knowledge and helping to mobilise both scientific and indigenous knowledge in a mutually beneficial manner.

(2554) Proposal to conserve the name *Schoenus hornei* (Cyperaceae) with a conserved type.

Larridon*, I., Govaerts*, R. & Goetghebeur, P. (2017). *Taxon* 66 (5): 1225–1226. DOI: 10.12705/665.21.

No abstract available.

(2555) Proposal to conserve the name *Tetraria* (Cyperaceae) with a conserved type.

Larridon*, I., Verboom, G. A. & Muasya, A. M. (2017). *Taxon* 66 (5): 1226–1227. DOI: 10.12705/665.21.

No abstract available.

Revised delimitation of the genus *Tetraria*, nom. cons. prop. (Cyperaceae, tribe Schoeneae, *Tricostularia* clade).

Larridon*, I., Verboom, G. A. & Muasya, A. M. (2018). *South African Journal of Botany* 118: 18–22. DOI: 10.1016/j.sajb.2018.06.007.

Tetraria as currently circumscribed still is a polyphyletic genus restricted to the southern hemisphere. Besides several small independent evolutionary lineages, two larger multispecies lineages have been recognised from South Africa, identifiable by key morphological differences: the c. 30 *Tetraria* species in the *Tricostularia* clade tribe Schoeneae have noded culms and a reticulate tunic surrounding the culm base, while the c. 17 *Tetraria* species in the *Schoenus* clade of tribe Schoeneae have a culm without nodes and lack reticulate sheaths at the culm bases. Recently, both the 17 non-reticulate *Tetraria* species (including the original type of the genus, *T. thuarii*) and seven species of the closely related genus Epischoenus were transferred into *Schoenus*. This left the c. 30 species of the other lineages of *Tetraria* s.l. in need of new names. For nomenclatural consistency and since *Tetraria*, in particular the group known as reticulate-sheathed *Tetraria*, represent an important and well-known plant group of the Cape Floristic Region, a conservation proposal was submitted to conserve *Tetraria* with a new type, i.e. *T. thermalis*, which is part of the reticulate-sheathed *Tetraria* clade. This study presents a redelimitation of *Tetraria*, nom. cons. prop. reflecting the recent taxonomic changes, and formally transfers five species of *Costularia* subgenus *Lophoschoenus* and one species of *Epischoenus* to *Tetraria*.

Dicksonia utteridgei, a new species of hairy tree fern (Dicksoniaceae - Cyatheales) from New Guinea.

Lehnert, M. & Cámara-Leret*, R. (2018). *Blumea* 63: 140–143. DOI: 10.3767/blumea.2018.63.02.09.

A new species of hairy tree fern (Dicksoniaceae - Cyatheales) is described and illustrated: *Dicksonia utteridgei* from stunted ridge forest in central New Guinea. The species is the only one in the genus with a combination of fully pinnate to bipinnate-pinnatifid pinnules and bristly spreading petiole hairs.

The majestic canopy-emergent genus *Dinizia* (Leguminosae: Caesalpinioideae), including a new species endemic to the Brazilian state of Espirito Santo.

Lewis*, G. P., Siqueira, G. S., Banks*, H. & Bruneau, A. (2017). *Kew Bulletin* 72: 48. DOI: 10.1007/S12225-017-9720-7.

Since its description, almost 100 years ago, the genus *Dinizia* has been treated as monospecific, comprising the single canopy-emergent species *Dinizia excelsa* Ducke which grows in non-flooded Amazonian forests of Guyana, Suriname and seven states of northern and central-western Brazil. *Dinizia jueirana-facao* G. P. Lewis & G. S. Siqueira, which grows in a restricted area of semi-deciduous Atlantic rain forest in Espírito Santo state, Brazil, is described as a new species in the genus. The new species is also a canopy-emergent of impressive stature. We provide descriptions for both species, a key to species identification, a distribution map and the new species is illustrated. Fossil leaves, inflorescences and fruit provide evidence for a *Dinizia*-like ancestor occurring in south-eastern North America during the Eocene. In contrast to *D. excelsa* where pollen is dispersed in tetrads, the pollen of *D. jueirana-facao* is shed in monads. *D. jueirana-facao* is considered critically endangered following IUCN conservation criteria, whereas *D. excelsa* is assessed to be of least concern. A lectotype is designated for *D. excelsa*.

Taxonomic novelties in *Myrcia guianensis* and allied species (Myrtaceae: Myrteae), including mass-typification in a large and taxonomically challenging group.

Lima, D. F., Goldenberg, R. & Lucas*, E. (2018). *Kew Bulletin* 73: 5. DOI: 10.1007/s12225-017-9729-y.

The '*Myrcia guianensis* group', or *Guianensis* clade, comprises c. 30 species distributed mainly in the Cerrado and Atlantic Forest biomes of Brazil. The group is currently being monographed and during this process, type collections have been analysed and a thorough literature search completed; 36 new synonyms are recognised, and 95 lectotypifications and five neotypifications are made.

A new infra-generic classification of the species-rich Neotropical genus *Myrcia s.l.*

Lucas*, E. J. *et. al.* (including Lughadha*, E. N., Vasconcelos*, T. N. C.) (2018). *Kew Bulletin* 73: 9–21. DOI: 10.1007/S12225-017-9730-5.

A new classification of the large Neotropical genus *Myrcia s.l.* is proposed. Nine sections are presented that correspond to recently published clades. Of these nine sections, sects. *Myrcia*, *Aulomyrcia* and *Sympodiomyrcia* are already published, sects. *Reticulosae* and *Tomentosae* are new sections, sect. *Eugeniopsis* is a new combination whilst sects. *Aguava*, *Calyptranthes* and *Gomidesia* are new combinations at a new rank (comb. & stat. nov.). Six lectotypifications are made for sections or genera. Estimates of species per section are listed.

Formal description of sequence based voucherless Fungi: promises and pitfalls, and how to resolve them.

Lücking, R. & Hawksworth*, D. L. (2018). *IMA Fungus* 9: 143–166. DOI: 10.5598/imafungus.2018.09.01.09.

There is urgent need for a formal nomenclature of sequence-based, voucherless Fungi, given that environmental sequencing has accumulated more than one billion fungal ITS reads in the Sequence Read Archive, about 1,000 times as many as fungal ITS sequences in GenBank. These unnamed Fungi could help to bridge the gap between 115,000 to 140,000 currently accepted and 2.2 to 3.8 million predicted species, a gap that cannot realistically be filled using specimen or culture-based inventories. The Code never aimed at placing restrictions on the nature of characters chosen for taxonomy, and the requirement for physical types is now becoming a constraint on the advancement of science. We elaborate on the promises and pitfalls of sequence-based nomenclature and provide potential solutions to major concerns of the mycological community. Types of sequence-based taxa, which by default lack a physical specimen or culture, could be designated in four alternative ways: (1) the underlying sample ('bag' type), (2) the DNA extract, (3) fluorescent in situ hybridization (FISH), or (4) the type sequence itself. Only (4) would require changes to the Code and the latter would be the most straightforward approach, complying with three of the five principal functions of types better than physical specimens. A fifth way, representation of the sequence in an illustration, has been ruled as unacceptable in the Code. Potential flaws in sequence data are analogous to flaws in physical types, and artifacts are manageable if a stringent analytical approach is applied. Conceptual errors such as homoplasy, intragenomic variation, gene duplication, hybridization, and horizontal gene transfer, apply to all molecular approaches and cannot be used as a specific argument against sequence-based nomenclature. The potential impact of these phenomena is manageable, as phylogenetic species delimitation has worked satisfactorily in Fungi. The most serious shortcoming of sequence-based nomenclature is the likelihood of parallel classifications, either by describing taxa that already have names based on physical types, or by using different markers to delimit species within the same lineage. The probability of inadvertently establishing sequence-based species that have names available is between 20.4 % and 1.5 % depending on the number of globally predicted fungal species. This compares favourably to a historical error rate of about 30 % based on physical types, and this rate could be reduced to practically zero by adding specific provisions to this approach in the Code. To avoid parallel classifications based on different markers, sequence-based nomenclature should be limited to a single marker, preferably the fungal ITS barcoding marker; this is possible since sequence-based nomenclature does not aim at accurate species delimitation but at naming lineages to generate a reference database, independent of whether these lineages represent species, closely related species complexes, or infraspecies. We argue that clustering methods are inappropriate for sequence-based nomenclature; this approach must instead use phylogenetic methods based on multiple alignments, combined with quantitative species recognition methods. We outline strategies to obtain higher-level phylogenies for ITS-based, voucherless species, including phylogenetic binning, 'hijacking' species delimitation methods, and temporal banding. We conclude that voucherless, sequence-based nomenclature is not a threat to specimen and culture-based fungal taxonomy, but a complementary approach capable of substantially closing the gap between known and predicted fungal diversity, an approach that requires careful work and high skill levels.

Yanomami Vernacular of the Brazilian Amazon.

Milliken*, W. (2017). *In:* Piesik, S. (ed.) *HABITAT: Vernacular Architecture for a Changing Planet*. Thames and Hudson, pp.78–81.

No abstract available.

Grass survey of the Itremo Massif records endemic central highland grasses.

Nanjarisoa*, O. P., Besnard, G., Ralimanana*, H., Jeannoda, H. V. & Vorontsova*, M. S. (2017). *Madagascar Conservation & Development* 12: 34–40. DOI: 10.431 4/mcd.v12i1.6.

Despite the substantial area covered by grasslands in Madagascar (65%), the taxonomy of the grasses (Poaceae), which represent the main plant component of these vegetation types, is still understudied. Inventories and detailed specimen identification work from 1 2 localities in the Itremo Massif Protected Area allowed us to compile a list of grasses present in the area. In total, members of eight subfamilies, 56 genera, and 99 species have been recorded from the Itremo Massif. Grasslands cover 75% of the Itremo Massif Protected Area and are dominated by Panicoideae (65%) and by C4 plants. The genera *Eragrostis* and *Panicum*, with nine and eight species respectively, are the best represented genera in Itremo. Eragrostis betsileensis and Tristachya betsileensis are the two species known to be local endemics. Twenty species are endemic to the central highlands, and a further 1 4 species are restricted to Madagascar. Five ecological groups of grasses were identified in the Itremo Massif: shade species in gallery forests, open wet area species, fire grasses, anthropogenic disturbance associated grasses and rock-dwelling grasses. Grasslands of the Itremo Massif are likely to be at least partly natural as shown by their richness in terms of endemic and native grass species. Conservation of such grasslands is thus an important issue, not only for grasses but for all species that inhabit these open canopy habitats.

Phylogenetics of *Eria* and related genera (Orchidaceae: Podochileae).

Ng, Y. P., Schuiteman*, A., Pedersen, H. Æ., Petersen, G., Watthana, S., Seberg, O., Pridgeon*, A. M., Cribb*, P. J. & Chase*, M. W. (2018). *Botanical Journal of the Linnean Society* 186: 179–201. DOI: 10.1093/botlinnean/box088.

A phylogenetic hypothesis for tribe Podochileae with emphasis on subtribe Eriinae s.s. is based on nucleotide sequences of the nuclear ITS and four plastid regions (matK, trnL-F spacer, trnL intron and ycf1). The strict consensus tree based on parsimony is largely congruent with the maximum likelihood tree with a few major differences; most importantly, monophyly of Podochileae as recently circumscribed is strongly supported by the maximum likelihood tree but not recovered in the parsimony analysis. Monophyly of Thelasiinae s.s. (without *Ridleyella*) and Eriinae *s.l.* (including Podochilinae) is supported, whereas *Eria s.l.* appears polyphyletic. The generic circumscription of Eriinae *s.s.* (excluding Podochilinae) is revised, and 21 genera are accepted, including two not previously recognized. Nomenclatural changes and a key to genera in Eriinae are provided.

Identifying novel features from specimen data for the prediction of valuable collection trips.

Nicolson*, N. & Tucker, A. (2017). *In*: Adams, N., Tucker, A. & Weston, D. (eds.) *IDA 2017: Advances in Intelligent Data Analysis XVI*. London: Springer. 10584: pp. 235–246.

Primary biodiversity data provide "what, where, and when" data points: the assertion that a species occurred at a particular point in space and time. These are most valuable when associated with specimens stored in natural history museums and herbaria, which evidence the assertions with reference to a physical specimen. The research presented uses novel data-mining techniques to uncover two hidden dimensions in specimen data - who collected the specimens and how they were collected. A combination of unsupervised and supervised learning techniques are used, which establish two new entities: collector and collection trip. Features are defined against these higher order representations of the data, which support the use of the data to answer novel questions such as which collection trips discover the most new species? We explore the features by building classifiers to predict species discovery, and compare these with a baseline model grouped using collector team transcriptions derived from the raw specimen data. Preliminary results are promising and whilst the particular focus of this research was botanical specimens, the technique is equally applicable to datasets of field-collected specimens from other scientific domains.

New discoveries: Species of fungi described in 2017.

Niskanen*, T., Douglas*, B., Kirk*, P. M., Crous, P. D., Lücking, R., Matheny, P. B., Cai, L., Hyde, K. D. & Cheek*, M. (2018). *In:* Willis*, K. J. (ed.) *State of the World's Fungi*. Richmond: Royal Botanic Gardens, Kew, pp. 18–23.

How many new species of fungi were described in 2017? Which groups do they represent, where were they found and what are some of the more surprising discoveries?

Identifying and naming the currently known diversity of the genus *Hydnum* with an emphasis on North American and European materials.

Niskanen*, T., Liimatainen*, K., Nuytinck, J., Kirk*, P., Orijel, R., Norvell, L., Olariaga, I., Huhtinen, S., Kytovuori, I., Ruotsalainen, J., Niemela, T., Ammirati, J. & Tedersoo, L. (2018). *Mycologia*: DOI: 10.1080/00275514.2018.1477004.

In this study, 49 species of *Hydnum* are recognized worldwide. Twenty-two of them are described here as new species. Epitypes are proposed for *H. repandum* and *H. rufescens*. The majority of the species are currently known only from a single continent. The barcodes produced in this study are deposited in the RefSeq database and used as a basis to name species hypotheses in UNITE. Eleven infrageneric clades recovered in a phylogenetic analysis are supported by morphological characteristics and formally recognized: subgenera *Alba*, *Hydnum*, *Pallida*, and *Rufescentia*; sections *Hydnum*, *Olympica*, *Magnorufescentia*, and *Rufescentia*; and subsections *Mulsicoloria*, *Rufescentia*, and *Tenuiformia*.

Psychronectria hyperantarctica gen. comb. nov., epitypification and phylogenetic position of an Antarctic bryophilous ascomycete.

Pawłowska, J., Istel, L., Gorczak, M., Galera, H., Wrzosek, M. & Hawksworth*, D. L. (2017). *Mycologia* 109: 601–607. DOI: 10.1080/00275514.2017.1398575.

The holotype of *Thyronectria hyperantarctica* was re-examined, redescribed, and compared with new collections of an Antarctic bryophilous ascomycete from a similar area. Because the condition of type material was insufficient for molecular studies, the authors designated an epitype from newly collected material with a high degree of morphological similarity to the holotype and paratype material. Phylogenetic analysis of the epitype revealed that its closest phylogenetic affinity was with the family Tilachlidiaceae and it formed a monophyletic group in this lineage within other collections of the species. Therefore, the new monotypic genus *Psychronectria* is described to accommodate *Thyronectria hyperantarctica*. The fungus is superficially similar to *Thyronectria* species in Nectriaceae, but the ascospores differ in color, size, and type of septation.

A monograph of the *Hydriastele wendlandiana* group (Arecaceae: Hydriastele).

Petoe*, P., Cámara-Leret*, R. & Baker*, W. J. (2018). *Kew Bulletin* 73: 17. DOI: 10.1007/s12225-018-9736-7.

A taxonomic revision is presented of the *Hydriastele wendlandiana* group, a well-defined species grouping within the Indo-Pacific palm genus *Hydriastele* that occurs in New Guinea, the Bismarck Archipelago and northern Australia. We accept five species: *Hydriastele kasesa*, *H. rheophytica*, *H. variabilis*, *H. wendlandiana* and *H. apetiolata sp. nov.* and provide fundamental information about each of those taxa including a summary of the group's taxonomic history and phylogeny, a distribution map, a key to the species, species descriptions with scientific illustrations, and IUCN Red List assessments.

A monograph of *Hydriastele* (Areceae, Arecaceae) in New Guinea and Australia.

Petoe*, P., Heatubun*, C. D. & Baker*, W. J. (2018). *Phytotaxa* 370 (1): 1–92. DOI: 10.11646/phytotaxa.370.1.1.

A taxonomic revision of the genus *Hydriastele* H.Wendl. & Drude in New Guinea, Australia and immediately adjacent islands is presented. We recognise 25 species from this area including three new species of robust tree palms from New Guinea: *Hydriastele calcicola*, *H. lanata* and *H. wosimiensis*. All species are described in full in the taxonomic treatment, with accompanying botanical illustrations, photographs, distribution maps and preliminary IUCN Red List Assessments. In addition, a key to the species in New Guinea and Australia is provided as well as a systematic conspectus placing all 39 accepted species of *Hydriastele* in an informal infrageneric framework.

Mesanthemum tuberosum Lecomte resurrected from *M. prescottianum* (Bong.) Körn. (Eriocaulaceae), variation and lectotypification.

Phillips*, S. M., Fofana, F. & Cheek*, M. (2018). *Kew Bulletin* 73 (13): 9744-9747. DOI: 10.1007/s12225-018-9744-7.

Mesanthemum prescottianum is a West African species occurring in the uplands extending from Guinea to Ivory Coast. Variation within the species is discussed and the synonym *M. tuberosum* Lecomte is raised to specific status. The conservation status of the first species is assessed using the IUCN 2012 standard as Least Concern, and the second as Vulnerable. Lectotypes are selected for both names. The type location of *M. prescottianum*, claimed to be Brazil, is shown to be an error.

Pleistocene population expansions of shade-tolerant trees indicate fragmentation of the African rainforest during the Ice Ages.

Piñeiro*, R., Dauby, G., Kaymak, E. & Hardy, O. J. (2017). *Proceedings of the Royal Society B: Biological Sciences* 284 (1866): 20171800. DOI: 10.1098/rspb.2017.1800.

The fossil record in tropical Africa suggests that dry conditions during the Ice Ages caused expansion of savannahs and contraction of the rainforest. Forest refugia have been proposed to be located in areas of Central Africa that currently harbour high rates of endemic species. However, to what extent the forest was fragmented remains unknown. Nuclear microsatellites and plastid sequences of 732 trees of two species occurring in the same habitat—mature lowland evergreen rainforests—but with remarkably different dispersal capacities—animal versus gravity—were analysed. Geographical information system tools revealed intraspecific lineages partially congruent across the two species, suggesting common past barriers to gene flow in Central Africa. According to approximate Bayesian computation, the intraspecific genetic clusters diverged during the Pleistocene (less than 2 Ma), so that intraspecific differentiation is the appropriate scale to test the aridification effect of the Ice Ages on tree populations. Demographic tests revealed clear genetic signals of population expansion in both taxa, possibly following bottleneck events after forest fragmentation, with stronger evidence of expansion after the Penultimate rather than after the Last Glacial Maximum. The differential dispersal capacity may have modulated the particular response of each species to climate change, as revealed by the stronger evidence of expansion found in the animal-dispersed species than in the gravity-dispersed one.

A new species of *Panopsis* (Proteaceae) from Bahia, Brazil.

Prance*, G. T. (2017). *Brittonia* 70 (1): 111–114. DOI: 10.1007/s12228-017-9497-x.

Recent collections from Bahia, Brazil included a new species of *Panopsis* from the Atlantic rainforest. So far it is only known with fruits, which are much larger than in most species of the genus. *Panopsis magnifructa* is described and compared to other species in the genus. It is only the second species of the genus known in the State of Bahia, Brazil.

Aloe belitsakensis (Asphodelaceae): a new species from north-western Madagascar.

Rakotoarisoa*, S. & Grace*, O. M. (2017). *Phytotaxa* 328 (3): 276–282. DOI: 10.11646/phytotaxa.328.3.6.

Madagascar is a major centre of diversity for the leaf-succulent genus *Aloe* Linnaeus (1753: 319) accounting for roughly a third of *Aloe* species (Carter et al. 2011). Approximately 128 species and 161 taxa are known from the region and all are restricted to Madagascar (Rakotoarisoa. 2014) and/or the nearby Mascarene archipelago. New taxa are described from these islands at a rate that rivals the ongoing discovery of aloes elsewhere in their natural range, on the African continent or Arabian Peninsula (Crouch et al. 2013). Extinction risks are alarmingly high among species of Aloe in this region. Conservatively, 39% of species are known to be threatened, and this figure is likely to be significantly higher (Rakotoarisoa et al. 2014), since several species have not been observed or collected for many decades. The Kew Madagascar Conservation Centre (KMCC) aims to record and collect the rare and threatened flora of Madagascar to ensure its conservation, and the genus Aloe is a priority for the dryland programme.

Joseph D. Hooker's 1839 Cabo Verde Collections.

Rico Arce*, M., Duarte, M. C., Romeiras, M. M., Santos-Guerra, A., Nepi, C. & Francisco-Ortega, J. (2017). *Curtis's Botanical Magazine* 34 (3): 146–168. DOI: 10.1111/curt.12193.

Joseph Dalton Hooker (1817–1911) was 22 years old when he undertook his first natural history journey abroad. He was appointed 'Assistant Surgeon', under the command of James Clark Ross in the Antarctic Expedition 1838–1845, also known as the South Pole Magnetic Expedition. The two HMS ships The Terror and The Erebus made brief stops in the Macaronesian islands of Madeira, Tenerife (the Canaries), and Santiago (Cabo Verde) where Hooker took the opportunity to observe and collect animals, plants and minerals, so these were the first three collecting sites documented in his Antarctic Journal.

(2618) Proposal to conserve *Bulbostylis*, nom. cons. (Cyperaceae) against an additional name, *Nemum*.

Roalson, E. H., Simpson*, D. A. & Larridon*, I. (2018). *Taxon* 67 (3): 642. DOI: 10.12705/673.23.

No abstract available.

Elatostema muluense (Urticaceae), a new species from the extraordinary caves of Gunung Mulu National Park, Malaysia.

Rodda, M. & Monro*, A. K. (2018). *Kew Bulletin* 73: 41. DOI: 10.1007/s12225-018-9768-z.

A new species, *Elatostema muluense*, is described and illustrated. It is endemic to the limestone karst of Gunung Mulu National Park and most closely resembles *E. pinnativenium*, a species from Kinabalu Park in Sabah. An assessment of its conservation status using IUCN categories and methodologies evaluates the species as Vulnerable to extinction (VU).

Six new species of *Microlicia* (Melastomataceae) from Bahia, Brazil.

Romero, R. & Woodgyer*, E. M. (2018). *Kew Bulletin* 73: 22. DOI: 10.1007/S12225-018-9747-4.

Microlicia abairana, *M. aureoglandulosa*, *M. crispa*, *M. curticalycina*, *M. ganevii* and *M. restingae* are described from Bahia state, Brazil. Comprehensive descriptions of the species are provided, including detailed illustrations, and statements of geographical distribution, habitat and IUCN conservation status.

Recognition of the genus *Thaumatophyllum* Schott – formerly *Philodendron* subg. *Meconostigma* (Araceae) – based on molecular and morphological evidence.

Sakuragui, C. M., Calazans, L. S. B., Oliveira, L. L., Morais, E. B., Benko-Iseppon, A. M., Vasconcelos, S., Schrago, C. E. G. & Mayo*, S. J. (2018). *Phytokeys* 98: 51–71. DOI: 10.3897/phytokeys.98.25044.

Philodendron subgenus *Meconostigma* has been a well-circumscribed group since 1829. Members of this group are easily distinguished by diagnostic morphological characters as well as by a distinct ecology and geographical distribution. Based on molecular, morphological and cytological evidence, we propose the recognition of *P.* subg. *Meconostigma* as a distinct genus, *Thaumatophyllum* Schott. We also present the necessary new combinations, an emended key and some nomenclatural and taxonomic corrections regarding 21 names of *Thaumatophyllum*.

Diversity of *Chroogomphus* (Gomphidiaceae, Boletales) in Europe, and typification of *C. rutilus*.

Scambler*, R., *et al*. (including Niskanen*, T., Ainsworth*, A. M., Kirk*, P. M. & Liimatainen*, K. (2018). *IMA Fungus* 9 (2): 271–290. DOI: 10.5598/imafungus.2018.09.02.04.

In this study, eight species of *Chroogomphus* are recognized from Europe: *C. britannicus*, *C.* aff. *filiformis* 1, *C. fulmineus*, *C.* cf. *helveticus*, *C. mediterraneus*, *C.* cf. *purpurascens*, *C. rutilus*, and *C. subfulmineus*. Different candidates for the application of the name *C. rutilus* are evaluated and the best fit to the description is selected; lecto- and epitypes are chosen to fix the name. *Chroogomphus fulmineus* and *C. mediterraneus* are also epitypified and a new species, *C. subfulmineus*, is described. The infrageneric classification is revised and a new subgenus *Siccigomphus* and three new sections, *Confusi*, *Filiformes*, and *Fulminei* are introduced. The former sections *Chroogomphus* and *Floccigomphus* are elevated to subgeneric level. Comparison of the ITS regions (nuc rDNA ITS1-5.8S-ITS2) of all species studied shows that there is a minimum interspecific difference of 1.5 %, with the exception of the two species belonging to sect. *Fulminei* which differ by a minimum of 0.9 %. Ecological specimen data indicate that species of *Chroogomphus* form basidiomes under members of Pinaceae, with a general preference for species of *Pinus*. Five European species have been recorded under *Picea*, while *Abies* and *Larix* have also been recorded as tree associates, although the detailed nutritional relationships of the genus, involving other suilloid fungi in particular, have yet to be fully clarified.

Cortinarius conicoumbonatus (*Cortinarius* subgen. *Telamonia* sect. *Hinnulei*): A new species from spruce-beech forests of the East Black Sea Region of Turkey.

Sesli, E. & Liimatainen*, K. (2018). *Turkish Journal of Botany* 42: 327–334. DOI: 10.3906/bot-1710-8.

Cortinarius conicoumbonatus is described as new to science based on the material collected from spruce-beech forests of Maçka, Trabzon, Turkey. The new species belongs to subgenus *Telamonia* section *Hinnulei*. A full description, *in situ* and micromorphological illustrations, a phylogenetic tree, and a short discussion are provided.

Olinia chimanimani (Penaeaceae), a new species endemic to the Chimanimani Mountains of Mozambique and Zimbabwe.

Shah*, T., Darbyshire*, I. & Matimele, H. (2018). *Kew Bulletin* 73: 36. DOI: 10.1007/S12225-018-9757-2.

Olinia chimanimani T. Shah & I. Darbysh. is described as a distinct species from the Chimanimani mountains in Mozambique and Zimbabwe, based on morphological evidence. It differs from other species of *Olinia* sect. *Rochetiana* in its smaller leaf size, sessile leaf attachment, glabrous flowers and galled flowers becoming narrowly swollen without prominent tubercles when infected. A species description, key and illustration, distribution map and ecological information are provided. The populations have been studied in the field, and it is only known from two locations. It is potentially under threat from burning due to human activity associated with

illegal artisanal mining activity, and thus has been evaluated as Endangered (EN) using the IUCN Red List categories and criteria.

Sir Joseph Dalton Hooker in the Kew Archive.

Sharp Jones*, C. (2018). *Curtis's Botanical Magazine* 34 (3): 203–210.

Sir Joseph Dalton Hooker was born in Halesworth, Suffolk in 1917. The second son of Sir William Jackson Hooker, Joseph Hooker would, throughout the course of his life, become one of the most famous and lauded scientists of his day. At its pinnacle, Joseph Hooker's career would see him hold the post of Director of the Royal Botanic Gardens, Kew for 20 years (1865–1885), and be the first botanist after Joseph Banks to be elected President of the Royal Society between 1873 and 1878. His archives and letters, which are described here, are held in the Library, Art and Archives at Kew.

Typification of *Piper* species (Piperaceae) in Southeast Asia, especially Thailand.

Suwanphakdee, C., Simpson*, D. A., Hodkinson, T. R. & Chantaranothai*, P. (2018). *Kew Bulletin* 73 (33): DOI: 10.1007/s12225-018-9761-6.

A nomenclatural revision of 13 species of *Piper* is presented (*P. arcuatum*, *P. caninum*, *P. crassipes*, *P. griffithii*, *P. kurzii*, *P. longum*, *P. muricatum*, *P. pedicellatum*, *P. porphyrophyllum*, *P. ribesioides*, *P. ridleyi*, *P. rostratum* and *P. sylvaticum*). A total of 23 lectotypifications are made and many names are reduced to synonymy. Diagnostic characteristics, line drawings, colour illustrations and distributional information of each species are given.

Melanthiaceae.

Trias-Blasi*, A., Suksathan, P. & Tamura, M. N. (2017). *In: Flora of Thailand*. Bangkok: The Forest Herbarium. Vol. 13, pp. 520–524.

No abstract available.

A revised conspectus of *Uncaria* (Rubiaceae).

Turner*, I. M. (2018). *Webbia* 73 (1): 9–21. DOI: 10.1080/00837792.2018.1445363.

The outline revision of the genus *Uncaria* published by Ridsdale in 1978 is updated. Two taxa treated as synonyms by Ridsdale (*U. ovata* R.Br. ex Hook.f. and *U. rhynchophylloides* F.C.How) are recognised as good species. Three names are considered as synonyms of different taxa from those given by Ridsdale, so *U. ovalifolia* Roxb. is moved from *U. acida* (W.Hunter) Roxb. to *U. sessilifructa* Roxb., *Nauclea rotundifolia* Bartl. ex DC. and its homotypic synonyms are relocated to *U. longiflora* (Poir.) Merr. var. *longiflora* from *Uncaria cordata* f. *insignis* (Bartl. ex DC.) Ridsdale, and *Uncaria forbesii* Wernham is transferred from *U. acida* to *U. callophylla* Blume ex Korth. The names *Cinchona kattukambar* J.Koenig ex Retz., *U. rhynchophylla* (Miq.) Miq. and *U. scandens* (Sm.) Wall. were validated earlier than listed by Ridsdale. Lectotypes and neotypes are designated for various names.

From India to Madeira and back again: a new combination for a wide-ranging *Spergularia* (Caryophyllaceae).

Turner*, I. M. (2017). *Willdenowia* 47 (3): 213–216. DOI: 10.3372/wi.47.47303.

A recently published phylogenetic analysis strongly supports the inclusion of *Spergula fallax* (Lowe) E. H. L. Krause in the genus *Spergularia* (Pers.) J. Presl & C. Presl (Caryophyllaceae), where it was originally described. This species of spurrey, which occurs across North Africa, the Middle East and N India, has also been named *Arenaria flaccida* Roxb., which is a later homonym and therefore illegitimate. *Stipularia flaccida* Madden is an overlooked replacement name for *A. flaccida* and is the earliest legitimate name for the species. The new combination *Spergularia flaccida* (Madden) I. M. Turner is proposed here. In addition, lectotypes are designated for *A. flaccida* and its taxonomic synonyms *Lepigonum eximium* Kindb., *Spergula flaccida* f. *purpurascens* Maire & Sauvage, *Spergula pentandra* var. *intermedia* Boiss. and *Spergularia fallax* Lowe.

A new combination in *Genianthus* (Apocynaceae – Secamonoideae).

Turner*, I. M. (2018). *Thai Forest Bulletin (Botany)* 46 (1): 40–43. DOI: 10.20531/tfb.2018.46.1.06.

The new combination *Genianthus micranthus* (Roxb.) I.M.Turner is proposed to replace '*Genianthus laurifolius* (Roxb.) Hook.f.', the supposed basionym of which (*Asclepias laurifolia* Roxb.) is an illegitimate later homonym. A lectotype is designated for *Asclepias laurifolia* Roxb. to replace an earlier erroneous selection.

A new combination in *Pseuderanthemum* (Acanthaceae).

Turner*, I. M. (2018). *Reinwardtia* 17 (1): 55–57. DOI: 10.14203/reinwardtia.v17i1.3517.

A new combination is provided in *Pseuderanthemum* for *Eranthemum diantherum* Roxb., an Acanthaceae species from the Moluccas. *Pseuderanthemum depauperatum* Merr. is a synonym of *Pseuderanthemum diantherum*. Lectotypes for *Eranthemum diantherum* and *Pseuderanthemum depauperatum* are designated.

The importance of the plates in the Verhandelingen over de natuurlijke geschiedenis der Nederlandsche overzeesche bezittingen, Botanie for the nomenclature of South-East Asian plants.

Turner*, I. M. (2018). *Taxon* 67 (3): 621–631. DOI: 10.12705/673.14.

The botany volume of the Verhandelingen over de natuurlijke geschiedenis der Nederlandsche overzeesche bezittingen was written by P.W. Korthals. It contains accounts of nearly 200 plant species from what is now western Indonesia, and includes 70 plates. The volume was published in seven parts from 1840 to 1844. A large number of the plates were published before the text that included the subjects of the illustrations. As these mostly meet the requirements of an illustration with analysis, the species names on the plates were validated before the text descriptions. This includes a number of generic names validated by the equivalent of a descriptio generico-specifica. All such cases from Korthals's work are here listed with the correct publication date. Due to overlooked homonymy, *Ploiarium elegans* Korth. is the correct name for *P. alternifolium* (Szyszył.) Melch. The names *Gordonia ovalis* and *Mitragyna speciosa* should be attributed to Korthals. The new combination *Dissochaeta pachygyna* (Korth.) I.M. Turner is proposed. The combination *Polyspora vulcanica* is validated. Lectotypes are designated for 14 names, and 5 second-step designations of lectotype are proposed.

Notes on the genus *Uncaria* (Rubiaceae) in Singapore.

Turner*, I. M. (2018). *Gardens' Bulletin, Singapore* 70: 9–12.

Flora of Singapore precursors, 4. A summary of scandent *Psychotria* (Rubiaceae) in Singapore and Peninsular Malaysia.

Turner*, I. M. & Kumar, V. S. (2018). *Phytotaxa* 361 (2): 183–197. DOI: 10.11646/phytotaxa.361.2.4.

A total of 18 species of *Psychotria* with a climbing and/or hemi-epiphytic habit are enumerated as native to Peninsular Malaysia and Singapore. This number includes one newly described species, *Psychotria deltata*, known from Johore and Singapore; and one taxon raised to species rank, *Psychotria euosma* (based on *Psychotria sarmentosa* var. montana). A new record for *Psychotria serpens* from Peninsular Malaysia is presented, and a number of collections are tentatively placed in *Psychotria chartacea*, a species from Peninsular Thailand. Four species are added to the list of native taxa for Singapore. *Psychotria kunstleri* is synonymised with *Psychotria ridleyi* and *P. cantleyi* is reduced to *P. scortechinii*. Lectotypes are designated for nearly all names applied to climbing *Psychotria* taxa for Peninsular Malaysia and Singapore including the Linnaean species *P. serpens*.

From stowaways to karst-aways: unloading the Peninsular Malaysia endemic *Polyalthia brunneifolia* (Annonaceae).

Turner*, I. M., Tan*, J. P. C. & Utteridge*, T. M. A. (2018). *Nordic Journal of Botany* 36 (5): DOI: 10.1111/njb.01693.

Detailed examination of specimens collected from limestone outcrops in Peninsular Malaysia and previously included in *Polyalthia brunneifolia* shows that they do not belong in this species. Three new species are described to accommodate these collections: *Polyalthia chinii* I.M.Turner & Utteridge from Bukit Serdam, Raub, Pahang; *P. guabatuensis* I.M.Turner & Utteridge from Batu Caves, Selangor, and *P. guamusangensis* I.M.Turner & Utteridge from Gua Musang, Kelantan. Conservation assessments are included for the new species and the general threats faced by species confined to limestone hills are discussed. In addition, an updated key to all species of Polyalthia known from Peninsular Malaysia is provided.

A new species of *Alphonsea* (Annonaceae).

Turner*, I. M. & Utteridge*, T. M. A. (2017). *Thai Forest Bulletin (Botany)* 45 (1): 42–46. DOI: 10.20531/tfb.2017.45.1.08.

Alphonsea isthmicola I.M.Turner & Utteridge is described. It is a species of tree currently known from two limestone outcrops in Peninsular Thailand and one limestone hill near the Thai border in Peninsular Malaysia. A key to the *Alphonsea* species of Peninsular Malaysia and Southern Thailand is included.

Talbotiella cheekii (Leguminosae: Detarioideae), a new tree species from Guinea.

van der Burgt*, X. M., Molmou, D., Diallo, A., Konomou, G., Haba, P. M. & Magassouba, S. (2018). *Kew Bulletin* 73 (26). DOI: 10.1007/s12225-018-9755-4.

Talbotiella cheekii Burgt, a new tree species from Guinea, is described and illustrated. It is a tree to 24 m high, with a stem diameter to 83 cm, and occurs in forest dominated by tree species of the Leguminosae subfamily Detarioideae, on rocky stream banks and rocky hill slopes, at an altitude of 100 – 600 m. It is estimated that 1600 – 2400 mature trees have been seen, in about twelve forest patches; more trees may be present in places not yet visited. One of the localities of the new species is situated at only 46 km northeast of the centre of the capital Conakry and 6 km northeast of the town centre of Coyah, part of the Conakry urban agglomeration. Its distribution is 1400 km further west from the previous westernmost distribution of the genus. The current extent of occurrence is 166 km^2. *Talbotiella cheekii* is here assessed as Endangered (EN) following IUCN Red List categories.

One new species, two new combinations and taxonomic notes on the All-spice genus *Pimenta* (Myrtaceae) from Hispaniola.

Vasconcelos*, T. N. C., Lucas*, E. J. & Peguero, B. (2018). *Phytotaxa* 348: 32–40.

One new species and two new combinations are here published as taxonomic updates on the all-spice genus *Pimenta* (Myrtaceae) for the flora of Hispaniola, Greater Antilles. *Pimenta berciliae* is a small tree, the type of which was found in the vicinity of the National Botanical Gardens in Santo Domingo. Natural populations of this species are restricted to a small area in Samaná and Cordillera Septentrional, and the preliminary assessment of its conservation status indicates an endangered species. Additionally, *Eugenia yumana* and *Eugenia samanensis* are here formally transferred to *Pimenta* after molecular and morphological analyses demonstrate that they belong to this latter genus. Two new combinations, *Pimenta yumana* and *Pimenta samanensis* are here provided. These three additions to the flora of *Pimenta* in Hispaniola increase the known diversity of the genus on the island and are important to better understand the diversity of the all-spice genus in the region.

Identification guide to grasses and bamboos in Madagascar.

Vorontsova*, M. S., Dransfield*, S., Renvoize*, S. A., Besnard, G., McRobb*, A., Razanatsoa, J., Nanjarisoa*, O. P., Rakotoarisoa*, S. E. & Ralimanana*, H. (2018). Royal Botanic Gardens, Kew: Kew Publishing.

Grasses and bamboos are part of the same botanical group, the grass family, also called Poaceae, a family with an estimated 12,000 species. Grasses occur throughout the world with similar diversity in the tropical and temperate regions, in all climates, and at all elevations. Madagascar is no exception, and the grass family is the most economically important group of plants which has always been closely involved in people's lives. Madagascar's grasses are still poorly known and many endemic species have only been recorded once or twice, and more collections and records are necessary to understand the true diversity and species distribution. This guide hopes to encourage study and collecting of grasses by showing how beautiful and interesting these plants can be, and by providing a practical means of identification at the generic level. This book compiles and summarises the current available knowledge on the genera of Madagascar Poaceae, with an emphasis on easily visible characters to verify generic identity. 144 grass genera are described with colour scans to aid recognition.

Dovyalis keniensis (Salicaceae), a new species from the coastal forests of Kenya.

Williams*, E. V. (2017). *Kew Bulletin* 72: 51. DOI: 10.1007/s12225-017-9723-4.

Dovyalis keniensis E. V. Williams (Salicaceae) is described as a new species from the coastal forests of Kenya. The species is illustrated, its distribution mapped and conservation status assessed. It is compared with *D. mollis* (Oliv.) Warb. and *D. hispidula* Willd. A key to the four species of *Dovyalis* in Kenya is presented.

Salvia macrophylla.

Wood*, J. R. I. (2018). *Curtis's Botanical Magazine* 35 (1): 75–88. DOI: 10.1111/curt.12226.

Salvia macrophylla Benth. from the Andes of South America is described and illustrated. Information is provided about the life of the almost forgotten collector Andrew Mathews, who discovered the plant in 1833. It is placed within both traditional and newer infrageneric classifications of American *Salvia* and a key to distinguish it from similar species is provided. Current concepts of the genus *Salvia* are briefly discussed. *S. macrophylla* is commonly grown in the northern hemisphere and cultivation methods, horticultural varieties and hybrids with *S. sagittata* are described.

El género *Ipomoea* L. (Convolvulaceae) en Paraguay.

Wood*, J. R. I., Degen de Arrua, R. & Scotland, R. W. (2017). *Rojasia* 16: 9–22.

No abstract available.

Distribution and endemism of the genus *Ipomoea* (Convolvulaceae) in eastern Bolivia and its biogeographical implications.

Wood*, J. R. I. & Martinez-Ugartache, M. T. (2018). *Kempffiana* 14 (1): 13–21.

En Bolivia, el género *Ipomoea* L. es mucho más diverso en el departamento de Santa Cruz que en otras regiones del país. Según Wood et al., hasta el 2015, de las 102 especies registradas para Bolivia, 87 estaban presentes en el departamento de Santa Cruz. Sin embargo, recientemente, estas cifras han aumentado como resultado de la revisión de muestras de herbario y colecciones de campo, llegando a identificar 108 especies para Bolivia, de las cuales, 90 se encuentran en Santa Cruz, convirtiéndose de

esta manera en uno de los géneros más diversos a nivel nacional y departamental, y cuya diversidad, además, incluye una serie de especies endémicas y otras con patrones de distribución interesantes desde el punto de vista biogeográfico.

Proposal to reject the name *Ipomoea emetica* (Convolvulaceae).

Wood*, J. R. I. & McDonald, J. A. (2018). *Taxon* 67 (1): 210–211. DOI: 10.12705/671.22.

No abstract available.

New species of *Ipomoea* (Convolvulaceae) from Souh America.

Wood*, J. R. I., Muñoz-Rodríguez, P., Degen, R. & Scotland, R. W. (2017). *Phytokeys* 88: 1–38. DOI: 10.3897phyotkeys.88.12891.

The importance of discovering, describing and cataloguing poorly known species in herbarium collections is discussed. It is a spur to efforts at rediscovery and consequent conservation efforts. The problems faced in describing species from limited material are discussed and our methods and criteria in making a decision are described. Prospects for future novelties are briefly assessed. Fifteen new species are described and illustrated with line drawings and distribution maps: *Ipomoea attenuata* J.R.I. Wood & Scotland, *I. cuscoensis* J.R.I. Wood & P. Muñoz, *I. dasycarpa* J.R.I. Wood & Scotland, *I. dolichopoda* J.R.I. Wood & R. Degen, *I. ensiformis* J.R.I.Wood & Scotland, *I. fasciculata* J.R.I. Wood & Scotland, *I. graminifolia* J.R.I. Wood & Scotland, *I. kraholandica* J.R.I. Wood & Scotland, *I. longirostra* J.R.I. Wood & Scotland, *I. revoluta* J.R.I. Wood & Scotland, *I. scopulina* J.R.I. Wood &. Scotland, *I. uninervis* J.R.I. Wood & Scotland, *I. veadeirosii* J.R.I. Wood & Scotland, *I. velutinifolia* J.R.I. Wood & Scotland, *I. walteri* J.R.I. Wood & Scotland. All species are narrow endemics except *I. velutinifolia* which is found in Brazil and Peru; of the others, 12 are found in Brazil and one each in Paraguay and Peru.

Population and genetic features of *Cypripedium calceolus* L. in Russia.

Zheleznaya, E. L., Gargiulo*, R. & Fay*, M. F. (2017). *In* International Scientific Conference on the 100th Anniversary of the Department of Botany of the Tver State University Tver, Russia: Tver State University, pp. 97–100.

No abstract available.

2 What drivers and processes underpin global plant and fungal diversity?

Ophrys fusca and *Ophrys dyris* (Orchidaceae) – constancy of tetraploidy amongst populations in Central Portugal.

Abreu*, J. A., Hawkins, J. A., Cotrim, H., Fay*, M. F., Hidalgo*, O. & Pellicer*, J. (2017). *New Journal of Botany* 7: 94–100. DOI: 10.1080/20423489.2017.1408185.

Ophrys is amongst the best known orchid genera and is an established system for the study of pollinator-mediated floral evolution. Two species, *Ophrys fusca s.l.* and *Ophrys dyris* (= *O. omegaifera* subsp. *dyris*) belonging to *Ophrys* section *Pseudophrys* are the focus of this study. In the context of an integrative study of morphological and genetic diversity of *O. fusca* and *O. dyris*, genome size (GS) and cytotype diversity were surveyed from Portuguese populations. Flow cytometry methods were used to assess GS, and subsequently determine the ploidy level of 67 specimens, including the species and putative hybrids. Cytotypes were also confirmed based on chromosome counts from the roots of two specimens, one of each species. Constancy of nuclear DNA content (1C = 11.19 pg) and ploidy level (2n = 4x = 72, 74) was documented among all the individuals analysed. Implications are considered, in terms of interpreting the origin and predicting the persistence of putative hybrids.

Photo-oxidation modulates green fern spore longevity during dry storage.

Ballesteros*, D., Narayan, S., Varghese, B. & Sershen (2018). *Plant Cell, Tissue and Organ Culture* 133 (2): 165–175. DOI: 10.1007/s11240-017-1370-9.

Desiccation tolerance and longevity of plant propagules in the dry state have significant implications for biotechnological applications. In this study fern spores were used as a unicellular model to characterize some of the mechanisms of ageing during dry storage of plant propagules (at relative humidity ca. 15%). More specifically, we compared the potential relationships among indicators of photo-oxidative stress and spore viability during dry storage between green (chlorophyllous) spores of *Todea barbara* and non-green spores of *Christella dentata*. Green spores stored under the light aged faster than those stored in the dark, and faster than light- and dark-stored non-green spores of C. dentata. This rapid ageing in light-stored green spores was associated with significantly lower antioxidant activity (relative to time zero and dark-stored spores) during storage, and a burst of hydrogen peroxide during the latter stages of storage, which was not a feature of dark-stored spores. We attribute these signs of enhanced oxidative-stress mediated ageing in light-stored spores to photo-oxidative processes, similar to those described in other homoiochlorophyllous organisms. Additionally, high antioxidant activity and low levels of reactive oxygen species in green spores compared with non-green spores suggests differing mechanisms of coping with life in the dry state.

Phylogenetically informative pollen structures of ‘caesalpinioid’ pollen (Caesalpinioideae, Cercidoideae, Detarioideae, Dialioideae and Duparquetioideae: Fabaceae).

Banks*, H. & Lewis*, G. (2018). *Botanical Journal of the Linnean Society* 187 (1): 59–86. DOI: 10.1093/botlinnean/boy005.

We provide an overview of phylogenetically useful pollen structures in five out of the new six subfamily classification of the legume family (Fabaceae). A large and diverse range of pollen structures occurs in the five subfamilies under review. These were, until recently, all part of a much larger subfamily Caesalpinioideae, except for the ‘mimosoid clade’, previously recognized as subfamily Mimosoideae, but now part of a recircumscribed subfamily Caesalpinioideae. We do not here present any pollen data on subfamily Papilionoideae, and only consider preliminary data for pollen of the ‘mimosoid clade’. The most common pollen structures, and those that particularly identify each subfamily, are discussed, compared and illustrated for the five subfamilies: Caesalpinioideae, Cercidoideae, Detarioideae, Dialioideae and Duparquetioideae. Tricolporate pollen with perforate to microreticulate surface ornamentation occurs in at least some species of all the subfamilies under study except Duparquetioideae. The distribution of pollen structural diversity between and within the subfamilies is discussed. The aperture type, pollen-unit, polarity, symmetry, surface ornamentation and grain size of pollen in each subfamily is described and compared. Apertures are found to be more reliable sources of phylogenetic information than surface ornamentation.

Evolutionary and functional significance of ploidy increase occurring within individual plants: somatic ploidy mapping of the complex labellum of sexually deceptive bee orchids.

Bateman*, R. M., Guy, J. J., Rudall*, P. J., Leitch*, I. J., Pellicer*, J. & Leitch*, A. R. (2018). *Annals of Botany* 122 (1): 133–150. DOI: 10.1093/aob/mcy048.

Recent tissue-level observations made indirectly via flow cytometry suggest that endoreplication (duplication of the nuclear genome within the nuclear envelope in the absence of subsequent cell division) is widespread within the plant kingdom. Here, we also directly observe ploidy variation among cells within individual petals, relating size of nucleus to cell micromorphology and (more speculatively) to function.

In *Dactylorhiza*, endoreplication was comparatively infrequent, reached only low levels, and appeared randomly located across the labellum, whereas in *Ophrys* endoreplication was commonplace, being most frequent in large peripheral trichomes. Endoreplicated nuclei reflected both endomitosis and endocycling, the latter reaching the third round of genome doubling (16C) to generate polytene nuclei. All *Ophrys* individuals studied exhibited progressively partial endoreplication.

Comparison of the two genera failed to demonstrate the hypothesized pattern of frequent polyploid speciation in genera showing extensive endoreplication. Endoreplication in *Ophrys* appears more strongly positively correlated with cell size/complexity than with cell location or secretory role. Epigenetic control of gene overexpression by localized induction of endoreplication within individual plant organs may represent a significant component of a plant's developmental programme, contributing substantially to organ plasticity.

Integrating restriction site-associated DNA sequencing (RAD-seq) with morphological cladistic analysis clarifies evolutionary relationships among major species groups of bee orchids.

Bateman*, R. M., Sramkó, G. & Paun, O. (2018). *Annals of Botany* 121: 85–105. DOI: 10.1093/aob/mcx129.

Bee orchids (*Ophrys*) have become the most popular model system for studying reproduction via insect-mediated pseudo-copulation and for exploring the consequent, putatively adaptive, evolutionary radiations. However, despite intensive past research, both the phylogenetic structure and species diversity within the genus remain highly contentious. Here, we integrate next-generation sequencing and morphological cladistic techniques to clarify the phylogeny of the genus.

RAD-seq data strongly support the monophyly of nine out of ten groups previously circumscribed using nrITS and resolve three major clades; in contrast, supposed microspecies are barely distinguishable. Strong incongruence separated the RAD-seq trees from both the morphological trees and traditional classifications; mapping of the morphological characters across the RAD-seq topology rendered them far more homoplastic.

The comparatively high level of morphological homoplasy reflects extensive convergence, whereas the derived placement of the *fusca* group is attributed to paedomorphic simplification. The phenotype of the most recent common ancestor of the extant lineages is inferred, but it post-dates the majority of the character-state changes that typify the genus. RAD-seq may represent the high-water mark of the contribution of molecular phylogenetics to understanding evolution within *Ophrys*; further progress will require large-scale population-level studies that integrate phenotypic and genotypic data in a cogent conceptual framework.

Seed ecology of the geophyte *Conopodium majus* (Apiaceae), indicator species of ancient woodland understories and oligotrophic meadows.

Blandino*, C., Fernandez-Pascual, E., Marin, M., Vernet, A. & Pritchard*, H. W. (2018). *Plant Biology* DOI: 10.1111/plb.12872.

Conopodium majus is a geophyte with pseudomonocotyly, distributed in Atlantic Europe. It is an indicator of two declining European habitats: ancient woodland understories and oligotrophic hay meadows. Attempts to reintroduce it by seed have been hindered by scarce seedling emergence and limited knowledge of its seed biology.

Micro-CT scanning was used to assess pseudomonocotyly. Embryo growth and germination were studied in the laboratory and the field, using dissection and image analysis. The effects of temperature, light, nitrate and GA3 on germination were tested. Seed desiccation tolerance was investigated by storage at different RHs and by drying seeds at different stages of embryo growth.

Seeds possess morphological but not physiological dormancy. Embryo growth and germination were promoted by temperatures between 0 and 5°C, arrested above 10°C, and indifferent to alternating temperatures, light, nitrate and GA3. Pseudomonocotyly appears to result from cotyledon fusion. While seeds tolerated drying to 15% RH and storage for 1 year at 20°C, viability was lost when storage was at 60% RH. Seeds imbibed at 5°C for 84 days had significant internal embryo growth but were still able to tolerate drying to 15% RH.

Reproduction by seed in *C. majus* follows a strategy shared by geophytes adapted to deciduous temperate forests. The evolution of fused cotyledons may enable the radicle and the hypocotyl to reach deeper into the soil where a tuber can develop. The embryo is capable of growth within the seed at low temperatures so that germination is timed for early spring.

Anchored phylogenomics generated nuclear, plastid and mitochondrial markers resolve the *Lepanthes horrida* (Orchidaceae: Pleurothallidinae) species complex.

Bogarin, D., Pérez-Escobar*, O. A., Groenenberg, D., Holand, S. D., Karremans, A., Lemon, E. M., Lemon, A. R., Pupulin, F., Smets, E. & Gravendeel, B. (2018). *Molecular Phylogenetics & Evolution* 129: 27–47. DOI: 10.1016/j.ympev.2018.07.014.

Phylogenetic relationships in species complexes and lineages derived from rapid diversifications are often challenging to resolve using morphology or standard DNA barcoding markers. The hyper-diverse genus *Lepanthes* from Neotropical cloud forest includes over 1200 species and many recent, explosive diversifications that have resulted in poorly supported nodes and morphological convergence across clades. Here, we assess the performance of 446 nuclear-plastid-mitochondrial markers derived from an anchored hybrid enrichment approach (AHE) coupled with coalescence- and species network-based inferences to resolve phylogenetic relationships and improve species recognition in the *Lepanthes horrida* species group. In addition to using orchid-specific probes to increase enrichment efficiency, we improved gene tree resolution by extending standard angiosperm targets into adjacent exons. We found high topological discordance among individual gene trees, suggesting that hybridization/polyploidy may have promoted speciation in the lineage via formation of new hybrid taxa. In addition, we identified ten loci with the highest phylogenetic informativeness values from these genomes. Most previous phylogenetic sampling in the Pleurothallidinae relies on two regions (ITS and matK), therefore, the evaluation of other markers such as those shown here may be useful in future phylogenetic studies in the orchid family. Coalescent-based species tree estimation methods resolved the phylogenetic relationships of the *L. horrida* species group. The resolution of the phylogenetic estimations was improved with the inclusion of extended anchor targets. This approach produced longer loci with higher discriminative power. These analyses also disclosed two undescribed species, *L. amicitiae* and *L. genetoapophantica*, formally described here, which are also supported by morphology. Our study demonstrates the utility

of combined genomic evidence to disentangle phylogenetic relationships at very shallow levels of the tree of life, and in clades showing convergent trait evolution. With a fully resolved phylogeny, is it possible to disentangle traits evolving in parallel or convergently across these orchid lineages such as flower color and size from diagnostic traits such as the shape and orientation of the lobes of the petals and lip.

Evaluating methodologies for species delimitation: the mismatch between phenotypes and genotypes in lichenized fungi (*Bryoria* sect. *Implexae, Parmeliaceae*).

Boluda, C. G., Rico, V. J., Divakar, P. K., Nadyeina, O., Myllys, L., McMullin, R. T., Zamora, J. C., Scheidegger, C. & Hawksworth*, D. L. (2018). *Persoonia* 42: 75–100. DOI: 10.3767/persoonia.2019.42.04.

In many lichen-forming fungi, molecular phylogenetic analyses lead to the discovery of cryptic species within traditional morphospecies. However, in some cases, molecular sequence data also questions the separation of phenotypically characterised species. Here we apply an integrative taxonomy approach – including morphological, chemical, molecular, and distributional characters – to re-assess species boundaries in a traditionally speciose group of hair lichens, *Bryoria* sect. *Implexae*. We sampled multilocus sequence and microsatellite data from 142 specimens from a broad intercontinental distribution. Molecular data included DNA sequences of the standard fungal markers ITS, IGS, GAPDH, two newly tested loci (FRBi15 and FRBi16), and SSR frequencies from 18 microsatellite markers. Datasets were analysed with Bayesian and maximum likelihood phylogenetic reconstruction, phenogram reconstruction, STRUCTURE Bayesian clustering, principal coordinate analysis, haplotype network, and several different species delimitation analyses (ABGD, PTP, GMYC, and DISSECT). Additionally, past population demography and divergence times are estimated. The different approaches to species recognition do not support the monophyly of the 11 currently accepted morphospecies, and rather suggest the reduction of these to four phylogenetic species. Moreover, three of these are relatively recent in origin and cryptic, including phenotypically and chemically variable specimens. Issues regarding the integration of an evolutionary perspective into taxonomic conclusions in species complexes, which have undergone recent diversification, are discussed. The four accepted species, all epitypified by sequenced material, are *Bryoria fuscescens*, *B. glabra*, *B. kockiana*, and *B. pseudofuscescens*. Ten species rank names are reduced to synonymy. In the absence of molecular data, they can be recorded as the *B. fuscescens* complex. Intraspecific phenotype plasticity and factors affecting the speciation of different morphospecies in this group of *Bryoria* are outlined.

The inheritance of recessive and dominant mutations in daffodil cultivars.

Brandham*, P. E. (2017). *In Daffodil, Snowdrop and Tulip Yearbook.* London: Royal Horticultural Society, pp. 26–32.

No abstract available.

A new phylogeny-based tribal classification of subfamily Detarioideae, an early branching clade of florally diverse tropical arborescent legumes.

De la Estrella*, M., Forest*, F., Klitgard*, B., Lewis*, G. P., Mackinder*, B. A., de Queiroz, L. P., Wieringa, J. J. & Bruneau, A. (2018). *Scientific Reports* 8: 6884. DOI: 10.1038/s41598-018-24687-3.

Detarioideae (81 genera, c. 760 species) is one of the six Leguminosae subfamilies recently reinstated by the Legume Phylogeny Working Group. This subfamily displays high morphological variability and is one of the early branching clades in the evolution of legumes. Using previously published and newly generated sequences from four loci (matK-trnK, rpL16, trnG-trnG2G and ITS), we develop a new densely sampled phylogeny to assess generic relationships and tribal delimitations within Detarioideae. The ITS phylogenetic trees are poorly resolved, but the plastid data recover several strongly supported clades, which also are supported in a concatenated plastid+ITS sequence analysis. We propose a new phylogeny-based tribal classification for Detarioideae that includes six tribes: re-circumscribed Detarieae and Amherstieae, and the four new tribes Afzelieae, Barnebydendreae, Saraceae and Schotieae. An identification key and descriptions for each of the tribes are also provided.

A phylogenetic analysis of the genus *Aloe* (Asphodelaceae) in Madagascar and the Mascarene Islands.

Dee*, R., Malakasi*, P., Rakotoarisoa*, S. E. & Grace*, O. M. (2018). *Botanical Journal of the Linnean Society* 187 (3): 428–440. DOI: 10.1093/botlinnean/boy026.

Aloe (Asphodelaceae) is a typical element of the succulent flora of the eastern Indian Ocean islands of Madagascar, the Mascarene Islands of Mauritius, and Réunion and the Seychelles. In this region, there are 129 native *Aloe* spp., all of which are endemic. The most recent classification of *Aloe* in Madagascar, completed by Reynolds in the 1960s, defined nine morpho-groups. The present study is the first phylogenetic analysis of *Aloe* in Madagascar and the Mascarenes, encompassing approximately one-third of the regional species diversity. Bayesian inference and maximum likelihood analyses of ITS, matK and trnQ-rps16 DNA sequences suggest that numerous dispersal events occurred from the African continent to Madagascar. As a result, close evolutionary relationships exist among geographically distant aloes, such as *A. suzannae*, the nocturnal-flowered species and Kumara in southern Africa. *Aloe* section *Lomatophyllum* is the only morpho-group to correspond to a phylogenetic clustering. Our findings confirm that *Aloe* spp. native to the eastern Indian Ocean islands do not comprise a monophyletic unit and emphasize the need for a revised infrageneric classification of *Aloe*.

Shape-shifting in Solanaceae flowers: the influence of pollinators.

Dodsworth*, S., Orejuela, A., Pérez-Escobar*, O. A., Särkinen, T. & Knapp, S. (2018). *Evolution* 72 (3): 717–718. DOI: 10.1111/evo.13437.

No abstract available.

Understanding the cone scale in Cupressaceae: insights from seed-cone teratology in *Glyptostrobus pensilis*.

Dörken, V. & Rudall*, P. J. (2018). *PeerJ* 1 (6): e4948. DOI: 10.7717/peerj.4948.

Both wild-type and teratological seed cones are described in the monoecious conifer *Glyptostrobus pensilis* and compared with those of other Cupressaceae *sensu lato* and other conifers. Some Cupressaceae apparently possess a proliferation of axillary structures in their cone scales. In our interpretation, in *Glyptostrobus* each bract of both typical and atypical seed cones bears two descending accessory shoots, interpreted here as seed scales (ovuliferous scales). The primary seed scale is fertile

and forms the ovules, the second is sterile and forms characteristic tooth-like structures. The bract and the two axillary seed scales are each supplied with a single distinct vascular bundle that enters the cone axis as a separate strand; this vasculature also characterises the descending accessory short shoots in the vegetative parts of the crown. In wild-type seed cones, the fertile seed scale is reduced to its ovules, and the ovules are always axillary. In contrast, the ovules of some of the teratological seed cones examined were located at the centre of the cone scale. An additional tissue found on the upper surface of the sterile lower seed scale is here interpreted as the axis of the fertile seed scale. Thus, the central position of the ovules can be explained by recaulescent fusion of the upper fertile and lower sterile seed scales. In several teratological cone scales, the ovules were enveloped by an additional sterile tissue that is uniseriate and represents an epidermal outgrowth of the fertile seed scale. Close to the ovules, the epidermis was detached from lower tissue and surrounded the ovule completely, except at the micropyle. These teratological features are potentially significant in understanding seed-cone homologies among extant conifers.

Origin of the Taxaceae aril: evolutionary implications of seed-cone teratologies in *Pseudotaxus chienii*.

Dörken, V. H., Nimsch, H. & Rudall*, P. J. (2018). *Annals of Botany*. DOI: 10.1093/aob/mcy150.

Fleshy structures that promote biotic dispersal by ingestion have evolved many times in seed plants. Within the yew family Taxaceae *sensu lato* (six genera, including *Cephalotaxus*), it remains controversial whether the characteristic fleshy structure surrounding the seed is interpreted as a novel outgrowth of the base of the ovule (i.e. an aril) or a fleshy seed coat that is entirely derived from the integument (i.e. a sarcotesta). This paper presents a detailed study of both wild-type and teratological seed cones of *Pseudotaxus chienii*, including morphology, anatomy and ontogeny.

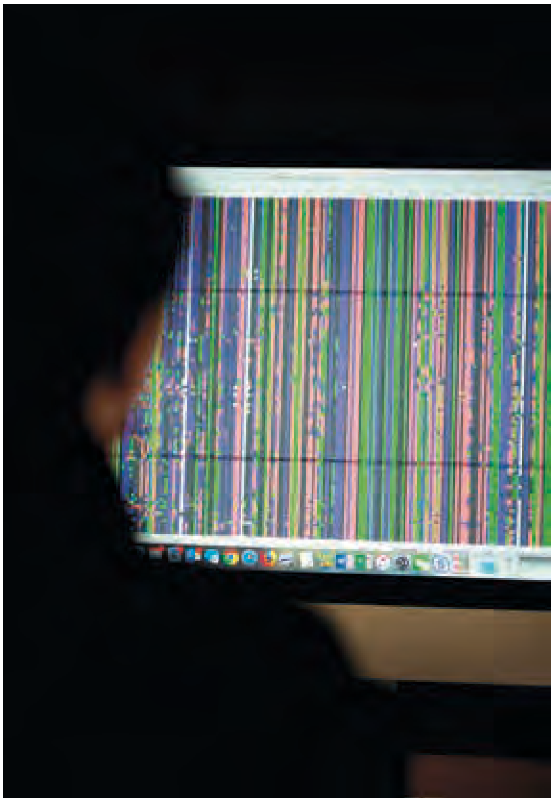
The wild-type seed cone of *Pseudotaxus* possesses a fleshy white aril that is cup-like and not entirely fused to the seed. In the teratological seed cones investigated, the aril was bilobed and consisted of two free halves. In both wild-type and teratological cones, the aril was initiated as two lateral primordia in a transverse plane, but in wild-type cones the two primordia became extended into a ring primordium, which grew apically, leading to the cup-like shape. The teratological seed cones lacked a ring primordium and the two lateral aril lobes remained free throughout their entire ontogeny, alternating with the scale-like leaves inserted below them on the same branch; in some cases, these leaves also became fleshy.

Based on the ontogeny and arrangement of the two fleshy aril lobes in the teratological seed cones of *Pseudotaxus*, we suggest that the typical aril of Taxaceae could be readily interpreted as a fused pair of strongly swollen leaves rather than a modified integument. Our investigations of the cup-like aril of *Pseudotaxus* demonstrate a similarity not only with other Taxaceae but also with relatively distantly related conifers such as *Phyllocladus* (Podocarpaceae).

A roadmap for global synthesis of the plant tree of life.

Eiserhardt* W.L. *et. al.* (including Botigué*, L. R., Dodsworth*, S., Forest*, F., Kim*, J. T., Leitch*, I. J., Pérez-Escobar*, O. A., Pokorny*, L., Baker*, W. J.) (2018). *American Journal of Botany* 105 (3): 614–622. DOI: 10.1002/ajb2.1041.

Providing science and society with an integrated, up-to-date, high quality, open, reproducible and sustainable plant tree of life would be a huge service that is now coming within reach. However, synthesizing the growing body of DNA sequence data in the public domain and disseminating the trees to a diverse audience are often not straightforward due to numerous informatics barriers. While big synthetic plant phylogenies are being built, they remain static and become quickly outdated as new data are published and tree-building methods improve. Moreover, the body of existing



phylogenetic evidence is hard to navigate and access for non-experts. We propose that our community of botanists, tree builders, and informaticians should converge on a modular framework for data integration and phylogenetic analysis, allowing easy collaboration, updating, data sourcing and flexible analyses. With support from major institutions, this pipeline should be re-run at regular intervals, storing trees and their metadata long-term. Providing the trees to a diverse global audience through user-friendly front ends and application development interfaces should also be a priority. Interactive interfaces could be used to solicit user feedback and thus improve data quality and to coordinate the generation of new data. We conclude by outlining a number of steps that we suggest the scientific community should take to achieve global phylogenetic synthesis.

Systematics of *Pochonia.*

Evans, H. C. & Kirk*, P. M. (2017). *In:* Manzanilla-Lopez, R. H. & Lopez-Llorca, L. V. (eds). *Pochonia chlamydosporia: Root and Rhizosphere Health Perspectives in Sustainable Nematode Management* Cham, Switzerland: Springer International Publishing, pp. 21–43.

This book is a multidisciplinary treatise with contributions by experts presented in a single volume and concerning the biology, physiology, ecology, protocols for production, integrated pest management strategies compatibility with *Pochonia chlamydosporia*, and other practical aspects of *P. chlamydosporia* use. There is a growing interest in the biopesticides market on products based on *Pochonia chlamydosporia* formulations. This volume covers those key aspects necessary to work with this biocontrol agent. The potential use of the fungus, not only as biological control agent but as a plant growth promoter and biofertilizer, will help to diversify the application of the fungus in crop management. The phasing-out of methyl bromide and nematicides has intensified the search for chemical or biological alternatives to maintain crop production under more strict policies to control pests and diseases using innovative environmentally friendly approaches for which *Pochonia chlamydosporia* is capable of playing an important role.

Inferring the mycorrhizal status of introduced plants of *Cypripedium calceolus* (Orchidaceae) in northern England using stable isotope analysis.

Fay*, M. F., Feustel, M., Newlands, C. & Gebauer, G. (2018). *Botanical Journal of the Linnean Society* 186 (4): 587–590. DOI: 10.1093/botlinnean/box104.

As part of the conservation programme for *Cypripedium calceolus* in England, seedlings have been produced in axenic culture and grown in pots prior to planting out at putatively suitable locations in northern England; the success of these introductions is expected to be dependent on the presence of appropriate mycorrhizal fungi at the introduction sites and the re-establishment of mycorrhizal associations by the introduced plants. To investigate mycorrhizal function, leaf samples of *C. calceolus* and associated non-orchid species were collected from the native wild site and from plants at three of the introduction sites and screened for enrichment in isotopes of carbon (C), nitrogen (N) and hydrogen (H) that are indicative of an exchange of matter between fungi and orchids in orchid mycorrhizal associations. Total N concentration was also measured. At all sites, plants of *C. calceolus* were enriched in 2H and, to a lesser extent, 15N relative to the associated species and had higher concentrations of total N. There was no apparent enrichment in 13C. Together, these results indicate that all the screened individuals of *C. calceolus* (wild and introduced) are likely to have formed a mycorrhizal association with a *Rhizoctonia*. Thus, after introduction the axenically produced seedlings may have established a mycorrhizal relationship with the same type of fungus utilized by *C. calceolus* elsewhere in its range.

Seeds of future past: climate change and the thermal memory of plant reproductive.

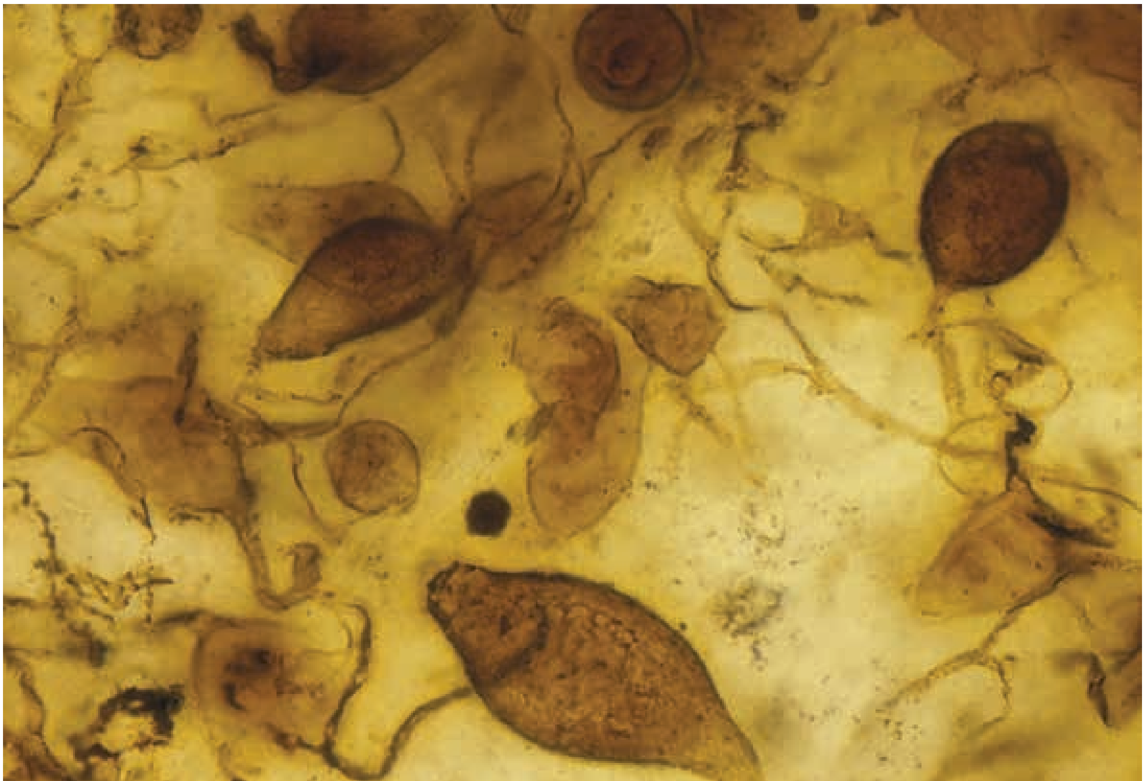
Fernandez-Pascual, E., Mattana*, E. & Pritchard*, H. W. (2018). *Biological Reviews*: DOI: 10.1111/brv.12461.

Plant persistence and migration in face of climate change depends on successful reproduction by seed, a central aspect of plant life that drives population dynamics, community assembly and species distributions. Plant reproduction by seed is a chain of physiological processes, the rates of which are a function of temperature, and can be modelled using thermal time models. Importantly, while seed reproduction responds to its instantaneous thermal environment, there is also evidence of phenotypic plasticity in response to the thermal history experienced by the plant's recent ancestors, by the reproducing plant since seedling establishment, and by its seeds both before and after their release. This phenotypic plasticity enables a thermal memory of plant reproduction, which allows individuals to acclimatise to their surroundings. This review synthesises current knowledge on the thermal memory of plant reproduction by seed, and highlights its importance for modelling approaches based on physiological thermal time. We performed a comprehensive search in the Web of Science and analysed 533 relevant articles, of which 81 provided material for a meta-analysis of thermal memory in reproductive functional traits based on the effect size Zr. The articles encompassed the topics of seed development, seed yield (mass and number), seed dormancy (physiological, morphological and physical), germination, and seedling establishment. The results of the meta-analysis provide evidence for a thermal memory of seed yield, physiological dormancy and germination. Seed mass and physiological dormancy appear to be the central hubs of this memory. We argue for integrating thermal memory into a predictive framework based on physiological time modelling. This will provide a quantitative assessment of plant reproduction, a complex system that integrates past and present thermal inputs to achieve successful reproduction in changing environments. The effects of a warming environment on plant reproduction cannot be reduced to a qualitative interpretation of absolute positives and negatives. Rather, these effects need to be understood in terms of changing rates and thresholds for the physiological process that underlie reproduction by seed.

Evolutionary diversity patterns in the Cape flora of South Africa.

Forest*, F., Colville, J. F. & Cowling, R. M. (2018). *In:* Scherson, R. & Faith, D. P. (eds). *Phylogenetic diversity: applications and challenges in biodiversity science.* Switzerland: Springer, pp. 167–187.

The Greater Cape Floristic Region of South Africa is a relatively small area found in the south-western corner of the African continent. It is characterised by a Mediterranean-type climate and harbours an incredible floral diversity with almost 11,500 species of plants, of which more than three-quarters are found nowhere else in the world. The floristic composition of the region is very distinctive with families not



dominant in other floras, such as Iridaceae, Aizoaceae, Ericaceae, Proteaceae and Restionaceae. In addition, small-leaved, sclerophyllous low shrubs and geophytes are by far the predominant growth forms with a low proportion of tree and annual species present. Understandably, this flora has attracted a lot of interest, and many have pondered what environmental and ecological factors could be responsible for its richness and uniqueness and the resulting biodiversity patterns observed today. In this chapter, the current state of knowledge of large-scale evolutionary patterns, investigated using phylogenetic diversity metrics, within the Cape region are reviewed. As well as published works, we report on ongoing studies examining biodiversity patterns using phylogenetic diversity, phylogenetic endemism and phylobetadiversity, both in plants and animals. We also review how these phylogeny-based approaches have been used to address applied questions (e.g. biodiversity surrogates, phytogeographical delimitations).

Fungal tree of life.

Gaya*, E., Kooij*, P. W., Dentinger, B. T. M., Grigoriev, I. V., Nagy, L., Stajich, J., Coker*, T. & Leitch*, I. J. (2018). *In:* Willis*, K. J. (ed.) *State of the World's Fungi.* Richmond: Royal Botanic Gardens, Kew, pp. 12–17.

How are different species of fungi related to each other? What do we know about the major steps in fungal evolution and when they occurred? What are we doing about filling the knowledge gaps in the fungal tree of life?

The role of chemical signalling in maintenance of the fungus garden by leaf-cutting ants.

Green*, P. W. C. & Kooij*, P. W. (2018). *Chemoecology* 28 (3): 101–107. DOI: 10.1007/s00049-018-0260-x.

How foraging trails are formed and the chemical communication between individual ants is well known. However, communication between partners in mutualistic relationships, such as the leaf-cutting ants (LCA) and their symbiotic fungus, is less studied. There is a feedback mechanism that operates in LCA colonies, with the fungus garden communicating its condition to the ants, most probably using chemicals. We discuss the literature on the chemistry of the LCA–forage–fungus system starting from selection of plants and its effect on the fungus garden. We suggest, using chemical examples, how the fungus might communicate with attendant ants and suggest areas for future research into this fascinating and complex system.

Characters of the inferior ovary of Myrteae (Myrtaceae) and their implication in the evolutionary history of the tribe.

Harthman, V. D. C., de Souza, L. A. & Lucas*, E. J. (2018). *Australian Systematic Botany* 31 (3): 252–261. DOI: 10.1071/SB17059.

Myrtaceae is commonly known to have an inferior ovary of appendicular, receptacular or mixed origin. Other characters of the ovary, such as the number of carpels, number of locules, vascularisation pattern, number of ovules, placentation and presence of compitum have also been of interest to researchers aiming to better understand the evolutionary history of the tribe. In the present study, aspects of the structure of the inferior ovary of 21 species of Myrteae are analysed and reviewed as potential characters for better understanding the evolutionary history of Myrteae. Flower buds were embedded in historesin and paraplast and sectioned transversely and longitudinally with a rotary microtome. Results suggested that most species have an inferior ovary of appendicular origin and that a compitum, or compitum tissue, is present in all species analysed, differing only in the degree of development. Number of carpels and locules vary, with most species having two locules. Vascular supply is transeptal and axial, the latter being the most common condition in the investigated species. Data presented here enhance current evolutionary understanding of the tribe and its history. Results indicated that the inferior ovary of ancestral Myrteae may has had an appendicular origin, that the presence and nature of the compitum may have a positive effect on fertilisation efficiency and a relationship with number of ovules and that transepetal vascular supply may be taxonomically useful to define large groups such as *Pimenta* and *Eugenia*.

Molecular phylogenetics of the genus *Costularia* (Schoeneae, Cyperaceae) reveals multiple distinct evolutionary lineages.

Larridon*, A. *et. al.* (including Prychid*, C. J.) (2018). *Molecular Phylogenetics & Evolution* 126: 196–209. DOI: 10.1016/j.ympev.2018.04.016.

We investigated the monophyly of *Costularia* (25 species), a genus of tribe Schoeneae (Cyperaceae) that illustrates a remarkable distribution pattern from southeastern Africa, over Madagascar, the Mascarenes and Seychelles, to Malesia and New Caledonia. A further species, *Tetraria borneensis*, has been suggested to belong to *Costularia*. Relationships and divergence times were inferred using an existing four marker phylogeny of

Cyperaceae tribe Schoeneae expanded with newly generated sequence data mainly for *Costularia s.l.* species. Phylogenetic reconstruction was executed using Bayesian inference and maximum likelihood approaches. Divergence times were estimated using a relaxed molecular clock model, calibrated with fossil data. Based on our results, *Tetraria borneensis* is not related to the species of *Costularia*. *Costularia s.l.* is composed of four distinct evolutionary lineages. Two lineages, one including the type species, are part of the *Oreobolus* clade, i.e. a much reduced genus *Costularia* restricted to southeastern Africa, Madagascar, the Mascarenes and Seychelles, and a small endemic genus from New Caledonia for which a new genus *Chamaedendron* is erected based on *Costularia* subgenus *Chamaedendron*. The other two lineages are part of the *Tricostularia* clade, i.e. a separate single-species lineage from the Seychelles for which a new genus (*Xyroschoenus*) is described, and *Costularia* subgenus *Lophoschoenus*. For the latter, more research is needed to test whether they are congeneric with the species placed in the reticulate-sheathed *Tetraria* clade.

Evolutionary trends in the columnar cactus genus *Eulychnia* (Cactaceae) based on molecular phylogenetics, morphology, distribution, and habitat

Larridon*, I., Walter, H. E., Rosas, M., Vandomme, V. & Guerrero, P. C. (2018). *Systematics and Biodiversity*. DOI: 10.1080/14772000.2018.1473898.

Populations of the columnar cactus genus *Eulychnia* (Cactaceae) are an iconic sight in the Chilean Atacama Desert. The most recent taxonomic treatment of the genus suggested to accept up to seven taxa at species level based on morphological data. To date, species boundaries and infrageneric relationships in *Eulychnia* have not been investigated using a molecular approach. In this study, sequence data were generated for six chloroplast markers (rpl32-trnL, trnH-psbA, trnL-trnF, trnQ-rps16, trnS-trnG, and ycf1) for the seven species. Where possible, samples were collected from the south and north of the distribution range of widely distributed species, as well as plants from two morphologically distinct populations in the Atacama and Coquimbo Regions. Evolutionary trends of morphological characters were investigated using ancestral state reconstruction, and the habitat of the Chilean taxa was taken into account based on latitudinal and altitudinal distribution, precipitation regime, and vegetation zones. Two major clades were retrieved in the molecular phylogenetic hypotheses, a northern clade and a southern clade, which can easily be distinguished morphologically by differences in rib shape and type of the indumentum of the pericarpel and the hypanthium. The only *Eulychnia* taxon found outside Chile is most commonly accepted as *Eulychnia iquiquensis* subsp. *ritteri*. However, its isolated geographic distribution and the fact that this taxon is not most closely related to *E. iquiquensis* but was retrieved as sister to the rest of the northern clade in our molecular phylogenetic results support the recognition of *E. ritteri* at species level. Our results also provide some support for the two recently published species, *E. chorosensis* (previously placed in *E. acida s.l.*) and *E. taltalensis* (previously considered to be part of *E. breviflora s.l.*). The relationships in the southern clade need further study.

Satellite DNA in *Paphiopedilum subgenus Parvisepalum* as revealed by high-throughput sequencing and fluorescent *in situ* hybridization.

Lee, Y.-I., Yap*, J. W., Izan, S., Leitch*, I. J., Fay*, M. F., Lee, Y.-C., Hidalgo* O., Dodsworth*, S., Smulders, M. J. M., Gravendeel, B. & Leitch*, A. R. (2018). *BMC Genomics* 19 (1): 578. DOI: 10.1186/s12864-018-4956-7.

Satellite DNA is a rapidly diverging, largely repetitive DNA component of many eukaryotic genomes. Here we analyse the evolutionary dynamics of a satellite DNA repeat in the genomes of a group of Asian subtropical lady slipper orchids (*Paphiopedilum* subgenus *Parvisepalum* and representative species in the other

subgenera/sections across the genus). A new satellite repeat in Paphiopedilum subgenus *Parvisepalum*, SatA, was identified and characterized using the RepeatExplorer pipeline in HiSeq Illumina reads from *P. armeniacum* (2n = 26). Reconstructed monomers were used to design a satellite-specific fluorescent in situ hybridization (FISH) probe. The data were also analysed within a phylogenetic framework built using the internal transcribed spacer (ITS) sequences of 45S nuclear ribosomal DNA.

SatA comprises c. 14.5% of the *P. armeniacum* genome and is specific to subgenus *Parvisepalum*. It is composed of four primary monomers that range from 230 to 359 bp and contains multiple inverted repeat regions with hairpin-loop motifs. A new karyotype of *P. vietnamense* (2n = 28) is presented and shows that the chromosome number in subgenus *Parvisepalum* is not conserved at 2n = 26, as previously reported. The physical locations of SatA sequences were visualised on the chromosomes of all seven Paphiopedilum species of subgenus *Parvisepalum* (2n = 26–28), together with the 5S and 45S rDNA loci using FISH. The SatA repeats were predominantly localised in the centromeric, peri-centromeric and sub-telocentric chromosome regions, but the exact distribution pattern was species-specific.

We conclude that the newly discovered, highly abundant and rapidly evolving satellite sequence SatA is specific to Paphiopedilum subgenus *Parvisepalum*. SatA and rDNA chromosomal distributions are characteristic of species, and comparisons between species reveal that the distribution patterns generate a strong phylogenetic signal. We also conclude that the ancestral chromosome number of subgenus *Parvisepalum* and indeed of all *Paphiopedilum* could be either 2n = 26 or 28, if *P. vietnamense* is sister to all species in the subgenus as suggested by the ITS data.

Fungal genomes: Exploring, understanding and utilising their diversity.

Leitch*, I. J., Kooij*, P. W., Coker*, T., Grigoriev, I. V., Nagy, L., Martin, F., Stajich, J., Dentinger, B. T. M. & Gaya*, E. (2018). *In:* Willis*, K. J. (ed.) *State of the World's Fungi.* Richmond: Royal Botanic Gardens, Kew, pp. 40–47.

How many whole fungal genomes have been sequenced to date. How is this information being used to enhance our insights into medicine and climate change resilience and to find new fungi for use in everyday life, from food to antibiotics and biofuels?

Desiccation tolerance in ferns: from the unicellular spore to the multi-tissular sporophyte.

López-Pozo, M., Fernández-Marín, B., García-Plazaola, J. I. & Ballesteros*, D. (2018). *In:* Fernández, H. (ed.) *Current Advances in Fern Research.* Cham: Springer, pp. 401–426.

Desiccation tolerance (DT) represents an ecophysiological strategy probably developed during land conquest by primitive plants that have been progressively lost in photosynthetic tissues throughout evolution, in parallel to the development of mechanisms for the control of water content (i.e., vascular system, cuticle, stomata). Currently, DT of photosynthetic organisms is common in algae but extremely rare in tracheophytes, especially in angiosperms. Moreover, when considering the different developmental stages of a photosynthetic organism, not all of them present the same response to desiccation. Ferns and lycophytes have three different life forms: (1) the unicellular spore – chlorophyllic or non-chlorophyllic – (2) the simple multicellular gametophyte, and (3) the complex multicellular and multi-tissular sporophyte. The three life forms comprise a wide extent of DT and particular adaptations to cope with the stresses produced by desiccation and life in the dry state. The intermediate position of ferns between bryophytes and spermatophytes in an evolutionary context, and the variation of responses to desiccation of the different life forms of ferns, allows us to use them as diverse models to study plant adaptations to terrestrial environment, as well as the evolution of the mechanisms of DT in land plants. The current knowledge on fern spore, gametophyte, and sporophyte DT and the mechanisms to survive in the dry state are reviewed in this chapter.

Morphological and functional seed traits of the wild medicinal plant *Dioscorea strydomiana*, the most threatened yam in the world.

Mattana*, E., Gomez-Barreiro*, P., Lotter, M., Hankey, A. J., Froneman, W., Mamatsharaga, A., Wilkin*, P. & Ulian*, T. (2018). *Plant Biology*: DOI: 10.1111/plb.12887.

Morphological and functional seed traits have important roles in characterising the species regeneration niche and help to understand the reproductive biology of rare and threatened plants, which can thus support appropriate plant conservation measures. Seed morphometric and dispersal kinetics of the critically endangered *Dioscorea strydomiana* were measured and compared with those of four other *Dioscorea* species, and seed germination response under constant temperatures (5–35 °C) was compared with that of the congeneric and widespread *D. sylvatica*. Seed mass of *D. strydomiana* (ca. 14 mg) was twice that of *D. sylvatica*, but similar to or smaller than the other species examined. Seeds of *D. strydomiana* have the lowest speed of descent and lowest variability in most of the morphological traits considered, suggesting lower phenotypic plasticity but higher variance in the wing-loading value. Seeds of *D. strydomiana* reached maximum germination at 15 °C (ca. 47%), which decreased slightly to ca. 37% at 25°C and was completely inhibited at 35 °C. D. sylvatica seeds started to germinate at 10 °C (ca. 3%), reached 75–80% germination at 15–20 °C and maximum (ca. 90%) at 25–30 °C. Base temperatures for germination (Tb) were 9.3 and 5.7 °C, for *D. strydomiana* and *D. sylvatica*, respectively. Due to the higher germination percentages of D. sylvatica, ceiling and optimum temperatures could also be modelled for this species, suggesting higher sensitivity to high temperature for seeds of *D. strydomiana*. The detected poor seed lot quality of *D. strydomiana* suggests difficulties in reproduction from seed, highlighting the need for further investigation and conservation actions for this threatened yam species.

Understanding biological and ecological factors affecting seed germination of the multipurpose tree *Anogeissus leiocarpa*.

Mattana*, E., Sacande*, M., G., B., Gomez-Barreiro*, P., Sanogo, S. & Ulian*, T. (2018). *Plant Biology* 20 (3): 602–609. DOI: 10.1111/plb.12702.

Anogeissus leiocarpa (DC.) Guill. & Perr. (Combretaceae) has important economic and cultural value in West Africa as source of wood, dye and medicine. Although this tree is in high demand by local communities, its planting remains limited due to its very low propagation via seed. In this study, X-rays were used to select filled fruits in order to characterise their morphology and seed germination responses to treatment with sulphuric acid and different incubation temperatures.

Morphological observations highlighted a straight orthotropous seed structure. The increase in mass detected for both intact and scarified fruits through imbibition tests, as well as morphological observations of fruits soaked in methylene blue solution, confirmed that they are water-permeable, although acid-scarified fruits reached significantly higher mass increment values than intact ones. Acid scarification (10 min soaking in 98% H_2SO_4) positively affected seed germination rate but not final germination proportions. When intact fruits where incubated at a range of temperatures, no seeds germinated at 10°C, while maximum seed germination (ca. 80%) was reached at 20°C. T50 values ranged from a minimum of ca. 12 days at 25°C to a maximum of ca. 34 days at 15 and 35°C. A theoretical base temperature for germination (Tb) of ca. 10°C and a thermal requirement for 50% germination (S) of ca. 195°C were also identified for intact fruits. The results of this study revealed the seed germination characteristics driven by fruit and seed morphology of this species, which will help in its wider propagation in plantations.

Phylogeny and biogeography of the hyper-diverse genus *Eugenia* (Myrtaceae: Myrteae), with emphasis on *E.* sect. *Umbellatae*, the most unmanageable clade.

Mazine, F. F., Faria, J. E. Q., Giaretta, A., Vasconcelos*, T., Forest*, F. & Lucas*, E. (2018). *Taxon* 67 (4): 752–769. DOI: 10.12705/674.5.

Eugenia, comprising ca. 1100 species, is the largest genus of Neotropical Myrtaceae. *Eugenia* sect. *Umbellatae* (formerly referred to as “clade 9”) is the most speciose lineage of *Eugenia*. This study aims to better delimit *E.* sect. *Umbellatae*, to identify and understand relationships between manageable subgroups of this large clade for future discrete

systematic studies and to explain biogeographical patterns in the genus. In total, 103 samples were used in this study. These include representatives of the nine clades of the "*Eugenia* group" with a particular focus on Eugenia clade 9, representing the morphological and geographical diversity found in the genus. Phylogenetic reconstructions were performed using maximum likelihood (ML) and Bayesian inference (BI) for the combined dataset, using the markers ITS, rpl16, psbA-trnH, rpl32-trnL, trnQ-rps16. The resultant tree was fossil calibrated and used for historical biogeographical analysis using DEC implemented in RASP. The mid Oligocene is the most likely period in which the crown node of *Eugenia s.l.* diversified. The earliest Eugenia appear to be associated with dry biomes and to have arisen from non-tropical southern South America, as did ancestors of the earliest American Myrteae. *Eugenia* subg. *Pseudeugenia* also most likely diversified in dry biomes, while *E.* subg. *Hexachlamys* and *E.* subg. *Eugenia* are likely to have diverged in the Atlantic Forests biome. *Eugenia* sect. *Umbellatae* is morphologically very variable; some clades can be circumscribed based on morphology while some remain morphologically undiagnosable. The study presented here provides discussion of the earliest origins of *Eugenia* and its response to climate-driven changes in the Neotropics as humid, forest biomes became more widespread in the Miocene. In addition, important practical conclusions are drawn regarding relationships within *Eugenia*. Three clades are newly classified as subgenera: *E.* subg. *Pseudeugenia* (including species of *E.* sect. *Pseudeugenia*); *E.* subg. *Hexachlamys* (including *E.* sect. *Hexachlamys*) and *E.* subg. *Eugenia* (including *E.* sect. *Umbellatae*, *E.* sect. *Jossinia*, *E.* sect. *Phyllocalyx*, *E.* sect. *Pilothecium*, *E.* sect. *Racemosae*, *E.* sect. *Schizocalomyrtus*, *E.* sect. *Speciosae* and *Eugenia* sect. *Excelsae*). Two previously unidentified clades are published as *E.* sect. *Excelsae* and recognized as *E.* sect. *Jossinia*, the latter consisting entirely of Old World species.

On the monophyly of *Macrolobium Schreb.*, an ecologically diverse neotropical tree genus (Fabaceae-Detarioideae).

Murphy*, B., de la Estrella*, M., Schley*, R., Forest*, F. & Klitgård*, B. (2018). *International Journal of Plant Sciences* 179 (1): 75–86. DOI: 10.1086/695338.

Premise of research. The Neotropical endemic *Macrolobium* is one of the most species-rich genera (ca. 75 species) within subfamily Detarioideae (Fabaceae, alternatively Leguminosae). Two sections distinguished by floral morphology have been recognized in the past. Although morphologically diverse, species within the genus share several characters, including a single well-developed petal in adaxial position. However, previous analyses based on plastid markers have suggested that the genus is not monophyletic. We produce the most densely sampled molecular phylogeny of *Macrolobium* and test the monophyly of the genus and the two sections.

The combined analysis retains *Macrolobium* as a monophyletic genus, with two well-supported subclades corresponding to the two recognized sections. *Macrolobium* pendulum is the only species placed in a section different from its taxonomic treatment. The relationships recovered with the plastid markers differ slightly from the combined and ITS analyses, but without significant support.

Macrolobium is shown to be a monophyletic genus and to contain two well-supported and morphologically defined sections with differing Amazonian and Andean/Central American distributions corresponding to the Gentry pattern. Species are also found to group partly according to habitat preferences and leaf morphology. Both sections contain groups of multijugate and unijugate species, and there appear to have been multiple shifts of this character.

Exploring the ecological history of a tropical agroforestry landscape using fossil pollen and charcoal analysis from four sites in Western Ghats, India.

Nogué, S., Tovar, C., Bagwhat, S., Finsinger, W. & Willis*, K. J. (2017). *Ecosystems* 21 (1): 45–55. DOI: 10.1007/s10021-017-0132-1.

Contrary to expectations, some human-modified landscapes are considered to sustain both human activities and biodiversity over the long-term. Agroforestry systems are among these landscapes where crops are planted under native shade trees. In this context, ancient agroforestry systems can provide insight into how farmers managed the landscape over time. Such insight can help to quantify the extent to which tropical forests (especially habitat-specialist trees) are responding to local and landscape-level management. Here, we extracted fossil pollen (indicator of past vegetation changes) and macroscopic charcoal (indicator of biomass burning) from four forest hollows' sedimentary sequences in an ancient agroforestry system in Western Ghats, India. We used a mixed-modelling approach and a principal components analysis (PCA) to determine past trajectories of forest change and species composition dynamics for the last 900 years. In addition, we reconstructed the long-term forest canopy dynamics and examined the persistence of habitat-specialist trees over time. Our results show that the four sites diverged to a surprising degree in both taxa composition and dynamics. However, despite these differences, forest has persisted over 900 years under agricultural activities within agroforestry systems. This long-term analysis highlights the importance of different land-use legacies as a framework to increase the effectiveness of management across tropical agricultural lands.

An assessment of seed viability, germination and vegetative propagation requirements for least water-lily (*Nuphar pumila*) (NECR244)

Peach*, J., Davies*, R., Walmisley, J. & Chapman*, T. (2017). *In: Natural England Commissioned Reports*, York.

Although fairly widespread in Scotland, Northern Europe and Asia, *Nuphar pumila* (Timm) DC., Least Water-lily, is considered Critically Endangered in England with its distribution restricted to a single site at Cole Mere, Shropshire (Stroh, 2014; Padgett, 2007; Preston and Croft, 1997). The isolation of this population has driven interest in its conservation and potential introduction to other sites, with both sexual reproduction by seed and clonal spread by rhizome fragments likely to play a part in establishing new plants and populations (Lansdown, 2017). In 2016, seeds were taken from Cole Mere for study at the Millennium Seed Bank (MSB) to assess the viability of seeds produced by this population and to examine the factors necessary for germination. Viability tests have found that 92% of the seeds collected were viable. The experimental work carried out for this study has provided an effective germination protocol resulting in maximum germination of 96%. Large variations in germination levels between seed batches were also observed and this is discussed with particular reference to seed maturity and port-harvest handling for optimum germination. Six rhizome fragments from Cole Mere were also sent to the nursery at Wakehurst Place in 2016, providing an opportunity to monitor their establishment in cultivation and trial further division of the rhizomes in spring 2017. Results to date suggest larger rhizome sections with a visible, healthy growth point are able to root and establish well, but that smaller sections and those without visible growth points are not. Division of rhizomes with more than one growing point appears to be feasible, and may occur spontaneously through the formation of natural breakage points within the rhizome. Experience gained during the seed germination and vegetative propagation trials enables a simple comparison of the advantages and disadvantages of each technique. Plants produced using both methodologies are being retained as part of the living collections at Wakehurst Place and RBG Kew.

Genome size diversity and its impact on the evolution of land plants.

Pellicer*, J., Hidalgo*, O., Dodsworth*, S. & Leitch*, I. J. (2018). *Genes* 9 (2): 88. DOI: 10.3390/genes9020088.

Genome size is a biodiversity trait that shows staggering diversity across eukaryotes, varying over 64,000-fold. Of all major taxonomic groups, land plants stand out due to their staggering genome size diversity, ranging ca. 2400-fold. As our understanding of the implications and significance of this remarkable genome size diversity in land plants grows, it is becoming increasingly evident that this trait plays not only an important role in shaping the evolution of plant genomes, but also in influencing plant community assemblages at the ecosystem level. Recent advances and improvements in novel sequencing technologies, as well as analytical tools, make it possible to gain critical insights into the genomic and epigenetic mechanisms underpinning genome size changes. In this review we provide an overview of our current understanding of genome size diversity across the different land plant groups, its implications on the biology of the genome and what future directions need to be addressed to fill key knowledge gaps.

Drivers of coral diversification in a major marine biodiversity hotspot.

Pérez-Escobar*, O. A., Cass, S. & Dodsworth*, S. (2018). *Evolution* 72 (2): 406–408. DOI: 10.1111/evo.13419.

Coral reefs are of great ecological importance to marine ecosystems, yet their origins are still poorly understood. Using a robust phylogenetic framework, Huang *et al*. (2017) show that most diversity within the Indo-Pacific Coral Triangle region is driven by range expansions of lineages from outside the region, rather than rapid diversification within. This highlights the need for macroevolutionary studies to fully understand species assemblages in biodiversity hotspots, and the potential importance of adjacent areas for conservation.

Multiple geographical origins of environmental sex determination enhanced the diversification of Darwin's favourite orchids.

Pérez-Escobar*, O. A., Chomicki, G., Condamine, F. L., de Vos*, J. M., Martins, A., Smidt, E., Klitgård*, B., Gerlach, G. & Heinrichs, J. (2017). *Scientific Reports* 7: 1.2878. DOI:10.1038/s41598-017-12300-y.

Environmental sex determination (ESD) – a change in sexual function during an individual life span driven by environmental cues – is an exceedingly rare sexual system among angiosperms. Because ESD can directly affect reproduction success, it could influence diversification rate as compared with lineages that have alternative reproductive systems. Here we test this hypothesis using a solid phylogenetic framework of Neotropical Catasetinae, the angiosperm lineage richest in taxa with ESD. We assess whether gains of ESD are associated with higher diversification rates compared to lineages with alternative systems while considering additional traits known to positively affect diversification rates in orchids. We found that ESD has evolved asynchronously three times during the last ~5 Myr. Lineages with ESD have consistently higher diversification rates than related lineages with other sexual systems. Habitat fragmentation due to mega-wetlands extinction, and climate instability are suggested as the driving forces for ESD evolution.

Evolutionary history and systematics of *Campylocentrum* (Orchidaceae: Vandeae: Angraecinae): a phylogenetic and biogeographical approach.

Pessoa, E. M., Viruel*, J., Alves, M., Bogarín, D., Whitten, M. W. & Chase*, M. W. (2018). *Botanical Journal of the Linnean Society* 186: 158–178. DOI: 10.1093/botlinnean/box089.

Subtribe Angraecinae (Orchidaceae: Vandeae) are mainly distributed in Africa, but with two genera, *Campylocentrum* and *Dendrophylax*, restricted to the Neotropics. As a widespread Neotropical genus, *Campylocentrum* constitutes an appropriate model for revealing biogeographical patterns in this area and investigating routes of colonization and dispersal. In this study, we reconstructed phylogenetic relationships of the genus with Bayesian inference and maximum parsimony analyses of combined nuclear (ITS rDNA and Xdh) and plastid (matK exon, rpl32-trnL spacer, trnL intron, trnL-trnF spacer and ycf1 exon) DNA datasets, aimed at establishing a new infrageneric classification for this taxonomically complex genus. Based on the most comprehensive phylogenetic tree, we investigated the biogeographical history of *Campylocentrum* by estimating divergence times, inferred using fossil and secondary calibrations applying a relaxed-clock model approach, and reconstructing ancestral areas of distribution under a time-stratified likelihood model. The phylogenetic analyses provided strong support for the majority of the clades. *Campylocentrum* is monophyletic, and we recognize five sections based upon strongly supported clades. We conclude that the African angraecoid ancestor of *Campylocentrum* and *Dendrophylax* dispersed to the Antilles. *Campylocentrum* is estimated to be a relatively young genus (late Miocene, c. 8.2 Mya) and its most recent common ancestor had a disjunct distribution in the Antilles and Parana dominion. During the Pliocene, the five sections diverged and expanded their distributions in the Neotropics, and in the Pleistocene diversification was experienced by some of the terminal clades. We hypothesize that the evolutionary history of *Campylocentrum* was strongly influenced by orogenic events during the Pliocene and climatic fluctuations during the Pleistocene.

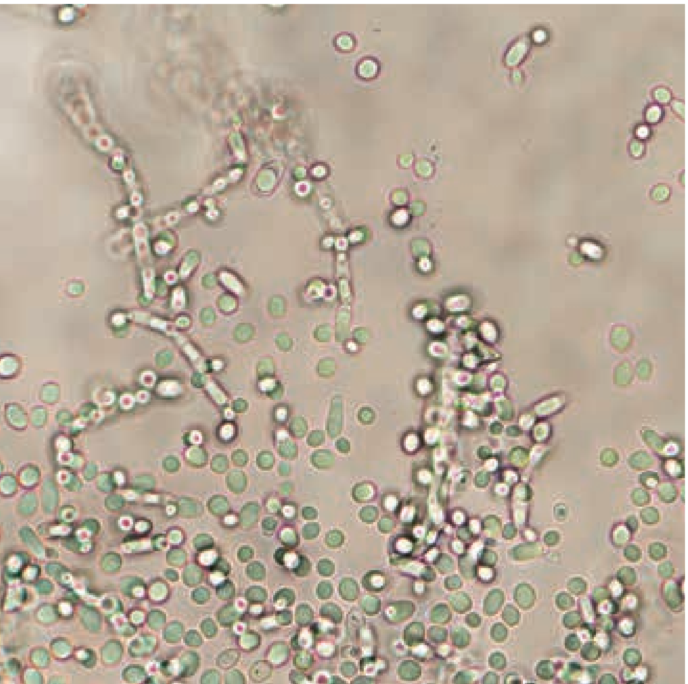
Ultrastructure and development of non-contiguous stomatal clusters and helicocytic patterning in *Begonia*.

Rudall*, P. J., Julier, A. C. M. & Kidner, C. A. (2018). *Annals of Botany* 122 (5) 767–776. DOI: 10.1093/aob/mcx146.

Helicocytic stomata are characterized by an inward spiral of mesogenous cells surrounding a central stomatal pore. They represent a relatively rare feature that occurs in some drought-tolerant angiosperm species. In some *Begonia* species with thick leaves, the stomata are not only helicocytic but also clustered into groups that are spaced apart by at least one cell. This paper presents a detailed ontogenetic study of this characteristic non-contiguous stomatal patterning in a developmental and phylogenetic context.

Light microscopy and both scanning and transmission electron microscopy were used to examine stomatal development in several species of *Begonia*. Published reports of stomatal development in *Begonia* and other angiosperms were reviewed to provide a comprehensive discussion of the evolution of stomatal patterning.

Helicocytic stomata develop from meristemoids that undergo a series of oriented asymmetric divisions to produce a spiral of mesogene stomatal lineage ground cells (SLGCs) surrounding a stoma. A clear developmental similarity between anisocytic and helicocytic stomata is positively correlated with the number of iterations of amplifying divisions that result in SLGCs. Stomatal clusters develop from asymmetric divisions in neighbouring SLGCs. Within each cluster, non-contiguous spacing of meristemoids is maintained by asymmetric divisions oriented away from each developing meristemoid.



Formation of non-contiguous stomatal clusters in *Begonia* relies on two primary developmental factors in the epidermis: an inwardly spiralling series of amplifying divisions that result in helicocytic stomata, and the development of a variable number of meristemoids from neighbouring SLGCs within each cluster. Optimization of these features on an angiosperm phylogeny indicates that the occurrence of amplifying divisions could be pre-adaptive for these factors. Both factors have been thoroughly studied in terms of developmental genetics in *Arabidopsis*, suggesting gene orthologues that could be implicated in *Begonia* stomatal patterning.

Phylogenetic systematics of subtribe Spiranthinae (Orchidaceae: Orchidoideae: Cranichideae) based on nuclear and plastid DNA sequences of a nearly complete generic sample.

Salazar, G. A. *et. al.* (including Chase*, M. W.) (2018). *Botanical Journal of the Linnean Society* 186 (3): 273–303. DOI: 10.1093/botlinnean/box096.

Subtribe Spiranthinae is the most species-rich lineage of terrestrial Neotropical orchids, encompassing > 500 species and 40 genera. We conducted maximum parsimony and maximum likelihood phylogenetic analyses of DNA sequence data of plastid matK-trnK and trnL-trnF and nuclear ribosomal ITS sequences for 36 genera and 182 species of Spiranthinae plus appropriate outgroups. The results strongly support monophyly of Spiranthinae (minus *Discyphus*, Discyphinae and Galeottiella, Galeottiellinae) and five major lineages, namely monospecific *Cotylolabium* (sister to the remaining Spiranthinae) and the *Eurystyles*, *Pelexia*, *Spiranthes* and *Stenorrhynchos* clades. Eighteen of the 27 genera of Spiranthinae for which more than one species was included in our analyses are monophyletic. Paraphyly of large genera, such as *Cyclopogon* and *Sarcoglottis*, resulted from segregation of particular species or groups of species exhibiting minor modifications of structures directly involved in pollination (e.g. nectary, rostellum and viscidium). Conversely, polyphyly has resulted from convergent evolution of floral attributes in distantly related species (e.g. *Mesadenus*). Some of the morphological characters used traditionally for generic delimitation and in non-molecular cladistic analyses of Spiranthinae are discussed against the evolutionary framework set by our molecular trees, emphasizing putative synapomorphies and problems derived from inappropriate character coding or incorrect homology assessments. Our ancestral area analysis indicates that Spiranthinae originated in eastern South America, with subsequent migrations and secondary

radiations in Mesoamerica and North America, plus a derived migration from the latter region to the Old World (*Spiranthes*).

Is Amazonia a 'museum' for Neotropical trees? The evolution of the *Brownea* clade (Detarioideae, Leguminosae).

Schley*, R. J., de la Estrella*, M., Pérez-Escobar*, O. A., Bruneau, A., Barraclough, T., Forest*, F. & Klitgård*, B. (2018). *Molecular Phylogenetics & Evolution* 126: 279–292. DOI: 10.1016/j.ympev.2018.04.029.

The flora of the Neotropics is unmatched in its diversity, however the mechanisms by which diversity has accumulated are debated and largely unclear. The *Brownea* clade (Leguminosae) is a characteristic component of the Neotropical flora, and the species within it are diverse in their floral morphology, attracting a wide variety of pollinators. This investigation aimed to estimate species divergence times and infer relationships within the group, in order to test whether the *Brownea* clade followed the 'cradle' or 'museum' model of diversification, i.e. whether species evolved rapidly over a short time period, or gradually over many millions of years. We also aimed to trace the spatio-temporal evolution of the clade by estimating ancestral biogeographical patterns in the group. We used BEAST to build a dated phylogeny of 73 *Brownea* clade species using three molecular markers (ITS, trnK and psbA-trnH), resulting in well-resolved phylogenetic relationships within the clade, as well as robust divergence time estimates from which we inferred diversification rates and ancestral biogeography. Our analyses revealed an Eocene origin for the group, after which the majority of diversification happened in Amazonia during the Miocene, most likely concurrent with climatic and geological changes caused by the rise of the Andes. We found no shifts in diversification rate over time, suggesting a gradual accumulation of lineages with low extinction rates. These results may help to understand why Amazonia is host to the highest diversity of tree species on Earth.

Seed germination niche of the halophyte *Suaeda maritima* to combined salinity and temperature is characterised by a halothermal time model.

Seal*, C. E., Barwell*, L. J., Flowers, T. J., Merrett Wade*, E. & Pritchard*, H. W. (2018). *Environmental and Experimental Botany* 155: 177–184. DOI: 10.1016/j.envexpbot.2018.06.035.

Sensitivity to salinity during seed germination potentially serves as a niche specifier for halophytes. Quantification of germination niche with respect to salinity, and any interaction with temperature, is therefore important to understand, particularly regarding the impacts of sea level rise in response to climate change. Population-based germination models quantify the response to temperature and water potential. However, there is limited applicability to salinity. Here, we develop a new approach considering thermal time (for temperature), halo time (for salinity) and halothermal time (for combined temperature and salinity), to quantify the germination of *Suaeda maritima*, a model halophyte with a worldwide distribution. We find salt concentration has a profound effect on the estimated base temperature for germination, Tb, being c. −4 °C in 600 mM NaCl compared with c. 1 °C in water. The predicted maximum concentration of NaCl for 50% germination to occur (NaClmax50) is 1280 mM at 5 °C and decreases (lower concentration) as the temperature increases. Overall, germination becomes slower as the concentration of salt increases (i.e., longer halo time) or the temperature decreases (i.e., longer thermal time). Combining all parameters into a halothermal time model is most successful at 5 and 10 °C. However, Na+ accumulation in the seed which coincides with maintained seed moisture content, regardless of salt concentration, influences the model fit. The models reveal two different germination niches: at cold temperatures, germination is slow but temperature and salinity are not necessarily limiting; and at warmer temperatures, germination is fastest but constrained by NaClmax50.

Phylogeny and systematics of Cyperaceae, the evolution and importance of embryo morphology.

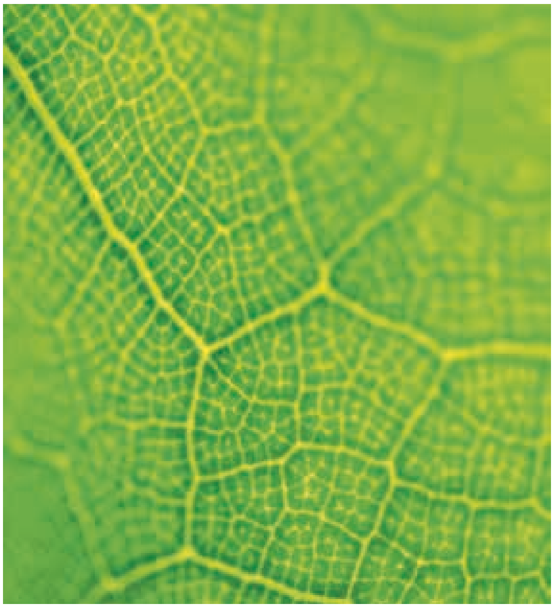
Semmouri, I., Bauters, K., Léveillé-Bourret, É., Starr, J. R., Goetghebeur, P. & Larridon*, I. (2018). *The Botanical Review*: 1–39. DOI: 10.1007/s12229-018-9202-0.

Despite recent advances in molecular phylogenetic studies, deep evolutionary relationships in Cyperaceae are still not entirely resolved. Reduction of floral morphology and complex inflorescences pose difficulties to unravel relationships based on morphology alone. One of the most phylogenetically informative structures in Cyperaceae are the embryos. The utility of embryo characters and types in Cyperaceae systematics is reviewed in a molecular phylogenetic context using a DNA supermatrix incorporating sequences from five plastid (matK, ndhF, rbcL, rps16, trnL-F) and two nuclear ribosomal (ETS, ITS) regions. The phylogenetic hypothesis presented includes the most extensive sampling of the family to date. Fourteen qualitative morphological embryo characters were coded, ancestral state reconstructions were performed, and the embryo of each sampled genus was classified in a typological system based on key morphological features. Embryo morphology provides a valuable source of independent data for Cyperaceae systematics that can be used to place species with unknown affinities, when molecular data is not available, or when results of analyses are inconclusive or conflicting. Integrating embryo data will remain critical for future higher level studies of Cyperaceae evolution and classification.

Was the ancestral angiosperm flower whorled throughout?

Sokoloff, D. D., Remizowa, M. V., Bateman*, R. M. & Rudall*, P. J. (2018). *American Journal of Botany* 105 (1): 5–15. DOI: 10.1002/ajb2.1003.

Inferring directions of character transformation during angiosperm evolution is widely appreciated as one of the most important goals of systematic botany, offering the potential to resolve the enigma of the origin of flowering plants. Many theories on the evolution of floral characters that were developed during the 20th century, such as those of Engler (1904), Takhtajan (1991), and Cronquist (1988), were based entirely on expert opinion. The subsequent cladistic approach to morphological character coding and use of topologies of molecular phylogenies as a framework for mapping phenotypic characters opened a more objective era in generating such reconstructions.



Pine mycorrhizal communities in pure and mixed pine-oak forests: abiotic environment trumps neighboring oak host effects.

Suz*, L. M., Kallow*, S., Reed, K., Bidartondo*, M. I. & Barsoum, N. (2017). *Forest Ecology and Management* 406: 370–380. DOI: 10.1016/j.foreco.2017.09.030.

Scots pine (*Pinus sylvestris*) is frequently planted as a monoculture, but it is also grown in mixed plantations with other native trees such as pedunculate oak (*Quercus robur*). Both pine and oak form ectomycorrhizas that cover their roots and extend into the soil, facilitating tree water and nutrient uptake in exchange for photosynthetic carbon. Forming the interface between the soil and tree roots, mycorrhizal fungi are key drivers of biogeochemical cycling in terrestrial ecosystems and play an important role in the successful establishment of tree seedlings. They can, however, be susceptible to changes in the soil environment and in their hosts. Both environment and neighboring hosts affect how fungi colonize roots and may affect their host preference. Despite the importance of mycorrhizal fungi in forest ecosystems, little is known about the biodiversity and functional effects of mycorrhizal communities in mixed compared with monoculture plantations. Changes in mycorrhizal richness and composition can result in changes in functional groups with consequences for forest ecosystem stability and functioning. We compared pine mycorrhizas in eight mixed plantations of pine and oak and eight pine monocultures in two forests in England, and we investigated the main factors driving their taxonomic and functional composition. Geographical location and litter pH explained over 50% of the variation in pine mycorrhizal communities.

Different environmental factors affected taxonomic and functional composition across stands, indicating functional redundancy. Pine tended to associate with more fungi in the presence of oak, but the abiotic environment exerted a stronger influence than oak presence on pine mycorrhizal diversity.

Positive plant–fungal interactions.

Suz*, L. M., Sarasan*, V., Wearn*, J. A., Bidartondo*, M. I., Hodkinson, T. R., Kowal, J., Murphy, B. R., Rodriguez, R. J. & Gange, A. (2018). *In:* Willis*, K. J. (ed.) *State of the World's Fungi.* Richmond: Royal Botanic Gardens, Kew, pp. 32–39.

How do plants benefit from fungal interactions and vice versa? What is the role of these positive interactions in supporting vital ecosystem processes?

Environment and host as large-scale controls of ectomycorrhizal fungi.

van der Linde*, S. *et. al.* (including Suz*, L. M., Bidartondo*, M. I.) (2018). *Nature* 558: 243–248. DOI: 10.1038/s41586-018-0189-9.

Explaining the large-scale diversity of soil organisms that drive biogeochemical processes—and their responses to environmental change—is critical. However, identifying consistent drivers of belowground diversity and abundance for some soil organisms at large spatial scales remains problematic. Here we investigate a major guild, the ectomycorrhizal fungi, across European forests at a spatial scale and resolution that is—to our knowledge—unprecedented, to explore key biotic and abiotic predictors of ectomycorrhizal diversity and to identify dominant responses and thresholds for change across complex environmental gradients. We show the effect of 38 host, environment, climate and geographical variables on ectomycorrhizal diversity, and define thresholds of community change for key variables. We quantify host specificity and reveal plasticity in functional traits involved in soil foraging across gradients. We conclude that environmental and host factors explain most of the variation in ectomycorrhizal diversity, that the environmental thresholds used as major ecosystem assessment tools need adjustment and that the importance of belowground specificity and plasticity has previously been underappreciated.

Floral heterochrony promotes flexibility of reproductive strategies in the morphologically homogeneous genus *Eugenia* (Myrtaceae).

Vasconcelos*, T. N., Lucas*, E. J., Faria, J. E. & Prenner*, G. (2018). *Annals of Botany* 121 (1): 161–174. DOI: 10.1093/aob/mcx142.

Comparative floral ontogeny represents a valuable tool to understand angiosperm evolution. Such an approach may elucidate subtle changes in development that discretely modify floral architecture and underlie reproductive lability in groups with superficial homogeneous morphology. This study presents a comparative survey of floral development in *Eugenia* (Myrtaceae), one of the largest genera of angiosperms, and shows how previously undocumented ontogenetic trends help to explain the evolution of its megadiversity in contrast to its apparent flower uniformity.

Eugenia flowers show similar organ arrangement patterns: radially symmetrical, (most commonly) tetramerous flowers with variable numbers of stamens and ovules. Despite a similar general organization, heterochrony is evident from size differences between tissues and structures at similar developmental stages. These differences underlie variable levels of investment in protection, subtle modifications to symmetry, herkogamic effects and independent androecium and gynoecium variation, producing a wide spectrum of floral display and contributing to fluctuations in fitness. During *Eugenia*'s bud development, the hypanthium (as defined here) is completely covered by stamen primordia, unusual in other Myrtaceae. This is the likely plesiomorphic state for Myrteae and may have represented a key evolutionary novelty in the tribe.

Floral evolution in *Eugenia* depends on heterochronic patterns rather than changes in complexity to promote flexibility in floral strategies. The successful early establishment of Myrteae, previously mainly linked to the key innovation of fleshy fruit, may also have benefitted from changes in flower structure.

Floral uniformity through evolutionary time in a species-rich tree lineage.

Vasconcelos*, T. N. C., Chartier, M., Prenner*, G., Martins, A. C., Schoenenberger, J., Wingler, A. & Lucas*, E. (2018). *New Phytologist*: DOI: 10.1111/nph.15453.

Changes in floral morphology are expected across evolutionary time and are often promoted as important drivers in angiosperm diversification. Such a statement, however, is in contrast to empirical observations of species-rich lineages that show apparent conservative floral morphologies even under strong selective pressure to change from their environments.

Here, we provide quantitative evidence for prolific speciation despite uniform floral morphology in a tropical species-rich tree lineage. We analyse floral disparity in the environmental and phylogenetic context of *Myrcia* (Myrtaceae), one of the most diverse and abundant tree genera in Neotropical biomes.

Variation in floral morphology among *Myrcia* clades is exceptionally low, even among distantly related species. Discrete floral specialisations do occur, but these are few, present low phylogenetic signal, have no strong correlation with abiotic factors, and do not affect overall macroevolutionary dynamics in the lineage.

Results show that floral form and function may be conserved over large evolutionary time scales even in environments full of opportunities for ecological interactions and niche specialisation. Species accumulation in diverse lineages with uniform flowers apparently does not result from shifts in pollination strategies, but from speciation mechanisms that involve other, nonfloral plant traits.

A role for fruit structure in seed survival and germination of *Swartzia langsdorffii* Raddi beyond dispersal.

Vaz, T. A. A., Rodrigues-Junior, A. G., Davide, A. C., Nakamura, A. T. & Toorop*, P. E. (2018). *Plant Biology* 20 (2): 263–270. DOI: 10.1111/plb.12671.

Diaspore structure has been hypothesised to play a role in seed viability and/or germination of recalcitrant seeds, especially for *Swartzia langsdorffii*. Thus, this work aims to (i) investigate the *in situ* contribution of pericarp and aril on seed viability and germination, and (ii) identify morphoanatomical traits of *S. langsdorffii* diaspores that allow its desiccation-sensitive seeds to remain viable.

The role of the pericarp and aril in seed survival and germination was investigated by placing the whole fruit, whole seeds (arillate seed) and bare seeds (without aril) in soil in the forest understorey, assessing germination, emergence, dead, firm and predated seeds, and water content of pericarps, arils and seeds. Correlation analysis was performed between environmental variables and physiological parameters. Histochemical features of diaspores were also investigated.

Pericarp water content fell after several months, while the aril maintained its water content. Seeds did not lose water even without the presence of the pericarp and aril. However, presence of the pericarp promoted seed water content, viability and germination long after dispersal. The embryo had a thickened outer periclinal cell wall.

Pericarp and aril are not essential to prevent water loss in seeds, but do help to retain seed moisture, favouring viability maintenance and promoting germination during the rainy season. Morphoanatomical features of seeds are suggested as main factors that reduce water loss. Survival of these desiccation-sensitive seeds upon dispersal during the dry season appears to be facilitated by multiple diaspore features that prevent viability loss.

Dry heat exposure increases hydrogen peroxide levels and breaks physiological seed coat-imposed dormancy in *Mesembryanthemum crystallinum* (Aizoaceae) seeds.

Visscher*, A. M., Yeo*, M., Gomez Barreiro*, P., Stuppy*, W., Latorre Frances*, A., Di Sacco*, A., Seal*, C. E. & Pritchard*, H. W. (2018). *Environmental and Experimental Botany* 155: 272–280. DOI: 10.1016/j.envexpbot.2018.07.009.

Seeds from many Aizoaceae species are characterized by their ability to survive extremely

high temperatures. In addition, physiological seed dormancy has been described for some members of the family. In this study, we investigated whether we could identify Aizoaceae species with physiological seed dormancy that can be broken by heat exposure. Furthermore, we explored the morphological and biochemical mechanisms through which heat may break this dormancy.

Three Aizoaceae species showed an increase in total germination following dry heat treatment. The physiological seed coat-imposed dormancy of *Mesembryanthemum crystallinum* seeds was found to be broken completely by dry heat exposure, which imposes both high temperature and ultra-drying stress, but not by high temperature or ultra-drying alone. Although no structural changes of the outer seed surface were detected using SEM, imbibition of water increased after dry heat treatment, whilst the seed coats remained impermeable to high-molecular-weight compounds. Analysis of H2O2 levels indicated that exposure to dry heat increased levels of this reactive oxygen species in *M. crystallinum* seeds relative to control conditions.

Here we describe for the first time in a species of the Aizoaceae family that exposure of seeds to dry heat can break physiological seed coat-imposed dormancy completely. Although *M. crystallinum* seeds became more permeable to water following dry heat treatment, this was not the case for methylene blue dye, suggesting that dry heat does not remove a potential barrier to diffusion of high-molecular-weight compounds. However, the observed elevation in H2O2 levels following dry heat treatment, possibly enabled by enhanced oxygen uptake through increased seed permeability, indicates a potential mechanism by which physiological dormancy is released in *M. crystallinum* seeds.

Ecological correlates of seed dormancy differ among dormancy types: a case study in the legumes.

Wyse*, S. V. & Dickie*, J. (2017). *New Phytologist* 217: 477–479. DOI: 10.1111/nph.14777.

No abstract available.

Taxonomic affinity, habitat and seed mass strongly predict seed desiccation response: a boosted regression trees analysis based on 17,539 species.

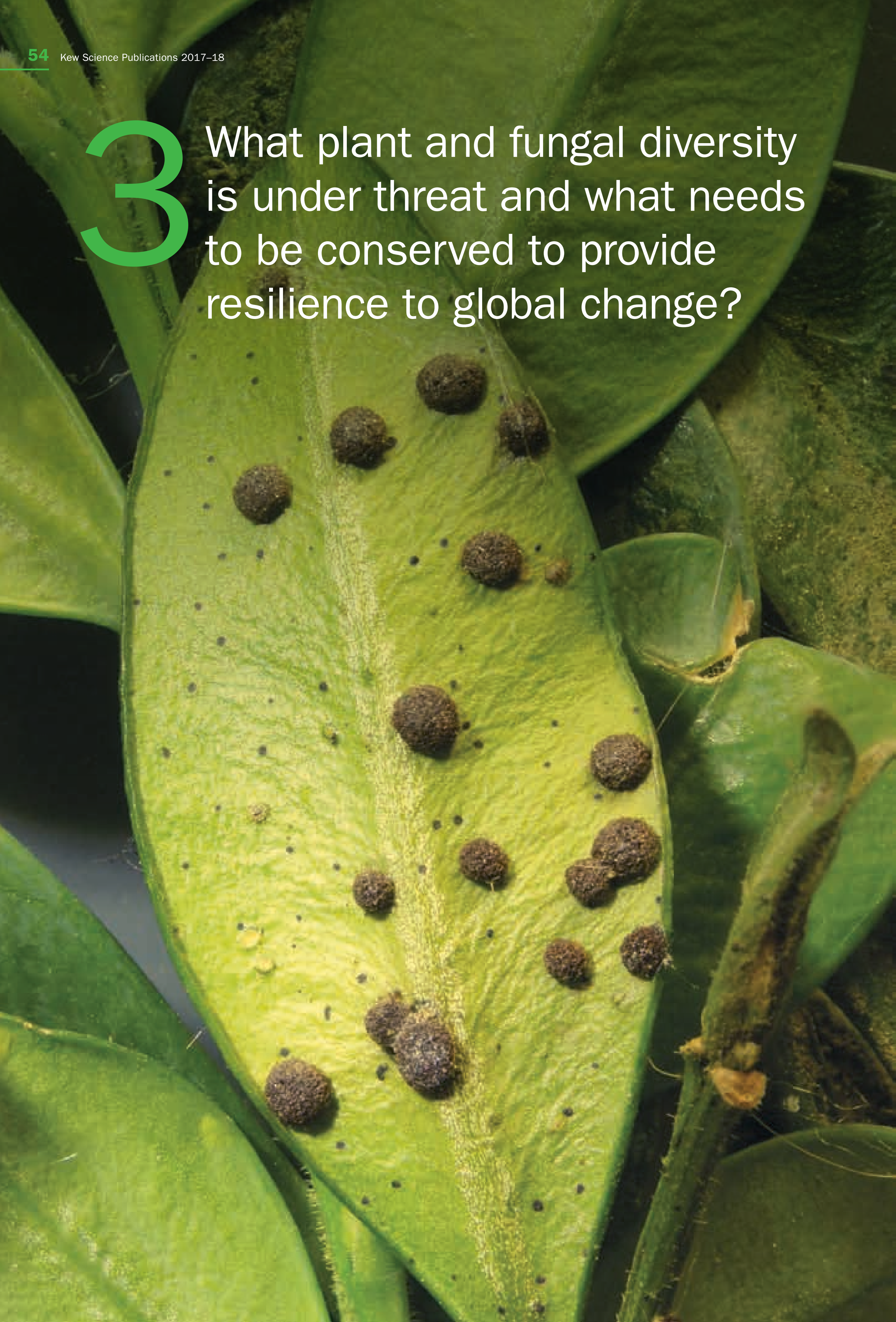
Wyse*, S. V. & Dickie*, J. B. (2018). *Annals of Botany* 121: 71–83. DOI: 10.1093/aob/mcx128.

Seed desiccation response plays an important role in plant regeneration ecology, and has significant implications for species conservation. The majority of seed plants produce desiccation-tolerant (orthodox) seeds, whilst comparatively few produce desiccation-sensitive (recalcitrant) seeds that are unable to survive dehydration, and which cannot be conserved in traditional seed banks. This study develops a set of models to predict seed desiccation response in unstudied species.

The three models had varying success rates for identifying the desiccation-sensitive species: 89 % for the genus-level model, 79 % for the family-level model and 60 % for the order-level model. The most important predictor variables were the seed desiccation responses of a species' relatives, seed mass and annual precipitation. It is predicted that 10 % of seed plants from Ecuador and 1.2 % of those from Britain and Ireland produce desiccation-sensitive seeds. Due to data availability, prediction accuracy is likely to be higher for the British and Irish flora, where it is estimated that a desiccation-sensitive species had a 96.7 % chance of being correctly identified, compared with 80.8 % in the Ecuador flora. These models can utilize existing data to predict species' likely seed desiccation responses, providing a gap-filling tool for global studies of plant traits, as well as critical decision-making support for plant conservation activities.

3

What plant and fungal diversity is under threat and what needs to be conserved to provide resilience to global change?



Conservation of fungi.

Ainsworth*, A. M., Canteiro*, C., Dahlberg, A., Douglas*, B., Furci, G., Minter, D., Mueller, G. M., Scheidegger, C., Senn-Irlet, B., Wilkins, T. & Williams*, E. (2018). *In:* Willis*, K. J. (ed.) *State of the World's Fungi.* Richmond: Royal Botanic Gardens, Kew, pp. 70–77.

How many species of fungi are threatened with extinction and why are they so difficult to assess? What threats are fungi facing and what are the conservation challenges?

Rarer than we thought: a DNA-based reassessment of UK *Amanita friabilis* collections.

Ainsworth*, M. & Suz*, L. M. (2018). *Field Mycology* 19 (3): 93–100. DOI: 10.1016/j.fldmyc.2018.07.010.

Following our DNA-based analyses of *Hohenbuehelia culmicola* and *Entoloma bloxamii*, which resulted in the description of two new species (Ainsworth et al., 2016; 2018), we are now reporting the results of similar work carried out on another species of conservation concern, Fragile Amanita, *Amanita friabilis*. This is generally regarded as an *Alnus*-associated ectomycorrhizal fungus with relatively small, greyish-brown, fragile sporophores. The stipe lacks an annulus (suggesting affinities with section *Vaginatae*) but it has a slightly bulbous base and lacks a cohesive and membranous volva (unlike section *Vaginatae*), although there may be a few scaly belts around the upper part of the bulb. It is widespread but rare, and hence poorly known, across its entire European range (Bas, 1974; Reid, 1987; Breitenbach & Kränzlin, 1995; Dahlberg & Croneborg, 2006). *Amanita friabilis* is known from around 100 sites in Europe, but it is reportedly declining in France and Sweden and is now regarded as extinct in the Netherlands (Fraiture & Otto, 2015). It was reported as new to Britain in Reid (1987) based on material collected in 1986 from Gait Barrows in NW England which is now preserved in Kew. There is an earlier (1957) collection catalogued as *A. friabilis* in the Royal Botanic Garden Edinburgh (http://data.rbge.org.uk/herb/E00252923) found in Norfolk by Peter Orton (which we have not studied), and an apparently unsubstantiated Scottish find documented in *Mycologia Scotica*, which could possibly refer to a 1979 Scottish record on the FRDBI (see links in reference list). These finds were not considered by Reid (1987) or by Legon & Henrici (2005) and so the possibility remains that there could be one or two pre-1986 British records. As with our two previous studies, this investigation began as a Natural England Species Recovery Project (SRP) in which we generated DNA barcode sequences (ITS region, Schoch et al., 2012) from non-lichenised fungi officially regarded as conservation priority species in England, i.e. those named on Section 41 of the NERC Act 2006. Historically, *A. friabilis* is unofficially assessed in Great Britain as Endangered (Ing, 1992; Evans et al., 2006). More recently it was selected as one of the 100 target species in RBG Kew's Lost and Found Fungi (LAFF) Project (see link in reference list). It is also the subject of significant international conservation interest and it is: currently proposed for assessment in the global red-listing project; one of the 33 fungal candidates unsuccessfully proposed for listing on Appendix 1 of the Bern Convention (Dahlberg & Croneborg, 2006); one of the 51 macrofungi recently mapped across Europe (Fraiture & Otto, 2015); red-listed in 14 European countries (Fraiture & Otto, 2015); and, a characteristic species of *Alnus* woodlands and is threatened by deforestation and drainage (Fraiture & Otto, 2015).

Quantifying progress toward a conservation assessment for all plants.

Bachman*, S. P., Nic Lughadha*, E. M. & Rivers, M. C. (2018). *Conservation Biology* 32 (3): 516–524. DOI: 10.1111/cobi.13071.

The Global Strategy for Plant Conservation (GSPC) set an ambitious target to achieve a conservation assessment for all known plant species by 2020. We consolidated digitally available plant conservation assessments and reconciled their scientific names and assessment status to predefined standards to provide a quantitative measure of progress toward this target. The 241,919 plant conservation assessments generated represent 111,824 accepted land plant species (vascular plants and bryophytes, not algae). At least 73,081 and up to 90,321 species have been assessed at the global scale, representing 21–26% of known plant species. Of these plant species, at least 27,148 and up to 32,542 are threatened. Eighty plant families, including some of the largest, such as Asteraceae, Orchidaceae, and Rubiaceae, are underassessed and should be the focus of assessment effort if the GSPC target is to be met by 2020. Our data set is accessible online (ThreatSearch) and is a baseline that can be used to directly support other GSPC targets and plant conservation action. Although around one-quarter of a million plant assessments have been compiled, the majority of plants are still unassessed. The challenge now is to build on this progress and redouble efforts to document conservation status of unassessed plants to better inform conservation decisions and conserve the most threatened species.

UAVs in pursuit of plant conservation - Real world experiences.

Baena*, S., Boyd, D. S. & Moat*, J. (2017). *Ecological Informatics*: 47: 2–9. DOI: 10.1016/j.ecoinf.2017.11.001.

Small Unmanned Aerial Systems (UASs) (more commonly called Unmanned Aerial Vehicles, UAVs or drones), have the potential to enhance current understanding and management of a range of environmental applications. There has been much coverage on the use of UAVs for conservation applications in the recent years, yet little on specific applications in plant conservation. Here we present our experience of using an off-the-shelf fixed wing UAV for plant conservation projects ranging from Peru's hyper-arid vegetation to the dry forests of the Caribbean and finally to the humid forest of South Africa and the Brazilian Amazon. We present our findings from over ten successful (but also our unsuccessful) field work campaigns flying over 4500 km. We show how the technology is being used for mapping, quantifying and monitoring plant species, but also review the real-world issues of using UAVs, particularly in remote areas.

Identifying species from the air: UAVs and the very high resolution challenge for plant conservation.

Baena*, S., Moat*, J., Whaley*, O. & Boyd, D. S. (2017). *PLoS One* 12 (11): e0188714. DOI: 10.1371/journal.pone.0188714.

The Pacific Equatorial dry forest of Northern Peru is recognised for its unique endemic biodiversity. Although highly threatened the forest provides livelihoods and ecosystem services to local communities. As agro-industrial expansion and climatic variation transform the region, close ecosystem monitoring is essential for viable adaptation strategies. UAVs offer an affordable alternative to satellites in obtaining both colour and near infrared imagery to meet the specific requirements of spatial and temporal resolution of a monitoring system. Combining this with their capacity to produce three dimensional models of the environment provides an invaluable tool for species level monitoring. Here we demonstrate that object-based image analysis of very high resolution UAV images can identify and quantify keystone tree species and their health across wide heterogeneous landscapes. The analysis exposes the state of the vegetation and serves as a baseline for monitoring and adaptive implementation of community based conservation and restoration in the area.

Fern conservation: spore, gametophyte, and sporophyte *ex situ* storage, in vitro culture, and cryopreservation.

Ballesteros*, D. & Pence, V. (2018). *In:* Fernández, H. (ed.) *Current Advances in Fern Research*. Springer, Cham, pp.227–249.

Many species of ferns and lycophytes are threatened by habitat destruction, over-collecting, invasive species, and climate change, and plans to secure their *in situ* and *ex situ* conservation are urgently needed. However, there has not been a development of standard methods for fern *ex situ* storage and conservation, as there has been for seed plants. This is likely due to the fact that ferns have been less studied and are less understood than seed plants and that there has been less funding and institutional focus on them for conservation purposes when compared with domesticated or wild seed plants. Tissues from different stages of the fern and lycophyte life cycle can be used as a ready source of germplasm for *ex situ* conservation. Spore storage is generally the most efficient method for *ex situ* fern conservation, but there are also situations where storing gametophytes or sporophytes can be extremely useful. The longevity of spores at –20 °C, the standard seed banking temperature, may vary with the species. Storage in LN should improve longevity in spores and is likely necessary for non-spore tissues. Recent results of a study on the viability of spores, gametophytes, and sporophytes after 20 years of storage in liquid nitrogen is used as a case study to illustrate the potential of these methods. The state of current methods and needs for further research and application are discussed. While there is much more to learn, these tools are available for fern *ex situ* conservation and should be implemented on a broader scale to preserve rare fern taxa and provide materials for future restoration and research.

Climate change: Fungal responses and effects.

Bidartondo*, M. I., Ellis*, C., Kauserud, H., Kennedy, P. G., Lilleskov, E. A., Suz*, L. M. & Andrew, C. (2018). *In:* Willis*, K. J. (ed.) *State of the World's Fungi.* Richmond: Royal Botanic Gardens, Kew, pp. 62–69.

What impact is climate change having on fungal communities across the globe and where are our greatest knowledge gaps?

Ex situ conservation of native plant species in Europe: The ENSCONET Consortium.

Breman*, E., Carta, A., Kiehn, M. & Miranto, M. (2018). *In* MNHN (ed.) EuroGard VII Congress Paris, France: The European Botanic Gardens Consortium, pp. 290–296.

High-standard seed collecting and storage activities are important elements of *ex situ* conservation and, ideally, should be fully integrated into overarching conservation actions. Consequently, European seed banks and other bodies with an interest in seed banking and conservation of Europe's native flora started the European Native Seed Conservation NETwork (ENSCONET) Consortium (2010-present), an extension of the FP6 funded ENSCONET project (2004-2009). Its aims are to improve quality, co-ordination and integration of European seed conservation practice, policy and research for native plant species. It also intends to enable the exchange of information, equipment and staff, the sharing of data, collaborations at the European level and interactions with *in situ* conservation initiatives.

Safe for the future: seed conservation standards developed for the Millennium Seed Bank Partnership.

Breman*, E. & Way*, M. (2018). *In* MNHN (ed.) EuroGard VII Congress Paris, France: The European Botanic Gardens Consortium, pp. 267–274.

The Millennium Seed Bank Partnership (MSBP) Seed Conservation Standards provide a framework within which member organisations cooperate to ensure the quality of their collections. Making conservation seed collections from wild populations faces very different challenges from banking agricultural collections, highlighting the need for standards tailored to such collections. The Seed Conservation Standards developed for the MSBP represent current best practice for long-term conservation of orthodox seeds from wild plants. They draw on and reference various existing protocols and guidelines and can be applied and monitored at an international scale. We provide an introduction to the Standards, which cover all aspects of long-term seed conservation, from collection to seed bank management. In addition to ensuring the quality of the collections, the Standards also provide a basis for technology transfer amongst partners and capacity development within the MSBP network as a whole. The ability of the Standards to improve facilities across the network is discussed. Up to 50% of the indicators used to monitor the Standards can be assessed by routine collection data exchange, such as through the MSBP Data Warehouse, a BRAHMS database containing seed collection data from across the MSBP. The remainder are assessed as part of regular partnership cooperation visits. An annual questionnaire records developments across the MSBP, and has been used to gauge response to the Standards. Eighty five percent of respondents to the 2014 survey supported the development and implementation of the Standards. Standards which were deemed easiest to meet included those associated with collecting, processing and data management, while ‘viability and monitoring’ was seen as the hardest group of Standards to meet, followed by ‘distribution’, ‘storage and duplication’, and ‘seed bank management’. In 2015, 40% of respondents to a survey felt ready for a Standards review, while 33% preferred to defer for a year.

Diachronic analysis using aerial photographs across fifty years reveals significant land use and vegetation changes on a Mediterranean island.

Carta, A., Taboada, T. & Müller*, J. V. (2018). *Applied Geography* 98: 78–86. DOI: 10.1016/j.apgeog.2018.07.010.

Understanding land use changes provides data suitable for decision making processes in biodiversity conservation and landscape planning. We examined temporal change in landscape and vegetation formations on Elba Island (Tyrrhenian Sea, Italy) using digital aerial photographs (1954, 1978, 2000) and deriving land-use maps from photo interpretation. The detected variations of landscape composition, patch size and isolation revealed that the decline of agriculture is the main anthropogenic driver causing significant changes in the landscape, leading to a complete shift from an island under cultivation to a largely naturally vegetated island. The patchiness and the fragmentation have decreased so that natural vegetation with localized intensive cultivation and settlements, especially along the coast, remained the dominant elements of the mosaic. These changes in landscape composition and pattern are expected to have dramatic functional consequences and a landscape management plan avoiding land-use polarization through tourism is needed.

Reversing land degradation and desertification in Africa’s drylands.

Ceci*, P., Sanogo, S., Ambrose*, E., Sacande, M., Sanou, L., Adda M. & Ulian*, T. (2018). *BGJournal* 15 (2): 19–22.

The knowledge of plant diversity and conservation by experts at the Royal Botanic Gardens, Kew, working with in-country partners in Burkina Faso, Mali and Niger, supports land restoration and livelihoods enhancement in sub-Saharan Africa.

Capturing, protecting and restoring plant diversity in the UK: RBG Kew and the Millennium Seed Bank.

Chapman*, T., Miles*, S. & Trivedi*, C. (2018). *Plant Diversity* 40. DOI: 10.1016/j.pld.2018.06.001.

Ex situ seed banking is a practical and cost-effective means of preserving wild plant diversity and a crucial complement to the *in situ* conservation and restoration of species and habitats. As pressures on the natural environment have grown, so has the call for seed banks to provide scientifically-robust, practical solutions to seed-related problems in nature conservation, from single-species recovery and reintroduction to the restoration of complex, dynamic communities at the largest scales. In this paper, we discuss how the Royal Botanic Gardens, Kew and its Millennium Seed Bank have responded to this call in the United Kingdom. We demonstrate that banked seed collections can provide a range of otherwise-unavailable, high quality, known-origin, genetically-diverse biological materials. The data, expertise and specialist facilities that accompany these collections are also valuable, helping overcome constraints to the collection, production and effective use of native seed. Challenges remain - to ensure *ex situ* collections protect the species and genetic diversity that will enable plants to adapt to a changing environment, and to find new ways for seed banks to mobilise their resources at a landscape scale.

Cola dorrii sp. nov. (Sterculiaceae), a threatened Maputaland Forest endemic of South Africa.

Cheek*, M., Lawrence*, P. & McCleland, W. (2018). *Kew Bulletin* 73 (2): 25. DOI: 10.1007/s12225-018-9749-2.

Cola dorrii Cheek sp. nov. is described from Maputaland Sand and Northern Coastal Forest types in KwaZulu-Natal of South Africa. Formerly treated as *Cola greenwayi* Brenan, it differs in much shorter leaf-blades and petioles, and in the fruitlets which are stipitate, with apices that are rounded and forward-facing. The indumentum has stellate hairs which are soft, with sinuate arms, rather than subscabrid with stiff arms. The species is assessed as Vulnerable using the IUCN 2012 standard due to habitat modification and loss due to humans, elephants and due to the invasive shrub *Chromolaena odorata*.

Endangered fairies: two new species of *Caladenia* (Orchidaceae; Orchidoideae; Diurideae), from the bauxite plateaux of southwestern Western Australia.

Dixon, K. W. & Christenhusz*, M. J. M. (2018). *Phytotaxa* 334: 87–90. DOI: 10.11646/phytotaxa.334.1.15.

Two new sympatric species of *Caladenia* from relatively inaccessible, high lateritic plateaux in a high rainfall area in southwestern Western Australia are described here as new to science. The species occur in a restricted area, c. 100 km southeast of Perth, south of Dwellingup and northeast of Waroona. The two species co-occur and are associated with putative floral model species that they are mimicking. *Caladenia lateritica* mimics *Conostylis setosa* (Haemodoraceae) in terms of flowering time, height, colour and fragrance. *Caladenia rosea* mimics the flowers of *Hypocalymma robustum* (Myrtaceae) in terms of flowering time, colour and scent. We assume that these orchids share a pollinator with their mimics and attract the pollinator via food deception as the ‘hosts’ are sources of nectar and pollen for visiting native bees. Because the species co-occur and exhibit a remarkable evolutionary ‘arms race’, they would make an ideal model for further study of the processes driving sympatric speciation. Unfortunately, both new species are under threat from mining activities and poorly informed burning regimes.

Enhancing accessibility and conservation of plant tissue samples stored in silica gel, and developing a disaster plan for this collection at Royal Botanic Gardens, Kew.

Duque-Thüs*, R. & Fulcher*, T. K. (2018). *Journal of Natural Science Collections* 5: 35–40.

Many specimens in the Royal Botanic Gardens (RBG), Kew Plant Tissue Collection represent rare and endangered species from difficult to access regions of the world, including unique samples from a diversity of taxonomic groups. Whilst storing research materials in individual laboratories during use is accepted practice, it is unsuitable for safe long-term preservation. This paper describes the process for deposition of plant materials into the tissue collections, best practice in recuration to ensure long-term preservation and storage, and disaster planning.

Orchid conservation: how can we meet the challenges in the twenty-first century?

Fay, M. F. (2018). *Botanical Studies* 59: 16. DOI: 10.1186/s40529-018-0232-z.

With c. 28,000 species, orchids are one of the largest families of flowering plants, and they are also one of the most threatened, in part due to their complex life history strategies. Threats include habitat destruction and climate change, but many orchids are also threatened by unsustainable (often illegal and/or undocumented) harvest for horticulture, food or medicine. The level of these threats now outstrips our abilities to combat them at a species-by-species basis for all species in such a large group as Orchidaceae; if we are to be successful in conserving orchids for the future, we will need to develop approaches that allow us to address the threats on a broader scale to complement focused approaches for the species that are identified as being at the highest risk.

Quest for adequate biodiversity surrogates in a time of urgency.

Forest*, F. (2017). *PNAS* 114 (48): 12638-12640. DOI: 10.1073/pnas.1717722114.

Earth’s biodiversity is declining at an alarming rate, in what some have dubbed the “sixth mass extinction” that life has faced in the history of our planet (1). This rapid decline of biodiversity, the realization that some of its components, such as fungi, remain relatively poorly known, and limited resources are rendering the process of prioritizing conservation efforts more challenging. The expression “agony of choice,” put forward by Vane-Wright et al. (2) to describe the context in which these decisions have to be made, has become even more pertinent. In this time of urgency and scarce resources, conservation practitioners have been seeking methods and indices that can accelerate the selection of species and areas, which are to be the focus of conservation actions. These approaches include the identification of surrogates, which can either mirror the distribution patterns of other features that are less readily accessible, but potentially more informative or relevant in a particular context, or more easily represent biodiversity as a whole. Surrogates are expected to save time and resources compared with more conventional methods and have attracted increasing interest among conservation planners. These surrogates are generally of two broad types, taxonomic and environmental (3). Taxonomic surrogates are using a particular group of organisms and extrapolate the patterns observed in this group as representing overall biodiversity (e.g., ref. 4). Environmental surrogates usually comprise an amalgam of physical

and biological information, such as ecological classifications (e.g., ref. 5), which have been widely employed in conservation planning as they are assumed to represent adequately groups of species, communities, and ecosystems.

Gymnosperms on the EDGE.

Forest*, F. *et al.* (including Moat*, J.) (2018). *Scientific Reports* 8: 1–11. DOI: 10.1038/s41598-018-24365-4.

Driven by limited resources and a sense of urgency, the prioritization of species for conservation has been a persistent concern in conservation science. Gymnosperms (comprising ginkgo, conifers, cycads, and gnetophytes) are one of the most threatened groups of living organisms, with 40% of the species at high risk of extinction, about twice as many as the most recent estimates for all plants (i.e. 21.4%). This high proportion of species facing extinction highlights the urgent action required to secure their future through an objective prioritization approach. The Evolutionary Distinct and Globally Endangered (EDGE) method rapidly ranks species based on their evolutionary distinctiveness and the extinction risks they face. EDGE is applied to gymnosperms using a phylogenetic tree comprising DNA sequence data for 85% of gymnosperm species (923 out of 1090 species), to which the 167 missing species were added, and IUCN Red List assessments available for 92% of species. The effect of different extinction probability transformations and the handling of IUCN data deficient species on the resulting rankings is investigated. Although top entries in our ranking comprise species that were expected to score well (e.g. *Wollemia nobilis*, *Ginkgo biloba*), many were unexpected (e.g. *Araucaria araucana*). These results highlight the necessity of using approaches that integrate evolutionary information in conservation science.

European Red List of lycopods and ferns.

García Criado, M., Väre, H., Nieto, A., Bento Elias, R., Dyer, R., Ivanenko, Y., Ivanova, D., Lansdown*, R., Molina, J. A., Rouhan, G., Rumsey, F., Troia, A., Vrba J. & Christenhusz*, M. J. M. (2017). Brussels, IUCN.

In recent years, awareness has risen surrounding the crucial role of plants in providing ecosystem services and on their decline – they are one of the essential foundations of healthy ecosystems that we depend on. However, significant gaps in knowledge still remain. In this context, the European Red List of lycopods and ferns provides the first ever comprehensive assessment of the extinction risk of all native lycopod and fern species to Europe. With 194 species assessed, this assessment highlights that 19.9% of lycopod and fern species are threatened with extinction in Europe. This is mainly due to urban and infrastructure development, human intrusions and disturbance, pollution, and water use and management.

High genetic diversity in a threatened clonal species, *Cypripedium calceolus* (Orchidaceae), enables long-term stability of the species in different biogeographical regions in Estonia.

Gargiulo*, R., Ilves A., Kaart T., Fay* M. F. & T., K. (2018). *Botanical Journal of the Linnean Society* 186 (4): 560–571. DOI: 10.1093/botlinnean/box105.

In plants capable of clonal reproduction, demographic and ecological investigations are essential for understanding the factors contributing to population diversity. The perennial, clonal orchid *Cypripedium calceolus* has a variable status in Europe and Asia, being threatened with extinction in some countries and abundant in others. In Estonia, thriving populations can be observed in different biogeographical regions. The aim of this study was to characterize genetic diversity and differentiation in Estonian populations, by comparing the current variation with long-term observations of the clonal system and taking into account climatic variables. Diversity at 11 microsatellite loci for 11 populations representing the boreal and nemoral regions was investigated. Some signatures of bottleneck and recent founder events were detected, with a high genetic diversity in terms of heterozygosity and allele diversity and a pattern of differentiation not strictly correlated with geographical factors. Globally, information regarding population dynamics in *C. calceolus* provides the possibility to inform conservation management, prevent loss of ancestral variation and promote intra-population divergence through the combination of gene flow and ecological change related to the clonal system.

Evaluation of genetic diversity and admixture in the only English population of *Nuphar pumila*.

Gargiulo*, R., Lansdown*, R. V. & Fay*, M. F. (2017). *Natural England Commissioned Report NECR245*. York: Natural England.

No abstract available.

First report of cobweb disease caused by *Cladobotryum dendroides* on shiitake mushroom (*Lentinula edodes*) in Spain.

Gea, F. J., Navarro, M. J. & Suz*, L. M. (2018). *Plant Disease* 102: 1030. DOI: 10.1094/PDIS-09-17-1481-PDN.

Lentinula edodes, known as shiitake, is the most cultivated edible mushroom worldwide, representing about 22% of the world's output, with China being the major producer. In 2017, symptoms of cobweb were observed on cultivated shiitake mushrooms in Castilla-La Mancha (Spain), affecting more than 30% of the blocks of pasteurized substrate.

Implementing a new approach to effective conservation of genetic diversity, with ash (*Fraxinus excelsior*) in the UK as a case study.

Hoban, S., Kallow*, S. & Trivedi*, C. (2018). *Biological Conservation* 225: 10–21. DOI: 10.1016/j.biocon.2018.06.017.

Gene conservation programs help safeguard species and tangibly benefit ecological restoration, agriculture, forestry, and horticulture. Here we describe a new method for deciding which and how many populations and individuals to conserve *ex situ*, and we demonstrate the method by evaluating collections of European Ash (*Fraxinus excelsior*) for an ongoing seed-banking project, the UK National Tree Seed Project (NTSP). The method uses simulations and geographic distribution data, and does not require (but can utilize) genetic data. We estimate that NTSP collections have captured >90% of all alleles and of locally common alleles. We identified optimal sampling solutions at large and small spatial scales, and for northern isolated vs. southern core populations. We also quantified genetic "points of diminishing returns" with a more precise method than previous studies. This analysis revealed that (for European ash, for a goal of capturing one copy of each allele) an optimal "stopping point" is approximately 35 populations, 10 to 30 trees per population, and 30 seeds per tree. Overall, we conclude that the NTSP protocol of random sampling of at least 15 trees per population from two populations per seed zone is effective. We demonstrated how collectors can adjust the number of populations, individuals and seeds sampled using the concept of “genetic equivalence”, allowing projects to accommodate practical or ecological constraints. Lastly we showed that for a conservation goal of 50 allele copies rather than one copy, a much larger sampling effort is needed (>150 populations). This new approach can be tailored to any species. It is applicable to any seed collection seeking to capture genetic diversity, as well as *in situ* gene conservation approaches. We emphasize that the ability to quantitatively estimate the outcome of gene conservation activities can help design, justify, or evaluate future programs.

Hybridisation and the conservation of *Nuphar pumila* (least water-lily).

Lansdown*, R., Cousins, M., Gargiulo*, R. & Fay*, M. (2018). *BSBI News* 137: 14–19.

No abstract available.

Development of a conservation plan for Least Water-lily (*Nuphar pumila*) in England.

Lansdown*, R. V., Natural England Commissioned Reports & York., N. (2017). *In: Natural England Commissioned Report*, York.

No abstract available.

The conservation value of germplasm stored at the Millennium Seed Bank, Royal Botanic Gardens, Kew, UK.

Liu*, U., Breman*, E., Cossu*, T. A. & Kenney, S. (2018). *Biodiversity and Conservation*: DOI: 10.1007/s10531-018-1497-y.

The Millennium Seed Bank (MSB) Partnership, developed and managed by the Royal Botanic Gardens, Kew (RBG Kew), conserves propagules primarily from orthodox seed-bearing wild vascular plants. It is the largest *ex situ* conservation programme in the world, currently involving 96 countries and territories. Where possible, seeds are collected and conserved in the country of origin with duplicates being sent to RBG Kew’s MSB for storage. In this paper we assess the conservation value of the germplasm stored at the MSB using both quantitative and qualitative methods. The MSB holdings represent a high quality, rich biological resource. Substantial and unique taxonomic diversity exists amongst the collections, representing 365 families, 5813 genera, 36,975 species and 39,669 taxa conserved. The collections cover a wide geographic range, originating from 189 countries and territories, representing all nine bio-geographic regions and all 35 biodiversity hotspots. The collections possess significant natural capital and population value: 32% of taxa, representing 49% of collections, have at least one identified use to humans; and 74% of taxa, representing 78% of collections, are either endemic, endangered (nationally or globally) and/or have an economic, ecological, social, cultural or scientific value. While 10% of taxa, representing > 8% of collections, are either extinct, rare or vulnerable to extinction at the global and/or national level, 20% of taxa, representing 13% collections, are endemic at the country or territory scale. Over the 17-year period since 2000 at least 11,182 seed samples, representing 12% of taxa and 8% of collections, have been distributed globally for conservation, research, education and display. This analysis highlighted collection gaps in MSB holdings in relation to their geographic representativeness, the taxonomic diversity of large families and genera of angiosperms, and coverage of threatened taxa. Further analysis across the entire MSB Partnership is required to underpin future collection activities and maximize the usefulness of collections.

LEFT—A web-based tool for the remote measurement and estimation of ecological value across global landscapes.

Long, P. R., Benz, D., Martin, A. C., Holland, P. W. A., Macias-Fauria, M., Seddon, A. W. R., Hagemann, R., Frost T.K, Simpson, A., Power, D. J., Slaymaker, M. A. & Willis*, K. J. (2018). *Methods in Ecology and Evolution* 9 (3): 571–579. DOI: 10.1111/2041-210X.12924.

The overall aim in the development of the Local Ecological Footprinting Tool (LEFT) was to design a web-based tool that could provide quickly obtained quantitative data on ecological risk to assist landowners when making land-use change decisions. The Local Ecological Footprinting Tool works for almost any region in the world and uses freely available satellite imagery, biotic and abiotic data from existing global databases, models and algorithms to deliver a customised report for a selected area within one hour of job submission. Biotic data automatically obtained for a selected landscape includes terrestrial vertebrate and plant species occurrence data, information on their conservation status and remotely sensed vegetation productivity. Abiotic information obtained includes temperature, precipitation, water availability, insolation, topography, elevation, distribution of urban infrastructure and location of wetlands. The tool performs a number of analyses on the biotic and abiotic data to produce maps for the selected area at a 30 m resolution depicting land cover type, numbers of globally threatened terrestrial vertebrate and plant species, beta-diversity of terrestrial vertebrates and plants, habitat intactness, wetland habitat connectivity, numbers of migratory species and vegetation resilience. Results are also aggregated to produce a summary map demonstrating areas of high and low ecological risk across the selected area.

The Local Ecological Footprinting Tool has been designed to be intuitive to use, requiring no specialised software or user expertise. Input is extremely easy and requires the user to highlight the area of interest on a map or using grid co-ordinates. Output is delivered via the web application and comprises a customised PDF containing the maps and a zip file of geographical information system (GIS) data for the area requested. Users may run an unlimited number of LEFT analyses and download reports free of charge. In addition to the free tool described in this paper, there is also a paid service: individual LEFT analyses can be upgraded for a charge to allow access to the geographically subsetted datasets generated for each report. These data are supplied as a zip file containing raster datasets for the layers in the LEFT analysis in GeoTIFF format. These can be opened and queried in a GIS software package.

Refining area of occupancy to address the modifiable areal unit problem in ecology and conservation.

Moat*, J., Bachman*, S. P., Field, R. & Boyd, D. S. (2018). *Conservation Biology*. DOI: 10.1111/cobi.13139.

The 'modifiable areal unit problem' is prevalent across many aspects of spatial analysis within ecology and conservation. The problem is particularly manifest when calculating metrics for extinction risk estimation, for example, area of occupancy (AOO). Although embedded into the International Union for the Conservation of Nature (IUCN) Red List criteria, AOO is often not used or is poorly applied. Here we evaluate new and existing methods for calculating AOO from occurrence records and present a method for determining the minimum AOO using a uniform grid. We evaluate the grid cell shape, grid origin and grid rotation with both real-world and simulated data, reviewing the effects on AOO values, and possible impacts for species already assessed on the IUCN Red List.

We show that AOO can vary by up to 80% and a ratio of cells to points of 1:1.21 gives the maximum variation in the number of occupied cells. These findings potentially impact 3% of existing species on the IUCN Red List, as well as species not yet assessed. We show that a new method that combines both grid rotation and moving grid origin gives fast, robust and reproducible results and, in the majority of cases, achieves the minimum AOO. As well as reporting minimum AOO, we outline a confidence interval which should be incorporated into existing tools that support species risk assessment. We also make further recommendations for reporting AOO and other areal measurements within ecology, leading to more robust methods for future species risk assessment.

Comparative biology of cycad pollen, seed and tissue – a plant conservation perspective.

Nadarajan*, J., Benson, E. E., Xaba, P., Harding, K., Lindstrom, A., Donaldson, J., Seal*, C. E., Kamoga, D., Agoo, E. M. G., Li, N., King, E. & Pritchard*, H. W. (2018). *Botanical Review* 84 (3): 295–314. DOI: 10.1007/s12229-018-9203-z.

Cycads are the most endangered of plant groups based on IUCN Red List assessments; all are in Appendix I or II of CITES, about 40% are within biodiversity ‘hotspots,’ and the call for action to improve their protection is long-standing. We contend that progress in this direction will not be made until there is better understanding of cycad pollen, seed and tissue biology, which at the moment is limited to relatively few (<10%) species. We review what is known about germplasm (seed and pollen) storage and germination, together with recent developments in the application of contemporary technologies to tissues, such as isotype labelling, biomolecular markers and tissue culture. Whilst progress is being made, we conclude that an acceleration of comparative studies is needed to facilitate the integration of *in situ* and *ex situ* conservation programmes to better safeguard endangered cycads.

Mining threatens Colombian ecosystems.

Pérez-Escobar*, O. A., *et al.*, (including Cámara-Leret*, R., Bateman* R.M., Bellot*, S. & Diazgranados*, M. (2018). *Science* 359 (6383): 1475. DOI: 10.1126/science.aat4849.

The American tropics are home to about 10% of Earth’s species and several biodiversity hotspots of global importance for conservation (1, 2), including high-elevation tropical alpine ecosystems (páramos) and Andean forests. These ecosystems deliver numerous services, such as providing water to millions of people (3). They are also extremely sensitive to perturbations and difficult to restore (4). Despite their importance and fragility, a goldmining company has proposed a project that will put Colombia’s montane and páramos environments at risk.

Plant-killers: Fungal threats to ecosystems.

Rafiqi*, M., Saunders, D., McMullan, M., Oliver, R., Bone*, R. E., Fones, H., Gurr, S., Vincent, D., Coker*, T. & Buggs*, R. J. A. (2018). *In:* Willis*, K. J. (ed.) *State of the World’s Fungi.* Richmond: Royal Botanic Gardens, Kew, pp. 56–61.

Which fungal diseases pose the greatest threats to global ecosystems? Why are these threats on the increase and what biosecurity is urgently needed to reduce their global spread?

How to meet the 2020 GSPC target 8 in Europe: priority-setting for seed banking of native threatened plants.

Riviere, S., Breman*, E., Kiehn, M., Carta, A. & Muller*, J. V. (2018). *Biodiversity and Conservation* 27 (8): 1873–1890. DOI: 10.1007/s10531-018-1513-2.

The contribution of the European Native Seed Conservation Network (ENSCONET, 2004-2009) and the ENSCONET Consortium (since 2010) towards meeting the 2020 Global Strategy for Plant Conservation (GSPC) target 8 was assessed in 2017. While the outcome was positive (62.7% of European threatened species already conserved *ex situ* in seed banks), the analysis showed that it was essential to provide guidance on which European native threatened species should be collected as a priority if the target was to be reached by 2020. In this paper we present a priority-setting method and its result, designed to guide collecting strategies across Europe to meet the 2020 GSPC target 8. The result of our study is a country-based checklist of European threatened taxa to be collected and stored *ex situ* across the seed banks of the ENSCONET Consortium by 2020. After discussing the results of the applied method, the ENSCONET Consortium Steering Committee has identified some key action points to support the implementation of such a collecting strategy across Europe in order to meet the 2020 GSPC target 8 for Europe.

Predicting aboveground forest biomass with topographic variables in human-impacted tropical dry forest landscapes.

Salinas-Melgoza, M., Skutsch, M. & Lovett*, J. C. (2018). *Ecosphere* 9 (1): e02063. DOI: 10.1002/ecs2.2063.

Topographic variables such as slope and elevation partially explain spatial variations in aboveground biomass (AGB) within landscapes. Human activities that impact vegetation, such as cattle grazing and shifting cultivation, often follow topographic features and also play a key role in determining AGB patterns, although these effects may be moderated by accessibility. In this study, we evaluated the potential to predict AGB in a rural landscape, using a set of topographical variables in combination with indicators of accessibility. We modeled linear and non-linear relationships between AGB, topographic variables within the territorial boundaries of six rural communities, and distance to roads. Linear models showed that elevation, slope, topographic wetness index, and tangential curvature could explain up to 21% of AGB. Non-linear models found threshold values for the relationship between AGB and diffuse insolation, topographic position index at 19 × 19 pixels scale and differentiated between groups of communities, improving AGB predictions to 33%. We also found a continuous and positive effect on AGB with increased distance from roads, but also a piecewise relationship that improves the understanding of intensity of human activities. These findings could enable AGB baselines to be constructed at landscape level using freely available data from topographic maps. Such baselines may be of use in national programs under the international policy Reducing Emissions from Deforestation and Forest Degradation.

Conserving and restoring the Caicos pine forests: The first decade.

Sanchez*, M. D., Manco, B. N., Blaise, J., Corcoran*, M. & Hamilton*, M. A. (2018). *Plant Diversity*. DOI: 10.1016/j.pld.2018.05.002.

The severe and rapid attack on the Caicos pine *Pinus caribaea* var. *bahamensis* (Pinaceae) by the non-native invasive pine tortoise scale, *Toumeyella parvicornis*, has resulted in the death of most of the trees in the Turks and Caicos Islands (TCI) in just over a decade. Local and international conservation

efforts have enabled the necessary multi-disciplinary research, data gathering, and monitoring to develop and implement a restoration strategy for this endemic tree from the Bahaman archipelago. The native plant nursery established on North Caicos and horticultural expertise acquired throughout the years were crucial to the successful rescue of Caicos pine saplings from the wild populations and cultivation of new saplings grown from locally sourced seeds. These saplings have been used to establish six Restoration Trial Plots on Pine Cay and a seed orchard on North Caicos in TCI. Core Conservation Areas (CCAs) for the Caicos pine forests have been identified and mapped. To date, forest within the Pine Cay CCA has been supplemented by planting more than 450 pine trees, which have survived at a high (>80%) rate.

Cryopreservation without vitrification suitable for large scale cryopreservation of orchid seeds.

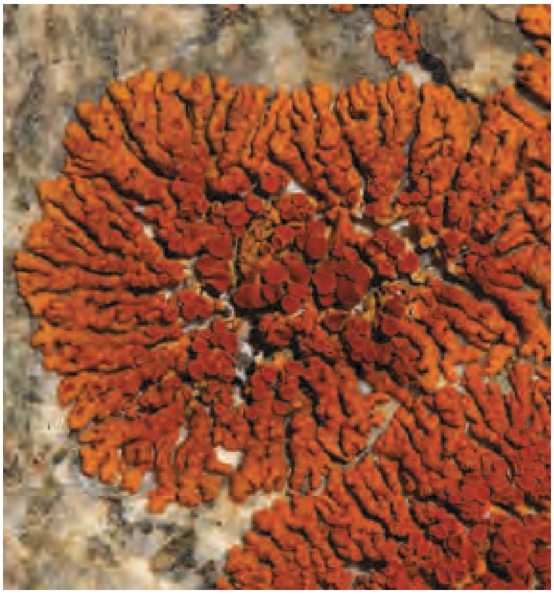
Schofield*, E., Jones*, E. P. & Sarasan*, V. (2018). *Botanical Studies* 59: 13. DOI: 10.1186/s40529-018-0229-7.

Orchids are under threat from human activities and climate change, with populations limited to small geographic hotspots. This makes them ideal candidates for *ex situ* conservation. Orchid seeds are desiccation tolerant, but often have poor longevity in seed banks and cryopreservation of orchid protocorms is complex and expensive. Therefore, simple methods for large-scale storage programs are essential to store orchid seeds of different life forms. Seeds of five species representing epiphytic, lithophytic and terrestrial orchids from the Central Highlands of Madagascar were studied to find a simple and effective system of cryopreservation. The use of a vitrification solution prior to cryopreservation to improve survival was investigated, as well as the use of symbiotic and asymbiotic germination media to maximise germination after cryopreservation. Using the filter paper packet method, dried seeds were stored in vapour phase above liquid nitrogen and recovered after thawing with both symbiotic and asymbiotic media.

Orchid seed and pollen: a toolkit for long-term storage, viability assessment and conservation.

Seaton, P. T., Hosomi, S. T., Custódio, C. C., Marks, T. R., Machado-Neto, N. B. & Pritchard*, H. W. (2018). *In:* Lee, Y. I., Yeung, E.T. (ed.) *Orchid Propagation: From Laboratories to Greenhouses—Methods and Protocols.* Springer Protocols Handbooks. New York: Humana Press.

The development of *ex situ* preservation techniques for seed and pollen provides a vital addition to orchid conservation using *in situ* and living collection approaches. The ability to both store and later efficiently distribute germplasm for reintroductions and maintenance of genetic diversity provides a powerful tool that can usefully operate beyond the confines of habitat loss and climate change. Currently a wealth of data and experience exists in both professional and amateur fields alike that requires effective global networking and sustainable resourcing to ensure that all practitioners of orchid conservation benefit. In this chapter we have summarised the current state of knowledge concerning the practice of both orchid seed and pollen storage, emphasising some of the problems that may be encountered. We also describe how current research shows that dry seeds, and potentially pollen, of many species have the capacity to survive in storage for a number of decades, if not longer, at low and cryogenic temperatures. Although within the plant kingdom orchid seeds may still be described as being short-lived, we highlight new techniques for storage and assessment of viability and germination that are continually being developed and applied more broadly to a wider range of species, to improve longevity and enhance measurement techniques. We emphasise throughout the need for more comparative data acquisition, information and interpretation of the variation in responses across the family, so as to help inform the global community of how best to handle orchid germplasm.



Genome-wide epigenetic variation among ash trees differing in susceptibility to a fungal disease.

Sollars, E. S. A. & Buggs*, R. J. A. (2018). *BMC Genomics* 19: 502. DOI: 10.1186/s12864-018-4874-8.

European ash trees (*Fraxinus excelsior*) are currently threatened by ash dieback (ADB) caused by the fungus *Hymenoscyphus fraxineus* but a small percentage of the population possesses natural low susceptibility. The genome of a European ash tree has recently been sequenced. Here, we present whole genome DNA methylation data for two *F. excelsior* genotypes with high susceptibility to ADB, and two genotypes with low susceptibility, each clonally replicated. We also include two genotypes of Manchurian ash (*F. mandshurica*), an ash species which has co-evolved with *H. fraxineus* and also has low susceptibility to ADB.

In *F. excelsior*, we find an average methylation level of 76.2% in the CG context, 52.0% in the CHG context, and 13.9% in the CHH context; similar levels to those of tomato. We find higher methylation in transposable elements as opposed to non-mobile elements, and high densities of Non-Differentially Methylation Positions (N-DMPs) in genes with housekeeping functions. Of genes putatively duplicated in whole genome duplication (WGD) events, an average of 25.9% are differentially methylated in at least one cytosine context, potentially indicative of unequal silencing. Variability in methylation patterns exists among clonal replicates, and this is only slightly less than the variability found between different genotypes. Of twenty genes previously found to have expression levels associated with ADB susceptibility, we find only two of these have differential methylation between high and low susceptibility *F. excelsior* trees. In addition, we identify 1683 significant Differentially Methylated Regions (DMRs) (q-value<0.001) between the high and low susceptibility genotypes of *F. excelsior* trees, of which 665 remain significant when *F. mandshurica* samples are added to the low susceptibility group.

We find a higher frequency of differentially methylated WGD-derived gene duplicates in ash than other plant species previously studied. We also identify a set of genes with differential methylation between genotypes and species with high versus low susceptibility to ADB. This provides valuable foundational data for future work on the role that epigenetics may play in gene dosage compensation and susceptibility to ADB in ash.

Plant community dynamics of lomas fog oasis of Central Peru after the extreme precipitation caused by the 1997-98 El Niño event.

Tovar*, C., Sánchez-Infantas, E. & Texeira-Roth, V. (2018). *PLoS One* 13 (1): e0190572.

Despite El Niño events being one of the main forces shaping the coastal desert vegetation in South America, the impacts of the high precipitation typical of this rare but recurrent climatic event remain understudied. Here we monitored the plant community of a coastal lomas, a seasonal desert ecosystem, during 1998 and 2001 to analyse its changes during the 1997–98 El Niño and the following La Niña events. We measured species abundance and vegetation cover in 31 plots, and recorded climate variables in Lomas de Lachay, Peru. We found a significant positive correlation between precipitation and vegetation cover, density, alpha diversity (species diversity at the plot level), total richness and abundance of several key species but no correlation with gamma diversity (species diversity at the whole loma level). During the El Niño event, the seasonality, typical of the lomas ecosystem, disappeared, as evidenced by both the similarity of species composition and mean vegetation cover values between most sampling campaigns of 1998 and 1999. Moreover, total richness was lower during the El Niño event than during the humid season of 2000 and 2001 resulting from the dominance of only a few species, such as *Nicotiana paniculata* and *Loasa urens*. Temporal-spatial changes in the abundance of the dominant species caused the differences between alpha and gamma diversity, especially during 1999. Within that year, mean alpha diversity showed similar values whilst gamma diversity values were different. The reestablishment of the seasonality of most plant community characteristics and a clear difference between species composition of the humid and the dry season occurred two years after the El Niño event, suggesting a resilient community. This study provides one of the few quantifications of the Peruvian lomas' response to the 1997–98 El Niño event and the following La Niña, one of the most extreme climatic events in the last century.

Benefits and challenges for gene conservation: a view from the UK national tree seed project.

Trivedi*, C. & Kallow*, S. (2017). *In:* Sniezko, R. A., Man, G., Hipkins, V., Woeste, K., Gwaze, D., Kliejunas, J. T. & McTeague, B. A. (eds) *Gene conservation of tree species—banking on the future. Proceedings of a workshop. Gen. Tech. Rep.* Portland: U.S. Department of Agriculture, Forest Service, Pacific Northwest Research Station, pp.44–47.

No abstract available.

Collecting genetic variation on a small island.

Trivedi*, C. & Kallow*, S. (2017). *In:* Sniezko, R. A., Man, G., Hipkins, V., Woeste, K., Gwaze, D., Kliejunas, J. T. & McTeague, B. A. (eds) *Gene conservation of tree species—banking on the future. Proceedings of a workshop. Gen. Tech. Rep.* Portland: U.S. Department of Agriculture, Forest Service, Pacific Northwest Research Station, pp.129–136.

No abstract available.

Natural history of Cerrado Mutun: VI Checklist, status of conservation and new records for Bolivia.

Villaroel, D., Aramayo, G. M., Martinez, M. T., Proenca, C. E. B., Munhoz, C. B. R., Klitgård*, B. B., Pinto-Ledezma, J. N. & Nee, M. H. (2017). *Kemppfiana* 13 (2): 29–74.

In this study, we present the checklist for plant species in the Cerro Mutún, obtained through floristic inventories made between 2008 and 2015 in six plant communities (bosque semideciduo chiquitano, BCh; bosque chiquitano dafohidrófilo, BChE; cerradão, Ce; cerrado sensu stricto, CSS; campo sujo, CS; and vegetación de bancadas lateríticas, VS). We also present the results of the analysis of the taxonomic similarities among genus and species, taxonomic importance at family level, number of species by life form into communities, and of the conservation status of the registered species according to the IUCN, at national and international level. A total of 559 species and 21 morphospecies were recorded (332 genus and 77 families), of which seven are considered endemic to Bolivia and 34 are new records for the Bolivian flora. The similarity of genera and species between communities was low (<50%, except for CSS vs. CS and CSS vs. Ce), highlighting the existence of taxonomic particularities. More than 50% of the genera and species were grouped into a small number of families (10), whose taxonomic identities differed between forest and savanna-grasslands communities, except for family Fabaceae, which ranked as the most important family of plants in the Mutún. The number

of species by life forms was different between one physiognomy and another, being the trees, shrubs and lianas the most diverse in the forests, and the sub-shrub and herbaceous in the savannas and grasslands. Finally, only 12 species were categorized as threatened in Bolivia and nine at international level, among which *Discocactus ferricola* stands out due its restricted distribution to the Cerro Mutún in Bolivia and Urucún in Brazil.

Orchid conservation – science and practice.

Gale, S. W. & Fay* M. F. (eds.). (2018). *Botanical Journal of the Linnean Society* 186 (4): 168.

Threats to orchid survival continue to intensify, with > 50% of the orchids that have been assessed for the IUCN Global Red List falling in to one of the categories of threat. Despite the best efforts of the orchid conservation community, the capacity to develop solutions at the species-level will be outstripped by the sheer scale and pace of change. In response to these challenges, scientists and conservation practitioners must make difficult choices in prioritizing their work. Following the 6th International Orchid Conservation Congress, we call for greater overlap between science-driven research objectives and real conservation needs.

Seed Banks.

Way*, M. (2018). *In:* Poff, D. & Michalos, A. (*eds*). *Encyclopedia of Business and Professional Ethics.* Cham: Springer.

No abstract available.

Shoot-level flammability of species mixtures is driven by the most flammable species: implications for vegetation-fire feedbacks favouring invasive species.

Wyse*, S. V., Perry, G. L. W. & Curran, T. J. (2017). *Ecosystems* 21 (5): 886–900. DOI: 10.1007/s10021-017-0195-z.

Invasive species can cause shifts in vegetation composition and fire regimes by initiating positive vegetation-fire feedbacks. To understand the mechanisms underpinning these shifts, we need to determine how invasive species interact with other species when burned in combination and thus how they may influence net flammability in the communities they invade. Previous studies using litter and ground fuels suggest that flammability of a species mixture is nonadditive and is driven largely by the more-flammable species. However, this nonadditivity has not been investigated in the context of plant invasions nor for canopy fuels. Using whole shoots, we measured the flammability of indigenous-invasive species pairs for six New Zealand indigenous and four globally invasive plant species, along with single-species control burns. Our integrated measure of flammability was clearly nonadditive, and the more-flammable species per pairing had the stronger influence on flammability in 83% of combinations. The degree of nonadditivity was significantly positively correlated with the flammability difference between the species in a pairing. The strength of nonadditivity differed among individual flammability components. Ignitability and combustibility were strongly determined by the more-flammable species per pair, yet both species contributed more equally to consumability and sustainability. Our results suggest mechanisms by which invasive species entrain positive vegetation-fire feedbacks that alter ecosystem flammability, enhancing their invasion. Of the species tested, *Hakea sericea* and *Ulex europaeus* are those most likely to increase the flammability of New Zealand ecosystems and should be priorities for management.

Techniques for the collection, transportation, and isolation of orchid endophytes from afar: a case study from Madagascar.

Zettler, L. W., Rajaovelona*, L., Kazutomo*, Y., Kendon*, J. P., Stice, A. L., Radcliffe, E. N., Amanda, E. W. & Sarasan*, V. (2017). *Botanical Studies* 58: 54. DOI: 10.1186/s40529-017-0209-3.

Tropical orchids need more study with respect to their mycorrhizal associations. For researchers in distant countries who aspire to study these orchids augmenting their conservation, the great distances involved, coupled with limited funds, pose formidable challenges. These challenges are sometimes exacerbated by political unrest, delays in securing permits, unexpected hardships, and the risk that the biological samples collected (e.g., roots harboring mycorrhizal fungi) will not survive long-distance transport.

We describe a protocol for the collection and transport of root samples from Madagascar orchids to labs in the United Kingdom (Kew) and the United States (Illinois) where *Rhizoctonia*-like fungi were subsequently isolated. Three separate trips were made spanning 4 years (2012–2015), with emphasis on the collection of roots from epiphytic, lithophytic, and terrestrial orchids inhabiting the Itremo Massif of the Central Highlands. Collectively, the trips to Madagascar resulted in the isolation of all major groups of *Rhizoctonia*-like fungi (*Ceratobasidium*, *Tulasnella*, *Sebacina*) from all three orchid growth forms (terrestrials, epiphytes and lithophytes). Sampling of terrestrial and epiphytes during the rainy season (January) yielded best results. Our study demonstrates that peloton-forming fungi in root samples can retain viability up to 3 weeks after collection.

4

Which plants and fungi contribute to important ecosystem services, sustainable livelihoods and natural capital and how do we manage them?

Multi-cropping edible truffles and sweet chestnuts: production of high-quality *Castanea sativa* seedlings inoculated with *Tuber aestivum*, its ecotype *T. uncinatum*, *T. brumale*, and *T. macrosporum*.

Álvarez-Lafuente, A., Benito-Matías, L. F., Peñuelas-Rubira, J. L. & Suz*, L. M. (2017). *Mycorrhiza* 28 (1): 29–38. DOI: 10.1007/s00572-017-0805-9.

The plantation and management of sweet chestnut (*Castanea sativa* Mill.) orchards is a common and traditional land use system in many areas of Europe that offers the advantage of simultaneous production of nuts and timber. During the last decades, sweet chestnut has declined dramatically in many regions because of the profound social changes in rural areas coupled with pathogen attacks. Truffles, the hypogeous ascocarps of the ectomycorrhizal genus *Tuber*, are currently cultivated using host trees inoculated with these fungi for improving production in truffle orchards. The production of good forestry quality chestnut seedlings inoculated with European truffles in nurseries is essential for multi-cropping plantation establishment, but so far, it has not been implemented in agroforestry practices. Moreover, it is necessary to assess the physiological condition of the seedlings due to the high calcium amendment needed for the growth of *Tuber* spp. mycelium that can become toxic for the host plants. In this study, seedlings of *C. sativa* were inoculated with *Tuber aestivum* and its ecotypes *T. uncinatum*, *T. brumale*, and *T. macrosporum* and were grown in a greenhouse using culture conditions favorable for the production of high-quality plants for forestry purposes. At the end of the assay, levels of root colonization and morphological and physiological parameters of the seedlings were measured. The colonization of *C. sativa* with *T. aestivum*, its ecotype *T. uncinatum*, and *T. brumale* was successful, and the seedlings showed normal growth. Inoculation protocols with *T. macrosporum* need to be improved. *Tuber* species formed well-developed ectomycorrhizae on *C. sativa* in nursery conditions.

The significance of climate in the pollinator dynamics of a tropical agroforestry system.

Arnold, S. E. J., Perry, G. B., Spinelli, G. R., Pierre, B., Murray, F., Haughton, C., Dockery, O., Grey, L., Murphy, S. T., Belmain, S. R. & Stevenson*, P. C. (2018). *Agriculture Ecosystems and Environment* 254: 1–9. DOI: 10.1016/j.agee.2017.11.013.

Even though many globally important tropical agroforestry crops are partially or completely dependent on insect pollination, the conditions influencing pollinator abundance in these systems are often incompletely understood. This is particularly the case for cocoa midges (Diptera: Ceratopogonidae), which are essential for cocoa pollination and thus yield, but agro-ecological management frequently neglects them. We report the first assessment of cocoa midge population dynamics from two Caribbean countries across a full year, and relate this to seasonal climate variables.

We used static suction traps along transects to sample insects monthly, from six cocoa farms across three Caribbean islands, with a particular focus on known pollinators of cocoa. A total of over 87,000 insects were captured, including more than 1800 cocoa midges. Midges were present in all months of the survey and on all sites, but typically comprised less than 2% of the total insects caught. At least twelve different species of cocoa midges were identified from this survey. The previous month’s rainfall positively predicted cocoa midge absolute abundance and further analysis also revealed a relationship between rainfall and relative midge abundance. In particular, during drought periods, midge numbers were very low, consistent with their larval ecology. Humidity and mean daily maximum and minimum temperatures did not relate to midge abundance. Rainfall negatively influenced the Shannon-Weaver index. The findings highlight the possible threat of droughts to cocoa pollination services and the importance of proactive farm management to support them.

A comparison of milk yields and methane production from three contrasting high-yielding dairy cattle feeding regimes: Cut-and-carry, partial grazing and total mixed ration.

Cameron, L., Chagunda, M. G. G., Roberts, D. J. & Lee*, M. A. (2018). *Grass and Forage Science* 73 (3): 789–797. DOI: 10.1111/gfs.12353.

There have been reductions in grazing cattle and corresponding increases in mixed diets across many regions. Mixed diets consist of silage, grains, legumes and other herbaceous plants (termed total mixed ration, TMR). TMR has been associated with increased milk yields but has also been linked to increased enteric methane production. We measured milk yields and methane production from high-yielding Holstein-Friesian cattle after substituting 29%–36% of a TMR diet with grass. Two feeding treatments were compared with a diet of TMR: grass grazed at pasture and grass cut in the field and delivered to housed cattle (termed cut-and-carry). Each feeding treatment was fed to 15 cattle, and the experiment was conducted in South-west Scotland. Using a laser methane detector, we measured a twofold and fourfold decline in enteric methane production for the cut-and-carry and grazing groups, respectively, when the animals consumed grass. TMR was consumed by both grass-fed groups overnight, so daily values were adjusted to include elevated methane production during this period. This revealed that methane production for the cut-and-carry and grazing groups was 17% and 39% lower than for the TMR-fed group respectively. Milk yields were maintained for all three groups, and the efficiency of milk production per unit of methane was substantially greater for the two grass-fed groups. A shift away from exclusively feeding TMR by adding fresh grass to the diets of cattle could contribute to meeting emissions targets and could also represent an economically sustainable climate change mitigation strategy.

The life cycle of a museum.

Cornish*, C. & Nesbitt*, M. (2018). *In:* von Zinnenburg Carroll, K. (ed.) *Botanical Drift: Protagonists of the Invasive Herbarium*. Berlin: Sternberg Press, pp. 19–28.

No abstract available.

Twists, turns and trade: a new look at the Indian Screw tree (*Helicteres isora*).

Cunningham, A. B., Ingram, W., Brinckmann, J. A. & Nesbitt*, M. (2018). *Journal of Ethnopharmacology* 225: 126–135. DOI: 10.1016/j.jep.2018.06.032.

This is the first study of global trade in fruits of the widely used traditional medicine, *Helicteres isora* L. It is used in Ayurvedic, Siddha, Unani medical systems and/or local folk traditional medicines in Bangladesh, India and Pakistan. The roots are used in Traditional Chinese Medicines in China and the fruits in jamu products in Indonesia, Malaysia and Thailand. In addition, *H. isora* fruits are also used in “traditional” medical systems far beyond the natural distribution of this species, for example in Zulu herbal medicine (South Africa) and Kurdish herbal medicines (Iraq).

This study had three aims: (i) to assess the global trade in *H. isora* fruits; (ii) to study the *H. isora* trade from West Timor to Java in terms of actors and prices along the value chain and (iii) to get a better understanding of the potential of this species to improve household income in eastern Indonesia. This study uses historical records, a contemporary analysis of global trade data (2014–2016) and field assessments of value chains and the biological factors influencing *H. isora* fruit production.

Globally, the major exporter of *H. isora* fruits is India, which exports *H. isora* fruits to 19 countries, far beyond the natural geographical distribution of this species. Over a 36-month period (January 2014–December 2016), India exported 392 t of

H. isora fruits, with a Free-On-Board (FOB) value of Indian rupiah (INR) 18,337,000 (US$ 274,055). This represents an average annual export quantity of about 130,526 kg/year. Over this three year period, most of these exports (85.5%) were to Indonesia (346.58 t), followed by Thailand (6.85%). Indian *H. isora* exports are also used in many other medical systems, including Kurdish and Zulu "traditional" medicines in Iraq and South Africa. Formation of an Indian diaspora in Bahrain, Mauritius, South Africa, Tanzania and Trinidad and Tobago over the past 130 years is one of the drivers of *H. isora* fruit trade outside the natural geographic distribution of the species. In Indonesia, demand for *H. isora* fruits is supplemented by an intra-island trade in Java and an inter-island trade from East Nusa Tenggara. West Timor, for example, exports around 31–37 t of air-dried *H. isora* fruits per year to Java. At the farm gate, local harvesters in West Timor get 4000 IDR (c. 0.3 US$) per kg, with businesses in Java paying 25,000 IDR (c. 2 US$) per kg for *H. isora* fruits. This is similar to the price paid for *H. isora* fruits imported from India to Java.

India is the major exporter of whole dried *H. isora* fruits, including to countries where this species has never been in traditional use. In Indonesia, *H. isora* fruit extracts are used in the cosmetic industry as well as in jamu herbal medicines, including "Tolak Angin", the country's most popular commercial "jamu" preparation. Indonesia also is the major importer of *H. isora* fruits from India. In eastern Indonesia, improved income to local villagers from the *H. isora* fruit trade could come from improved *H. isora* fruit quality due to better drying techniques. This would also reduce health risks along the supply chain from to mycotoxins that have been recorded on poorly dried *H. isora* fruits. There also is an opportunity for cultivation of *H. isora* in small-holder teak plantations in Indonesia, with harvest of *H. isora* fruits as well as the medicinal bark

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Coffee atlas of Ethiopia.

Davis*, A. P., Wilkinson*, T., Challa, Z. K., Williams*, J., Baena*, S., Gole, T. W. & Moat*, J. (2018). Richmond: Royal Botanic Gardens, Kew.

This richly illustrated volume is the first complete atlas of coffee production in Ethiopia, birth-place of coffee drinking and the main home of wild arabica coffee (*Coffea arabica*). Around 15 million Ethiopians are coffee farmers, and Ethiopia is Africa's largest coffee producer and one of the most important coffee-growing regions of the world, renowned for its diversity of flavour profiles, including those of the celebrated coffees of Harar, Limu, Sidamo, and Yirgacheffe. The aim of the Coffee Atlas of Ethiopia is to inform the reader about the coffee landscape of Ethiopia. It shows where coffee is grown, where the natural coffee forests are located, and where coffee could be grown. The atlas maps are accompanied by information on coffee farming, environment and climate, and a description of the main coffee areas. Also included in the atlas are key coffee origins, coffee towns and coffee delivery centres, as well as other useful items. The atlas can be used to assess the potential and vulnerability for coffee farming in Ethiopia, as well as provide a logistics resource for the coffee sector and those otherwise working with, or interested in, coffee. It is also an essential reference for resource managers.

Cataloguing nature's 'library': The doctrine of signatures in Western thought and practice.

Durant*, O. (2017). *Pharmaceutical Historian* 47 (4): 95–98.

Generally viewed as a quaint, if puzzling, relic of the folk medical tradition, the Doctrine of Signatures and wider concepts of 'sympathetic magic' have informed selection patterns of natural medicines the world over. Associations between form and perceived medical value are idiosyncratic and culture specific. Briefly considered here are the factors that led to the development of a Doctrine of Signatures in the western tradition and what lessons it might impart when re-considered as an evolving series of ideas, rather than as a single doctrine.

"Foreign herbs supriz'd in English ground": the life and work of George D. Ehret (1708–1770).

Edmondson*, J. R. (2018). *In* Köhler, M. & Wolschke-Bulmahn, J. (*eds*). *Hanover and England - a garden and personal union?* Munich: Akademische Verlagsgemeinschaft München, pp. 121–132.

No abstract available.

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Crop domestication alters floral reward chemistry with potential consequences for pollinator health.

Egan, P., Adler, L. S., Irwin, R. E., Farrel*, I. W., Palmer-young, E. & Stevenson*, P. C. (2018). *Frontiers in Plant Science* 9 (1357): PMC6169423. DOI: 10.3389/fpls.2018.01357.

Crop domestication can lead to weakened expression of plant defences, with repercussions for herbivore and pathogen susceptibility. However, little is known about how domestication alters traits that mediate other important ecological interactions in crops, such as pollination. Secondary metabolites, which underpin many defence responses in plants, also occur widely in nectar and pollen and influence plant-pollinator interactions. Thus, domestication may also affect secondary compounds in floral rewards, with potential consequences for pollinators. To test this hypothesis, we chemically analysed nectar and pollen from wild and cultivated plants of highbush blueberry (*Vaccinium corymbosum* L.), before conducting an artificial diet bioassay to examine pollinator-pathogen interactions. Our results indicated that domestication has significantly altered the chemical composition of *V. corymbosum* nectar and pollen, and reduced pollen chemical diversity in cultivated plants. Of 20 plant metabolites identified in floral rewards, 13 differed significantly between wild and cultivated plants, with a majority showing positive associations with wild compared to cultivated plants. These included the amino acid phenylalanine (4.5 times higher in wild nectar, 11 times higher in wild pollen), a known bee phagostimulant and essential nutrient; and the antimicrobial caffeic acid ester 4-O-caffeoylshikimic acid (two times higher in wild nectar). We assessed the possible biological relevance of variation in caffeic acid esters in bioassays, using the commercially available 3-O-caffeoylquinic acid. This compound reduced Bombus impatiens infection by a prominent gut pathogen (*Crithidia*) at concentrations that occurred in wild but not cultivated plants, suggesting that domestication may influence floral traits with consequences for bee health. Appreciable levels of genetic variation and heritability were found for most floral reward chemical traits, indicating good potential for selective breeding. Our study provides the first assessment of plant domestication effects on floral reward chemistry and its potential repercussions for pollinator health. Given the central importance of pollinators for agriculture, we discuss the need to extend such investigations to pollinator-dependent crops more generally and elaborate on future research directions to ascertain wider trends, consequences for pollinators, mechanisms, and breeding solutions.

Country focus: China.

Fang*, R., Kirk*, P. M., Wei, J.-C., Li, Y., Cai, L., Fan, L., Wei, T.-Z., Zhao, R.-L., Wang, K., Yang, Z.-L., Li, T.-H., Li, Y., Phurbu-Dorji & Yao, T.-H. (2018). *In:* Willis*, K. J. (ed.) *State of the World's Fungi.* Richmond: Royal Botanic Gardens, Kew, pp. 48–55.

What is the current status of knowledge of fungi in China? How many different Chinese fungal species are currently known, where are they distributed, which are most important economically, and how do they help combat the effects of desertification?

Compounds contributing to the insecticidal activity of extracts from *Tithonia diversifolia* and *Vernonia amygdalina*.

Green*, P. W. C., Ndakidemi, P., Farrell*, I., Belmain, S. R. & Stevenson*, P. C. (2017). *Industrial Crops and Products* 110: 15–21. DOI: 10.1016/j.indcrop.2017.08.021.

The diversity of synthetic pesticides has been reduced through regulation especially in the European Union, leading to a resurgence of interest in natural plant products for pest control. Here we investigated two Asteraceae species, *Tithonia diversifolia* and *Vernonia amygdalina* that are used by farmers in Africa in bio-rational pest control to determine the chemical basis of activity against pests of stored legumes and identify plant compounds with commercial potential. The cowpea beetle, *Callosobruchus maculatus*, an ubiquitous pest of African stored grain legumes, was exposed to extracts of both plant species at 10, 1 and 0.1% w/v and fractions of these extracts at representative concentrations. Extracts and fractions were toxic to recently emerged adults, but did not reduce oviposition by those females that survived. The sesquiterpene, tagitinin A, was isolated from one of the active fractions and identified using H1 and C13-NMR and shown also be toxic to C. maculatus and so partially explains the activity of the whole plant. Other compounds in the active fractions were identified, at least to structural class, using high resolution mass spectroscopy (HRESI-MS). Sequiterpenes and flavones were common to fractions from both plants. Stigmostane steroidal saponins were the most abundant secondary metabolites in *V. amygdalina*.

Flower preferences and pollen transport networks for cavity-nesting solitary bees: Implications for the design of agri-environment schemes.

Gresty, C. E. A., Clare, E., Devey*, D. S., Cowan*, R. S., Csiba*, L., Malakasi*, P., Lewis, O. T. & Willis*, K. J. (2018). *Ecology and Evolution*: DOI: 10.1002/ece3.4234.

Floral foraging resources are valuable for pollinator conservation on farmland, and their provision is encouraged by agri-environment schemes in many countries. Across Europe, wildflower seed mixtures are widely sown on farmland to encourage pollinators, but the extent to which key pollinator groups such as solitary bees exploit and benefit from these resources is unclear. We used high-throughput sequencing of 164 pollen samples extracted from the brood cells of six common cavity-nesting solitary bee species (*Osmia bicornis*, *Osmia caerulescens*, *Megachile versicolor*, *Megachile ligniseca*, *Megachile centuncularis* and *Hylaeus confusus*) which are widely distributed across the UK and Europe. We documented their pollen use across 19 farms in southern England, UK, revealing their forage plants and examining the structure of their pollen transport networks. Of the 32 plant species included currently in sown wildflower mixes, 15 were recorded as present within close foraging range of the bees on the study farms, but only *Ranunculus acris* L. was identified within the pollen samples. *Rosa canina* L. was the most commonly found of the 23 plant species identified in the pollen samples, suggesting that, in addition to providing a nesting resource for *Megachile* leafcutter bees, it may be an important forage plant for these species. Higher levels of connectance and nestedness were characteristic of pollen transport networks on farms with abundant floral resources, which may increase resilience to species loss. Our data suggest that plant species promoted currently by agri-environment schemes are not optimal for solitary bee foraging. If a diverse community of pollinators is to be supported on UK and European farmland, additional species such as *R. canina* should be encouraged to meet the foraging requirements of solitary bees.

Characterisation of biomass resources in Nepal and assessment of potential for increased charcoal production.

Hammerton, J., Joshi, L. R., Ross, A. B., Pariyar, B., Lovett*, J. C., Shrestha, K. K., Rijal, B., Li, H. & Gasson*, P. E. (2018). *Journal of Environmental Management* 223: 358–370. DOI: 10.1016/j.jenvman.2018.06.028.

Characterisation of 27 types of biomass was performed together with an assessment of regional resource availability. Charcoal was produced under two conditions from all samples and their yields were compared. Sugarcane bagasse, sal and pine produced the best charcoal with a low volatile matter and high calorific value. The amount of high-quality charcoal which can be made within Nepal from the biomass types tested is equivalent to 8,073,000 tonnes of firewood a year or 51% of the yearly demand. The areas which would benefit the most from charcoal making facilities are the Mid-hills of the Western, Central and Eastern Development Regions, as well as the Terai in the Central and Eastern Development Regions. The main potential benefit is to convert agricultural residues which are underutilised because, in their original form, produce large quantities of smoke, to cleaner burning charcoal. The conversion of agricultural residues to charcoal is also a viable alternative to anaerobic digestion in the Mid-hills.

Phytochemicals as anti-inflammatory nutraceuticals and phytopharmaceuticals.

Howes*, M.-J. R. (2018). *In:* Chatterjee, S., Jungraithmayr, W. & Bagchi, D. (eds). *Immunity and Inflammation in Health and Disease. Emerging Roles of Nutraceuticals and Functional Foods in Immune Support.* UK: Academic Press (Elsevier), pp. 363–388.

Inflammatory processes have been associated with a wide range of chronic diseases including cardiovascular disease, cancer, dementia, and diabetes. Emerging evidence from mechanistic, clinical, and epidemiological studies associates some dietary factors, including a diverse array of phytochemicals, with effects relevant to modulating inflammatory processes that may contribute to their suggested health benefits. In this context, there is much interest in the use of dietary phytochemicals as nutraceuticals that are considered to maintain health or prevent disease, although the scientific evidence to support their use is often variable. Inflammation may also occur in other circumstances such as following injury or in other pathologies. Plants have been used for centuries for their reputed medicinal effects and scientific evidence is also emerging to explain their medicinal uses, including studies that suggest some plant species and their constituents have anti-inflammatory effects relevant for a particular therapeutic use. In these circumstances, plants may be used as phytopharmaceuticals to treat or alleviate inflammatory diseases. This chapter describes some plant constituents that have been associated with anti-inflammatory effects relevant for use as nutraceuticals, phytopharmaceuticals, or as both.

The evolution of anticancer drug discovery from plants.

Howes*, M.-J. R. (2018). *The Lancet Oncology* 19: 293–294. DOI: 10.1016/S1470-2045(18)30136-0.

Compared with human beings, plants are arguably superior synthetic chemists. Plants have evolved to produce an extremely diverse range of chemical compounds, often with steric complexity, as a strategy to survive and protect against challenges in their environments. For example, many plant alkaloid chemicals are associated with toxic effects, considered an evolutionary strategy to deter predators. It is therefore not surprising that many plant chemicals have potent activities that target human diseases, including cancer. Indeed, almost 50% of the plant-derived natural products that have pharmaceutical and biological applications are alkaloids. It is this chemical diversity and pharmacological potency that provides the scientific basis for why plants have been an important source of medicines throughout history. Records of the use of plants to treat cancer date back to the Ebers papyrus in 1500 BCE, and for many cultures plants remain a primary or complementary source of medicines.

Balancing conservation and livelihoods in the Chimanimmani Forest Belt, Mozambique.

Hudson*, A., Timberlake, J., Chipanga, H. & Ulian*, T. (2018). *BGJournal* 15 (1): 18–21.

Mozambique is one of the least developed countries in the world, recently ranked 181st of 188 by the United Nations' human development index (Jahan, 2016). Much of the population live in poverty, many living in rural areas as smallholder farmers with an average of just 1.2 hectares of land (Anderson & Learch, 2016). Historic migration has been an important driver of instability for these farmers. This continues today as large economic interests, such as government or private backed farms, push farmers onto marginalised land, like that found in protected areas. The Chimanimani Trans-Frontier Conservation Area (TFCA) is a protected area that brings together the Chimanimani National Park (Zimbabwe) with the Reserva Nacional de Chimanimani (Mozambique). This creates a crossborder protected area. It is divided into two zones: the core zone, for strict nature protection; and the buffer zone, where current communities are allowed the sustainable use of resources as long as tropical lowland rain forest and the core zone are protected (SADC, 2013). For local TFCA communities,

farming is important to their daily lives. Maize provides the main staple crop, although production is low. Communities still use forests and natural areas to supplement their food, and to get materials and medicines. Population expansion, some of which is due to migration, has gradually increased farmland and pressure on wild harvested species (Ghiurghi et al., 2010). Under these conditions the reserve is in need of new sustainable options that provide for communities and keep natural areas safe. Conservation in protected areas can prove to be a problem to local communities when access to resources is restricted. This is particularly damaging to those already in or close to poverty. Compromises need to be found that allow both the continued survival of people as well as protection for nature. Working with communities to decide how they use and conserve their resources, with scientific evidence and technical support, offers a way to try to tackle these issues.

Chemical variation and insecticidal activity of *Lippia javanica* essential oil against *Sitophilus zeamais*.

Kamanula, J. F., Belmain S.R., H., D.R., Farman, D. I., Goyder*, D. J., Mvumi, B. M., Masumbu, F. F. & Stevenson*, P. C. (2017). *Industrial Crops and Products* 11: 75–82. DOI: 10.1016/j.indcrop.2017.06.036.

Lippia javanica (Burm. f.) Spreng is used commercially as an herbal tea and medicinal plant in sub-Saharan Africa. Here we investigated the chemical variation and pesticidal potential of *L. javanica* essential oils against a major stored product pest, *Sitophilus zeamais* Motschulsky. We identified two morphologically distinct varieties of *L. javanica* growing at different locations in Malawi. Perillaldehyde was the major constituent in oil of *L. javanica* var. *javanica* while myrcenone (ipsdienone) was the major compound in oils of *L. javanica* var. *whytei*. Myrcene, linalool, carvone, β-caryophyllene and germacrene D were identified as the other most significant components in oils from both varieties. The yields of oil and the chemical composition also varied significantly with time of harvest during the season in both cases. In contact toxicity tests against *S. zeamais*, oils from both varieties were active. However, whereas perillaldehyde, linalool and carvone, components of the oil of *L. javanica* var. *javanica*, were all toxic against adult *S. zeamais*, myrcenone, the main component of oil from *L. javanica* var. *whytei*, was not. The oil from *L. javanica* var. *javanica* also showed some fumigant toxicity against *S. zeamais*. The high efficacy of *L. javanica* oil against *S. zeamais* suggests it is suitable to be used as a botanical insecticide to control *S. zeamais* in stored maize. However, further research is required to optimise and standardise the variety and harvest time to be recommended and to evaluate its activity against *S. zeamais* and other storage insect pests under farm conditions before it can be adopted by farmers more widely.

A global comparison of the nutritive values of forage plants grown in contrasting environments.

Lee*, M. A. (2018). *Journal of Plant Research* 131 (4): 641–654. DOI: 10.1007/s10265-018-1024-y.

Forage plants are valuable because they maintain wild and domesticated herbivores, and sustain the delivery of meat, milk and other commodities. Forage plants contain different quantities of fibre, lignin, minerals and protein, and vary in the proportion of their tissue that can be digested by herbivores. These nutritive components are important determinants of consumer growth rates, reproductive success and behaviour. A dataset was compiled to quantify variation in forage plant nutritive values within- and between-plant species, and to assess variation between plant functional groups and bioclimatic zones. 1255 geo-located records containing 3774 measurements of nutritive values for 136 forage plant species grown in 30 countries were obtained from published articles. Spatial variability in forage nutritive values indicated that climate modified plant nutritive values. Forage plants grown in arid and equatorial regions generally contained less digestible material than those grown in temperate and tundra regions; containing more fibre and lignin, and less protein. These patterns may reveal why herbivore body sizes, digestion and migration strategies are different in warmer and drier regions. This dataset also revealed the capacity for variation in the nutrition provided by forage plants, which may drive consumer species coexistence. The proportion of the plant tissue that was digestible ranged between species from 2 to 91%. The amount of fibre contained within plant material ranged by 23–90%, protein by 2–36%, lignin by 1–21% and minerals by 2–22%. On average, grasses and tree foliage contained the most fibre, whilst herbaceous legumes contained the most protein and tree foliage contained the most lignin. However, there were individual species within each functional group that were highly nutritious. This dataset may be used to identify forage plant species or mixtures of species from different functional groups with useful nutritional traits which can be cultivated to enhance livestock productivity and inform wild herbivore conservation strategies.

Medicinal Mascarene *Aloes*: An audit of their phytotherapeutic potential.

Lobine, D., Cummins, I., Govinden-Soulange, J., Ranghoo-Sanmukhiya, M., Lindsey, K., Chazot, P. L., Ambler, C. A., Grellscheid, S., Sharples, G., Lall, N., Lambrechts, I. & Howes*, M.-J. R. (2017). *Fitoterapia* 124: 120–126. DOI: 10.1016/j.fitote.2017.10.010.

A phytochemical and biological investigation of the endemic Mascarene Aloes (*Aloe* spp.), including *A. tormentorii* (Marais) L.E.Newton & G.D.Rowley, *A. purpurea* Lam, *A. macra* Haw., *A. lomatophylloides* Balf.f and *A. vera* (synonym *A. barbadensis* Mill.), which are used in the traditional folk medicine of the Mascarene Islands, was initiated. Methanolic extracts of the Aloes under study were analysed using high resolution LC-UV-MS/MS and compounds belonging to the class of anthraquinones, anthrones, chromones and flavone C-glycosides were detected. The Mascarene Aloes could be distinguished from *A. vera* by the absence of 2″-*O*-feruloylaloesin and 7-*O*-methylaloeresin. GC–MS analysis of monosaccharides revealed the presence of arabinose, fucose, xylose, mannose and galactose in all the Mascarene Aloes and in *A. vera*. The crude extracts of all Aloes analysed displayed antimicrobial activity against Bacillus cereus, Staphylococcus aureus, Escherichia coli and Pseudomonas aeruginosa. Only extracts of *A. macra* were active against P. aeruginosa and Klebsiella pneumoniae, while none of the Aloe extracts inhibited Propionibacterium acnes. *A. macra* displayed anti-tyrosinase activity, exhibiting 50% inhibition at 0.95 mg/mL, and extracts of *A. purpurea* (Mauritius) and *A. vera* displayed activity in a wound healing-scratch assay. In vitro cytotoxicity screening of crude methanolic extracts of the Aloes, using the MTT (3-(4, 5-dimethylthiazolyl-2)-2, 5-diphenyltetrazolium bromide) showed that only *A. purpurea* (Réunion) elicited a modest toxic effect against HL60 cells, with a percentage toxicity of 8.2% (*A. purpurea* - Réunion) and none of the Aloe extracts elicited a toxic effect against MRC 5 fibroblast cells at a concentration of 0.1 mg/mL. Mascarene Aloe species possess noteworthy pharmacological attributes associated with their rich phytochemical profiles.

Plants in the built environment

Milliken*, W. (2017). *In:* Piesik, S. (ed.) *HABITAT: Vernacular Architecture for a Changing Planet*. Thames and Hudson, pp. 38–41.

No abstract available.

Impact of management regime and frequency on the survival and productivity of four native tree species used for fuelwood and charcoal in the caatinga of northeast Brazil.

Milliken*, W., Gasson*, P., Pareyn, F., Sampaio, E. V. S. B., Lee*, M., Baracat, A., de Lima Araújo, E. & Cutler*, D. (2018). *Biomass and Bioenergy* 116: 18–25. DOI: 10.1016/j.biombioe.2018.05.010.

The seasonally dry deciduous forest (Caatinga) of northeast Brazil is under intense human pressure, and sustainable use of its tree resources for fuelwood is a pressing concern. An experiment was conducted to ascertain which management techniques (coppicing, pollarding or crown-thinning) permit the highest survival of trees and optimal timber production. Four much-utilised tree species: *Croton sonderianus*, *Mimosa ophthalmocentra*, *Mimosa tenuiflora* and *Poincianella pyramidalis* (syn. *Caesalpinia pyramidalis*) were studied at two sites in Pernambuco State. The impact of each harvesting regime was evaluated over a six-year period, with additional variables including wet-season versus dry-season harvesting, and three-year versus six-year harvesting cycles. The best performing tree species varied between sites, with *M. tenuiflora* providing the highest yields with all treatments at Sertânia and *M. tenuiflora* and *Poincianella pyramidalis* at Serra Talhada. The optimal management regime did not vary between species. Crown-thinned trees produced limited regrowth with the lowest mortality rates, and when ultimately coppiced growth appeared to have been stimulated. Pollarding was intermediate and coppicing was the poorest management strategy. Trees which were harvested twice, in both 2005 and 2008, had much lower overall production than those which had only been harvested once in 2008. The highest yields were obtained from crown-thinned trees which were coppiced in 2005 or 2008. Management decisions

must consider local environmental conditions in the selection of the tree species used to produce fuelwood, however, the optimal management strategy for high production and low mortality is consistently low impact, infrequent crown thinning. There was considerable difference in the findings between the study sites (e.g. in the distribution of statistically significant results), and also in the impacts of treatments on mortality between the four species. The results can be used to guide species-level management regimes that minimise tree mortality, contributing to long-term fuelwood productivity.

Exploring the genetic and adaptive diversity of a pan-Mediterranean crop wild relative: Narrow-leafed lupin.

Mousavi-Derazmahalleh, M. *et al.* (including Nelson*, M. N.) (2018). *Theoretical and Applied Genetics* 131 (4): 887–901. DOI: 10.1007/s00122-017-3045-7.

Most grain crops suffer from a narrow genetic base, which limits their potential for adapting to new challenges such as increased stresses associated with climate change. Plant breeders are returning to the wild ancestors of crops and their close relatives to broaden the genetic base of their crops. Understanding the genetic adaptation of these wild relatives will help plant breeders most effectively use available wild diversity. Here, we took narrow-leafed lupin (*Lupinus angustifolius* L.) as a model to understand adaptation in a wild crop ancestor. A set of 142 wild accessions of narrow-leafed lupin from across the Mediterranean basin were subjected to genotyping-by-sequencing using Diversity Arrays Technology. Phylogenetic, linkage disequilibrium and demographic analyses were employed to explore the history of narrow-leafed lupin within the Mediterranean region. We found strong genetic differentiation between accessions from the western and eastern Mediterranean, evidence of an historic West to East migration, and that eastern Mediterranean narrow-leafed lupin experienced a severe and recent genetic bottleneck. We showed that these two populations differ for flowering time as a result of local adaptation, with the West flowering late while the East flowers early. A genome-wide association study identified single nucleotide polymorphism markers associated with climatic adaptation. Resolving the origin of wild narrow-leafed lupin and how its migration has induced adaptation to specific regions of the Mediterranean serves as a useful resource not only for developing narrow-leafed lupin cultivars with greater resilience to a changing climate, but also as a model which can be applied to other legumes.

Everlasting flowers in Kew's Economic Botany Collection.

Nesbitt*, M. (2017). *In:* Law, R. L. (ed.) *Life in Death*. Kew: Kew Publishing, pp.4–7.

No abstract available.

Botany in Victorian Jamaica.

Nesbitt*, M. (2018). *In:* Barringer, T. & Modest, W. (eds). *Victorian Jamaica.* Durham: Duke University Press, pp.209–239.

No abstract available.

Essential oils and aromas that affect mood and cognition.

Okello, E. J. & Howes*, M.-J. R. (2018). *In:* Murphy, P. N. (ed.) *The Routledge International Handbook of Psychobiology*. UK: Routledge, Taylor & Francis Group, pp. 195–208.

No abstract available.

A phylogenetic road map to antimalarial *Artemisia* species.

Pellicer*, J., Saslis-Lagoudakis, C. H., Carrió, E., Ernst, M., Garnatje, T., Grace*, O. M., Gras, A., Mumbru, M., Vallès, J., Vitales, D. & Rønsted, N. (2018). *Journal of Ethnopharmacology* 225: 1–9. DOI: 10.1016/j.jep.2018.06.030.

The discovery of the antimalarial agent artemisinin is considered one of the most significant success stories of ethnopharmacological research in recent times. The isolation of artemisinin was inspired by the use of *Artemisia annua* in traditional Chinese medicine (TCM) and was awarded a Nobel Prize in 2015. Antimalarial activity has since been demonstrated for a range of other *Artemisia* species, suggesting that the genus could provide alternative sources of antimalarial treatments. Given the stunning diversity of the genus (c. 500 species), a prioritisation of taxa to be investigated for their likely antimalarial properties is required.

Yeast chemogenomic profiling reveals iron chelation to be the principle cell inhibitory mode of action of gossypol.

Prescott*, T. A. K., Jaeg, T. & Hoepfner, D. (2018). *Journal of Medicinal Chemistry* 61 (16): 7381–7386. DOI: 10.1021/acs.jmedchem.8b00692.

Gossypol is an inhibitor of eukaryotic cells with an undetermined mode of action. Here we show that the chemogenomic profile of gossypol is strikingly similar to that of the iron chelators deferasirox and desferricoprogen. Iron import channels Fet1 and Fet3 are prominent in all three profiles. Furthermore, yeast inhibited by gossypol and deferasirox is rescued by the addition of Fe2+. We propose that Fe2+ chelation is in fact the principle mode of action of gossypol.

Useful fungi.

Prescott*, T., Wong, J., Panaretou, B., Boa, E., Bond*, A., Chowdhury*, S., Davies*, L. & Østergaard, L. (2018). *In:* Willis*, K. J. (ed.) *State of the World's Fungi* Richmond: Royal Botanic Gardens, Kew, pp.24–31.

What makes a species of fungus economically valuable? What daily products utilise fungi and what are the useful fungi of the future for food, medicines and fungal enzymes?

Potential of goat weed (*Ageratum conyzoides* L.) as a non-food crop for increased food productivity and ecosystem balance among smallholder farmers: a review.

Rioba, N. B. & Stevenson*, P. C. (2017). *Industrial Crops and Products* 110: 22–29. DOI: 10.1016/j.indcrop.2017.06.068.

Ageratum conyzoides L. (Asteraceae) is an aromatic, annual herb and cosmopolitan weed commonly known as billygoat weed or goat weed and is typically found in cultivated fields and other disturbed ecosystems. The species has been studied widely owing to its biological properties and its potential application in medicine and agriculture. Due to its importance and use in the treatment of burns and wounds, arthrosis, malaria, asthma, leprosy and dermatitis, its medicinal properties have been reviewed. *A. conyzoides*, however, also has insecticidal activity against a range of major pests of field crops and stored products including *Callosobruchus chinensis* L. (Coleoptera: Chrysomelidae), *Chilo partellus* Swinhoe (Lepidoptera: Crambidae), *Sitophilus oryzae* L. (Coleoptera: Curculionidae), *Panonychus citri* McGregor (Tetranychidae: Panonychus), *Sitophilus zeamais* Motchulsky (Coleoptera: Curculionidae), *Plutella xylostella* L. (Lepidoptera: Plutellidae) and *Brevicoryne brassicae* L. (Hemiptera: Aphididae). Evidence suggests that its efficacy is comparable to synthetic pesticides and that it is economically viable too while its impact on beneficial insects including ladybirds, hoverflies and spiders is much reduced compared to synthetics. Anti-microbial activity against important agricultural disease agents is also reviewed here including against *Fusarium oxysporum* Schltdl., (Hypochreales: Nectriaceae), *Phytophthora citrophthora* (R.E. Sm. & E.H. Sm.) Leonian, (Phythiales: Phythiaceae), *Pythium aphanidermatum* (Edson) Fitzp., (Peronosporales: Pythium), *Fusarium solani* Mart (Sacc.) (Hypochreales: Nectriaceae) and *Gibberella zeae* (Schwein.) Petch (*Fusarium graminearum* (Schwabe) (Hypochreales: Nectriaceae). These activities suggest a compelling multipurpose plant that has merit as a potential commercial species. Since earlier reviews have focused on medicinal properties of *A. conyzoides* and less on its potential value in agriculture, this review seeks to bridge this gap by reviewing research on the various properties of this species that are relevant to food production. The review presents updated information on the use of this species as an agricultural resource and emphasizes its potential as an industrial crop.

Pesticidal plants in Africa: a global vision from local uses.

Stevenson*, P. C., Isman, M. B. & Belmain, S. R. (2017). *Industrial Crops and Products* 110: 2–9. DOI: 10.1016/j.indcrop.2017.08.034.

Botanical insecticides provide a multitude of chemistries for the development of new pest management products. Despite relatively low rates of expansion of botanically based pesticides, regulatory changes in many parts of the world are driving a renaissance for the development of new natural pest control products that are safer for human health and the environment. Africa is arguably the continent with the most to gain from developing natural plant-based pesticides. Hundreds of indigenous and exotic species with pesticidal properties have been reported from Africa through various farmer surveys and subsequent research, many of which have been confirmed to be active against a range of arthropod pests. On-farm use of pesticidal plants, particularly among resource-poor small-holder farmers, is widespread and familiar to many African farmers. Until recently, the pyrethrum industry was dominated by East African production through small holder farmers, showing that non-food cash crop production of pesticidal plants is a realistic prospect in Africa when appropriate entrepreneurial investment and regulatory frameworks

are established. This paper reviews the current status of research and commercialisation of pesticidal plant materials or botanically active substances that are used to control pests in Africa and establishes where major gaps lie and formulates a strategy for taking research forward.

The Yucatan Peninsula is the place of origin of sisal (*Agave sisalana*, Asparagaceae): historical accounts, phytogeography and current populations.

Trejo-Torres, J. C., Gann., G. D. & Christenhusz*, M. J. M. (2018). *Botanical Sciences* 96 (2): 366–379. DOI: 10.17129/botsci.1928.

Agave sisalana is a cultigen from Mexico. In 1833 it was brought to Florida by Henry Perrine as an experimental crop. From there it was introduced to tropical Africa and Asia in the late 19th Century, where it became established as a fiber crop. Paradoxically, in the Yucatan it meanwhile evanesced from its already scanty presence. Because material was collected from cultivated stock in Chiapas in the 1950s and a neotype from there was selected in 1988, it was assumed to have originated in Chiapas. Did *A. sisalana* originate in the Yucatan Peninsula following Perrine (1838a, 1938b) rather than from Chiapas *sensu* Gentry (1988)? *Agave sisalana* (sisal), one of the strongest natural fibers in the world and a commercially important crop. Live plants were located in the Yucatan between 2013–2017. Eleven localities in the Yucatan Peninsula still have extant populations of sisal. We uncovered herbarium specimens from the region, including an original specimen by Perrine, from Campeche, which is selected as the lectotype for the name, superseding the neotype from Chiapas. We demonstrate the continued presence of *Agave sisalana* in the Yucatan Peninsula, even though it has now become rare. It is most likely that the crop was first domesticated there.

A nuclear Xdh phylogenetic analysis of yams (*Dioscorea*: Dioscoreaceae) congruent with plastid trees reveals a new Neotropical lineage.

Viruel*, J., Forest*, F., Paun, O., Chase*, M. W., Devey*, D., Sousa Couto, R., Segarra-Moragues, J. G., Catalán, P. & Wilkin*, P. (2018). *Botanical Journal of the Linnean Society* 187 (2): 232–246. DOI: 10.1093/botlinnean/boy013.

Due to its economic value and evolutionary importance among monocots and Dioscoreales, *Dioscorea* has been extensively studied phylogenetically. All analyses have produced congruent results resolving ten consistent main clades but were based solely on plastid data. Here we present the first phylogenetic tree of *Dioscorea* based on a low-copy nuclear gene, xanthine dehydrogenase (Xdh). The Xdh topology and the divergence order of the main *Dioscorea* clades are congruent with those of the plastid-based trees, showing an early diverging position of *Stenophora*, followed by those of the two

New World clades (NW I, NW II) and a still unresolved relationship between the African and Mediterranean clades plus *D. tentaculigera*. Subsequent branches include a more recently evolved clade B of *Dioscorea* comprising all cultivated species, the well-supported Malagasy, compound-leaved (CL) and *Rajania* clades and a clade composed of mixed *Birmanica* and *Enantiophyllum* accessions. We also identified a more recently evolved New World clade (NW III), represented by *D. anomala*, nested in clade B.

A botanical exception. The award of First World War campaign medals to Sir Arthur Hill.

Wearn*, J. & Hudson, J. (2017). *Medal News* 56: 29–31.

The Royal Botanic Gardens, Kew, is widely known as a delightful, publicly accessible green space and scientific research institution. However, the unique and often secret involvement of Kew's staff in the First World War has remained a forgotten chapter in the institution's rich history, until now. The two world wars shaped Kew's activities – at home and away – leaving a unique legacy, which we have recently been uncovering. Among these was an intriguing exception made by the award of the Victory Medal to a temporarily commissioned non-combatant, who was not actively serving in a recognised military unit in a theatre of war. This was Honorary Captain Arthur William Hill (1875–1941), Assistant Director of Kew.

Hyphaene thebaica (Doum palm) in First World War medicine.

Wearn*, J. A. & Hudson, J. (2018). *Palms* 62 (3): 138–144.

The Doum palm, *Hyphaene thebaica* (L.) Mart., has long been used for local medicinal applications, and phytochemical analyses have provided supporting evidence of therapeutic effectiveness. During the First World War, a novel medicinal use was employed for the powdered fruits of this palm, forming an extension of biocultural knowledge within former French colonies in west Africa, from where it was derived.

What makes a terrestrial ecosystem resilient?

Willis*, K. J., Jeffers, E. S. & Tovar*, C. (2018). *Science* 359 (6379): 988–989. 10.1126/science.aar5439.

With increasing incidence of extreme climatic events, disease outbreaks, and other environmental perturbations, conservation of terrestrial ecosystems that can retain their structure and function despite environmental shocks has moved rapidly up the international political agenda. International environmental policies and targets such as the Aichi Biodiversity Targets and the Sustainable Development Goals include conserving resilient ecosystems as a key priority.

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Editorial team: Dr James Wearn, Prof. Monique Simmonds, Dr Ilia Leitch
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