

A close-up photograph of a laboratory setting. A pipette is positioned at the top, dispensing a small drop of liquid into a microcentrifuge tube held by a hand wearing a blue nitrile glove. The background is a soft, out-of-focus gradient of light blue and white.

Royal Botanic Gardens

Kew

**Kew Science
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For the academic year 2016–17

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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.com) and web-based portals (e.g. plantsoftheworldonline.org) to academic papers.

In the academic year 2016-2017, Kew scientists, in collaboration with numerous national and international research partners, published 350 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

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:

- 1** What plants and fungi occur on Earth and how is this diversity distributed? **p2**
- 2** What drivers and processes underpin global plant and fungal diversity? **p26**
- 3** What plant and fungal diversity is under threat and what needs to be conserved to provide resilience to global change? **p50**
- 4** Which plants and fungi contribute to important ecosystem services, sustainable livelihoods and natural capital and how do we manage them? **p62**

Professor Katherine Willis (Director of Science)
& **Dr James Wearn** (Business Analyst)

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



Coelogyne putaoensis (Orchidaceae), a new species from Myanmar.

Aung, Y. L., Jin, X. & Schuiteman*, A. (2017). *Phytokeys* 82: 27–34. DOI: 10.3897/phytokeys.82.13172.

Coelogyne putaoensis, a new species of section *Ocellatae* from Putao, Kachin State, Myanmar, is described and illustrated. It is morphologically similar to *C. taronensis* and *C. weixiensis*, presumably its nearest relatives. An identification key and colour photographs are provided. A preliminary risk-of-extinction assessment according to the IUCN Red List categories and criteria is given for the new species.

More new rattans from New Guinea and the Solomon Islands (Calamus, Arecaceae).

Baker*, W. J. & Dransfield*, J. (2017). *Phytotaxa* 305: 61–86. DOI: 10.11646/phytotaxa.305.2.1.

As part of current research on the taxonomy of the palms (Arecaceae or Palmae) of New Guinea, ten new species of the rattan genus *Calamus* are described and illustrated here: *Calamus baiyerensis*, *Calamus capillosus*, *Calamus erythrocarpus*, *Calamus heatubunii*, *Calamus jacobsii*, *Calamus katikii*, *Calamus kostermansii*, *Calamus papyraceus*, *Calamus pintaudii* and *Calamus superciliatus*. An eleventh species, *Calamus novae-georgii*, from the neighbouring Solomon Islands is also included here. The palm flora of New Guinea now includes 62 species of *Calamus*, 34 of which have been described since 2002, demonstrating the remarkable scale of botanical discovery on the island.

Flore d'Afrique Centrale: Pandanaceae.

Beentje*, H. J. (2016). Belgium: Jardin Botanique Meise.

A flora treatment for the Pandanaceae occurring in the Democratic Republic of the Congo, Rwanda and Burundi is given. The family is represented by 3 indigenous species of trees or sometimes shrubs of the genus *Pandanus*, with possibly an additional one or even two new species but these with inadequate material.

The orchid hunter.

Bersweden*, L. (2017). London: Short Books.

In the summer after leaving school, a young botanist sets out to fulfil a childhood dream – to find every species of orchid native to the British Isles.

Battling the vagaries of the British climate in his clapped-out car, Leif Bersweden has just a few months to do what no one has ever done before: to complete this quest within one growing season.

This study of the 52 native species is a fantastic gateway into the compendious world of orchids, and one that will open your eyes to the rare hidden delights to be found on the doorstep.

Telamonioid Cortinarius species of the C. puellaris group from calcareous Tilia forests.

Brandrud, T. E., Dima, B., Liimatainen, K. & Niskanen*, T. (2016). *Sydowia* 69: 37–45. DOI: 10.12905/0380.sydowia69-2017-0037.

Four species belonging to the *Cortinarius puellaris* group are presented, including the two new species *C. biriensis*, *C. subpuellaris* and the recently described *C. puellaris*. Based on type studies, it is shown that the fourth species in the group should be named *C. intemptivus* (= *C. cristatosporus*). The species co-occur and are all studied mainly from SE Norwegian calcareous *Tilia* forests, but at least some of them also occur in *Quercus(-Carpinus)* forests in temperate-mediterranean areas of C-S Europe, and are apparently widespread and much overlooked. These are all tiny, small, ochre-redbrown telamonioid cortinariid with strongly to spiny ornamented spores. Phylogenetically, the taxa are well-distinguished by 8 to 22 ITS differences. Together with two taxa only known from ectomycorrhizal ITS sequences, they constitute an apparently well-supported clade with uncertain affinity.

Sedge (Cyperaceae) Genera of Africa and Madagascar.

Browning*, J. & Goetghebeur, P. (2017). Leicester: Troubador Publishing Ltd.

Sedges (of the plant family Cyperaceae) can appear seemingly insignificant. On closer inspection, however, their hidden, complex and remarkable constructive design is revealed.

In order to facilitate identification of the 63 genera occurring in Africa and Madagascar, this book includes, for the first time, photographs of the living sedge plants in their natural habitats and line drawings of their morphology. Additionally, photographs of small fruits, as they appear under a microscope, are included as well as full botanical descriptions, so that a detailed assessment of these plants is possible.

The genera illustrated and accounted for here, carry the names that were applied at the turn of the century. Most of these names are still in use today, however, due to recent and on-going research there have been changes, not only to genera, but also to species within these genera. A list of these name changes is included so that the work is fully up to date at this time.

Sedges are widely distributed in a number of diverse habitats (most often found in wetlands and on the margins of lakes, rivers and streams). This publication focuses on those genera occurring in Africa and Madagascar, however, as these plants are also represented on other continents, the taxonomic tools for identification presented here will be useful to those further afield.

Three new species of *Ventilago* (Rhamnaceae) from South-East Asia.

Cahen*, D. & Utteridge*, T. M. A. (2017). *Phytotaxa* 307: 171–182. DOI: 10.11646/phytotaxa.307.3.1.

Three new species of *Ventilago* from Malesia are described and illustrated here: *V. crenata* from New Guinea, *V. ferruginea* from Borneo, Singapore and Sumatra and *V. flavovirens* from Borneo. The morphology of *V. dichotoma*, *V. ferruginea* and *V. flavovirens* is compared, and a key to the *Ventilago* species of Borneo is presented. An IUCN conservation status assessment is given for each new species.

The book of orchids.

Chase*, M. W., Christenhusz*, M. J. M. & Miranda, T. (2017). London & Chicago: Ivy Press and University of Chicago Press.

One of every seven flowering plants on earth is an orchid. Some are stunningly over the top; others almost inconspicuous. The Orchidaceae is the second most widely geographically distributed family, after the grasses, yet remains one of the least understood. This book will profile 600 species, representing the remarkable and unexpected diversity and complexity in the taxonomy and phylogeny of these beguiling plants, and the extraordinary means they have evolved in order to ensure the attraction of pollinators. Each species will be photographed to capture its delicate detail, and shown life-size, giving a strong visual theme to the book, and each is accompanied by text offering an in-depth species profile.

A synoptic revision of *Inversodicraea* Engl. ex R.E. Fries (Podostemaceae).

Cheek*, M., Feika, A., Lebbie, A., Goyder*, D., Tchiengue, B., Sene, O., Choutou, P. & van der Burgt*, X. (2017). *Blumea* 62: 125–156. DOI: 10.3767/blumea.2017.62.02.07.

Six new species of *Inversodicraea* (*I. feika* from Sierra Leone, *I. liberia* from Liberia, and *I. ebo*, *I. eladii*, *I. tchoutoi*, and *I. xanderi* from Cameroon) are described as new to science in the context of a synoptic revision



of this African genus, now comprising 30 species, including *I. cussetiana* comb. nov., newly transferred from *Macropodiella*. *Inversodicraea* is now equal in number of species to *Ledermanniella* (as redefined), as the largest genus of the family in Africa. Terete or slightly dorsiventrally flattened leaf petioles (not sheathing and/or stipulate) are newly discovered to distinguish the genus from *Ledermanniella*, in addition to the presence of scale-leaves. *Inversodicraea boumiensis*, *I. annithomae*, and *I. bosii* are redelimited in this paper. Examples of species hybrids are discussed. Eighteen species are point endemics. A key and IUCN 2012 standard conservation assessments for all species are included. 28 of the 30 species have been assessed as Threatened or Near Threatened. Hydroelectric projects are the biggest source of extinction risk to species of the genus, threatening 19 of the 30 species.

Spiny African *Allophylus* (Sapindaceae): a synopsis.

Cheek*, M. & Haba, P. (2016). *Kew Bulletin* 71 (4): DOI: 10.1007/s12225-016-9672-3.

Allophylus samoritourei from the lowland and submontane forests of the Loma-Man highlands in Guinea-Conakry and Liberia, Africa and *Allophylus bertoua* from lowland eastern Cameroon are described and illustrated as part of a synoptic revision of the four spiny African species of *Allophylus*. IUCN conservation assessments are given for all species. The phenomena of androgynophores and of spiny structures in the Sapindaceae, and the possibility of monophyly of spiny *Allophylus* are discussed.

***Inversodicraea* Engl. resurrected and *I. pepehabei* sp. nov. (Podostemaceae), a submontane forest species from the Republic of Guinea.**

Cheek*, M. & Haba, P. (2016). *Kew Bulletin* 71 (55): DOI: 10.1007/s12225-016-9673-2.

Inversodicraea, shown by previous workers to merit resurrection, is restored here, to include all those species previously included in *Ledermanniella* subg. *Phyllosma*. The final seven species remaining in subg. *Phyllosma* are formally transferred to *Inversodicraea* as *I. mortonii*, *I. gabonensis*, *I. boumiensis*, *I. harrisii*, *I. paulsitae*, *I. torrei* and *I. thollonii*. A new species from the submontane forest of Mt Ziama, in Guinea-Conakry is formally described as *I. pepehabei*. Similar to *I. adamesii*, it is assessed as Endangered according to the IUCN 2012 standard.

New plant species discovered in 2016.

Cheek*, M., Lindon*, H. & Nic Lughadha*, E. (2017). In: Willis*, K. J. (ed.) *State of the World's Plants 2017*. Richmond: Royal Botanic Gardens, Kew, pp.10–15.

1,730 vascular plant species new to science in 2016 were logged in the International Plant Names Index by March 2017. They include those of interest for horticulture, plants of economic importance (food, fodder, medicinal plants, timber, and herbs and spices) and country-based novelties.

852. *Kewa acida*: Kewaceae Plant in Peril 39.

Christenhusz*, M. J. M., Clubbe*, C., Hilgenhof*, R. & Fay*, M. F. (2016). *Curtis's Botanical Magazine* 33 (4): 327–337 [with plate 852]. DOI: 10.1111/curt.12167.

Recent studies showed that a group of *Hypertelis* species was neither related to the type of that genus or to other members of Molluginaceae. As a result, these species were segregated as a new genus in its own family, Kewaceae. The St Helenan endemic *Kewa acida* (Hook.) Christenh. is illustrated here and its relationships, status, cultivation and conservation are discussed.

***Erythrostemon sousanus* (Leguminosae: Caesalpinioideae), a new species from the Río Papagayo Basin in Guerrero, México.**

Contreras-Jiménez, J. L., Sotuyo, S., Calvillo-Canadell, L. & Lewis*, G. P. (2017). *Phytotaxa* 308 (2): 289–294. DOI: 10.11646/phytotaxa.308.2.11.

A new legume species, *Erythrostemon sousanus*, from seasonally dry forest of the Río Papagayo Basin in Guerrero, Mexico is described and illustrated. The new species is morphologically similar to *E. mexicanus*, from which it is distinguished by its glabrous leaves with a greater number of pairs of pinnae (6–11 vs 5–7) and each pinna with more pairs of leaflets (5–7 vs 2–4); by flowers, inflorescences and fruits densely pubescent; and by larger flowers (13–17 vs 12 mm long), fruits (8 × 2 vs 4 × 1.5 cm) and seeds (12 × 9 × 2 vs 9–10 × 7.5 × 1.5 mm).

Slipper orchids of the tropical Americas.

Cribb*, P. & Purver, C. (2017). Natural History Publications (Kota Kinabalu, Borneo) and The Orchid Digest (Laguna Niguel, USA) in association with Royal Botanic Gardens (Kew, UK).



Slipper orchids are amongst the most popular of all cultivated orchids. They are widely grown and have been hybridised for almost a century and a half. Slipper Orchids of the Tropical Americas covers the tropical American species of three genera of slipper orchids, *Selenipedium*, *Mexipedium* and *Phragmipedium*. Until fairly recently the slipper orchid scene has been dominated by the tropical Asian species of the genus *Paphiopedilum*, however the discovery of a suite of spectacular new species, particularly in the genus *Phragmipedium* and of the monotypic *Mexipedium xerophyticum* a true missing link, has transformed appreciation of the tropical American slipper orchid species. The new generation of hybrids that have resulted are showy, brightly coloured and long-lasting – favourites on the show bench and in the amateur greenhouse.

This is the first monograph in English to cover the tropical American slipper orchids. Written by Phillip Cribb, perhaps the leading orchid taxonomist in the world, together with Christopher Purver, Director of the Eric Young Orchid Foundation, on the Isle of Jersey, renowned for its *Phragmipedium* breeding program.

The authors provide a detailed systematic treatment of the genera and species, including their history, taxonomy, description, keys, distribution, cytology and ecology. A history of the breeding of *Phragmipedium* hybrids since the second half of the 19th century deals with the revolution brought about by the discovery of the amazing scarlet-flowered *P. besseae* and the spectacular royal purple *P. kovachii*. Future breeding trends are also covered and the cultivation of these desirable plants is also discussed.

The enigma of *Pleione* 'Frank Kingdon Ward'.

Cribb*, P. J. & Butterfield, I. (2017). *Curtis's Botanical Magazine* 34 (2): 133–138. DOI: 10.1111/curt.12190.

Pleione 'Frank Kingdon Ward' first appeared in collections in the 1950s and has persisted. It has been considered to be a form of the spring flowered *Pleione humilis* but cytological examination shows it to be a triploid hybrid. Its identity is examined here and a formal hybrid name is proposed for it.

Phragmipedium hirtzii.

Cribb*, P. J. & Rankou*, H. (2017). *Curtis's Botanical Magazine* 34 (2): 90–97. DOI: 10.1111/curt.12185.

Alex Hirtz (born 1945), a professional geologist in Ecuador, has been the most prolific discoverer of new orchid species in that country in modern times with

eponymous species in 51 orchid and three bromeliad genera. Orchids are his first love and his knowledge of the Ecuadorian orchid flora, habitats and ecology is comprehensive and perspicacious. He has also developed his own ideas on orchid evolution in the Andes which, while contentious, are nevertheless stimulating. The slipper orchid featured here and named in his honour is one of his most spectacular discoveries.

Cypripedium fargesii.

Cribb*, P. J. & Schuiteman*, A. (2017). *Curtis's Botanical Magazine* 34 (2): 81–89. DOI: 10.1111/curt.12184.

Cypripedium fargesii Franch., an endangered species from West China, is described and illustrated. Notes on its discovery, taxonomy, habitat, conservation status, and cultivation are provided.

A new species of *Craterostigma* (Linderniaceae) from Kenya.

Darbyshire*, I. & Fischer, E. (2017). *Phytotaxa* 306: 91–95. DOI: 10.11646/phytotaxa.306.1.8.

The new species *Craterostigma loitense* from the Loita Hills in Kenya is described and illustrated. It differs from *Craterostigma purpureum* in the two abaxial staminodes, the basal tufts of hairs on the anthers, and the subentire to serrulate leaf margin.



A synopsis of *Chlamydocardia* (Acanthaceae) including *Linocalix*.

Darbyshire*, I. & Govaerts*, R. (2017). *Kew Bulletin* 72 (37): DOI 10.1007/S12225-017-9711-8.

Linocalix Lindau, one of the few remaining unplaced genera for the World Checklist of Selected Plant Families database, is found to be a synonym of *Chlamydocardia* Lindau (Acanthaceae). An extant type at the BR herbarium of *Linocalix albus* Lindau is referable to *Chlamydocardia subrhomboidea* Lindau. A synopsis of the two species of *Chlamydocardia*, *C. buettneri* Lindau (including *C. lanciformis* Lindau) and *C. subrhomboidea* is provided, together with an identification key and a discussion of their status. Neotypes are selected for *C. buettneri* and *C. subrhomboidea*, and *C. lanciformis* and *Linocalix albus* are lectotypified.



Pleurostyliya serrulata and two allied new species from Africa are actually members of the New World *Crossopetalum* (Celastraceae).

Darbyshire*, I., Simmons, M. P., Cappa, J. J., Breteler, F. J. & Buerki, S. (2016). *Systematic Botany* 41: 851–864. DOI 10.1600/036364416X693955.

Based on phylogenetic analyses using rDNA and plastid sequence data, and the examination of morphological characters, we infer that *Pleurostyliya*, as currently delimited, is a polyphyletic group. *Pleurostyliya serrulata* and two newly described species from Africa are part of the New World *Crossopetalum* lineage. By contrast, *Pleurostyliya* s.s. consists of all remaining species, which form a clade nested within a primarily Malagasy lineage. We present preliminary evidence that *Pleurostyliya opposita*, the most geographically widespread species in the entire Celastraceae family, may include cryptic species. Although molecular evidence supports the monophyly of *Crossopetalum*, this genus does not appear to be well defined by a single morphological synapomorphy, rather the following combination of character states is diagnostic: 4-merous flowers; stamens inserted in the sinuses of a \pm 4-lobed intrastaminal floral disk; pistil (2- or) 4-locular with one atropous ovule per locule; stigma conspicuously (2-) 4-branched; drupe usually single seeded and asymmetric with an excentric style remnant; and seeds exarillate with ramified postchalazal bundles visible on the surface and with endosperm present. A taxonomic treatment of *Crossopetalum* in Africa is presented, in which the new combination *Crossopetalum serrulatum* is proposed and two new species, *C. bokdamii* and *C. mossambicense*, are described and their conservation status assessed.

Ruellia domatiata (Acanthaceae), a striking new species from Madagascar.

Darbyshire*, I., Tripp, E. A. & Onjalalaina*, G. E. (2017). *Kew Bulletin* 72 (13): DOI: 10.1007/s12225-017-9676-7.

The new species *Ruellia domatiata* I. Darbysh. & E. Tripp from northern Madagascar is described and illustrated and its affinities within the genus are discussed. This striking new species is currently assessed as Critically Endangered using the categories and criteria of the IUCN Red List. The presence of tuft-domatia on the undersurface of the leaves, a rare occurrence in the Acanthaceae family, is noted.

Espeletia praesidentis, a new species of Espeletiinae (Millerieae, Asteraceae) from northeastern Colombia.

Diazgranados*, M. & Sánchez, L. R. (2017). *Phytokeys* 76: 1–12. DOI: 10.3897/phytokeys.76.11220.

A new species of *Espeletia* from the Páramo de Presidente in northeastern Colombia is described. The species is named *Espeletia praesidentis* after the name of the páramo, and it is dedicated to the President Juan Manuel Santos, for his persistent efforts in working for peace for Colombia. The new species is closely related to *Espeletia dugandii*, but differs in the shape and colour of the leaves and arrangements of the capitulescences. A large population was found, but its total extension is yet to be determined.

848. *Platystele misera*: Orchidaceae.

Dodsworth*, S. (2016). *Curtis's Botanical Magazine* 33 (4): 294–302 [with plate 848]. DOI: 10.1111/curt.12163.

Platystele misera (Lindl.) Garay is illustrated as the first of two species of *Platystele* Schltr., a genus of tiny Pleurothallid orchids from South and Central America. The ecology and distribution of *Platystele* are discussed, accompanied by brief notes on the cultivation of this species.

849. *Platystele ovatilabia*: Orchidaceae.

Dodsworth*, S. (2016). *Curtis's Botanical Magazine* 33 (4): 303–309 [with plate 849]. DOI: 10.1111/curt.12164.

Platystele ovatilabia (Ames & C. Schweinf.) Garay is illustrated, as the second of two *Platystele* species. The history, taxonomy and phylogenetic relationships of *Platystele* are discussed further.

The flora and fauna of the Euphrates Expedition of 1836.

Edmondson*, J. R. (2017). *Israel Journal of Plant Sciences*: DOI: 10.1080/07929978.2017.1288467.

In 1836 Col. Francis Rawson Chesney, a British army officer, led an expedition to test the proposition that large iron vessels could successfully navigate the river Euphrates from southern Turkey to the Persian Gulf. The naturalist Dr Johann Wilhelm Helfer, his wife Pauline (later Countess Nostitz), and the surgeon-geologist William Francis Ainsworth made field observations and gathered natural history collections from along the banks of the Euphrates. Botanical specimens were processed by John Lindley and made available to Antonio Bertoloni of Bologna, who described a number of new species

from the material. A partial catalog of this material has been compiled, noting the location of type specimens, and the collections have been localized as far as possible given the scanty evidence from the labels. A bibliography of references relevant to natural history from the extensive literature on the expedition is provided.

Raman spectroscopic analysis of the effect of the lichenicolous fungus *Xanthoriicola physciae* on its lichen host.

Edwards, H. G. M., Seaward, M. R. D., Preece, T. F., Jorge-Villar, S. E. & Hawksworth*, D. L. (2016). *Symbiosis* 71: 57–63. DOI: 10.1007/s13199-016-0447-2.

Lichenicolous (lichen-dwelling) fungi have been extensively researched taxonomically over many years, and phylogenetically in recent years, but the biology of the relationship between the invading fungus and the lichen host has received limited attention, as has the effects on the chemistry of the host, being difficult to examine in situ. Raman spectroscopy is an established method for the characterization of chemicals in situ, and this technique is applied to a lichenicolous fungus here for the first time. *Xanthoriicola physciae* occurs in the apothecia of *Xanthoria parietina*, producing conidia at the hymenium surface. Raman spectroscopy of apothecial sections revealed that parietin and carotenoids were destroyed in infected apothecia. Those compounds protect healthy tissues of the lichen from extreme insolation and their removal may contribute to the deterioration of the apothecia. Scytonemin was also detected, but was most probably derived from associated cyanobacteria. This work shows that Raman spectroscopy has potential for investigating changes in the chemistry of a lichen by an invading lichenicolous fungus.





A Handbook of the World's Conifers.

Farjon*, A. (2017). Vol. 1 & 2. Brill, Leiden & Boston. Second, revised edition.

Conifers are known to everyone as a conspicuous kind of evergreen trees or shrubs that feature prominently in gardens and parks as well as in many managed forests in the cool to cold temperate regions of the Northern Hemisphere. Numerous books have been written about them and continue to appear, mostly with a bias towards these uses in Europe and North America. This second edition, revised and updated, of *A Handbook of the World's Conifers* is departing from this traditional approach in that it includes all the world's 615 species of conifers, of which some 200 occur in the tropics. It gives as much information about these and the Southern Hemisphere conifers as about the better known species, drawing on research into the taxonomy, biology, ecology, distribution and uses by the author over nearly 35 years.

Ancient Oaks in the English Landscape.

Farjon*, A. (2017). Royal Botanic Gardens, Kew: Kew Publishing.

England has more ancient native oak trees than the rest of Europe combined. How did that come about? The reasons are all historical, and nothing to do with climate or soil factors. This story goes back to the Norman conquest of England in 1066. They created Royal Forests, chases and deer parks, where only the nobility could hunt or keep deer and it was forbidden to cut the trees. This was, if you like, an early form of nature conservation, but for the sake of privileged hunting.

Preservation of these oaks further continued through a combination of private ownership of thousands of parks, conservatism of the landowners, overseas timber availability and the absence of ruining wars on

the English landscape; the majority of which had been confined to the continent. Modernisation of forestry in England only took hold after 1920, and by that stage too late to destroy all of the old and worthless hollow trees. In contrast, modern forestry was introduced on the continent at least 200 years earlier, with devastating results for ancient trees. We owe the ancient oaks to all these circumstances which created a unique 'population' of ancient oaks, highly important for biodiversity and an asset unique to England.

A new generic system for the pantropical *Caesalpinia* group (Leguminosae).

Gagnon, E., Bruneau, A., Hughes, C. E., De Queiroz, L. P. & Lewis*, G. P. (2016). *Phytokeys* 71: 1–60. DOI: 10.3897/phytokeys.71.9203.

The *Caesalpinia* group is a large pantropical clade of ca. 205 species in subfamily Caesalpinioideae (Leguminosae) in which generic delimitation has been in a state of considerable flux. Here we present new phylogenetic analyses based on five plastid and one nuclear ribosomal marker, with dense taxon sampling including 172 (84%) of the species and representatives of all previously described genera in the *Caesalpinia* group. These analyses show that the current classification of the *Caesalpinia* group into 21 genera needs to be revised. Several genera (*Poincianella*, *Erythrostemon*, *Cenostigma* and *Caesalpinia sensu* Lewis, 2005) are non-monophyletic and several previously unclassified Asian species segregate into clades that merit recognition at generic rank. In addition, the near-completeness of our taxon sampling identifies three species that do not belong in any of the main clades and these are recognised as new monospecific genera. A new generic classification of the *Caesalpinia* group is presented including a key for the identification of genera, full generic descriptions, illustrations (drawings and photo plates of all genera), and (for most genera) the nomenclatural transfer of species to their correct genus. We recognise 26 genera, with reinstatement of two previously described genera (*Biancaea* Tod., *Denisophytum* R. Vig.), re-delimitation and expansion of several others (*Moullava*, *Cenostigma*, *Libidibia* and *Erythrostemon*), contraction of *Caesalpinia* s.s. and description of four new ones (*Gelrebia*, *Paubrasilia*, *Hererolandia* and *Hultholia*), and make 75 new nomenclatural combinations in this new generic system.

Validating the combination *Cerastium dichotomum* var. *inflatum* (Caryophyllaceae).

Ghazanfar*, S. A. (2017). *Kew Bulletin* 72 (16): DOI: 10.1007/s12225-017-9684-7.



A new combination *Cerastium dichotomum* var. *inflatum* invalidly published in Flora of Iraq Volume 5 Part 1 is here validated.

The Plants of Jordan: an annotated checklist.

Ghazanfar*, S. A. (ed.) (2017). Royal Botanic Gardens, Kew: Kew Publishing.

This is the first up to date and comprehensive checklist of the vascular plants of Jordan. The book covers 112 families and all species (including ferns and gymnosperms) recorded for Jordan, with at least one specimen for each species cited.

***Scrophularia amadiyana* (Scrophulariaceae), a new species from Iraq and a key to *Scrophularia* in Iraq.**

Ghazanfar*, S. A. & Haloob, A. (2017). *Kew Bulletin* 72 (17): DOI: 10.1007/s12225-017-9683-8.

A new species, *Scrophularia amadiyana* is described and illustrated. It resembles *S. gracilis* Blakelock in habit but can be differentiated by its glandular-pubescent, oblong calyx lobes which are without scarious margins, smaller glandular capsules and seeds that are longitudinally ridged and obscurely pitted. The species is known so far from a single location in Iraq growing on mountain slopes in Kurdistan where it is reported to be frequent, and is assessed here as Data Deficient.

Naming and counting the world's plant families.

Govaerts*, R., Hind*, N., Lindon*, H., Chase*, M. W., Baker*, W. J., Lewis*, G., Vorontsova*, M., Nicolson*, N., Christenhusz*, M. J. M., Barker*, A. M. & Paton*, A. (2017). In: Willis*, K. J. (ed.) *State of the World's Plants 2017*. Richmond: Royal Botanic Gardens, Kew, pp.4–9.

80% of the food derived from plants comes from 17 plant families. In total, 452 vascular plant families have been identified by botanists across the world.

Bizarre Botany: An A-Z Adventure through the Plant Kingdom.

Harrison*, C. & Gardiner*, L. M. (2016). Royal Botanic Gardens, Kew, UK: Kew Publishing.

Take a journey through a forest of fascinating facts and explore the wonders of the plant kingdom – from the tallest and smallest, to the smelliest and deadliest. This A to Z gift book reveals some of the most quirky and awe-inspiring stories about plants and will give you a whole new appreciation of all things floral.

Fungal diversity revisited: 2.2 to 3.8 million species.

Hawksworth*, D. L. & Lücking, R. (2017). *Microbiology Spectrum* 5 (4): DOI: 10.1128/microbiolspec.FUNK-0052-2016.

The question of how many species of Fungi there are has occasioned much speculation, with figures mostly posited from around half a million to 10 million, and in one extreme case even a sizable portion of the spectacular number of 1 trillion. Here we examine new evidence from various sources to derive an updated estimate of global fungal diversity. The rates and patterns in the description of new species from the 1750s show no sign of approaching an asymptote and even accelerated in the 2010s after the advent of molecular approaches to species delimitation. Species recognition studies of (semi-)cryptic species hidden in morpho-species complexes suggest a weighted average ratio of about an order of magnitude for the number of species recognized after and before such studies. New evidence also comes from extrapolations of plant:fungus ratios, with information now being generated from environmental sequence studies, including comparisons of molecular and fieldwork data from the same sites. We further draw attention to undescribed species awaiting discovery in biodiversity hot spots in the tropics, little-explored habitats (such as lichen-inhabiting fungi), and material in collections

awaiting study. We conclude that the commonly cited estimate of 1.5 million species is conservative and that the actual range is properly estimated at 2.2 to 3.8 million. With 120,000 currently accepted species, it appears that at best just 8%, and in the worst case scenario just 3%, are named so far. Improved estimates hinge particularly on reliable statistical and phylogenetic approaches to analyze the rapidly increasing amount of environmental sequence data.

Fungal nomenclature evolving: changes adopted by the 19th International Botanical Congress in Shenzhen 2017, and procedures for the Fungal Nomenclature Session at the 11th International Mycological Congress in Puerto Rico 2018.

Hawksworth*, D. L., May, T. W. & Redhead, S. A. (2017). *IMA Fungus* 8: 211–218. DOI: 10.5598/ima fungus.2017.08.02.01.

This article summarizes the key changes in the rules relating to the nomenclature of fungi made at the XIX International Botanical Congress in Shenzhen, China, in July 2017. Most significant was the decision to transfer decision-making on matters related only to the naming of fungi from International Botanical to International Mycological Congresses (IMCs). The rules relating to fungi are to be grouped together in a separate section of the International Code of Nomenclature for algae, fungi, and plants (ICN). The way in which the Fungal Nomenclature Session will operate at the upcoming IMC in Puerto Rico in 2018



is summarized and the timetable for new proposals is presented. In addition, approval for names included on lists of protected names to be protected against unlisted as well as known competing names were passed, as were some simplifications relating to the naming of pleomorphic fungi. From 1 January 2019, it will also be necessary to deposit details of lecto-, neo-, and epitypifications in one of the recognized repositories of fungal names in order for them to be validly published and to establish their priority. Various aspects relating to typifications were referred to a new Special Committee, with a separate Special Subcommittee charged with addressing the issue of using DNA sequences as types for all groups covered by the ICN. It is anticipated that the Shenzhen Code will be published in the first half of 2018.

Fixing the application of the generic name *Naematelia* (Tremellales) by lectotypification.

Hawksworth*, D. L., Millanes, A. M. & Wedin, M. (2016). *Taxon* 65 (5): 1093–1096. DOI: 10.12705/655.10.

The place of publication and typification of the generic name *Naematelia* is discussed, and *N. encephala* is confirmed as the correct name of the type of the genus name. That name was a replacement name for the earlier *N. encephaliformis*, which is lectotypified by a Willdenow plate; as selection of an epitype cannot be justified at present, a sequenced specimen from Sweden is selected as a reference specimen to represent the molecular application of the name in our sense. As the name *N. encephala* is a sanctioned name, it must be retained over *N. encephaliformis*. The species is fungicolous, widespread, growing mainly on *Stereum sanguinolentum* on conifers, but also reported on deciduous trees.

The enigma of the *Diporothea* palynomorph.

Hawksworth*, D. L., van Geel, B. & Wiltshire, P. E. J. (2016). *Review of Palaeobotany and Palynology* 235: 94–98. DOI: 10.1016/j.revpalbo.2016.09.010.

In the Quaternary palynological literature, the name *Diporothea rhizophila* has come to be applied for fungal spores labelled in the Hugo de Vries-Laboratory (HdV) in Amsterdam (The Netherlands) as Type HdV-143. The widespread occurrence of this taxon in palynological preparations was difficult to understand as the species is definitely known only from *Solanum* species in Washington State in the USA. Comparison of spores found in palaeoecological and forensic samples with those of the original material (holotype) of *D. rhizophila* established that the name had been misapplied. Type HdV-143 is distinguished from the

holotype by the shape, size, and ornamentation of the ascospores. The spores in the palaeoecological material are navicular to fusiform, and not oval when mature. They develop robust, dark brown, anastomosed ridges from an early stage, and are much longer, measuring 44–59 μm and not 25–37 μm in length. Similarities in spore structure and development indicate that both can be accommodated in the same genus, but as different species. The specimens from palynological preparations are described here as *D. webbii* sp. nov. Circumstantial evidence, gained from palaeoecological analysis, suggests that the new species may be associated with the fern genus *Thelypteris*, and today occurs most commonly in wet *Alnus* carr. Similar spores have been reported from the pre-Quaternary fossil record under the generic name *Striadiporites*.

***Areca jokowi*: a new species of betel nut palm (Arecaceae) from Western New Guinea.**

Heatubun*, C. D. (2016). *Phytotaxa* 288 (2): 175–180. DOI: 10.11646/phytotaxa.288.2.8.

A new species of betel nut palm, *Areca jokowi*, is described and illustrated here. This is the third species of *Areca* to have been described recently from New Guinea that is closely related to the widespread, economically important species *A. catechu*, the cultivated betel nut palm. A discussion of its morphological characters, distribution, ecology, habitat, uses and conservation status is provided, as well as a new identification key for western New Guinean *Areca*.

New species and nomenclatural changes in *Cynorkis* (Orchidaceae: Orchidoideae) from Madagascar and the Mascarenes.

Hermans*, J., Andriantiana, J., Sieder, A., Kiehn, M., Cribb*, P., Rajavelona*, L. & Gardiner*, L. M. (2017). *Kew Bulletin* 72. DOI: 10.1007/s12225-017-9715-4.

Ten new species, *Cynorkis aconitiflora*, *C. christae*, *C. elephantina*, *C. jackyi*, *C. lentiginosa*, *C. mammuthus*, *C. mangabensis*, *C. sanguinolenta*, *C. siederi* and



C. syringescens, are described for the first time. The identity of *C. elegans* is clarified. The status of *Arnottia* and *Physoceras* are discussed and both subsumed into *Cynorkis*, with the necessary taxonomic changes made.

***Ardisia gasingoides* (Primulaceae-Myrsinoideae), a new species from southern Peninsular Malaysia.**

Julius, A., Kajita, T. & Utteridge*, T. M. A. (2017). *Phytotaxa* 291: 281–286. DOI: 10.11646/phytotaxa.291.4.5.

Ardisia gasingoides Julius & Utteridge sp. nov. (Primulaceae-Myrsinoideae) is described and illustrated as a new species; it is endemic to the state of Johor from southern Peninsular Malaysia. The new species belongs to subgenus *Stylardisia* and is morphologically similar to *Ardisia cockburniana*, *A. crassa* and *A. crassiuscula* in having obconically flared and thickened pedicels but differs in smaller leaves with fewer veins, few flowers in shorter inflorescences and, especially, the 5-sided turbinate fruits. A preliminary conservation status and key to related taxa are provided.

***Lysimachia kraduengensis* (Primulaceae), a new species from northeast Thailand.**

Julius, A., Tagane, S., Naiki, A., Gutiérrez-Ortega, J. S., Suddee, S., Rueangruea, S., Yahara, T. & Utteridge*, T. M. A. (2016). *Phytotaxa* 289: 69–76. DOI: 10.11646/phytotaxa.289.1.5.

A new species of Primulaceae from Thailand, *Lysimachia kraduengensis*, is described and illustrated. It is morphologically similar to *L. engleri*, *L. lancifolia*, *L. laxa* and *L. sikokiana* in having solitary and axillary flowers, a yellow corolla, relatively long pedicels and basifixed anthers. The new species can be distinguished by the combination of its height, leaf texture, petiole, calyx and anther length, and brown coloration on the flowers. In addition, the conservation status, an updated key to *Lysimachia* species in



Thailand, and discussion of the systematic placement of the new species based on the trnL-F marker of chloroplast DNA are provided.

Leontidine-type quinolizidine alkaloids in *Orphanodendron* (Leguminosae).

Kite*, G. C. (2017). *Biochemical Systematics and Ecology* 73: 47–49. DOI: 10.1016/j.bse.2017.06.002.

Herbarium leaf fragments of the two known species of *Orphanodendron* (Leguminosae), *O. bernalii* and *O. grandiflorum*, were found to contain the quinolizidine alkaloids camoensine (1), camoensidine (2) and guianodendrine (3), supporting the recent phylogenetic placement of the genus in the genistoid clade of subfamily Papilionoideae rather than its traditional placement in subfamily Caesalpinioideae.

Compositae (Asteraceae).

Koyama, H., Bunwong, S., Pornpongrungrueng, P. & Hind*, D. J. N. (2016). In: *Flora of Thailand*. Bangkok, Thailand: Forest Herbarium, Department of National Parks, Wildlife and Plant Conservation. Vol. 13 (2), pp.143–428.

This volume deals with the family Compositae (Asteraceae), which is one of the largest families of flowering plants, with approximately 24,000 known species and an estimated total of as many as 30,000. One hundred and seven genera with 240 species are enumerated in Thailand and some of them are endemic to the country. Many introduced species are newly recognised to the flora in the tribes Heliantheae, Eupatorieae and Senecioneae. Some of them are cultivated as garden ornamentals and others have medicinal uses.

Notes on the genus *Callitriche* (Plantaginaceae) in South Africa.

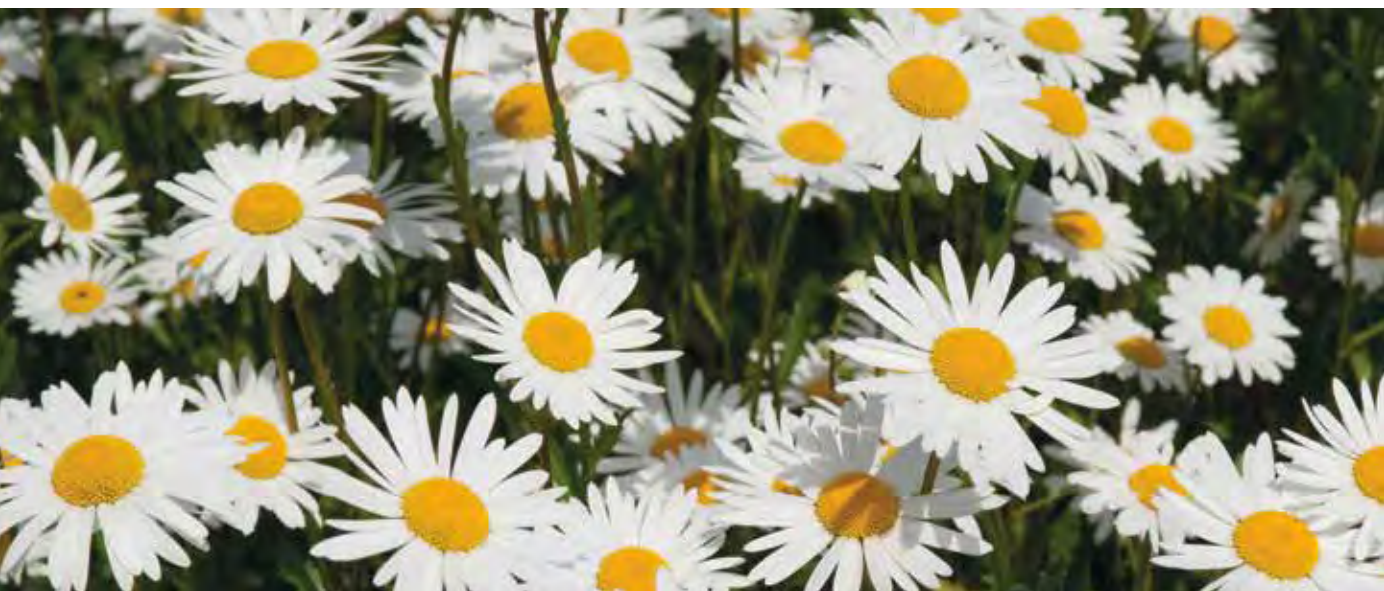
Lansdown*, R. V., Glen, R. & Hassemer, G. (2017). *Phytotaxa* 317 (3): 219–225. DOI: 10.11646/phytotaxa.317.3.6.

Historically there has been confusion over the status and identification of *Callitriche* species in South Africa. Review of herbarium specimens and fieldwork have enabled confirmation of the presence of *C. deflexa* as a naturalised species in this country and confirmed that *C. compressa* and specimens named as *C. bolusii* are conspecific. Field surveys showed that *C. compressa* still occurs in the areas from which most historic collections were made with no evidence of a decline, it is widespread but local in Kwa-Zulu Natal and Eastern Cape Provinces and extends into eastern Western Cape Province. However because it is known from only five widely scattered sites, it is classed as Vulnerable under the IUCN Red List. We also typify here the names *C. compressa* and *C. deflexa*.

Taxonomic notes on the genus *Premna* L. (Lamiaceae) in Thailand.

Leeratiwong, C., Chantaranothai, P. & Paton*, A. (2016). *Thai Forest Bulletin (Botany)* 44: 122–124. DOI: 10.20531/tfb.2016.44.2.06.

The following 10 species in the genus *Premna* (Lamiaceae) are lectotypified: *Premna annulata*, *P. collinsiae*, *P. dubia*, *P. fulva*, *P. garrettii*, *P. paniculata*, *P. quadridentata*, *P. repens*, *P. serrata* and *P. siamensis*. *Premna collinsiae* is reduced to the synonymy of *P. pubescens* and *P. paniculata* is also fully described for the first time following the discovery of complete flowers. Photographs of *P. paniculata* and *P. pubescens* are provided.





A Conspectus of *Myrcia* sect. *Aulomyrcia* (Myrtaceae) 1.

Lucas*, E., Wilson, C. E., Lima, D. F., Sobral, M. & Matsumoto, K. (2016). *Annals of the Missouri Botanical Garden* 101 (4): 648–698. DOI: 10.3417/2014015.

An annotated conspectus of 124 species is presented for *Myrcia* DC. sect. *Aulomyrcia* (O. Berg) Griseb. This list is published for use as a basis for future revisionary work and presents the species of this evolutionary group together for the first time. Publication and type information, habitat and distribution, preliminary conservation assessments, and diagnostic notes are provided for each species.

Four new combinations in Argentinian Heliotropiaceae.

Luebert, F. & Frohlich*, M. W. (2016). *Darwiniana, nueva serie* 4 (2): 192–194. DOI: 10.14522/darwiniana.2016.42.717.

Four new combinations in the genera *Euploca* and *Myriopus* (Heliotropiaceae) are established: *Euploca aurata*, *E. catamarcense*, *Myriopus breviflorus* and *M. paniculatus* var. *austrinus*.

A new species of *Myrcia* sect. *Aulomyrcia* (Myrtaceae) from the restingas of Bahia, Brazil.

Marinho, L. C. & Lucas*, E. J. (2016). *Phytotaxa* 280 (3): 285–291. DOI: 10.11646/phytotaxa.280.3.7.

The new species *Myrcia ramifinita* is described and illustrated; diagnostic characters such as large solitary bracts subtending auxotelic inflorescences and striking bracts covered in silky silver hairs are contrasted to closely related *M. micropetala*. Both species belong to *Myrcia* section *Aulomyrcia* and share persistent bracts, bilocular ovaries and covered by the indumentum peduncles, hypanthia and calyx lobes. The species occurs in Southern Bahian restinga (Brazil).

Mapania jongkindii (Cyperaceae), a new species from Liberia.

Mesterházy, A., Kim, C. & Browning*, J. (2017). *Kew Bulletin* 72 (36): DOI: 10.1007/S12225-017-9707-4.

A new species of *Mapania*, *M. jongkindii* is described and illustrated from the Nimba Mts, Liberia. It is separated from the related species, *M. baldwinii* and *M. linderi*, by characteristics of both leaf and fruit. Confirmation of this separation and the phylogenetic position of *M. jongkindii* was determined by phylogenetic analyses of DNA sequences from nuclear ribosomal Internal Transcribed Spacer and two chloroplast regions (rpoB and trnL-F IGS).

A first checklist to the vascular plants of La Amistad International Park (PILA), Costa Rica-Panama.

Monro*, A. K., Santamaría-Aguilar, D., González, F., Chacón, O., Solano, D., Rodríguez, A., Zamora,

N., Fedele, E. & Correa, M. (2017). *Phytotaxa* 332: 1–283. DOI: 10.11646/phytotaxa.322.1.1.

La Amistad International Park is a World Heritage Site, which comprises 401,000 ha of mainly upland continuous natural vegetation straddling the Costa Rica and Panama border. We present a first checklist of vascular plant diversity for the park and a brief discussion of how this diversity is distributed by elevation and vegetation type together with a superficial assessment of floristic affinities. The checklist recognises 3,046 vascular plant species, 26 of which are lycopods, 433 are ferns and 2,586 are seed plants. Of these, 16 are new records for Costa Rica and 39 are for the flora of Panama; 14 represent undescribed or new species to science and 73 are endemic to La Amistad or its buffer zone. For each species we document its presence within the Park by citing herbarium specimens and the associated elevational range, together with their global distribution, extinction risk assessments where undertaken, whether the taxon is exotic.

Impact of e-publication changes in the International Code of Nomenclature for algae, fungi and plants (Melbourne Code, 2012) - did we need to “run for our lives”?

Nicolson*, N., Challis, K., Tucker, A. & Knapp, S. (2017). *BMC Evolutionary Biology* 17: 116. DOI: 10.1186/s12862-017-0961-8.

Background

At the Nomenclature Section of the XVIII International Botanical Congress in Melbourne, Australia (IBC), the botanical community voted to allow electronic publication of nomenclatural acts for algae, fungi and plants, and to abolish the rule requiring Latin descriptions or diagnoses for new taxa. Since the 1st



January 2012, botanists have been able to publish new names in electronic journals and may use Latin or English as the language of description or diagnosis.

Results

Using data on vascular plants from the International Plant Names Index (IPNI) spanning the time period in which these changes occurred, we analysed trajectories in publication trends and assessed the impact of these new rules for descriptions of new species and nomenclatural acts. The data show that the ability to publish electronically has not “opened the floodgates” to an avalanche of sloppy nomenclature, but concomitantly neither has there been a massive expansion in the number of names published, nor of new authors and titles participating in publication of botanical nomenclature.

Conclusions

The e-publication changes introduced in the Melbourne Code have gained acceptance, and botanists are using these new techniques to describe and publish their work. They have not, however, accelerated the rate of plant species description or participation in biodiversity discovery as was hoped.

Field-based species identification of closely-related plants using real-time nanopore sequencing.

Parker*, J., Helmstetter*, A. J., Devey*, D., Wilkinson*, T. & Papadopoulos*, A. S. T. (2017). *Scientific Reports* 7: 8345. DOI: 10.1038/s41598-017-08461-5.

Advances in DNA sequencing and informatics have revolutionised biology over the past four decades, but technological limitations have left many applications unexplored. Recently, portable, real-time, nanopore sequencing (RTnS) has become available. This offers opportunities to rapidly collect and analyse genomic data anywhere. However, generation of datasets from large, complex genomes has been constrained to laboratories. The portability and long DNA sequences of RTnS offer great potential for field-based species identification, but the feasibility and accuracy of these technologies for this purpose have not been assessed. Here, we show that a field-based RTnS analysis of closely-related plant species (*Arabidopsis* spp.) has many advantages over laboratory-based high-throughput sequencing (HTS) methods for species level identification and phylogenomics. Samples were collected and sequenced in a single day by RTnS using a portable, “al fresco” laboratory. Our analyses demonstrate that correctly identifying unknown reads from matches to a reference database with RTnS reads enables rapid and confident species identification. Individually annotated RTnS reads can

be used to infer the evolutionary relationships of *A. thaliana*. Furthermore, hybrid genome assembly with RTnS and HTS reads substantially improved upon a genome assembled from HTS reads alone. Field-based RTnS makes real-time, rapid specimen identification and genome wide analyses possible.

A new species of *Telipogon* from the Paramos of Colombia.

Pérez-Escobar*, O. A., Rodríguez, L. K. & Martel, C. (2017). *Phytotaxa* 305: 262–268. DOI: 10.11646/phytotaxa.305.4.2.

Telipogon heinrichsii from the paramo of the western slope of the Central Andean Cordillera in Colombia is proposed as a new species. The new taxon is similar to *T. puruantensis* and *T. vollesii*, but differs by the triquetrous peduncle of the inflorescence, a widely ovate labellum, and the column completely surrounded by uniformly distributed setae. A description, illustrations, and notes on the ecology and distribution are provided.

Eight new synonyms in the genus *Pycurus* (Cyperaceae).

Prasad, V. P & Simpson*, D. A. (2016). *Rheedea* 26 (2): 12–16.



Pycurus plicatus Govind. is reduced to the synonym of *P. diaphanus* (Schrad. ex Schult.) S.S. Hooper & T. Koyama. *Cyperus latovaginatatus* Govind. [*Pycurus latovaginatatus* (Govind.) P. Singh & V. Singh], *C. plumbeonucea* Govind. [*P. plumbeonuceus* (Govind.) P. Singh & V. Singh], *C. curvibracteatus* Govind. [*P. curvibracteatus* (Govind.) P. Singh & V. Singh], *Pycurus apiculatus* Govind. and *P. opulentus* Govind. are reduced to the synonyms of *P. diaphanus* var. *gracilescens* (Kük.) S.S. Hooper. *Pycurus palghattensis* Govind. is reduced to the synonym of *P. pumilus* (L.) Nees, *P. membranaceus* (Vahl) Govind. is treated as a variety, i.e., *P. pumilus* var. *membranaceus* (Vahl) Karthik. and *P. similinervulosus* Govind. is reduced to the synonym of *P. pumilus* var. *membranaceus*. Also lectotype is designated for *P. similinervulosus*.

Notes on the taxonomy and lectotypification of *Cyperus macer* (Cyperaceae).

Prasad, V. P & Simpson*, D. A. (2017). *Kew Bulletin* 72 (33): DOI: 10.1007/s12225-017-9702-9.

Cyperus macer C. B. Clarke is lectotypified, and its taxonomy and distribution are discussed.

Ilex pubifructa (Aquifoliaceae), a new species from northern Thailand.

Pruesapan, K., Andrews, S. & Simpson*, D. A. (2017). *Kew Bulletin* 72 (21): DOI: 10.1007/s12225-017-9692-7.

A new species of the genus *Ilex* is recorded for northern Thailand. *Ilex pubifructa* is closely allied to *I. denticulata* but is immediately recognisable by the dense pubescence covering many parts of the plant.

Computational Botany: Methods for Automated Species Identification.

Remagnino, P, Mayo*, S., Wilkin*, P, Cope, J. & Kirkup*, D. (2017). Berlin: Springer-Verlag.

This book discusses innovative methods for mining information from images of plants, especially leaves, and highlights the diagnostic features that can be implemented in fully automatic systems for identifying plant species. Adopting a multidisciplinary approach, it explores the problem of plant species identification, covering both the concepts of taxonomy and morphology. It then provides an overview of morphometrics, including the historical background and the main steps in the morphometric analysis of leaves together with a number of applications. The core of the book focuses on novel diagnostic methods for plant species identification developed from a



computer scientist's perspective. It then concludes with a chapter on the characterization of botanists' visions, which highlights important cognitive aspects that can be implemented in a computer system to more accurately replicate the human expert's fixation process.

853. *Sophora cassioides* (Leguminosae).

Rix, M. & Lewis*, G. (2016). *Curtis's Botanical Magazine* 33 (4): 338–346 [with plate 853]. DOI: 10.1111/curt.12168.

Sophora cassioides (Phil.) Sparre, from Chile, is illustrated and suggestions for its cultivation are given. The history of *Sophora* sect. *Edwardsia* is discussed briefly.

857. *Platanus orientalis* (Platanaceae).

Rix*, M. & Fay*, M. F. (2017). *Curtis's Botanical Magazine* 32: 29–40 [with plate 857]. DOI: 10.1111/curt.12177.

The oriental plane tree, *Platanus orientalis* L., is illustrated. Its phylogenetic position is discussed, and its cultural history and early literature references are mentioned; its geography and ecology are described.

New records of Orchidaceae from Cambodia IV.

Schuiteman*, A., Jenny, R., Khou, E. H., Nay, S. & Att, S. (2017). *Cambodian Journal of Natural History* 2017 (1): 4–9.

The previous article in this series on new orchid records from Cambodia is Schuiteman et al. (2016). We here report on eight new records, including

the following three new generic records: *Ania*, *Cylindrolobus*, and *Hetaeria*. All were found by the authors, together with Mr Neang Thy, during field trips to western and southern Cambodia in November 2016. Two species (*Cylindrolobus biflorus* and *Hetaeria oblongifolia*) were not seen in flower in the field but flowered in cultivation at the Royal Botanic Gardens, Kew, from collected living specimens, while a third, *Tropidia angulosa*, was observed only as sterile specimens. In the interests of conservation we do not provide exact localities. Global distribution data follow Govaerts et al. (2017), unless indicated otherwise. Vouchers of all specimens mentioned are kept in the Kew Spirit Collection.

Checklist of lichen-forming, lichenicolous and allied fungi of Eagle Hill and its vicinity, Maine.

Seaward, M. R. D., Richardson, D. H. S., Brodo, I. M., Harris, R. C. & Hawksworth*, D. L. (2017). *Northeastern Naturalist* 24: 349–379. DOI: 10.1656/045.024.0305.

600 lichens and 82 lichenicolous and allied fungi have been recorded from Eagle Hill in Steuben, ME, and its vicinity over the past 25 years, mainly as a consequence of courses and research centered upon the Eagle Hill Institute (formerly the Humboldt Field Research Institute). Of the 682 taxa listed, 331 have been recorded within the Institute's boundary, of which 27 were not found elsewhere in the vicinity; a further 66 taxa recorded but lacking voucher material are listed. One lichen, *Lambiella fuscosora*, and 7 lichenicolous fungi, *Cornutispora pyramidalis*, *Epicladonia stenospora*, *Monodictys epilepraria*, *Muellerella polyspora*, *Taeniolella cladinicola*, and *Tremella coppinsii*, are additional to the North American checklist; *Lambiella fuscosora* and

Cornutispora pyramidalis are also recorded as new for Canada. Five lichens, *Alyxoria ochrocheila*, *Cladonia albonigra*, *Ephebe solida*, *Myriolecis schofieldii*, and *Parmotrema stuppeum*, are new for Maine. Notes on new records and interesting taxa are provided.

A synopsis of *Coulteria* (Leguminosae), including new names and synonyms.

Sotuyo, S., Contreras, J. L., Gagnon, E. & Lewis*, G. P. (2017). *Phytotaxa* 291 (1): 33–42. DOI: 10.11646/phytotaxa.291.1.3.

As a result of ongoing studies in *Caesalpinia sensu lato*, new combinations and synonyms are proposed in the reinstated segregate genus *Coulteria*.



A new species of *Erythrostemon* (Leguminosae, Caesalpinioideae) from the western Río Balsas Depression, Mexico.

Sotuyo, S., Contreras-Jiménez, J. L. & Lewis*, G. P. (2017). *Phytokeys* 76: 31–38. DOI: 10.3897/phytokeys.76.10921.

A new legume species from a seasonally dry forest of the Western Río Balsas Depression, in the states of Guerrero and Michoacán, Mexico, *Erythrostemon guevarafeferii*, is herein described and illustrated. The new species shows morphological affinities with *E. hintonii*, from which it is distinguished in having fewer leaflets per pinna, mature leaflets disposed toward the upper half of the pinnae rachises, long inflorescences on curved slender peduncles, abundant red glands on its flowers and inflorescences, and its fruit glabrous with red stipitate glands at maturity. A taxonomic key to the Río Balsas Depression species of *Erythrostemon* is included.

Eulophia obtusa (Orchidaceae: Epidendroideae: Cymbideae) an addition to the flora of Bangladesh, with notes on its ecology and conservation status.

Sourav, M. S. H., Halder, R., Kumar, P. & Schuiteman*, A. (2017). *Kew Bulletin* 72 (19): DOI: 10.1007/S12225-017-9689-2.

Little published information exists about *Eulophia obtusa*, a showy and distinctive species previously recorded from North India and Nepal. It is here reported from Bangladesh for the first time. The population occurring in Bangladesh may represent a distinct colour form, with pure white instead of bright yellow sepals and petals as in previous records. A species growing in seasonally waterlogged grassland, its only known site in Bangladesh has already been destroyed for agricultural development. No reliable data on its present day occurrence in India and Nepal could be obtained. However, the most recent of only three collections in the Kew Herbarium dates from 1902, which suggests that it is quite a rare species. It must be assessed as critically endangered (CR) in Bangladesh, according to the IUCN Red Listing criteria.

Urticaceae-feeders from the family Tischeriidae: descriptions of two new species and new genus *Paratischeria* gen. nov.

Stonis, J. R., Diskus, A., Paulaviciute, B. & Monro*, A. K. (2017). *Biologija* 63 (1): 1–22. DOI: 10.6001/biologija.v63i1.3470.

We describe a new genus *Paratischeria* Diškus & Stonis, gen. nov. and present the first observations of Urticaceae-feeding Tischeriidae species in South America and two new Urticaceae feeding species (*Paratischeria fasciata* sp. nov. and *P. ferruginea* Diškus & Stonis, sp. nov. from the Andes of Bolivia and Ecuador). Together with the African *P. urticolella* (Ghesquière) (comb. nov.) from Congo, they are attributed to the newly designated *ferruginea* species group.

The mystery of the tiny Urticaceae-feeders: documentation of the first leaf-mining Nepticulidae (Lepidoptera) species from equatorial America associated with *Phenax*, *Boehmeria* and *Pilea*.

Stonis, J. R., Diskus, A., Remeikis, A. & Monro*, A. K. (2017). *Biologija* 63 (2): 105–125. DOI: 10.6001/biologija.v63i2.3523.

The paper presents the first documentation of Urticaceae-feeding Nepticulidae species in South

America and describes four new species: two species feeding on *Phenax* Wedd. (*Stigmella singularia* Diškus & Stonis, sp. nov. and *S. lata* Diškus & Stonis, sp. nov.), one species on *Boehmeria* Jacq. (*S. boehmeriphaga* Diškus & Stonis, sp. nov.), and one species on *Pilea* Lindl. (*S. auripurpurata* Diškus & Stonis, sp. nov.); all from the equatorial Andes. In addition, leaf-mines of an unknown *Stigmella* taxa feeding on *Phenax* are documented. The newly discovered Urticaceae-feeding Nepticulidae exhibit some morphological and taxonomical diversity: two species groups, *Stigmella singularia* and *S. marmorea*, are revealed (the latter is designated in the current paper).



Vitaceae.

Trias Blasi*, A. (2017). In Watson, M. F., Akiyama, S., Ikeda, H., Pendry, C. A., Rajbhandari, K. R. & Shrestha, K. K. (eds). *Flora of Nepal*. Royal Botanic Garden Edinburgh. Webedition 1 edn.

Woody or herbaceous climbers. Hermaphroditic, or polygamo-dioecious. Stems generally conspicuously lenticellate, bark sometimes shredding. Tendrils simple, bifurcate, 2–14 branched (adhesive discs on each tip in *Parthenocissus* and *Tetrastigma obtectum*), usually leaf-opposed, rarely absent, sometimes associated with the inflorescence. Leaves petiolate, simple and palmately veined or digitately or pedately compound, lobed or unlobed, usually with ‘pearl glands’ (small multicellular, stalked, caducous spherical structures), margin variously toothed. Inflorescences paniculate, corymbose or thyrsoid, leaf-opposed, pseudo-terminal, or axillary. Flowers small, generally pedicellate, sometimes sessile, actinomorphic, hypogynous, 4–5-merous. Calyx cupuliform, sometimes with 4–5 small lobes. Petals valvate, 4–5, free or connate and forming a calyptra, apex generally cucullate. Stamens 4–5, antepetalous, anthers medifixed dehiscing longitudinally, tetrasporangiate. Disc intrastaminal, cupular or annular, entire or lobed, mostly adnate to the ovary; sometimes inconspicuous. Ovary superior, 2-locular; style simple, stigma mostly inconspicuous, sometimes capitate or discoid, 4-lobed in *Tetrastigma*. Fruit a 1–4-seeded berry, seeds endotestal with an abaxial chalazal knot and an adaxial raphe. A family of approximately 14 genera and 900 species distributed pantropically in Asia, Africa, Australia, the Neotropics and the Pacific with some species in temperate areas. Eight genera and 27 species in Nepal, including 2 cultivated species.

Nomenclatural notes on species of Asian Vitaceae.

Trias-Blasi*, A., Parnell, J. A. N. & Watson, M. F. (2017). *Taxon* 66 (3): 718–733. DOI: 10.12705/663.12.

Lectotypifications, neotypifications, epitypifications, and nomenclatural corrections are provided for fifty-eight Asian Vitaceae names (excluding those belonging to *Tetrastigma*) for the forthcoming floristic account in the Flora of Thailand. A total of fifty-four lectotypes, three neotypes, and one epitype are designated here and two nomenclatural clarifications and corrections are also proposed.

Phylogenetic relationships among Old World *Ruellia* L.: a new classification and reinstatement of the genus *Dinteracanthus* Schinz.

Tripp, E. A. & Darbyshire*, I. (2017). *Systematic Botany* 42: 470–483. DOI 10.1600/036364417X695961.

The genus *Ruellia* (Acanthaceae) consists of some ca. 350 species that are concentrated in tropical and subtropical regions of the world. Old World *Ruellia* have never been the focus of explicit phylogenetic study, yet comprise the earliest diverging lineages in the genus and contain upwards of 100 species. We sampled 52 accessions representing 29 OW species of *Ruellia* for phylogenetic analysis. Results yielded five clades that were strongly supported and marked by morphological synapomorphies. Analyses additionally recovered a newly recognized lineage within the tribe Ruellieae, a small radiation of plants in the deserts of Namibia and Angola, and the name *Dinteracanthus* is available for reinstatement. Divergence time analysis using a primary fossil calibration revealed relatively young estimates for crown ages of all five clades of OW *Ruellia* (2.5 Ma - 630,000 ypb) as well as for *Dinteracanthus* (2.0

Ma). Ancestral state reconstruction of pollination systems among OW *Ruellia* suggest a minimum of two transitions from short-tongued insect pollination to nocturnal moth pollination, one from short-tongued insect to bird pollination, and one reversal from nocturnal moth pollination back to short-tongued insect pollination. We formally delimit the five clades of OW *Ruellia* as sections and present a key to aid in their identification: sect. *Eusiphon*, sect. *Dipteracanthus*, sect. *Madagasikara*, sect. *Pseudoruellia*, and sect. *Discifolia*. We provisionally treat 77 of 97 species of OW *Ruellia* among these five sections, with the remaining names considered to be unresolved.

New combinations and new synonyms in Asian Annonaceae with a bibliographical note.

Turner*, I. M. (2016). *Webbia* 71 (2): 229-323. DOI: 10.1080/00837792.2016.1241516.

Four species are transferred from *Polyalthia* to *Huberantha*. Four names are reduced to synonymy for the first time: *Alphonsea sessiliflora* to *Meiogyne cylindrocarpa*, *Anaxagorea meyeriana* to *Marsypopetalum pallidum*, *Cyathostemma acuminatum* to *Uvaria wrayi* and *Polyalthia schefferi* to *Marsypopetalum littorale*. Six names are lectotypified. A paper on Asian Annonaceae by Scheffer that appeared in volume 2 of the *Annales du Jardin Botanique de Buitenzorg* is shown to have been published in 1881 rather than 1885 as generally cited.



Species names attributed to Bentham & Hooker's *Genera Plantarum*.

Turner*, I. M. (2016). *Annales Botanici Fennici* 53: 285-337. DOI: 10.5735/085.053.0604.

Genera Plantarum by George Bentham and Joseph Hooker is a highly influential work in the history of plant classification. However, the importance of the work for names at the rank of species is equivocal. Bentham and Hooker proposed transferring many species to different genera without making the required new combinations. Many such supposed combinations were attributed to *Genera Plantarum*, particularly in *Index Kewensis*. Species names attributed to *Genera Plantarum* are reviewed herein. Typification of species described in *Genera Plantarum* is also analysed. Many citations of the valid publication of combinations are listed that should replace the incorrect ones still given in reference works. *Simira podocarpa* (Benth.) I.M. Turner, comb. nova and *Erigeron emodi* I.M. Turner, nom. nov. are proposed. *Litsea elongata* (Nees) Benth. ex Hook. f. is a later homonym that should be replaced by *Litsea faberi* Hemsl. *Peucedanum diversifolium* H. Wolff is not a later homonym and should be used rather than *P. chinense* M. Hiroe.

Rather for the nomenclaturist than for the scientific botanist: The *Botanical Cabinet* of Conrad Loddiges & Sons.

Turner*, I. M. (2016). *Taxon* 65: 1107–1149. DOI: 10.12705/655.13.

A selection of names appearing in the *Botanical Cabinet*, a serial work published by the nursery company of Conrad Loddiges & Sons between 1817 and 1833, is reviewed. Many names are here



lectotypified to plates published in the Botanical Cabinet. The new combinations *Pseuderanthemum maculatum* (G.Lodd.) I.M.Turner and *Wahlenbergia loddigesii* (A.DC.) I.M.Turner are made. *Erica aristata* var. *parva* I.M.Turner is proposed as an avowed substitute for *E. coruscans* var. *minor* L. Bolus. The accepted name for a number of species should change for a variety of nomenclatural reasons: *Cirrhaea loddigesii* Lindl. becomes *Cirrhaea obtusata* Lindl., *Erica peziza* G.Lodd. becomes *Erica nivalis* Andrews, *Passiflora racemosa* Brot. becomes *Passiflora princeps* G.Lodd., *Phyllanthus lanceolarius* (Roxb.) Müll.Arg. becomes *Phyllanthus fraxinifolius* G.Lodd., *Rhododendron myrtifolium* Schott & Kotschy ex Schott becomes *Rhododendron kotschyi* Simonk.

A new combination for a subspecies of *Radermachera quadripinnata* (Bignoniaceae).

Turner*, I. M. (2017). *Reinwardtia* 16 (1): 47–48. DOI: 10.14203/reinwardtia.v16i1.3001.

A new combination for a subspecies of *Radermachera quadripinnata* (Bignoniaceae).

Reinwardtia 16(1): 47 – 48. — The new combination *Radermachera quadripinnata* subsp. *lobbii* is made to replace subsp. *acuminata* as the autonym *Radermachera lobbii* subsp. *lobbii* has priority over *R. lobbii* subsp. *acuminata*. Lectotypes are designated for *Spathodea lobbii* Teijsm. & Binn. and *Radermachera lobbii* subsp. *acuminata* Steenis.

Nomenclatural note on a Brazilian aroid.

Turner*, I. M. (2017). *Skvortsovia* 4 (2): 38–39.

The correct name for the Brazilian species of Araceae known as *Asterostigma lividum* (G.Lodd.) Engl. is shown to be *Asterostigma luridum* (Kunth) Kuntze. A lectotype is designated.

Annonaceae in the Western Pacific: geographic patterns and four new species.

Turner*, I. M. & Utteridge*, T. M. A. (2017). *European Journal of Taxonomy* 339: 1–44. DOI: 10.5852/ejt.2017.339.



The taxonomy and distribution of Pacific Annonaceae are reviewed in light of recent changes in generic delimitations. A new species of the genus *Monoon* from the Solomon Archipelago is described, *Monoon salomonicum* I.M.Turner & Utteridge sp. nov., together with an apparently related new species from New Guinea, *Monoon pachypetalum* I.M.Turner & Utteridge sp. nov. The confirmed presence of the genus in the Solomon Islands extends the generic range eastward beyond New Guinea. Two new species of *Huberantha* are described, *Huberantha asymmetrica* I.M.Turner & Utteridge sp. nov. and *Huberantha whistleri* I.M.Turner & Utteridge sp. nov., from the Solomon Islands and Samoa respectively. New combinations are proposed: *Drepananthus novoguineensis* (Baker f.) I.M.Turner & Utteridge comb. nov., *Meiogyne punctulata* (Baill.) I.M.Turner & Utteridge comb. nov. and *Monoon merrillii* (Kaneh.) I.M.Turner & Utteridge comb. nov. One neotype and four lectotypes are designated. The geographic patterns exhibited by nine native Annonaceae genera, that range in the Pacific beyond New Guinea, are discussed.

Field Guide to the Introduced Flora of South Georgia.

Upson*, R., Myer, B., Floyd, K., Lee, J. & Clubbe*, C. (2017). Richmond: Kew Publishing.

Non-native plants have been introduced to South Georgia since the first sealers inhabited the island in the late eighteenth century. The number of species and their impacts have varied over the years and today 41 non-native plant species are established and many threaten the native species and habitats of South Georgia.

The correct name for Schumannianthus dichotomus (Marantaceae).

Veldkamp, J. F. & Turner*, I. M. (2016). *Kew Bulletin* 71 (4): 47. DOI: 10.1007/s12225-016-9660-7.

The genus *Schumannianthus* Gagnep. (Marantaceae) is typified by *S. dichotomus* Gagnep. This is a new genus and species for the material of *Phrynium dichotomum* auct. non Roxb. *Phrynium dichotomum*



Roxb. and derivatives are superfluous names for *Donax canniformis* (G. Forst.) K. Schum. The correct name for *S. dichotomus* is *Schumannianthus benthamianus* (Kuntze) Veldkamp & I. M. Turner comb. nov. Lectotypes are designated for *Arundastrum benthamianum* Kuntze and *Schumannianthus dichotomus* Gagnep., and a second-step lectotypification is proposed for *Thalia canniformis* G. Forst.

Digitaria bosseri (Poaceae: Panicoideae), a new species from Madagascar.

Vorontsova*, M. S. (2017). *Kew Bulletin* 72 (29): DOI: 10.1007/s12225-017-9700-y.

A new panicoid grass species of uncertain generic affiliation is described and illustrated from the dry and spiny forest ecosystems of southern Madagascar. It is tentatively placed in the genus *Digitaria* based on its spikelet structure, pending DNA sequence data.

World Checklist of Bamboos and Rattans.

Vorontsova*, M. S., Clark, L. G., Dransfield*, J., Govaerts*, R. & Baker*, W. J. (2016). International Network of Bamboo and Rattan & Royal Botanic Gardens, Kew.

This book contains a global checklist of all known species of bamboos and rattans. It is an authoritative source of information on accepted species of bamboos and rattans, the correct names that should be applied to them, and the incorrect names that should not be used. It has been compiled from expert data sources, edited extensively by the authors, with additional contributions from numerous reviewers. Together with the accompanying World Atlas of Bamboos and Rattans, it serves as a fundamental biodiversity resource for anybody with an interest in bamboos and rattans. The classification of plants and the recording of their distributions is a growing area of human knowledge. Extensive knowledge gaps are unfortunately still present, especially for diverse tropical plants that are difficult to classify and often impossible to identify by non-specialists.

The data are available in searchable format via the World Checklist of Selected Plant Families web site at <http://apps.kew.org/wcsp>.

World Atlas of Bamboos and Rattans.

Vorontsova*, M. S., Clark, L. G., Dransfield*, J., Govaerts*, R., Wilkinson*, T. & Baker*, W. J. (2016). International Network of Bamboo and Rattan & Royal Botanic Gardens, Kew.



This book contains a global atlas of all known species of bamboos and rattans. It has been produced to accompany the World Checklist of Bamboos and Rattans (Vorontsova et al. 2016) and should be used in conjunction with that volume. For general information about bamboos and rattans, please see the introductory section of the World Checklist of Bamboos and Rattans. The World Atlas of Bamboos and Rattans consists entirely of maps documenting the known distribution of all 1,642 species of bamboo and all 631 species, subspecies and varieties of rattan and rattan-like palm. The geographical information used to generate the maps is primarily derived from a database called the World Checklist of Selected Plant Families. The data are available in searchable format via the World Checklist of Selected Plant Families web site at <http://apps.kew.org/wcsp>.

A revision of the spiny solanums, *Solanum* subgenus *Leptostemonum* (Solanaceae) in Africa and Madagascar.

Vorontsova*, M. S. & Knapp, S. (2016). In: *Systematic Botany Monographs*. Vol. 99, pp.432.

Solanum subgenus *Leptostemonum* (Solanaceae) in continental Africa and Madagascar contains 76 native and 10 introduced species; the native species form part of a monophyletic clade of Old World spiny solanums, while the introduced taxa are from the New World and are members of other spiny *Solanum* clades. Subgenus *Leptostemonum* (the spiny solanums) is characterized by the possession of stellate trichomes, long tapering anthers with distally directed pores, and the usual presence of epidermal prickles. African members of subgenus *Leptostemonum* have long been perceived as difficult due to great morphological variability and lack of

modern collections. The treatment is based on the examination of over 10,000 herbarium specimens and on field work in the center of species diversity in the group. All species from the region are included in this treatment to assist with identification. The center of both richness and endemism of native species is in East Africa (with 33 endemic species, focused on Kenya and Tanzania); secondary centers of diversity occur in South Africa (12 endemic species) and Madagascar (10 endemic species). The introduced species are generally widespread and are often invasive weeds, but some are cultivated for ornament. Both a dichotomous key and a synoptic character list are presented to aid with identification of these highly variable species. Full descriptions and synonymies (including designation of lecto- and neotypes), illustrations, distribution maps, and discussion concerning similar and potentially related taxa are provided for all accepted species.

Taxonomy and phylogenetic position of *Fimbristylis fusiformis*, a new species of Cyperaceae from Thailand.

Wangwasit, K., Muasya*, A. M., Chantaranonthai*, P. & Simpson*, D. A. (2017). *Blumea* 62: 47–52. DOI: 10.3767/000651917X695209.

Fimbristylis fusiformis, an unusual new species of Cyperaceae from Thailand, is described and illustrated. This taxon has a single terminal spikelet per culm with a semi-distichous glume arrangement, bisexual flowers that lack perianth parts, and pistil with persistent style whose base is slightly

swollen and trigonous nutlets with pubescent ribs. Phylogenetic reconstruction using ITS sequence data places this taxon in Abildgaardieae and sister to the rest of *Fimbristylis*. The species has a conservation status of Least Concern (LC).

Nomenclatural novelties. *Cuphophyllus lepidopus* (Rea) A.M. Ainsw., comb.nov.

Ainsworth*, A. M. (2017). *Index Fungorum* 332.

No abstract available.

Orchid hunters and orchid cake eaters.

Bone*, R. E. (2016). *The Orchid Review* 124: 160–167.

No abstract available.

The deepening of Darwin's abominable mystery.

Buggs*, R. J. A. (2017). *Nature Ecology & Evolution* 1: 0169. DOI 10.1038/s41559-017-0169.

No abstract available.

Classifying wild and naturalised tulips.

Christenhusz*, M. J. M. & Fay*, M. F. (2016). In: *Daffodil, Snowdrop and Tulip Yearbook 2016*, pp.56–63.

No abstract available.





Common mistakes when using plant names and how to avoid them.

Dauncey*, E. A., Irving*, J., Allkin*, R. & Robinson, N. (2016). *European Journal of Integrative Medicine* 8 (5): 597–601. DOI: 10.1016/j.eujim.2016.09.005.

No abstract available.

Towards stable classifications.

Fay*, M. F. (2016). *Botanical Journal of the Linnean Society* 182: 719–722. DOI: 10.1111/boj.12488.

Editorial. No abstract available.

The mosses and liverworts of Kew Gardens.

Harrington, A. J. & Sheahan*, M. C. (2017). *London Naturalist* 95: 168–176.

No abstract available.

Nomenclatural novelties. 13 new species of *Cortinarius*.

Liimatainen*, K., Niskanen*, T. & Kytovuori, I. (2017). *Index Fungorum* 339.

No abstract available.

A guide to the exotic palms of Singapore.

Merklinger, F. F., Loo, A. H. B., Ang, W. F., Tan, H. T. W., Wong, K. M. & Baker*, W. J. (2017). Singapore: Science Centre.

No abstract available.

La Evolución y trascendencia de los herbarios en la época de la información tecnológica.

Rico*, M. (2016). *Boletín del Departamento de Matemáticas*, Facultad de Ciencias, UNAM 533: 2-4.

No abstract available.

Lady Tankervilles's Legacy. A Historical and Monographic Review of *Phaius* and *Gastrochis*.

Stone, J. & Cribb*, P. J. (2017). Kota Kinabalu & Royal Botanic Gardens, Kew: Natural History Publications.

No abstract available.

Phyllanthopsis (Phyllanthaceae).

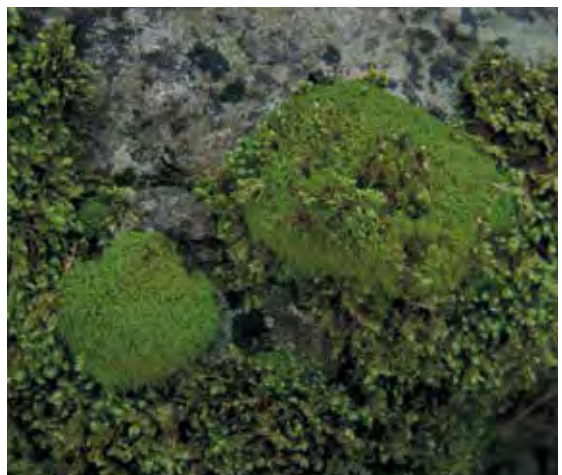
Vorontsova*, M. S. (2016). In: Committee, F. o. N. A. E. (ed.) *Flora of North America North of Mexico: Vitaceae to Garryaceae*. New York/Oxford: Oxford University Press. Vol. 12, pp.331–333.

No abstract available.

The Chimanimani Mountains: an updated checklist.

Wursten, B., Timberlake*, J. & Darbyshire*, I. (2017). *Kirkia* 19: 70–100.

No abstract available.



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



Distasteful nectar deters floral robbery.

Barlow*, S., Wright, G. A., Ma, C., Barberis, M., Farrell*, I. W., Marr, E. C., Brankin, A., Pavlik, B. M. & Stevenson*, P. C. (2017). *Current Biology* 27: 2552–2558. DOI: 10.1016/j.cub.2017.07.012.

Toxic nectar is an ecological paradox. Plants divert substantial resources to produce nectar that attracts pollinators, but toxins in this reward could disrupt the mutualism and reduce plant fitness. Alternatively, such compounds could protect nectar from robbers, provided that they do not significantly alter pollinator visitation to the detriment of plant fitness. Indeed, very few studies have investigated the role of plant toxins in nectar for defense against nectar robbers. Here, we compared two *Aconitum* species (*A. napellus* and *A. lycoctonum*) that have flowers specialized for long-tongued bumblebee pollinators (*Bombus hortorum*) but are occasionally robbed by short-tongued bumblebees (*B. terrestris*). Pollinator visits to flowers were much more frequent than by robbers, but visits correlated negatively with nectar alkaloid concentration and declined sharply between 200 and 380 ppm. However, alkaloid concentrations of >20 ppm were deterrent to *B. terrestris*, suggesting that robbers were less tolerant of nectar alkaloids. Nectar of both plant species contained similar concentrations of carbohydrates and toxic alkaloids, but *A. lycoctonum* was more likely to secrete nectar in each flower and was also visited more frequently by pollinators and robbers. We conclude that alkaloids in *Aconitum* spp. nectar affect rates of both pollinator visitation and robbery but may have co-evolved with nectar availability to maintain the fitness benefits of specialized plant-pollinator relationships. Chemical defense of nectar is, however, ultimately constrained by pollinator gustatory sensitivity.

Variation in limits to germination temperature and rates across the seed-seedling transition in the palm *Oenocarpus bataua* from the Brazilian Amazon.

Bastos, L. L. S., Ferraz, I. D. K., Junior, M. J. V. L. & Pritchard*, H. W. (2017). *Seed Science and Technology* 45 (1): 1–13. DOI: 10.15258/sst.2017.45.1.05.

Germination efficiency can be quantified using the optimal temperature and the temperature limits for germinating seeds. Such estimates generally pertain to the earliest phase of germination, that of radicle emergence. Few comparisons have been made on the subsequent stages of growth, even though the seed-seedling transition is critical for establishment. We assessed the thermal parameters for development of four developmental stages over the seed-seedling transition (germination button, primary root, 1st

cataphyll and 2nd cataphyll) in the Amazonian palm tree *Oenocarpus bataua*. Germination was observed under eight constant and two alternating temperatures with four replicates of 25 seeds for each condition. Constant temperatures of 25 and 30°C resulted in the highest final germination in the shortest time period for all four germination criteria. Alternating temperatures did not enhance germination and seedling development. The four germination stages differed in temperature tolerances. While the germination button formed over a large range of constant temperatures (10 to 40°C), development of the 2nd cataphyll (i.e., seedling development) over 60 days was limited to 25 to 30°C. These results indicate that the thermal responses for growth in this species vary with developmental stage and that early seedling growth, when seed reserves are being mobilised, occurs over the most restricted range of temperature across the four stages of development.

In situ morphometric survey elucidates the evolutionary systematics of the Eurasian *Himantoglossum* clade (Orchidaceae: Orchidinae).

Bateman*, R. M., Molnár, A. V. & Sramkó, G. (2017). *PeerJ* 5: e2893. DOI: 10.7717/peerj.2893.

Background and Aims

The charismatic *Himantoglossum s.l.* clade of Eurasian orchids contains an unusually large proportion of taxa that are of controversial circumscriptions and considerable conservation concern. Whereas our previously published study addressed the molecular phylogenetics and phylogeography of every named taxon within the clade, here we use detailed morphometric data obtained from the same populations to compare genotypes with associated phenotypes, in order to better explore taxonomic circumscription and character evolution within the clade.

Methods

Between one and 12 plants found in 25 populations that encompassed the entire distribution of the *Himantoglossum s.l.* clade were measured in situ for 51 morphological characters. Results for 45 of those characters were subjected to detailed multivariate and univariate analyses.

Key Results

Multivariate analyses readily separate subgenus *Barlia* and subgenus *Comperia* from subgenus *Himantoglossum*, and also the early-divergent *H. formosum* from the less divergent remainder of subgenus *Himantoglossum*. The sequence of divergence of these four lineages is confidently resolved. Our experimental approach to morphometric character analysis demonstrates clearly that

phenotypic evolution within *Himantoglossum* is unusually multi-dimensional.

Conclusions

Degrees of divergence between taxa shown by morphological analyses approximate those previously shown using molecular analyses. *Himantoglossum* s.l. is readily divisible into three subgenera. The three sections of subgenus *Himantoglossum*—*hircinum*, *caprinum* and *formosum*—are arrayed from west to east with only limited geographical overlap. At this taxonomic level, their juxtaposition combines with conflict between contrasting datasets to complicate attempts to distinguish between clinal variation and the discontinuities that by definition separate bona fide species. All taxa achieve allogamy via food deceit and have only weak pollinator specificity. Artificial crossing demonstrates that intrinsic sterility barriers are weak. Although we have found evidence of gene flow among and within the three sections of subgenus *Himantoglossum*, reports of natural hybrids are surprisingly rare, probably because putative parents are sufficiently similar to questionably warrant the status of species. Phenological separation and increased xeromorphy characterise the origin of subgenus *Barlia*. Several individual morphological characters show evidence of parallel acquisition, and loss of features is especially frequent in floral markings among members of section *caprinum*. Detailed patterns of gain and loss demonstrate that several different categories of flower markings are inherited independently. Along with the dimensions of labellar lobes, these pigmentation characters have been over-emphasised in previous taxonomic treatments. Increased plant vigour was a crucial element of the origin of the genus, but vegetative characters underwent remarkably little subsequent evolution. Attempts to reconstruct hypothetical ancestors at internal nodes of the phylogeny are weakened by (a) uncertain placement of *Steveniella*

as sister to *Himantoglossum* s.l. and (b) uncertain relationships among subtly different putative species within section *caprinum*. Nonetheless, heterochronic/allometric trends, ultimately limited by functional constraints, clearly dictate transitions between contrasting flower sizes and complex labellum shapes.

Modelling responses of western Amazonian palms to soil nutrients.

Cámara-Leret*, R., Tuomisto, H., Ruokolainen, K., Balslev, H. & Munch Kristiansen, S. (2017). *Journal of Ecology* 105: 367–381. DOI: 10.1111/1365-2745.12708.

Understanding the responses of individual plant species along different edaphic gradients is a key question in ecology, with implications to community assembly, functioning of forest ecosystems, niche theory and conservation planning. In tropical rain forests, responses to soil nutrients have been described only for a handful of species. Even abundant and conspicuous components of the forest, such as the palms (Arecaceae), remain largely unknown in this respect.

We inventoried all palm species and analysed soil chemistry in 96 sites across western Amazonia to (i) assess the relative importance of some micronutrients vs. macronutrients as drivers of patterns in palm species composition, (ii) model the response shapes of 61 palm taxa and of canopy vs. understorey palms along gradients of selected soil nutrients, (iii) determine if the response shapes of conspecific palm varieties differ in relation to the most important observed soil nutrient and (iv) assess if the rank order of the most abundant canopy species changes along edaphic gradients.

Patterns in palm species composition were best explained by Mehlich-III extractable exchangeable bases (Ca, K, Mg) and phosphorus (P), with the different palm species clearly separating along the soil cation concentration gradient. All 61 palm taxa exhibited statistical responses along soil nutrient gradients. Response shapes in relation to exchangeable bases varied among bimodal skewed (51% of species), unimodal skewed (47%) and monotonic (2%).

There were no significant differences between canopy vs. understorey species in their mean response shapes to the exchangeable bases, but canopy species had significantly higher mean optimum value for soil P and greater mean niche width along the Ca, K, Mg, P and boron (B) gradients. Varieties of the same species of *Bactris*, *Desmoncus* and *Geonoma* generally had different response shapes and different optima for the exchangeable bases.





Synthesis. Among the soil variables we studied, macronutrients (especially exchangeable bases and P) emerged as more important than micronutrients in predicting species abundances in palm communities of western Amazonian non-inundated forests. Non-Gaussian responses were predominant, conspecific palm varieties exhibited different response types, and the rank order of dominance of canopy palms varied along the gradients of exchangeable bases and P. Together, these findings advance niche theory about palms and may be used for generating better predictive models of palm species distributions and for experimental studies that search for the physiological mechanisms underlying inter- and infra-specific trade-offs along edaphic gradients.

Time-calibrated phylogenetic trees establish a lag between polyploidisation and diversification in *Nicotiana* (Solanaceae).

Clarkson*, J. J., Dodsworth*, S. & Chase*, M. W. (2017). *Plant Systematics and Evolution* 303: 1001–1012. DOI: 10.1007/s00606-017-1416-9.

We investigate the timing of diversification in allopolyploids of *Nicotiana* (Solanaceae) utilising sequence data of maternal and paternal origin to look for evidence of a lag phase during which diploidisation took place. Bayesian relaxed clock phylogenetic

methods show recent allopolyploids are a result of several unique polyploidisation events, and older allopolyploid sections have undergone subsequent speciation at the polyploid level (i.e. a number of these polyploid species share a singular origin). The independently formed recent polyploid species in the genus all have mean age estimates below 1 million years ago (Ma). *Nicotiana* section *Polydicliae* (two species) evolved 1.5 Ma, *N.* section *Repandae* (four species) formed 4 Ma, and *N.* section *Suaveolentes* (~35 species) is about 6 million years old. A general trend of higher speciation rates in older polyploids is evident, but diversification dramatically increases at approximately 6 Ma (in section *Suaveolentes*). *Nicotiana* sect. *Suaveolentes* has spectacularly radiated to form 35 species in Australia and some Pacific islands following a lag phase of almost 6 million years. Species have filled new ecological niches and undergone extensive diploidisation (e.g. chromosome fusions bringing the ancestral allotetraploid number, $n = 24$, down to $n = 15$ and ribosomal loci numbers back to diploid condition). Considering the progenitors of *Suaveolentes* inhabit South America, this represents the colonisation of Australia by polyploids that have subsequently undergone a recent radiation into new environments. To our knowledge, this study is the first report of a substantial lag phase being investigated below the family level.

Levyns' Law: explaining the evolution of a remarkable longitudinal gradient in Cape plant diversity.

Cowling, R. M., Bradshaw, P. L., Colville, J. F. & Forest*, F. (2017). *Transactions of the Royal Society of South Africa* 72: 184–201. DOI: 10.1080/0035919X.2016.1274277.

It has been known for many decades that the diversity of clades endemic to the Greater Cape Floristic Region (GCFR) declines along a longitudinal (west-east) gradient, in concert with a reduction in the proportion of winter rainfall. In honour of the pioneering work by Margaret Levyns, we recognise this pattern as Levyns' Law, and illustrate it with distribution data for 23 speciose endemic clades. All patterns were consistent with Levyns' Law. Here we assess explanations for Levyns' Law in terms of theories invoked to explain the evolution of diversity patterns along other diversity macro-gradients. Neither the metabolic nor the ecological opportunity hypotheses convincingly explain Levyns' Law. Surprisingly, almost no research has been done on the evolutionary opportunities associated with the Mid Miocene onset of a winter-rainfall regime in the western GCFR, despite this phenomenon being frequently invoked to explain the diversification of many GCFR clades. In all other respects, niche space both now and historically shows no major differences between the western, winter rainfall, and the eastern, year-round rainfall regions of the GCFR. We suggest that higher Pleistocene climatic and biome stability in the western GCFR – the age and area hypothesis – best explains Levyns' Law. Pronounced instability in the east reduced diversification rates via increased rates of extinction of lineages. Testing the age and area hypotheses will require, inter alia, proxy data for Pleistocene environmental and biotic dynamics, an analysis of diversification rates in relation to rainfall seasonality, and an assessment of the patterns of phylogenetic diversity in the GCFR.

The evolution of angiosperm trees: from palaeobotany to genomics.

Cronk*, Q. C. B. & Forest*, F. (2017). In: Groover, A. T. & Cronk*, Q. C. B. (eds). *Comparative and evolutionary genomics of angiosperm trees*. Switzerland: Springer International Publishing. pp.1–17.

Angiosperm trees now rival the largest conifers in height and many species reach over 80 m high. The large tree life form, with extensive secondary xylem, originated with the progymnosperms and gymnosperms in the Devonian and Carboniferous. However evidence suggests that the ancestor of extant angiosperms was not a tree but either a herb or understory shrub. Angiosperm fossil woods are rare in the early



Cretaceous but become common in the mid-Cretaceous. The “reinvention” of wood in the Cretaceous produced a novel xylary morphospace that has since been extensively explored by subsequent evolution. Today, large timber trees are absent in the early diverging lineages of the angiosperms, and conventional wood has been lost in the monocots. There are a few timber trees in the magnoliid clade. Most timber trees are in the rosid clade, particularly the fabids (e.g. Fabaceae) but also in the Malvids (e.g. Meliaceae). Timber trees are less common in the strongly herbaceous asterid clade but some important timbers are also found in this lineage such as teak, *Tectona grandis* (Lamiaceae). Genomic resources for angiosperm trees are developing rapidly and this, coupled with the huge variation in woody habit, make angiosperm trees a highly promising comparative system for understanding wood evolution at the molecular level.

The evolutionary history of *Eugenia* sect. *Phyllocalyx* (Myrtaceae) corroborates historically stable areas in the southern Atlantic forests.

de Oliveira Bünger, M., Mazine, F. F., Forest*, F., Bueno, M. L., Stehmann, J. R. & Lucas*, E. J. (2016). *Annals of Botany* 118: 1209–1223. DOI: 10.1093/aob/mcw209.

Background and Aims

Eugenia sect. *Phyllocalyx* Nied. includes 14 species endemic to the Neotropics, mostly distributed in the Atlantic coastal forests of Brazil. Here the first comprehensive phylogenetic study of this group is presented, and this phylogeny is used as the basis to evaluate the recent infrageneric classification in *Eugenia sensu lato* (s.l.) to test the history of the evolution of traits in the group and test hypotheses associated with the history of this clade.

Methods

A total of 42 taxa were sampled, of which 14 were *Eugenia* sect. *Phyllocalyx* for one nuclear (ribosomal

internal transcribed spacer) and four plastid markers (psbA-trnH, rpl16, trnL-rpl32 and trnQ-rps16). The relationships were reconstructed based on Bayesian analysis and maximum likelihood. Additionally, ancestral area analysis and modelling methods were used to estimate species dispersal, comparing historically climatic stable (refuges) and unstable areas.

Key Results

Maximum likelihood and Bayesian inferences indicate that *Eugenia* sect. *Phyllocalyx* is paraphyletic and the two clades recovered are characterized by combinations of morphological characters. Phylogenetic relationships support a link between Cerrado and south-eastern species and a difference in the composition of species from north-eastern and south-eastern Atlantic forest. Refugia and stable areas identified within unstable areas suggest that these areas were important to maintain diversity in the Atlantic forest biodiversity hotspot.

Conclusion

This study provides a robust phylogenetic framework to address important historical questions for *Eugenia* s.l. within an evolutionary context, supporting the need for better taxonomic study of one of the largest genera in the Neotropics. Furthermore, valuable insight is offered into diversification and biome shifts of plant species in the highly environmentally impacted Atlantic forest of South America. Evidence is presented that climate stability in the south-eastern Atlantic forest during the Quaternary contributed to the highest levels of plant diversity in this region that acted as a refugium.



Geography shapes the phylogeny of frailejones (Espeletiinae Cuatrec., Asteraceae): a remarkable example of recent rapid radiation in sky islands.

Diazgranados*, M. & Barber, J. C. (2017). *PeerJ* 5: e2968. DOI: 10.7717/peerj.2968

Background

The páramo ecosystem, located above the timberline in the tropical Andes, has been the setting for some of the most dramatic plant radiations, and it is one of the world's fastest evolving and most diverse high-altitude ecosystems. Today 144+ species of frailejones (subtribe Espeletiinae Cuatrec., Asteraceae) dominate the páramo. Frailejones have intrigued naturalists and botanists, not just for their appealing beauty and impressive morphological diversity, but also for their remarkable adaptations to the extremely harsh environmental conditions of the páramo. Previous attempts to reconstruct the evolutionary history of this group failed to resolve relationships among genera and species, and there is no agreement regarding the classification of the group. Thus, our goal was to reconstruct the phylogeny of the frailejones and to test the influence of the geography on it as a first step to understanding the patterns of radiation of these plants.

Methods

Field expeditions in 70 páramos of Colombia and Venezuela resulted in 555 collected samples from 110 species. Additional material was obtained from herbarium specimens. Sequence data included nrDNA (ITS and ETS) and cpDNA (rpl16), for an aligned total of 2,954 bp. Fragment analysis was performed with AFLP data using 28 primer combinations and yielding 1,665 fragments. Phylogenies based on sequence data were reconstructed under maximum parsimony, maximum likelihood and Bayesian inference. The AFLP dataset employed minimum evolution analyses. A Monte Carlo permutation test was used to infer the influence of the geography on the phylogeny.

Results

Phylogenies reconstructed suggest that most genera are paraphyletic, but the phylogenetic signal may be misled by hybridization and incomplete lineage sorting. A tree with all the available molecular data shows two large clades: one of primarily Venezuelan species that includes a few neighboring Colombian species; and a second clade of only Colombian species. Results from the Monte Carlo permutation test suggests a very strong influence of the geography on the phylogenetic relationships. Venezuelan páramos tend to hold taxa that are more distantly-related to each other than Colombian páramos, where taxa are more closely-related to each other.

Conclusions

Our data suggest the presence of two independent radiations: one in Venezuela and the other in Colombia. In addition, the current generic classification will need to be deeply revised. Analyses show a strong geographic structure in the phylogeny, with large clades grouped in hotspots of diversity at a regional scale, and in páramo localities at a local scale. Differences in the degrees of relatedness between sympatric species of Venezuelan and Colombian páramos may be explained because of the younger age of the latter páramos, and the lesser time for speciation of Espeletiinae in them.

Petal, Sepal, or Tepal? B-Genes and Monocot Flowers.

Dodsworth*, S. (2017). *Trends in Plant Science* 22: 8–10. DOI: 10.1016/j.tplants.2016.11.006.

In petaloid monocots expansion of B-gene expression into whorl 1 of the flower results in two whorls of petaloid organs (tepals), as opposed to sepals in whorl 1 of typical eudicot flowers. Recently, new gene-silencing technologies have provided the first functional data to support this, in the genus *Tricyrtis* (Liliaceae).

Digest: Salamanders' slow slither into genomic gigantism.

Dodsworth*, S., Guignard*, M. S., Hidalgo*, O., Leitch*, I. J. & Pellicer*, J. (2016). *Evolution* 70: 2915–2916. DOI: 10.1111/evo.13112.

Genome size varies enormously across the eukaryotic tree of life (c. 64,000-fold in animals alone), with the largest reported nuclear genomes found in vertebrates (e.g., salamanders, lungfish) and angiosperms (e.g., mistletoe, fritillaries). Yet despite this huge diversity, most genomes are considerably smaller than the largest reported (c. 150 Gb), with the mean size of both vertebrate and plant genomes being similar, c. 5 Gb.



Although clearly outliers, the existence of giant genomes in this subset of animals and plants provides excellent study systems to unpick those processes likely involved in genomic obesity and that may constrain genome size in most species over evolutionary timescales. Such genome expansion is governed predominantly by amplification of highly repetitive DNA, that is, transposable elements (TEs).

Among tetrapods, salamanders have the largest genomes found, including an average size much larger than related amphibians (Fig. 1). Phylogenetic reconstructions suggest that they have evolved large genome sizes since early in their evolutionary history, over a timescale of approximately 150–200 million years (Organ et al. 2011).

Genome-wide repeat dynamics reflect phylogenetic distance in closely related allotetraploid *Nicotiana* (Solanaceae).

Dodsworth*, S., Jang, T.-S., Struebig, M., Chase*, M. W., Weiss-Schneeweiss, H. & Leitch*, A. R. (2017). *Plant Systematics and Evolution* 303: 1013–1020. DOI: 10.1007/s00606-016-1356-9.

Nicotiana sect. *Repandae* is a group of four allotetraploid species originating from a single allopolyploidisation event approximately 5 million years ago. Previous phylogenetic analyses support the hypothesis of *N. nudicaulis* as sister to the other three species. This is concordant with changes in genome size, separating those with genome downsizing (*N. nudicaulis*) from those with genome upsizing (*N. repanda*, *N. nesophila*, *N. stocktonii*). However, a recent analysis reflecting genome dynamics of different transposable element families reconstructed greater similarity between *N. nudicaulis* and the Revillagigedo Island taxa (*N. nesophila* and *N. stocktonii*), thereby placing *N. repanda* as sister to the rest of the group. This could reflect a different phylogenetic hypothesis or the unique evolutionary history of these particular elements. Here we re-examine relationships in this group and investigate genome-wide patterns in

repetitive DNA, utilising high-throughput sequencing and a genome skimming approach. Repetitive DNA clusters provide support for *N. nudicaulis* as sister to the rest of the section, with *N. repanda* sister to the two Revillagigedo Island species. Clade-specific patterns in the occurrence and abundance of particular repeats confirm the original (*N. nudicaulis* (*N. repanda* (*N. nesophila* + *N. stocktonii*))) hypothesis. Furthermore, overall repeat dynamics in the island species *N. nesophila* and *N. stocktonii* confirm their similarity to *N. repanda* and the distinctive patterns between these three species and *N. nudicaulis*. Together these results suggest that broad-scale repeat dynamics do in fact reflect evolutionary history and could be predicted based on phylogenetic distance.

Plant phylogeny as a window on the evolution of hyperdiversity in the tropical rainforest biome.

Eiserhardt*, W. L., Couvreur, T. L. P. & Baker*, W. J. (2017). *New Phytologist* 214: 1408–1422. DOI: 10.1111/nph.14516.

Tropical rainforest (TRF) is the most species-rich terrestrial biome on Earth, harbouring just under half of the world's plant species in c. 7% of the land surface. Phylogenetic trees provide important insights into mechanisms underpinning TRF hyperdiversity that are complementary to those obtained from the fossil record. Phylogenetic studies of TRF plant diversity have mainly focused on whether this biome is an evolutionary 'cradle' or 'museum', emphasizing speciation and extinction rates. However, other explanations, such as biome age, immigration and ecological limits, must also be considered. We present a conceptual framework for addressing the drivers of TRF diversity, and review plant studies that have tested them with phylogenetic data. Although surprisingly few in number, these studies point to old age of TRF, low extinction and high speciation rates as credible drivers of TRF hyperdiversity. There is less evidence for immigration and ecological limits, but these cannot be dismissed owing to the limited



number of studies. Rapid methodological developments in DNA sequencing, macroevolutionary analysis and the integration of phylogenetics with other disciplines may improve our grasp of TRF hyperdiversity in the future. However, such advances are critically dependent on fundamental systematic research, yielding numerous, additional, well-sampled phylogenies of TRF lineages.

Insights on the evolutionary origin of Detarioideae, a clade of ecologically dominant tropical African trees.

Estrella*, M., Forest*, F., Wieringa, J. J., Fougère-Danezan, M. & Bruneau, A. (2017). *New Phytologist* 214: 1722–1735. DOI: 10.1111/nph.14523.

African tropical forests are generally considered less diverse than their Neotropical and Asian counterparts. By contrast, the Detarioideae is much more diverse in Africa than in South America and Asia. To better understand the evolution of this contrasting diversity pattern, we investigated the biogeographical and ecological origin of this subfamily, testing whether they originated in dry biomes surrounding the Tethys Seaway as currently hypothesized for many groups of Leguminosae.

We constructed the largest time-calibrated phylogeny for the subfamily to date, reconstructed ancestral states for geography and biome/habitat, estimated diversification and extinction rates, and evaluated biome/habitat and geographic shifts in Detarioideae.

The ancestral habitat of Detarioideae is postulated to be a primary forest (terra firme) originated in Africa–South America, in the early Palaeocene, after which several biome/habitat and geographic shifts occurred.

The origin of Detarioideae is older than previous estimates, which postulated a dry (succulent) biome origin according to the Tethys Seaway hypothesis, and instead we reveal a post Gondwana and terra firme origin for this early branching clade of legumes. Detarioideae include some of the most dominant trees in evergreen forests and have likely played a pivotal role in shaping continental African forest diversity.

Global land-cover change – wildfires.

Etherington*, T. R., Curran, T., Long, P. & Wyse*, S. V. (2017). In: Willis*, K. J. (ed.) *State of the World's Plants 2017*. Richmond: Royal Botanic Gardens, Kew, pp.50–57.

Each year around 340 million hectares of the Earth's vegetated surface burns. Fire is an emotive topic. Extreme wildfires can have massive economic, social and environmental impacts, and recent catastrophic fires, such as in Canada and Chile, demonstrate to

the public at large the rapid, dramatic and negative impacts of fires. But fire is also a naturally occurring global phenomenon that fundamentally affects many ecosystem patterns and processes, including the distribution and structure of vegetation.

Spatially adaptive probabilistic computation of a sub-kilometre resolution lightning climatology for New Zealand.

Etherington*, T. R. & Perry, G. L. W. (2016). *Computers & Geosciences* 98: 38-45. DOI: 10.1016/j.cageo.2016.09.010.

Lightning is a key component of the Earth's atmosphere and climate systems, and there is a potential positive feedback between a warming climate and increased lightning activity. In the biosphere, lightning is important as the main natural ignition source for wildfires and because of its contribution to the nitrogen cycle. Therefore, it is important to develop lightning climatologies to characterise and monitor lightning activity. While traditional methods for constructing lightning climatologies are suitable for examining lightning's influence on atmospheric processes, they are less well suited for examining questions about biosphere-lightning interactions. For example, examining the interaction between lightning and wildfires requires linking atmospheric processes to finer scale terrestrial processes and patterns. Most wildfires ignited by lightning are less than one hectare in size, and so require lightning climatologies at a comparable spatial resolution. However, such high resolution lightning climatologies cannot be derived using the traditional cell-count methodology. Here we present a novel geocomputational approach for analysing lightning data at high spatial resolutions. Our approach is based on

probabilistic computational methods and is capable of producing a sub-kilometre lightning climatology that honours the spatial accuracy of the strike locations and is adaptive to underlying spatial patterns. We demonstrate our methods by applying them to the mid-latitude oceanic landmass of New Zealand, an area with geographic conditions that are under-represented in existing lightning climatologies. Our resulting lightning climatology has unparalleled spatial resolution, and the spatial and temporal patterns we observe in it are consistent with other continental and tropical lightning climatologies. To encourage further use and development of our probabilistic approach, we provide Python scripts that demonstrate the method alongside our resulting New Zealand lightning climatology.

Seed carotenoid and tocochromanol composition of wild Fabaceae species is shaped by phylogeny and ecological factors.

Fernández-Marín, B., Míguez, F., Méndez-Fernández, L., Agut, A., Becerril, J. M., García-Plazaola, J. I., Kranner, I. & Colville*, L. (2017). *Frontiers in Plant Science* 8: 1428. DOI: 10.3389/fpls.2017.01428.

Carotenoids distribution and function in seeds have been very scarcely studied, notwithstanding their pivotal roles in plants that include photosynthesis and phytohormone synthesis, pigmentation, membrane stabilization and antioxidant activity. Their relationship with tocochromanols, whose critical role in maintaining seed viability has already been evidenced, and with chlorophylls, whose retention in mature seed is thought to have negative effects on storability, remain also unexplored. Here, we aimed at elucidating seed carotenoids relationship with tocochromanols and chlorophylls with regard to



phylogenetic and ecological traits and at understanding their changes during germination. The composition and distribution of carotenoids were investigated in seeds of a wide range of wild species across the Fabaceae (the second-most economically important family after the Poaceae). Photosynthetic pigments and tocopherols were analyzed by HPLC in mature dry seeds of 50 species representative of 5 subfamilies within the Fabaceae (including taxa that represent all continents, biomes and life forms within the family) and at key timepoints during seedling establishment in three species representative of distinct clades. Total-carotenoids content positively correlated with tocopherols in the basal subfamilies Detarioideae, Cercidoideae, and Dialioideae, and with chlorophylls in the Papilionoideae. Papilionoideae lacked tocotrienols and had the highest total-carotenoids, chlorophyll and γ -tocopherol contents. Interestingly, lutein epoxide was present in 72% of the species including several herbs from different subfamilies. Overall, species original from temperate biomes presented higher carotenoids and lower tocopherols levels than those from tropical biomes. Also shrub species showed higher carotenoids content than herbs and trees. During germination, total content of photosynthetic pigments increased in parallel to changes in relative abundance of carotenoids: zeaxanthin and antheraxanthin decreased and β -carotene augmented. Notably, the highest contents of nutritionally valuable carotenoids were found in Papilionoideae subfamily to which all pulses of socio-economic importance belong. The major differences in carotenoids and tocopherols composition across the Fabaceae are apparently related to phylogeny in conjunction with ecological traits such as biome and growth form.

Comparative biology of aloes and related genera in the context of recent phylogenetic evidence.

Grace*, O. M. & Rønsted, N. (2017). In: Campbell, L. M., Davis, J. I., Meerow, A. W., Naczi, R. F. C., Stevenson, D. W. & Thomas, W. W. (eds). *Diversity and Phylogeny of the Monocotyledons. Contributions from Monocots V*. Memoirs of the New York Botanic Garden Vol. 118.

The aloes are a major group of Old World succulents, comprising over 600 taxa in the genera *Aloe*, *Aloiampelos*, *Aloidendron*, *Aristaloe*, *Gonialoe*, and *Kumara*. Together with *Astroloba*, *Gasteria*, *Haworthia*, *Haworthiopsis*, and *Tulista*, they comprise a group known collectively as the alooids, after a Dahlgrenian concept, within Xanthorrhoeaceae subfam. Asphodeloideae. All alooids are, to varying extents leaf succulents and many exhibit other features typical of plants adapted to drought-prone environments, such as



a waxy cuticle and sunken stomata. The alooids share a southern African center of diversity, and *Aloe* is the most widespread of the representatives, as it is found throughout the Arabian Peninsula, Africa, Madagascar, and on islands in the western Indian Ocean. Members of the related genera of Xanthorrhoeaceae subfam. Asphodeloideae occur more widely in Africa, Asia, Australia, and New Zealand. Significant progress has recently been made toward a well-resolved phylogeny of the alooids, resulting in changes to the circumscription of the two most speciose genera, *Aloe* and *Haworthia*. The extensive literature on aloes and related genera is reviewed here in the context of recently defined generic concepts, in order to highlight current understanding of the biology, conservation concerns, and research questions, for this charismatic group.

Phylogenetic analyses of plastid DNA suggest a different interpretation of morphological evolution than those used as the basis for previous classifications of Dipterocarpaceae (Malvales).

Heckenhauer, J., Samuels R., Ashton*, P. S., Turner B., Barfuss, M. H. J., Jang T.S., Temsch, E. M., Salim, K. A., Attanayake, A. S. & Chase*, M. W. (2017). *Botanical Journal of the Linnean Society* 185 (1): 1–26. DOI: 10.1093/botlinnean/box044.

Phylogenetic and molecular clock analyses were performed including all genera except one (*Pseudomonotes*) for the three subfamilies of Dipterocarpaceae. We also included representatives of Sarcocaulaceae and Cistaceae with Bixaceae as the ultimate outgroup. Three plastid regions (six markers), partial *rbcl*, *trnK-matK-trnK* (partial *trnK* intron including complete *matK*) and *trnT-trnL-trnF* (partial *trnT*, complete *trnT-trnL* intergenic spacer, complete *trnL*, complete *trnL-trnF* intergenic spacer and partial



trnF), were analysed. We also investigated additional accessions for genome size and chromosome numbers. Our phylogenetic results differ in three important respects from previous interpretations of morphological characters, as reflected in recent classifications. First, our analyses strongly support assignment of *Pakaraimaea* (subfamily Pakaraimaeoideae) to Cistaceae. Second, the morphological concepts of Dipterocarpeae and Shoreeae in subfamily Dipterocarpoideae are not supported because *Dipterocarpus* is sister to *Dryobalanops* plus tribe Shoreeae. Our analysis revealed four clades: (1) Dipterocarpus; (2) *Dryobalanops*, for which tribal assignment has been contentious; (3) genera of Shoreeae; and (4) the remaining genera of Dipterocarpeae. Third, *Shorea* is not monophyletic. Monotoideae are weakly supported as sister to Dipterocarpoideae; Sarcolaenaceae (endemic to Madagascar) are sister to this pair. Divergence in extant Dipterocarpoideae occurred c. 55 Mya. Genome sizes for all accessions examined are small (0.3264–0.6724 pg), and the additional chromosome numbers we collected fit into the patterns previously observed for Dipterocarpaceae.

Is there an upper limit to genome size?

Hidalgo*, O., Pellicer*, J., Christenhusz, M. C., Schneider, H., Leitch, A. R. & Leitch*, I. J. (2017). *Trends in Plant Science* 22: 567–573. DOI: 10.1016/j.tplants.2017.04.005.

At 50-fold the size of the human genome (3 Gb), the staggeringly huge genome of 147.3 Gb recently discovered in the fern *Tmesipteris obliqua* is comparable in size to those of the other plant and animal record-holders (i.e., *Paris japonica*, a flowering plant with a genome size of 148.8 Gb, and *Protopterus aethiopicus*, a lungfish with a genome of 130 Gb). The synthesis of available information on giant genomes suggests that the biological limit to genome size expansion in eukaryotes may have been reached. We propose several explanations for why the genomes of ferns, flowering plants, and lungfish, all of which have independently undergone dramatic increases in genome size through a variety of mechanisms, do not exceed 150 Gb.

Cytogenetic insights into an oceanic island radiation: the dramatic evolution of pre-existing traits in *Cheirolophus* (Asteraceae, Cardueae-Centaureinae).

Hidalgo*, O., Viales, D., Vallès, J., Garnatje, T., Siljak-Yakovlev, S., Leitch*, I. J. & Pellicer*, J. (2017). *Taxon* 66: 146–157. DOI: 10.12705/661.8.

The genus *Cheirolophus* constitutes one of the most striking cases of species radiation in Macaronesia, where it diversified into a lineage of ca. 20 endemic species at a rate that is amongst the fastest reported for oceanic islands. Whilst the cytogenetic dynamics of many of the Macaronesian *Cheirolophus* species have been comparatively well studied, an overall vision of chromosome and genome evolution has been hampered by the lack of data for the earliest-diverging species, *Ch. crassifolius*. In this study, we have completed the cytogenetic survey of *Cheirolophus* to investigate how different cytogenetic traits may have contributed to the dramatic radiation of the genus in Macaronesia. We provide new cytogenetic data (i.e., chromosome counts, genome size estimates and physical mapping of 35S rDNA loci) for several key species, including *Ch. crassifolius*, and then model trait evolution within a phylogenetic context. Our results reveal a trend of genome downsizing accompanied by a dramatic increase in number of 35S rDNA loci which started early in the evolutionary history of the genus, before its radiation in Macaronesia. It is notable that the increasing number of 35S rDNA loci has not been driven by polyploidisation, in contrast to the more typical trend observed in many angiosperms. In addition, the number of 35S rDNA loci was observed to negatively correlate with genome size, which is also very unusual in angiosperms. It is suggested that non-homologous and unequal homologous recombination are the most likely mechanisms to explain these observations and we discuss whether the unique genomic architectures of *Cheirolophus* could have predisposed the genus to its successful and rapid speciation in Macaronesia.

Phylogenetic trends in the evolution of inflorescence odours in *Amorphophallus*

Kite*, G. C. & Hettterscheid, W. L. A. (2017). *Phytochemistry* 142: 126–142. DOI: 10.1016/j.phytochem.2017.06.006.

The chemical composition of inflorescence odours of 80 species of *Amorphophallus* (Araceae) were determined by headspace-thermal desorption GC-MS. When compared to published molecular phylogenies of the genus, the data reveal evidence both of phylogenetic constraint and plasticity of odours. Dimethyl oligosulphides were found as common constituents of *Amorphophallus* odours and were the most abundant components in

almost half of the species studied. Odours composed mainly of dimethyl oligosulphides, and perceived as being 'gaseous', were only found among Asian species, and some of these species clustered in certain clades in molecular phylogenies; e.g. in two clades in *Amorphophallus* subgenus *Metandrium*. However, some species with gaseous odours were found to be closely related to species producing odours more reminiscent of rotting meat in which various minor components accompany the dominant dimethyl oligosulphides. These two broad types of odours have co-evolved with other inflorescence characteristics such as colour, with species with rotting meat odours having darker inflorescences. Species producing pleasant odours characterised by benzenoid compounds constitute two broad groups that are not related in published phylogenies. Species having fruity odours containing 1-phenylethanol derivatives mainly occur in a clade in subgenus *Metandrium* while those with anise odours composed almost solely of the 2-phenylethanol derivative 4-methoxyphenethyl alcohol are restricted to a clade in subgenus *Scutandrium*. Phylogenetic mapping of odours also indicates that the evolution of some odour types is likely to have been influenced by ecological factors. For example, species producing fishy odours dominated by trimethylamine and occurring in N and NE Borneo are not all closely related. Conversely, two sister species, *A. mossambicensis* and *A. abyssinicus*, which are morphologically very similar and have overlapping geographical distribution, produce odours which are very different chemically. The pressure of pollinator resource has therefore been a factor influencing the evolution of odours in *Amorphophallus*, driving both the divergence of odour types in some taxa and the convergence of odour types in others..

Untangling the reticulate history of species complexes and horticultural breeds in *Abelia* (Caprifoliaceae).

Landrein, S., Buerki, S., Wang, H.-F. & Clarkson*, J. J. (2017). *Annals of Botany* 120: 257–269. DOI: 10.1093/aob/mcw279.

Background and Aims

The genetic and morphological consequences of natural selection and selective breeding are explored in the genus *Abelia*. The genus consists of ornamental shrubs endemic to China, which have been bred to create attractive and diverse cultivars.

Methods

DNA fingerprinting (AFLP) and DNA sequence data are used to investigate the genetic diversity among 46 accessions of *Abelia* (22 natural taxa and 24 horticultural breeds). In the cultivated varieties these data are used to explore taxon boundaries, hybridisation and backcrossing. The genetic analysis dataset is also used to investigate morphological

variation within natural species complexes and subsequently to inform a taxonomic treatment.

Key Results

Abelia comprises five species: *A. forrestii*, *A. schumannii*, *A. macrotera*, *A. uniflora* and *A. chinensis* and has a total of 11 varieties. *Abelia uniflora* and *A. macrotera* do not occur in sympatry and are disjunctly distributed to the east and west of the *A. chinensis* distribution range. *Abelia chinensis* is widespread in eastern China and creates hybrids and introgressive taxa, including *A. uniflora*, along the contact zones with the previous taxa. *Abelia* 'Maurice Foster' is a horticultural variety collected from wild stocks in Sichuan (China). Bayesian clustering methods (inferred in STRUCTURE based on AFLP data) indicate admixture between *A. macrotera* and *A. schumannii* in this variety. Hybridization probably occurred in the wild where these progenitor taxa co-occur and naturally form hybrids. AFLP results also reveal that a few diagnostic morphological characters such as sepal number or inflorescence structure were transferred between natural species and this is mirrored by taxa such as in *Abelia* 'Saxon Gold' and *A. forrestii*.

Conclusions

Studying both natural and cultivated species from the same group has helped understanding both differentiation mechanisms and how to improve cultivated plants in the future by studying which morphological characters are transferred between species and which taxa may already have arisen through hybridisation.

Plant genomes – progress and prospects.

Leitch*, I. J., Coker*, T. & Leitch*, A. R. (2017). In: Willis*, K. J. (ed.) *State of the World's Plants 2017*. Richmond: Royal Botanic Gardens, Kew, pp.16–21.

225 plant species now have whole genome sequences – and rising. The sequence of DNA in plants is a repository of huge amounts of useful information that can be put to a great variety of uses, from elucidating the evolutionary relationships between different plant species to determining the origin of tropical timber.

Endopolyploidy in Plants.

Leitch*, I. J. & Dodsworth*, S. (2017). *eLS*: 1–10. DOI: 10.1002/9780470015902.a0020097.pub2.

Endopolyploidy is a general term describing the multiplication of nuclear DNA within the cell. In plants, this takes place via several mechanisms but mainly through the process of endoreduplication. Endoreduplication involves the replication of chromosomal deoxyribonucleic acid (DNA) without intervening mitoses and no obvious chromatin condensation/decondensation, with chromatids staying united either at the centromere or rarely,

along their entire length. The occurrence of this form of endopolyploidy is uneven across plants; thus far, it has not been detected in some lineages (e.g. liverworts), whereas it is common in angiosperms (flowering plants), where very high levels (up to 24 567C) of endopolyploidy have been reported in some tissues. Internal and external factors contribute to the mechanisms underlying endopolyploidy, which can be seen as a key part of the developmental flexibility of plants. Recent work has shown that endopolyploidy may also play an important role in the response of plants to environmental stress.

Cortinarius section Bicolores and section Saturnini (Basidiomycota, Agaricales), a morphogenetic overview of European and north American species.

Liimatainen*, K., Carteret, X., Dima, B., Kytövuori, I., Bidaud, A., Reumaux, P., Niskanen*, T., Ammirati, J. F. & J-M., B. (2017). *Persoonia* 39: 175–200. 10.3767/persoonia.2017.39.08.

Cortinarius is the largest genus of ectomycorrhizal fungi worldwide. Recent molecular studies have shown high levels of morphological homoplasy within the genus. Importantly, DNA phylogenies can reveal characteristics that have been either over- or underemphasized in taxonomic studies. Here we sequenced and phylogenetically analysed a large set of pan-European and North American collections taxonomically studied and placed in *Cortinarius* sect. *Bicolores* and sect. *Saturnini*, according to traditional morpho-anatomical criteria. Our goal was to circumscribe the evolutionary boundaries of the two sections, to stabilize both the limits and nomenclature of relevant species, and to identify described taxa

which, according to our current understanding, belong to other lineages. Our analysis resolves two clades: */Bicolores*, including 12 species, one of which is new to science, and */Saturnini*, including 6 species. Fifteen binomials, traditionally treated in these two sections based on morphology, do not belong to the above two phylogenetic clades. Instead, six of these latter are clearly placed in other clades that represent sect. *Bovini*, sect. *Sciophylli*, sect. *Duracini* and sect. *Brunneotincti*. The presence or absence of blue pigments and the detection of specific odours emerge as clearly misleading taxonomic features, but more surprisingly, spore size and ecology can be misleading as well. A total of 63 type specimens were sequenced, 4 neotypes and 2 epitypes are proposed here, and 1 new combination is made.

Thermal requirements for seed germination of underutilized *Lippia* species.

Mattana*, E., Sacande*, M., Abdul Sanogo, K., Lira, R., Gomez-Barreiro*, P., Rogledi*, M. & Ulian*, T. (2017). *South African Journal of Botany* 109: 223–230. DOI: 10.1016/j.sajb.2016.12.020.

Seed germination requirements of three underutilized *Lippia* (Verbenaceae) species were investigated. Seeds of *L. graveolens*, *L. javanica* and *L. multiflora* were incubated at a range of constant temperatures (5–35 °C) in the light (12 h light/12 h darkness). The effect of GA3 and KNO3 on seed germination was also tested in the same range of germination temperatures. Germination responses to accumulated temperature were then characterized by a thermal time approach. Two different trends of germination response to temperature were detected among species, regardless of the applied treatment. Seeds of *L. graveolens* and *L. javanica* started to germinate at 15 °C, reached their maximum germination at 25 °C and then decreased at warmer temperatures, while those of *L. multiflora* reached their maximum at the highest tested temperature (35 °C). Base temperature for germination (Tb, °C) and the thermal constant for 50% germination (S, °Cd) of untreated seeds were ca. 2.5 and 7.5 °C and 76.92 and 84.3 °Cd, for *L. graveolens* and *L. javanica*, respectively. A Tb of ca. 20 °C could only be roughly estimated for *L. multiflora*, due to the low germination achieved at temperatures < 35 °C. GA3 and KNO3 had an overall inefficacy on enhancing seed germination of these species. Thermal thresholds of treated seeds could also be estimated for *L. javanica*, with a Tb of ca. 11 °C for both treatments and a S of 70.92 and 69.44 °Cd for GA3 and KNO3, respectively. Practical applications of the findings of this study may support the propagation of these underutilized *Lippia* species.





The biogeographic history of the interaction between mycoheterotrophic *Thismia* (Thismiaceae) plants and mycorrhizal *Rhizophagus* (Glomeraceae) fungi.

Merckx, V. S. F. T., Gomes, S., Wapstra, M., Hunt, C., Steenbeeke, G., Mennes, C. B., Walsh, N., Smissen, R., Hsieh, T.-H., Smets, E. F. & Bidartondo*, M. I. (2017). *Journal of Biogeography* 44. DOI: 10.1111/jbi.12994.

Aim

Achlorophyllous mycoheterotrophic plants and mycorrhizal fungi often have highly specific interactions that potentially limit the plants' distribution and diversification potential. However, specificity in biotic interactions may differ considerably over a species' distribution range and therefore interactions need to be studied over their entire range to assess their evolution in space and time. The present study investigates the biogeographical history of the interaction between five closely related mycoheterotrophic *Thismia* species and arbuscular mycorrhizal fungi over the distribution range of the plant species.

Location

Temperate south-east Australia and New Zealand.

Methods

Phylogenetic relationships of *Thismia* (nrITS and mtcob) and their arbuscular mycorrhizal fungi (partial nrSSU) were reconstructed based on data from 65 plant specimens. The diversification times in *Thismia* were estimated with a Bayesian relaxed clock approach using a Dioscoreales framework (nrSSU, mtatp1, mtmatR, mtnad1 b-c). Ancestral geographical ranges were reconstructed using a maximum likelihood approach. The same approach was used to reconstruct ancestral mycorrhizal associations.

Results

Our analysis shows that *Thismia* plants have highly specific, phylogenetically conserved and evolutionarily persistent interactions with *Rhizophagus* fungi.

Nevertheless, *Thismia* was able to diversify and radiate recently due to the wide geographical distribution of the host fungi. In addition, we find that although the mycorrhizal interactions of this clade of mycoheterotrophs are strictly bound to a fungal lineage, host switches remain possible.

Main conclusions

In this clade of closely related mycoheterotrophs, dependency on highly specific fungal interactions is the result of phylogenetic niche conservatism, acting over at least 12 million years. Nevertheless, plants that are dependent on highly specific fungal interactions have ample opportunities to disperse and radiate over the geographical range of their hosts. Our study highlights the need to link the ecology and evolution of species interactions over broad geographical and evolutionary scales for understanding mycorrhizal interactions.

Are landscape attributes a useful shortcut for classifying vegetation in the tropics? A case study of La Amistad International Park.

Monro*, A. K., Bystriakova, N. & González, F. (2017). *Biotropica* 49: 848–855. DOI: 10.1111/btp.12470.

Effective vegetation classification schemes identify the processes determining species assemblages and support the management of protected areas. They can also provide a framework for ecological research. In the tropics, elevation-based classifications dominate over alternatives such as river catchments. Given the existence of floristic data for many localities, we ask how useful floristic data are for developing classification schemes in species-rich tropical landscapes and whether floristic data provide support for classification by river catchment. We analyzed the distribution of vascular plant species within 141 plots across an elevation gradient of 130 to 3200 m asl within La Amistad National Park. We tested the hypothesis that river catchment, combined with elevation, explains much of the variation in species composition. We found that annual mean temperature, elevation, and river catchment variables best explained the variation within local species communities. However, only plots in high-elevation oak forest and Páramo were distinct from those in low- and mid-elevation zones. Beta diversity did not significantly differ in plots grouped by elevation zones, except for low-elevation forest, although it did differ between river catchments. None of the analyses identified discrete vegetation assemblages within mid-elevation (700–2600 m asl) plots. Our analysis supports the hypothesis that river catchment can be an alternative means for classifying tropical forest assemblages in conservation settings.

The loss of vernalization requirement in narrow-leaved lupin is associated with a deletion in the promoter and de-repressed expression of a *Flowering Locus T (FT)* homologue.

Nelson*, M. N., Książkiewicz, M., Rychel, S., Besharat, N., Taylor, C. M., Wyrwa, K., Jost, R., Erskine, W., Cowling, W. A., Berger, J. D., Batley, J., Weller, J. L., Naganowska, B. & Wolko, B. (2017). *New Phytologist* 213 (1): 220–232. DOI: 10.1111/nph.14094.

Summary

Adaptation of *Lupinus angustifolius* (narrow-leaved lupin) to cropping in southern Australian and northern Europe was transformed by a dominant mutation (Ku) that removed vernalization requirement for flowering. The Ku mutation is now widely used in lupin breeding to confer early flowering and maturity. We report here the identity of the Ku mutation.

We used a range of genetic, genomic and gene expression approaches to determine whether Flowering Locus T (FT) homologues are associated with the Ku locus.

One of four FT homologues present in the narrow-leaved lupin genome, LanFTc1, perfectly co-segregated with the Ku locus in a reference mapping population. Expression of LanFTc1 in the ku (late-flowering) parent was strongly induced by vernalization, in contrast to the Ku (early-flowering) parent, which showed constitutively high LanFTc1 expression. Co-segregation of this expression phenotype with the LanFTc1 genotype indicated that the Ku mutation impairs cis-regulation of LanFTc1. Sequencing of LanFTc1 revealed a 1.4-kb deletion in the promoter region, which was perfectly predictive of vernalization response in 216 wild and domesticated accessions. Linkage disequilibrium rapidly decayed around LanFTc1, suggesting that this deletion caused the loss of vernalization response.

This is the first time a legume FTc subclade gene has been implicated in the vernalization response.

Comparative germination responses to water potential across different populations of *Aegilops geniculata* and cultivar varieties of *Triticum durum* and *Triticum aestivum*.

Orsenigo, S., Guzzon, F., Abeli, T., Rossi, G., Vagge, I., Balestrazzi, A., Mondoni, A. & Müller*, J. V. (2017). *Plant Biology* 19: 165–171. DOI: 10.1111/plb.12528.

Crop Wild Relatives are often used to improve crop quality and yields because they contain genetically important traits that can contribute to stress resistance and adaptation.

Seed germination of different populations of *Aegilops geniculata* Roth collected along a latitudinal gradient

was studied under different drought stress in order to find populations suitable for improving drought tolerance in wheat. Different accessions of *Aegilops neglecta* Req. ex Bertol., *Triticum aestivum* L. and *T. durum* Desf. were used as comparison.

Under full hydration, germination was high in all populations, but increasing drought stress led to reduced and delayed germination. Significant differences in final germination and mean time to germinate were detected among populations. Wheat, durum wheat and the southern population of *Ae. geniculata* were not significantly affected by drought stress, germinating similarly under all treatments. However, seed germination of the northern populations of *Ae. geniculata* was significantly reduced under high water stress treatment. Differences between populations of the same species could not be explained by annual rainfall across populations' distributions, but by rainfall during seed development and maturation.

Differences in the germination responses to drought found here highlight the importance of source populations as criteria for genotype selection for pre-breeders.

Genome size dynamics in tribe Gilliesieae (Amaryllidaceae, subfamily Allioideae) in the context of polyploidy and unusual incidence of Robertsonian translocations.

Pellicer*, J., Hidalgo*, O., Walker, J., Chase*, M. W., Christenhusz*, M. J. M., Shackelford, G., Leitch*, I. J. & Fay*, M. F. (2017). *Botanical Journal of the Linnean Society* 184: 16–31.

This study focuses on tribe Gilliesieae (Amaryllidaceae, Allioideae), which stand out because of their karyotype diversity, constituting a textbook example of Robertsonian translocations (RTs), in which chromosomes fuse or break at the centromere.





Polyploidy (i.e. whole genome duplication, WGD) is also common in the tribe, hence making Gilliesieae particularly suitable for investigating two major processes of genome evolution in an integrated way. Our phylogenetic reconstruction supported a two subtribe classification, Gilliesiinae and Leucocoryninae, the latter taxonomically validated in this paper. Leucocoryninae are composed of three well-supported lineages, corresponding to the genera *Leucocoryne* + *Latace*, blue-flowered (typical) *Ipheion* + *Tristagma* and *Nothoscordum* (including yellow-flowered *Ipheion* = *Beauverdia*). Analysis of the chromosome data in Leucocoryninae indicates that WGDs have resulted in an almost proportional genome size (GS) increase in *Leucocoryne*, in contrast to the reduction in monoploid GS in polyploid *Nothoscordum*. Likewise, contrasting patterns of GS dynamics and extraordinary karyotype diversity have been recovered in *Ipheion*, *Tristagma* and *Nothoscordum*, clearly illustrating the impact of RTs in shaping genome evolution in these plants.

Recent origin and rapid speciation of Neotropical orchids in the world's richest plant biodiversity hotspot.

Pérez-Escobar*, O. A., Chomicki, G., Condamine, F. L., Karremans, A. P., Bogarín, D., Matzke, N. J., Silvestro, D. & Antonelli, A. (2017). *New Phytologist* 215: 891–905. DOI:10.1111/nph.14629.

The Andean mountains of South America are the most species-rich biodiversity hotspot worldwide with c. 15% of the world's plant species, in only 1% of the world's land surface. Orchids are a key element of the Andean flora, and one of the most prominent components of the Neotropical epiphyte diversity, yet very little is known about their origin and diversification.

We address this knowledge gap by inferring the biogeographical history and diversification dynamics of the two largest Neotropical orchid groups (Cymbidiaceae and Pleurothallidinae), using two

unparalleled, densely sampled orchid phylogenies (including more than 400 newly generated DNA sequences), comparative phylogenetic methods, geological and biological datasets.

We find that the majority of Andean orchid lineages only originated in the last 20–15 million yr. Andean lineages are derived from lowland Amazonian ancestors, with additional contributions from Central America and the Antilles. Species diversification is correlated with Andean orogeny, and multiple migrations and recolonizations across the Andes indicate that mountains do not constrain orchid dispersal over long timescales.

Our study sheds new light on the timing and geography of a major Neotropical diversification, and suggests that mountain uplift promotes species diversification across all elevational zones.

Andean mountain building did not preclude dispersal of lowland epiphytic orchids in the Neotropics.

Pérez-Escobar*, O. A., Gottschling, M., Chomicki, G., Condamine, F. L., Klitgaard*, B. B., Pansarín, E. & Gerlach, G. (2017). *Scientific Reports* 7: 4919. DOI: 10.1038/s41598-017-04261-z.

The Andean uplift is one of the major orographic events in the New World and has impacted considerably the diversification of numerous Neotropical lineages. Despite its importance for biogeography, the specific role of mountain ranges as a dispersal barrier between South and Central American lowland plant lineages is still poorly understood. The swan orchids (*Cycnoches*) comprise ca 34 epiphytic species distributed in lowland and pre-montane forests of Central and South America. Here, we study the historical biogeography of *Cycnoches* to better understand the impact of the Andean uplift on the diversification of Neotropical lowland plant lineages. Using novel molecular sequences (five nuclear and plastid regions) and twelve biogeographic models, we infer that the most recent common ancestor of *Cycnoches* originated in Amazonia ca 5 Mya. The first colonization of Central America occurred from a direct migration event from Amazonia, and multiple bidirectional trans-Andean migrations between Amazonia and Central America took place subsequently. Notably, these rare biological exchanges occurred well after major mountain building periods. The Andes have limited plant migration, yet it has seldom allowed episodic gene exchange of lowland epiphyte lineages such as orchids with great potential for effortless dispersal because of the very light, anemochorous seeds.



The “Hutchinsonian niche” as an assemblage of demographic niches: implications for species geographic ranges.

Pironon*, S., Villellas, J., Thuiller, W., Eckhart, V. M., Geber, M. A., Moeller, D. A. & García, M. B. (2017). *Ecography*: DOI: 10.1111/ecog.03414.

Hutchinson (1957) defined the ecological niche as a hypervolume shaped by the environmental conditions under which a species can “exist indefinitely”. Although several authors further discussed the need to adopt a demographic perspective of the ecological niche theory, very few have investigated the environmental requirements of different components of species’ life cycles (i.e. vital rates) in order to examine their internal niche structures. It therefore remains unclear how species’ demography, niches and distributions are interrelated. Using comprehensive demographic data for two well-studied, short-lived plants (*Plantago coronopus*, *Clarkia xantiana*), we show that the arrangement of species’ demographic niches reveals key features of their environmental niches and geographic distributions. In *Plantago coronopus*, opposing geographic trends in some individual vital rates, through different responses to environmental gradients (demographic compensation), stabilize population growth across the range. In *Clarkia xantiana*, a lack of demographic compensation underlies a gradient in population growth, which could translate in a directional geographic range shift. Overall, our results highlight that occurrence and performance niches cannot be assumed to be the same, and that studying their relationship is essential for a better understanding of species’ ecological niches. Finally, we argue for the value of considering the assemblage of species’ demographic niches when studying ecological systems, and predicting the dynamics of species geographical ranges.

Floral development in *Goniorrhachis marginata* reveals new insights into the evolution of the florally diverse detarioid legumes.

Prenner*, G. & Cardoso, D. (2017). *Annals of Botany* 119: 417–432. DOI: 10.1093/aob/mcw223.

Background and Aims

The study of floral morphology and ontogeny and the re-investigation of existing data help to uncover potential synapomorphic characters and foster our understanding of phylogenetic relationships that rely primarily on molecular analyses. *Goniorrhachis marginata* is a monotypic caesalpinoid legume (Leguminosae) that shows some interesting floral features, such as a long hypanthium and regular Rosaceae-like flowers. We studied the ontogeny and morphology of the flowers in detail and present our results in a broad phylogenetic context.

Methods

Flower buds were collected in the field, fixed in 70 % ethanol and investigated using scanning electron microscopy. Older buds in spirit were carefully opened to investigate the direction of style bending. Characters of the style from 131 taxa from the main legume lineages were analysed and mapped on a Bayesian molecular phylogeny.

Key Results

The tetramerous calyx is the result of complete loss of one sepal. The formation of the radially symmetrical corolla starts in a typical caesalpinoid pattern with the adaxial petal innermost (ascending aestivation). The young style bends in the abaxial direction, which is a character found exclusively in all studied detarioid legumes and therefore a newly described synapomorphy for the clade.

Conclusions

We show that investigation of unstudied taxa and reinvestigation of published data can uncover new, previously overlooked and important characters. Curvature of the style can be detected in young buds with a hand lens and therefore is an important character for field botanists. Our study reveals the importance of including poorly studied and/or phylogenetically enigmatic taxa in molecular phylogenies and in detailed morphological and ontogenetic analyses.

Morphological misfits and character evolution in monocots, with particular reference to Pandanales.

Rudall*, P. J. (2017). In: Campbell, L. M., Davis, J. I., Meerow, A. W., Naczi, R. F. C., Stevenson, D. W. & Thomas, W. W. (eds). *Diversity and Phylogeny of the Monocotyledons*. New York: NYBG Press.

Recent progress in clarifying relationships among the major groups of monocots has facilitated our understanding of morphological evolution. Morphological misfits are taxa whose phenotype is anomalous in the context of their phylogenetic placement and often does not fit readily into the conceptual framework of classical morphology. This paper focuses on reproductive structures in the order Pandanales. In some genera of Pandanales, notably *Cyclanthus*, *Lacandonia*, and *Sararanga*, interpretation of the boundaries of individual flowers is problematic. The flowers of *Lacandonia* are almost unique among extant angiosperms in that they are “inside-out,” with the carpels surrounding the stamens. These structures have been variously interpreted as either flowers or inflorescences, perhaps as an example of fasciation caused by changes in the reproductive apex. This paper revisits this debate in the context of recent phylogenetic data on monocots. It explores whether such anomalous taxa have a predictive value in highlighting significant developmental constraints, or limitations on phenotypic variability that can help to explain why evolution is apparently canalized in different lineages. An ultimate goal is to develop hypotheses of monocot evolution that are potentially testable using developmental genetics.

Evolution and development of monocot stomata.

Rudall*, P. J., Chen, E. D. & Cullen, E. (2017). *American Journal of Botany* 104 (8): 1–20. DOI: 10.3732/ajb.1700086.

Premise of the Study

Leaves of monocots are typically linear with parallel venation, though a few taxa have broad leaves. Studies of stomatal patterning and development in monocots required updating in the context of rapidly improving knowledge of both the phylogenetic and developmental context of monocots that facilitate studies of character evolution.

Methods

We used an existing microscope-slide collection to obtain data on stomatal structure across all the major monocot clades, including some species with relatively broad leaves. In addition, we used both light and electron microscopy to study stomatal development in 16 selected species. We evaluated these data in a phylogenetic context to assess stomatal character evolution.

Key Results

Mature stomatal patterning in monocots can be broadly categorized as anomocytic, paracytic-nonoblique, and paracytic/tetracytic oblique, depending on the presence, development, and arrangement

of lateral subsidiary cells. Stomatal meristemoids invariably result from an asymmetric mitosis in monocots. In species where lateral subsidiary cells are present, they are perigene cells. Among monocots with relatively broad leaves, stomatal orientation is linear-axial in most taxa, but transverse in *Lapageria* and *Stemona*, and random in *Dioscorea* and some Araceae. Amplifying divisions are apparently absent in monocots.

Conclusions

Anomocytic stomata represent the likely ancestral (plesiomorphic) condition in monocots, though multiple evolutionary transitions and reversals have occurred. Paracytic-nonoblique stomata with highly modified perigene lateral neighbor cells characterize grasses and other Poales. The presence of anomocytic stomata in *Japonolirion* and *Tofieldia* reinforces the concept that these two genera have retained many ancestral monocot features and are critical in understanding character evolution in monocots.



Floral ontogeny and vasculature in Xyridaceae, with particular reference to staminodes and stylar appendages.

Sajo*, M. G., Oriani A., Scatena, V. L. & Rudall*, P. J. (2017). *Plant Systematics and Evolution* 303: 1293–1310. DOI 10.1007/s00606-017-1438-3.

We provide a detailed comparative study of floral ontogeny and vasculature in Xyridaceae, including *Xyris*, *Abolboda* and *Orectanthe*. We evaluate these data in the context of a recent well-resolved phylogenetic analysis of Poales to compare floral structures within the xyrid clade (Xyridaceae and Eriocaulaceae).

Xyrids are relatively diverse in both flower structure and anatomy; many species incorporate diverse and unusual floral structures such as staminodes and stylar appendages. Xyridaceae possess three generally

epipetalous stamens in a single whorl; the “missing” stamen whorl is either entirely absent or transformed into staminodes. Fertile stamens each receive a single vascular bundle diverged from the median petal bundle. In *Xyris*, the stamen bundle diverges at the flower base, but it diverges at upper flower levels in both *Abolboda* and *Orectanthe*. In species of *Abolboda* that possess staminodes, staminode vasculature is closely associated with the lateral vasculature of each petal. Despite the likely sister-group relationship between Eriocaulaceae and Xyridaceae, our character optimization indicates that the stilar appendages that characterize some Xyridaceae (except *Xyris* and *Achlyphila*) are non-homologous with those of some Eriocaulaceae. On the other hand, it remains equivocal whether the loss of a fertile outer androecial whorl occurred more than once during the evolutionary history of the xyrid clade; this transition occurred either once followed by a reversal to fertile stamens in Eriocauloideae and staminodes in some Xyridaceae, or twice independently within both Xyridaceae and Eriocaulaceae.

Biogeographical patterns of *Myrcia* s.l. (Myrtaceae) and their correlation with geological and climatic history in the Neotropics.

Santos, M. F., Lucas*, E., Sano, P. T., Buerki, S., Staggemeier*, V. G. & Forest*, F. (2017). *Molecular Phylogenetics and Evolution* 108: 34–48. DOI: 10.1016/j.ympev.2017.01.012.

Many recent studies discuss the influence of climatic and geological events in the evolution of Neotropical biota by correlating these events with dated phylogenetic hypotheses. Myrtaceae is one of

the most diverse Neotropical groups and it therefore a good proxy of plant diversity in the region. However, biogeographic studies on Neotropical Myrtaceae are still very limited. *Myrcia* s.l. is an informal group comprising three accepted genera (*Calyptanthes*, *Marlierea* and *Myrcia*) making up the second largest Neotropical group of Myrtaceae, totalling about 700 species distributed in nine subgroups. Exclusively Neotropical, the group occurs along the whole of the Neotropics with diversity centres in the Caribbean, the Guiana Highlands and the central-eastern Brazil. This study aims to identify the time and place of divergence of *Myrcia* s.l. lineages, to examine the correlation in light of geological and climatic events in the Neotropics, and to explore relationships among Neotropical biogeographic areas. A dated phylogenetic hypothesis was produced using BEAST and calibrated by placing *Paleomyrtinaea princetonensis* (56 Ma) at the root of the tree; biogeographic analysis used the DEC model with dispersal probabilities between areas based on distance and floristic affinities. *Myrcia* s.l. originated in the Montane Atlantic Forest between the end of Eocene and early Miocene and this region acted as a secondary cradle for several lineages during the evolution of this group. The Caribbean region was important in the diversification of the *Calyptanthes* clade while the Guayana shield appears as ancestral area for an older subgroup of *Myrcia* s.l. The Amazon Forest has relatively low diversity of *Myrcia* s.l. species but appears to have been important in the initial biogeographic history of old lineages. Lowland Atlantic Forest has high species diversity but species rich lineages did not originate in the area. Diversification of most subgroups of *Myrcia* s.l. occurred throughout the Miocene, as reported for other Neotropical taxa. During the Miocene, geological events may have influenced the evolution of the Caribbean and Amazon forest lineages, but other regions were geological stable and climate changes were the most likely drivers of diversification. The evolution of many lineages in montane areas suggests that *Myrcia* s.l. may be particularly adapted to such environments.

Systematics of *Yuania prainii* (Orchidaceae: Calypsoinae).

Schuiteman*, A. & Averyanov, L. V. (2017). *Phytotaxa* 309: 288–290. DOI: 10.11646/phytotaxa.309.3.12.

Recently, two new genera of mycoheterotrophic orchids were described from China: *Danxiaorchis* Zhai, Xing & Liu (2013: e60371) and *Yunorchis* Liu, Zhang & Li (2015: e123382). Both were considered to be monospecific, and in each case the descriptions were accompanied by a phylogenetic analysis.





Museomics resolve the systematics of an endangered grass lineage endemic to north-western Madagascar.

Silva, C., Besnard, G., Piot, A., Razanatsoa, J., Oliveira, R. P. & Vorontsova*, M. S. (2017). *Annals of Botany* 119 (3): 339-351. DOI: 10.1093/aob/mcw208.

Background and Aims

Recent developments in DNA sequencing, so-called next-generation sequencing (NGS) methods, can help the study of rare lineages that are known from museum specimens. Here, the taxonomy and evolution of the Malagasy grass lineage *Chasechloa* was investigated with the aid of NGS.

Methods

Full chloroplast genome data and some nuclear sequences were produced by NGS from old herbarium specimens, while some selected markers were generated from recently collected Malagasy grasses. In addition, a scanning electron microscopy analysis of the upper floret and cross-sections of the rachilla appendages followed by staining with Sudan IV were performed on *Chasechloa* to examine the morphology of the upper floret and the presence of oils in the appendages.

Key Results

Chasechloa was recovered within tribe Paniceae, sub-tribe Boivinellinae, contrary to its previous placement as a member of the New World genus *Echinoalaena* (tribe Paspaleae). *Chasechloa* originated

in Madagascar between the Upper Miocene and the Pliocene. It comprises two species, one of them collected only once in 1851. The genus is restricted to north-western seasonally dry deciduous forests. The appendages at the base of the upper floret of *Chasechloa* have been confirmed as elaiosomes, an evolutionary adaptation for myrmecochory.

Conclusions

Chasechloa is reinstated at the generic level and a taxonomic treatment is presented, including conservation assessments of its species. Our study also highlights the power of NGS technology to analyse relictual or probably extinct groups.

Potential impacts of climate change on native plant distributions in the Falkland Islands.

Upson*, R., Williams*, J. J., Wilkinson*, T., Clubbe*, C. P., Maclean, I. M. D., McAdam, J. H. & Moat*, J. F. (2016). *PLoS One* 11 (11): e0167026. DOI: 10.1371/journal.pone.0167026.

The Falkland Islands are predicted to experience up to 2.2°C rise in mean annual temperature over the coming century, greater than four times the rate over the last century. Our study investigates likely vulnerabilities of a suite of range-restricted species whose distributions are associated with archipelago-wide climatic variation. We used present day climate maps calibrated using local weather data, 2020–2080



climate predictions from regional climate models, non-climate variables derived from a digital terrain model and a comprehensive database on local plant distributions. Weighted mean ensemble models were produced to assess changes in range sizes and overlaps between the current range and protected areas network. Target species included three globally threatened Falkland endemics, *Nassauvia falklandica*, *Nastanthus falklandicus* and *Plantago moorei*; and two nationally threatened species, *Acaena antarctica* and *Blechnum cordatum*. Our research demonstrates that temperature increases predicted for the next century have the potential to significantly alter plant distributions across the Falklands. Upland species, in particular, were found to be highly vulnerable to climate change impacts. No known locations of target upland species or the southwestern species *Plantago moorei* are predicted to remain environmentally suitable in the face of predicted climate change. We identify potential refugia for these species and associated gaps in the current protected areas network. Species currently restricted to the milder western parts of the archipelago are broadly predicted to expand their ranges under warmer temperatures. Our results emphasise the importance of implementing suitable adaptation strategies to offset climate change impacts, particularly site management. There is an urgent need for long-term monitoring and artificial warming experiments; the results of this study will

inform the selection of the most suitable locations for these. Results are also helping inform management recommendations for the Falkland Islands Government who seek to better conserve their biodiversity and meet commitments to multi-lateral environmental agreements.

Links between parallel evolution and systematic complexity in angiosperms—a case study of floral development in *Myrcia sl* (Myrtaceae).

Vasconcelos*, T. N., Prenner*, G., Santos, M. F., Wingler, A. & Lucas*, E. J. (2016). *Perspectives in Plant Ecology, Evolution and Systematics* 24: 11–24. DOI: 10.1016/j.ppees.2016.11.001.

Incongruence between morphological classification and molecular phylogenies is one of the biggest challenges to systematists. Such incongruence might be explained by underlying homologies, namely parallelisms. This study case shows how parallelisms and convergences are both related to taxonomic problems in systematic complex groups. Parallelism may be a feature of recent diversified lineages, where the molecular basis for the expression of a character can still be triggered. Re-expression of characters can make changes in early steps of development being less phylogenetically constraint than late stage ones.

Myrteae phylogeny, calibration, biogeography and diversification patterns: Increased understanding in the most species rich tribe of Myrtaceae.

Vasconcelos*, T. N. C., Proença, C. E. B., Ahmad, B., Aguilar, D. S., Aguilar, R., Amorim, B. S., Campbell, K., Costa, I. R., De-Carvalho, P. S., Faria, J. E. Q., Giaretta*, A., Kooij*, P. W., Lima, D. F., Mazine, F. F., Peguero, B., Prenner*, G., Santos, M. F., Soewarto, J., Wingler, A. & Lucas*, E. J. (2017). *Molecular Phylogenetics and Evolution* 109: 113–137. DOI: 10.1016/j.ympev.2017.01.002.

Myrteae (c. 2500 species; 51 genera) is the largest tribe of Myrtaceae and an ecologically important groups of angiosperms in the Neotropics. Systematic relationships in Myrteae are complex, hindering conservation initiatives and jeopardizing evolutionary modelling. A well-supported and robust phylogenetic hypothesis was here targeted towards a comprehensive understanding of the relationships within the tribe. The resultant topology was used as a base for key evolutionary analyses such as age estimation, historical biogeography and diversification rate patterns. One nuclear (ITS) and seven chloroplast

(psbA-trnH, matK, ndhF, trnI-trnF, trnQ-rps16, rpl16 and rpl32-trnL) DNA regions for 115 taxa representing 46 out of the 51 genera in the tribe were accessed and analysed using maximum likelihood and Bayesian inference tools for phylogenetic reconstruction. Dates of diversification events were estimated and contrasted using two distinct fossil sets (macro and pollen) in BEAST. The subsequent dated phylogenies were compared and analysed for biogeographical patterns using BioGeoBEARS and diversification rates using BAMM. Myrteae phylogeny presents strong statistical support for three major clades within the tribe: Australasian group, *Myrtus* group and Main Neotropical Lineage. Dating results from calibration using macrofossil are an average of 20 million years older and show an early Paleocene origin of Myrteae, against a mid-Eocene one from the pollen fossil calibration. Biogeographic analysis shows the origin of Myrteae in Zealandia in both calibration approaches, followed by a widespread distribution throughout the still-linked Gondwana continents and diversification of Neotropical endemic lineages by later vicariance. Best configuration shift indicates three points of acceleration in diversification rates, all of them occurring in the Main Neotropical Lineage. Based on the reconstructed topology, several new taxonomic placements were recovered, including: the relative position of *Myrtus communis*, the placement of the *Blepharocalyx* group, the absence of generic endemism in the Caribbean, and the paraphyletism of the former *Pimenta* group. Distinct calibration approaches affect biogeography interpretation, increasing the number of necessary long distance dispersal events in the topology with older nodes. It is hypothesised that biological intrinsic factors such as modifications of embryo type and polyploidy might have played a role in accelerating shifts of diversification rates in Neotropical lineages. Future perspectives include



formal subtribal classification, standardization of fossil calibration approaches and better links between diversification shifts and trait evolution.

Structural colour from helicoidal cell-wall architecture in fruits of *Margaritaria nobilis*.

Vignolini, S., Gregory, T., Kollé, M., Lethbridge, A., Moyroud, E., Steiner, U., Glover, B. J., Vukusic, P. & Rudall*, P. J. (2016). *Journal of the Royal Society Interface* 13: 20160645. DOI: 10.1098/rsif.2016.0645.

The bright and intense blue-green coloration of the fruits of *Margaritaria nobilis* (Phyllanthaceae) was investigated using polarization-resolved spectroscopy and transmission electron microscopy. Optical measurements of freshly collected fruits revealed a strong circularly polarized reflection of the fruit that originates from a cellulose helicoidal cell wall structure in the pericarp cells. Hyperspectral microscopy was used to capture the iridescent effect at the single-cell level.

Biospeckle activity in coffee seeds is associated non-destructively with seedling quality.

Vivas, P. G., Resende, L. S., Braga Jr, R. A., Guimaraes, R. M., Azevedo, R., da Silva, E. A. A. & Toorop*, P. E. (2017). *Annals of Applied Biology* 170 (2): 141–149. DOI: 10.1111/aab.12314.

Seeds age during storage, resulting in a decline in germination and seedling quality. Seed quality tests are important to monitor this decline. However, such tests are usually destructive and require large seed numbers and long time. For coffee seeds the standard germination test and assessment of seedling quality takes 30 days. Biospeckle has been used previously as a non-destructive optical tool to monitor biological activity in a range of tissues. Biospeckle was applied 3–6 days after imbibition (DAI) to investigate an association with coffee seedling quality after 30 days. Two distinct areas of biospeckle activity were demonstrated, concurring with the locations of the embryonic axis and the cotyledons in the apical and central seed parts, respectively. Moisture content analysis revealed that embryos of imbibed seeds contained more water than endosperm. Different areas within the endosperm did not differ in moisture content, while the moisture content of the axis was higher than that of the cotyledons, and this did not change from 4 DAI. Therefore, it was concluded that high biospeckle activity was not the result of increased water content in any seed part, but more likely of growth and metabolism in the axis and cotyledons, which had been described previously. A threshold biospeckle ratio apical: central of 1.02 after 6 days distinguished between seeds that produced dead and viable seedlings after 30 days and provided similar results as a tetrazolium test, a widely acknowledged but destructive test for seed quality. Thus, biospeckle data provided a non-destructive early parameter for seedling quality, based on embryo growth during germination.



Climate trends in the wood anatomy of *Acacia* s.s. (Leguminosae: Mimosoideae).

Warwick, N. M. W., Hailey, L., Clarke, K. L. & Gasson*, P. E. (2017). *Annals of Botany* 119: 1249-1266. DOI: 10.1093/aob/mcx019.

Background and Aims

This study investigates the structural diversity of the secondary xylem of 54 species of *Acacia* from four taxonomic sections collected across five climate regions along a 1200 km E-W transect from sub-tropical [approx. 1400 mm mean annual precipitation (MAP)] to arid (approx. 240 mm MAP) in New South Wales, Australia. *Acacia sensu stricto* (s.s.) is a critical group for understanding the effect of climate and phylogeny on the functional anatomy of wood.

Methods

Wood samples were sectioned in transverse, tangential and radial planes for light microscopy and analysis.

Key Results

The wood usually has thick-walled vessels and fibres, paratracheal parenchyma and uniseriate and biseriate rays, occasionally up to four cells wide. The greater abundance of gelatinous fibres in arid and semi-arid species may have ecological significance. Prismatic crystals in chambered fibres and axial parenchyma increased in abundance in semi-arid and arid species. Whereas vessel diameter showed only a small decrease from the sub-tropical to the arid region, there was a significant 2-fold increase in vessel frequency and a consequent 3-fold decrease in the vulnerability index.

Conclusions

Although the underlying phylogeny determines the qualitative wood structure, climate has a significant influence on the functional wood anatomy of *Acacia* s.s., which is an ideal genus to study the effect of these factors.

Biomechanical, biochemical, and morphological mechanisms of heat shock-mediated germination in *Carica papaya* seed.

Webster, R. E., Waterworth, W. M., Stuppy*, W., West, C. E., Ennos, R., Bray, C. M. & Pritchard*, H. W. (2016). *Journal of Experimental Botany* 67: 6373–6384. DOI: 10.1093/jxb/erw402.

Carica papaya (papaya) seed germinate readily fresh from the fruit, but desiccation induces a dormant state. Dormancy can be released by exposure of the hydrated seed to a pulse of elevated temperature, typical of that encountered in its tropical habitat. *Carica papaya* is one of only a few species known to germinate in response to heat shock (HS) and we know little of the mechanisms that control germination in tropical ecosystems. Here we investigate the mechanisms that mediate HS-induced stimulation of germination in pre-dried and re-imbibed papaya seed. Exogenous gibberellic acid (GA3 \geq 250 μ M) overcame the requirement for HS to initiate germination. However, HS did not sensitise seeds to GA3, indicative that it may act independently of GA biosynthesis. Seed coat removal also overcame desiccation-imposed dormancy, indicative that resistance to radicle emergence is coat-imposed.

Morphological and biomechanical studies identified that neither desiccation nor HS alter the physical structure or the mechanical strength of the seed coat. However, cycloheximide prevented both seed coat weakening and germination, implicating a requirement for de novo protein synthesis in both processes. The germination antagonist abscisic acid prevented radicle emergence but had no effect on papaya seed coat weakening. Desiccation therefore appears to reduce embryo growth potential, which is reversed by HS, without physically altering the mechanical properties of the seed coat. The ability to germinate in response to a HS may confer a competitive advantage to *C. papaya*, an opportunistic pioneer species, through detection of canopy removal in tropical forests.

Extraction of DNA from lichen-forming and lichenicolous fungi: a low-cost fast protocol using Chelex.

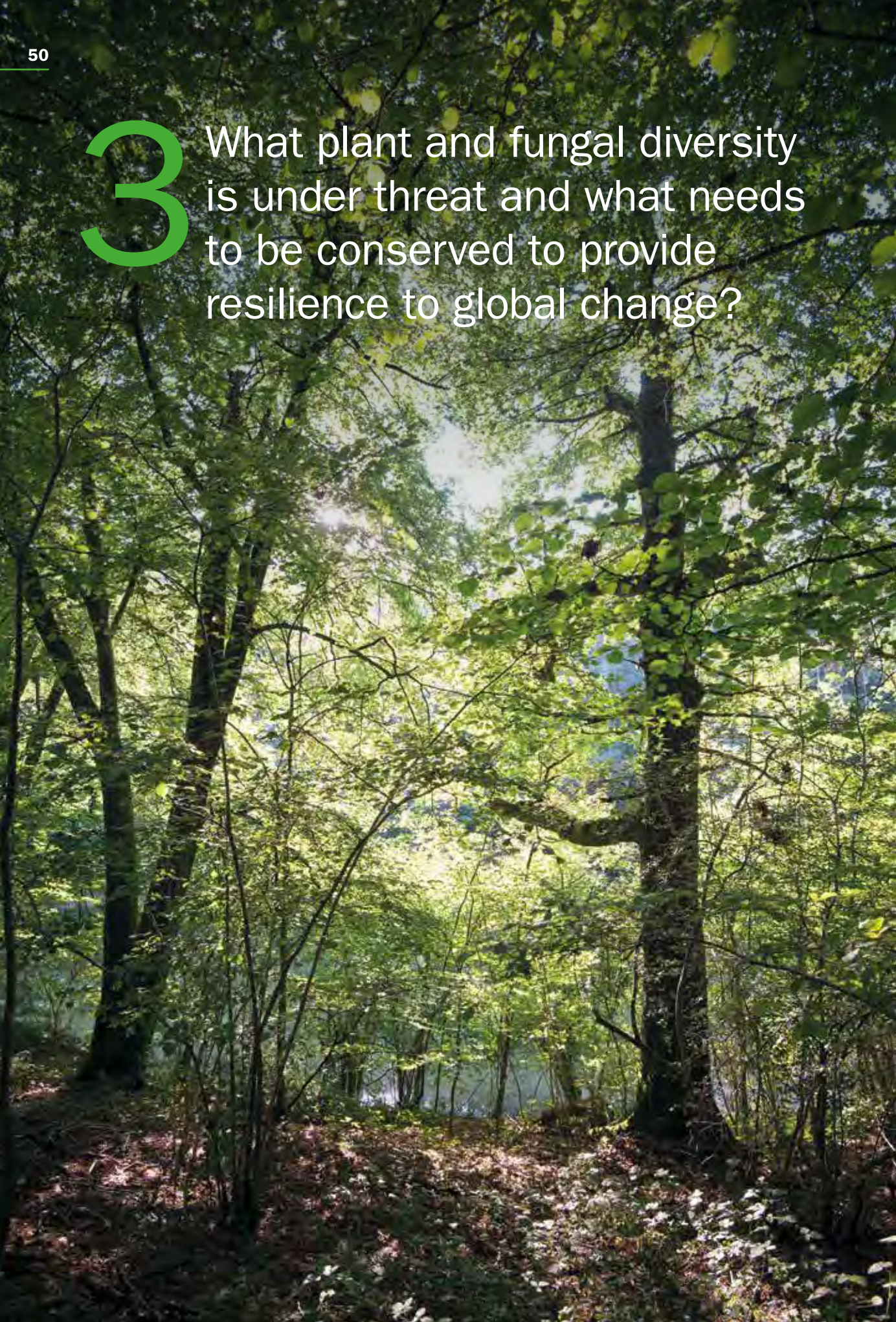
Ferencova, Z., Rico, V. J. & Hawksworth*, D. L. (2017). *The Lichenologist* 49 (5): 521–525. DOI: 10.1017/S0024282917000329.

No abstract available.



3

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



Plant health – state of research.

Buggs*, R. J. A., Coker*, T., Dennis, C., Walker, D., Smith, J., Mota-Sanchez, D. & Cock, M. (2017). In: Willis*, K. J. (ed.) *State of the World's Plants 2017*. Richmond: Royal Botanic Gardens, Kew, pp.64–71

There are potential costs of US \$540 billion per year to world agriculture if the spread of invasive pests and pathogens is not stopped, and introduced insects and diseases have effectively eliminated entire tree species from United States forests within decades.

Ternstroemia cameroonensis (Ternstroemiaceae), a new medicinally important species of montane tree, nearly extinct in the highlands of Cameroon.

Cheek*, M., Tchiengue, B. & Tacham, W. N. (2017). *Blumea* 62: 53–57. DOI: 10.3767/000651917X695362.

Ternstroemia cameroonensis sp. nov. (Ternstroemiaceae) is formally described from the Highlands of Cameroon and its conservation status is assessed as Critically Endangered using the IUCN 2012 standard. This is the third species of *Ternstroemia* known from Africa. The species is unusual in its genus in being monoecious, having Terminalia-branching (Aubreville's model), phyllotaxy of 1/3 (not pseudo-vericillate), flowers with a uniseriate androecium and a distinct intra-staminal disc, and in the stamens lacking a distinct apicular connective. The species is used locally for extensive medicinal purposes.

Important Plant Areas: revised selection criteria for a global approach to plant conservation.

Darbyshire*, I., Anderson, S., Asatryan, A., Byfield, A., Cheek*, M., Clubbe*, C., Ghrabi, Z., Harris, T., Heatubun, C. D., Kalema, J., Magassouba, S., McCarthy, B., Milliken*, W., Montmollin, B. d., Nic Lughadha*, E., Onana, J. M., Saidou, D., Sarbu, A., Shrestha, K. & Radford, E. A. (2017). *Biodiversity & Conservation* 26: 1767–1800. DOI: 10.1007/s10531-017-1336-6.

Despite the severe threats to plant habitats and high levels of extinction risk for plant species in many parts of the world, plant conservation priorities are often poorly represented in national and global frameworks because of a lack of data in an accessible and consistent format to inform conservation decision making. The Important Plant Areas (IPAs) criteria system offers a pragmatic yet scientifically rigorous means of delivering these datasets, enabling informed national- or regional-scale conservation prioritisation, and contributing significantly towards

global prioritisation systems including the International Union for Conservation of Nature Key Biodiversity Areas (KBAs) Standard. In this paper, we review the IPA rationale and progress on IPA identification to date, including the perceived limitations of the process and how these may be overcome. We then present a revised set of criteria for use globally, developed through the combined experiences of IPA identification over the past decade and a half and through a recent global consultation process. An overview of how the revised IPA criteria can work alongside the newly published KBA Standard is also provided. IPA criteria are based around a sound, scientific, global framework which acknowledges the practical problems of gathering plant and habitat data in many regions of the world, and recognises the role of peer reviewed expert opinion in the selection process. National and sub-national engagement in IPA identification is essential, providing a primary route towards long term conservation of key sites for plant diversity. The IPA criteria can be applied to the conservation of all organism groups within the plant and fungal kingdoms.

Important Plant Areas.

Darbyshire*, I., Halski, B., Williams*, J., Baines*, D., Clubbe*, C. & McCarthy, B. (2017). In: Willis*, K. J. (ed.) *State of the World's Plants 2017*. Richmond: Royal Botanic Gardens, Kew, pp.30–35.

There is only 53% overlap between Important Plant Areas (IPAs) and Important Bird and Biodiversity Areas (IBAs) across Europe and the Mediterranean region. IPAs include regions of internationally significant populations of threatened plant species, threatened habitats, and/or areas that exhibit exceptional botanical richness. In total, nearly 2,550 IPAs have been either fully or provisionally identified and published to date.





Barleria lebomboensis (Acanthaceae), an endangered new species from the Lebombo Mountains of Swaziland.

Darbyshire*, I., McClelland, W. & Foreman, W. (2017). *Phytotaxa* 323: 173–181. DOI: 10.11646/phytotaxa.323.2.5.

A new species, *Barleria lebomboensis*, restricted to the Lebombo Mountains of Swaziland, is described and illustrated. Its affinities to species in *Barleria* sect. *Somalia*, particularly *B. meyeriana* and *B. dolomiticola*, are discussed. Based upon current knowledge of its distribution, ecology and associated threats, *Barleria lebomboensis* is assessed as Endangered under criterion B of the IUCN Red List categories and criteria.

Using coarse-scale species distribution data to predict extinction risk in plants.

Darrah, S. E., Bland, L. M., Bachman*, S. P., Clubbe*, C. P. & Trias-Blasi*, A. (2017). *Diversity and Distributions* 23: 435–447. DOI: 10.1111/ddi.12532.

Aim

Less than 6% of the world's described plant species have been assessed on the IUCN Red List, leaving many species invisible to conservation prioritization. Large-scale Red List assessment of plant species is a challenge, as most species' ranges have only been

resolved to a coarse scale. As geographic distribution is a key assessment criterion on the IUCN Red List, we evaluate the use of coarse-scale distribution data in predictive models to assess the global scale and drivers of extinction risk in an economically important plant group, the bulbous monocotyledons.

Methods

Using coarse-scale species distribution data, we train a machine learning model on biological and environmental variables for 148 species assessed on the IUCN Red List in order to identify correlates of extinction risk. We predict the extinction risk of 6439 'bulbous monocot' species with the best of 13 models and map our predictions to identify potential hotspots of threat.

Results

Our model achieved 91% classification accuracy, with 88% of threatened species and 93% of non-threatened species accurately predicted. The model predicted 35% of bulbous monocots presently 'Not Evaluated' under IUCN criteria to be threatened and human impacts were a key correlate of threat. Spatial analysis identified some hotspots of threat where no bulbous monocots are yet on the IUCN Red List, for example central Chile.

Main conclusions

This is the first time a machine learning model has been used to determine extinction risk at a global scale in a species-rich plant group. As coarse-scale distribution data exist for many plant groups, our methods can be replicated to provide extinction risk predictions across the plant kingdom. Our approach can be used as a low-cost prioritization tool for targeting field-based assessments.

150-seed comparative longevity protocol – a reduced seed number screening method for identifying short-lived seed conservation collections.

Davies*, R. M., Newton*, R. J., Hay, F. R. & Probert, R. J. (2016). *Seed Science and Technology* 44 (3): DOI: 10.15258/sst.2016.44.3.13.

Comparative seed longevity testing is a useful tool for setting appropriate germination test intervals for viability monitoring of ex situ conservation collections. A reduced seed number comparative longevity protocol, designed to screen for short-lived species and which uses only 150 seeds sampled at just four intervals during controlled ageing, at 2, 10, 15 and 30 days, was compared with the standard comparative longevity protocol of nine or ten sampling intervals using a total of either 450 or 500 seeds, respectively. Reduced seed number longevity test survival curves differed

significantly ($P < 0.05$) from standard longevity test survival curves in only one of the 30 collections tested. Estimates of p_{50} for reduced seed number longevity tests were not significantly different from standard longevity tests. Adoption of this reduced seed number longevity test as a routine procedure in genebank management will identify conservation collections with potentially short-lived seeds and thereby reduce the risk of undetected viability loss. The reduced seed number longevity test will also reduce staff time and costs and use fewer seeds compared with standard seed longevity testing, thus enabling more effective management of conservation collections.

Plant conservation and Botanic Gardens.

Fay*, M. F. & Christenhusz*, M. J. M. (2016). eLS: 1–15. DOI: 10.1002/9780470015902.a0023748.

With a history dating back to the sixteenth century, modern botanic gardens have had an important role in plant conservation, most notably since the second half of the twentieth century. The formation of Botanic Gardens Conservation International in the 1980s and the development of the Global Strategy for Plant Conservation have led to many botanic gardens across the world now having conservation as a major focus. The combination of historical collections and expertise in areas including plant taxonomy, population genetics, propagation and seed banking mean that botanic gardens are ideally placed to play a major role in ex situ and in situ plant conservation. Maintaining living

collections of the rarest species in botanic gardens has been a way of saving these from extinction, albeit often in isolation from the other organisms (plants, animals and fungi) with which they would interact in nature.

Tahina spectabilis: a new discovery in Madagascar ten years on.

Gardiner*, L. M., Rabehevitra*, D., Letsara, R. & Shapcott, A. (2017). *Palms* 61 (2): 69–82.

A decade after the extraordinary hapaxanthic Coryphoid palm was discovered on a remote peninsula in northwest Madagascar, a team from Kew revisited the site to see how successful conservation activities have been and were able to confirm a stunning discovery back on the mainland.

Population genetics data help to guide the conservation of palm species with small population sizes and fragmented habitats in Madagascar.

Gardiner*, L. M., Rakotoarinivo, M., Rajaovelona*, L. R. & Clubbe*, C. (2017). *PeerJ*: 5:e3248 DOI: 10.7717/peerj.3248.

Background

The need to incorporate genetic data into conservation management decisions is increasingly recognised. However, many published studies represent a 'gold standard' of sampling, techniques, and analyses.



Such rigour is often not possible with limited funding and resourcing available for developing plans for the increasing number of threatened species requiring conservation management. Two endemic palm species of the Itremo Massif in central Madagascar, *Dypsis ambositrae* and *D. decipiens*, are known to be threatened with extinction and conservation management for these species is a priority for the newly created protected area in the region.

Methods

The genetic diversity of these two species was studied using the relatively low-cost and rapid AFLP technique. DNA fragments generated using three primer combinations were analysed for 20 and 50 individuals of the two species, respectively, from across their ranges.

Results

Genetic diversity was relatively low for both species. The two sites where the highly restricted *D. ambositrae* grows were found to be genetically distinct (although overall heterozygosity was low). Despite having a much wider distribution and relatively large population, *D. decipiens* did not show clear geographical nor genetic groupings and had similarly low genetic heterozygosity to *D. ambositrae*.

Discussion and Recommendations

With so few individuals remaining in the wild and two genetically distinct subpopulations, it is recommended that both sites of *D. ambositrae* are conserved and that seed are collected from both for ex situ conservation and potential future reintroduction. It may be less important to focus resources on conserving or collecting ex situ material from all sites where *D. decipiens* is found, as the genetic diversity represented by each subpopulation is limited and increasing sampling may not protect significantly higher levels of genetic diversity. This study provides data that inform and support conservation decisions taken for both species within

this region, and in the management of the newly designated Itremo Massif Protected Area, which covers most of the sites where these two species remain in the wild.

Country focus – status of knowledge of Madagascan plants.

Goyder*, D. J., Baker*, W. J., Besnard, G., Dransfield*, J., Gardiner*, L. M., Rabehevitra*, D., Rajaovelona*, L., Rakotoarisoa*, S., Rakotonasolo*, F., Ralimanana*, H., Randriamboavonjy*, T., Razanatsoa, J., Sarasan*, V., Vorontsova*, M., Wilkin*, P. & Cable*, S. (2017). *In: Willis*, K. (ed.) State of the World's Plants 2017*. Richmond: Royal Botanic Gardens, Kew, pp.37–41.

83% of Madagascar's 11,138 native species of vascular plant occur nowhere else on Earth. Madagascar is the world's fourth largest island, home to five unique plant families and three times as many palm species as continental Africa.

Collecting near mature and immature orchid seeds for ex situ conservation: 'in vitro collecting' as a case study.

Kendon*, J., Rajaovelona*, L., Sandford*, H., Fang*, R., Bell*, J. & Sarasan*, V. (2017). *Botanical Studies* 58 (34): DOI: 10.1186/s40529-017-0187-5.

Background

Lack of phenological information and efficient collecting methods are considered impediments for orchid seed collecting. This leads to opportunistic collecting as part of general seed collecting schedules that may last few weeks especially in remote areas. The study explored the feasibility of collecting near mature and immature seeds to support conservation action plans. Mature, near mature and immature seeds of orchids were collected from the wild in the Central Highlands of Madagascar (CHM). Seed capsules were collected in sterile culture medium in the wild, to prevent deterioration of seeds inside the capsule after collecting, later to be cultured under laboratory conditions.

Results

Seed capsules collected by the in vitro collecting (IVC) method were kept in very good condition for up to 4 weeks before germination under in vitro conditions. Significantly faster and higher germination rate ($p < 0.001$) than mature seeds was observed in a number of taxa collected during a 3 year-long study. In some taxa even immature seeds, with no apparent sign of testa covering the embryo, germinated following IVC where mature seeds failed to germinate.





Conclusions

We propose that IVC method has potential to complement conventional seed collecting by increasing the germplasm that can be used in integrated conservation action plans. Improvements can be made in developing collections for taxa from biodiversity hotspots and remote areas where collecting requires considerable resources. This method can further be used on a wider selection of plants from different geographic areas and on embryo rescue programmes for economically important plants.

Native seed supply and the restoration species pool.

Ladouceur, E., Jiménez-Alfaro, B., Marin, M., De Vitis, M., Abbandonato, H., Iannetta, P.P.M., Bonomi, C. & Pritchard*, H. W. (2017). *Conservation Letters*: DOI: 10.1111/conl.12381.

Globally, annual expenditure on ecological restoration of degraded areas for habitat improvement and biodiversity conservation is approximately \$18bn. Seed farming of native plant species is crucial to meet restoration goals, but may be stymied by the disconnection of academic research in seed science and the lack of effective policies that regulate native seed production/supply. To illustrate this problem, we identified 1,122 plant species important for European grasslands of conservation concern and found that only 32% have both fundamental seed germination data available and can be purchased as seed. The “restoration species pool,” or set of species available in practice, acts as a significant biodiversity selection filter for species use in restoration projects. For improvement, we propose: (1) substantial expansion of research and development on native seed quality, viability, and production; (2) open-source knowledge transfer between sectors; and (3) creation of supportive policy intended to stimulate demand for biodiverse seed.

Managing *ex situ* collections of wild species' seeds: Use of biodiversity informatics in the Millennium Seed Bank to address challenges.

Liu*, U. & Dickie*, J. B. (2017). *Biodiversity Information Science and Standards* 1: e20197 DOI: 10.3897/twdgproceedings.1.20197.

The Royal Botanic Gardens Kew manages the Millennium Seed Bank (MSB) Partnership, the largest *ex situ* conservation program for wild plant species in the world. The long-term storage of viable dry seed collections ('orthodox' seeds) in deep-freeze chambers and maintaining their quality, viability and longevity for future use are central to the conservation effort. Seed collections conserved within the vault of MSB represent the highest concentration of living seed-plant biodiversity on earth with over 83,500 collections from 37,940 vascular plant species originating from nine bio-geographical areas, 189 countries and territories, 35 biodiversity hotspots, 357 families and 5821 genera.

Curation of living seeds from such diversity and wide geographic origin is challenging and requires breadth and depth of knowledge, resources and experience in taxonomy and seed biology, physiology, morphology and ecology in order to understand taxon level seed traits related to seed viability, germination and survival in long-term storage. We describe how biodiversity informatics are integrated with collection and trait data to develop decision and prediction tools to support curators and collection professionals at MSB to address challenges in decision making during curatorial activities to best allocate their conservation effort. Bringing these disciplines together and bridging the gaps require accurate data acquisition, sharing, analysis and interoperability. MSB met these challenges through collaboration and establishing and sharing data standards, structures, algorithms and resources with MSB Partnership, currently across 95 countries.



A range of databases and tools are central to carrying out the daily routine work of curators at MSB. (1) The Seed Bank Database (SBD) captures collection level data from the point of sampling and throughout their lifespan in storage. It is the main data hub used to manage collections. SBD includes mathematical and statistical computations to monitor quality, quantity and viability of collections. (2) The Taxon Database (TDB) consolidates the plant name backbone with taxonomic identities of collections. It enables curators to identify the taxon to allocate the correct curation protocol for conservation. (3) The Seed Information Database (SID) serves as a main source of a variety of taxon-based biological information for use in large scale analysis and decision support. It is a compilation of seed biological trait data (weights, storage behavior, germination, viability constant, protein content, oil content, morphology, dispersal) from MSB Partnership collections and other published and unpublished sources. SID, which is in public domain (<http://data.kew.org/sid/>), also provides useful tools that incorporate mathematical models to predict viability of seeds after period of storage in range of environments. SID data are used at MSB to predict seed storage behavior and to identify short-lived taxa in long-term storage. (4) The Data Analysis and Reporting Tool (DART) serves as the user interface where SBD, TDB, SID and other Kew databases can be linked. It is the main tool used for data querying, analysis, and visualization. (5) The Germination Predictor Tool uses MSB Collection data (month of seed dispersal, geo-coordinates and seed germination) and world climatic data (precipitation and temperature) to

predict conditions and treatments that are required to germinate seeds based on taxonomy and geographic origin of collections. This enables curators to simulate conditions that trigger germination of seeds in their natural environment. Kew's UK Germination toolbox, which is in the public domain (<http://data.kew.org/ukgerm/search>), mostly uses SBD germination data and provides successful germination conditions for UK native species. (6) The Species Prioritization Tool ranks vascular plant taxa by using an integrative assessment technique that incorporates taxon level data compiled from several Kew and open databases to yield priority scores based on multiple priority-setting criteria. It is used by collection managers during collection acquisition and management to identify conservation priority taxa and collections.

The above examples of applications used at the MSB show clearly how biodiversity data provides essential systems for collection management in ex situ conservation.

rCAT: Conservation Assessment Tools.

Moat*, J. & Bachman*, S. (2017). *R package version 0.1.5*. <https://cran.r-project.org/package=rCAT>

A set of tools to help with species conservation assessments (Red List threat assessments). Includes tool for Extent of occurrence, Area of Occupancy, Minimum Enclosing Rectangle, a geographic Projection Wizard and Species batch processing.



The Alpine Seed Conservation and Research Network – a new initiative to conserve valuable plant species in the European Alps.

Müller*, J. V., Berg, C., Détraz-Méroz, J., Erschbamer, B., Fort, N., Lambelet-Haueter, C., Margreiter, V., Mombrial, F., Mondoni, A., Pagitz, K., Porro, F., Rossi, G., Schwager, P. & Breman*, E. (2017). *Journal of Mountain Science* 14 (4): 806–810. DOI: 10.1007/s11629-016-4313-8.

Safeguarding plants as seeds in ex situ collections is a cost effective element in an integrated plant conservation approach. The European Alps are a regional centre of plant diversity. Six institutions have established a regional network covering the European Alps which will conserve at least 500 priority plant species and which will improve the conservation status of plant species in grassland communities in the subalpine, alpine and nival altitudinal belts. Targeted research will expand the knowledge of the ecology of target species. Public engagement activities will raise the awareness for the importance of specific conservation actions in the European Alps.

Invasive species.

Newton*, R., Budden*, A. P., Petrokofsky, G., Nic Lughadha*, E. & Clubbe*, C. (2017). In: Willis*, K. J. (ed.) *State of the World's Plants 2017*. Richmond: Royal Botanic Gardens, Kew, pp.58–63.

6,075 species are now documented as invasive. Invasive plants are among the most important drivers of biodiversity loss. We examine the different methods used to control invasive species, the most studied invasive families, life forms, and the countries undertaking invasive species research, as well as providing an overview of new technologies that are helping with early detection, monitoring, control and elimination of new plant invasions.

Extinction risk and threats to plants.

Nic Lughadha*, E., Canteiro*, C., Bachman*, S., Baines*, D., Gardiner*, L. M., Meagher, T., Rivers, M., Schuiteman*, A., Williams*, E. & Hargreaves*, S. (2017). In: Willis*, K. J. (ed.) *State of the World's Plants 2017* Richmond: Royal Botanic Gardens, Kew, pp.72–77.

Plant traits help predict fates: epiphytes and late bloomers may be more vulnerable to extinction than other plants. Despite ongoing efforts to increase the rate at which plants are evaluated for their extinction risk, there is a widespread recognition that many plants may become extinct before they have been recognised as being at risk, and perhaps even before they have been discovered.



Island biodiversity conservation needs palaeoecology.

Nogué, S., de Nascimento, L., Froyd, C. A., Wilmshurst, J. M., de Boer, E. J., Coffey, E. E. D., Whittaker, R. J., Fernández-Palacios, J. M. & Willis*, K. J. (2017). *Nature Ecology & Evolution* 1: 0181. DOI: 10.1038/s41559-017-0181.

The discovery and colonization of islands by humans has invariably resulted in their widespread ecological transformation. The small and isolated populations of many island taxa, and their evolution in the absence of humans and their introduced taxa, mean that they are particularly vulnerable to human activities. Consequently, even the most degraded islands are a focus for restoration, eradication, and monitoring programmes to protect the remaining endemic and/or relict populations. Here, we build a framework that incorporates an assessment of the degree of change from multiple baseline reference periods using long-term ecological data. The use of multiple reference points may provide information on both the variability of natural systems and responses to successive waves of cultural transformation of island ecosystems, involving, for example, the alteration of fire and grazing regimes and the introduction of non-native species. We provide exemplification of how such approaches can provide valuable information for biodiversity conservation managers of island ecosystems.



Using network connectivity to prioritise sites for the control of invasive species.

Perry, G. L. W., Moloney, K. A. & Etherington*, T. R. (2017). *Journal of Applied Ecology* 54: 1238-1250. DOI: 10.1111/1365-2664.12827.

Habitat connectivity is a crucial determinant of population dynamics in fragmented landscapes. The corollary of the emphasis on maintaining connectivity to enhance the movement of organisms is that disrupting connectivity should minimise it. Here, we evaluate the efficiency of an invasive species control strategy that targets the most connected habitats in a landscape.

A network (spatial graph) provides an intuitive representation of a landscape, and the topology of this network can be used to identify the most connected patches. We implemented a simulation model of the spread of an invasive species on a network and used it to evaluate whether targeting the better-connected components of the landscape enhances control effectiveness.

Control strategies based on network topology consistently outperformed both a null strategy of random habitat selection and one based on separation distance alone. The advantages of the connectivity-based strategy were strongest in the early phases of the invasion process, when a small number of habitats are occupied at low population density. However, if long-distance dispersal events were common, the advantages of the connectivity approach weakened.

The performance of the connectivity-based strategy is robust to habitat-level demographic stochasticity. In

fact, connectivity-based targeting outperforms a strategy focussing on source habitats, with the additional benefit that it requires less information to be implemented.

Synthesis and applications. Our simulation model outcomes demonstrate that deliberately targeting the best-connected components of a landscape is an efficient control strategy for invasive species when long-distance dispersal is infrequent, and it is likely to be cheaper than other alternatives such as targeting population sources. Network scientists have developed a range of methods designed to identify the minimal set of nodes on a graph that will disrupt the network as a whole; these tools have potential to aid in the design of more effective control strategies.

Isolation and characterization of microsatellite loci in *Sorbus porrigentiformis* and cross-amplification in *S. aria* and *S. rupicola* (Rosaceae).

Piñeiro*, R., Karrman-Bailey*, F., Cowan*, R. S. & Fay*, M. F. (2017). *Applications in Plant Sciences* 5 (2): 1600150. DOI: 10.3732/apps.1600150.

Premise of the study

Southwestern Britain is an emblematic hotspot of polyploid diversity of whitebeams (*Sorbus aria* agg.: Rosaceae) with ca. 30 polyploid endemic species. The tetraploid *S. porrigentiformis* is postulated as one of the parents of most of these endemics, along with the sexual diploid *S. aria* s. str. and the tetraploid *S. rupicola*.





Methods and Results

We isolated 16 nuclear microsatellite loci from *S. porrigentiformis* and characterized them on 45 trees representing the three putative parental species. Eleven loci were polymorphic, and eight of them exhibited species-specific alleles. Allele numbers ranged from one to 11, and observed heterozygosity ranged from 0.40 to 1.00. The intraspecific levels of variation were very low, in agreement with the facultative apomictic reproduction hypothesized for this species.

Conclusions

The species-specific alleles will be useful for tracing the origin of the narrowly distributed *Sorbus* taxa. In addition, the assessment of diversity levels will help design a conservation strategy for the polyploid complex.

Conserving *Grammangis spectabilis*.

Rajaovelona*, L. R. & Gardiner*, L. M. (2017). *Orchid Review* 125: 20–23.

Landy R. Rajaovelona and Lauren M. Gardiner report on a project to save this critically endangered orchid from south Madagascar.

Thermal buffering capacity of the germination phenotype to global temperature change across the environmental envelope of the Cactaceae.

Seal*, C. E., Daws*, M. I., Flores, J., Ortega-Baes, P., Galíndez, G., León-Lobos, P., Sandoval, A., Stuva, A. C., Bullón, N. R., Dávila-Aranda, P., Ordoñez-Salanueva, C. A., Yáñez-Espinosa, L., Ulian*, T., Amosso, C., Zubani, L., Bilbao, A. T. & Pritchard*, H. W. (2017). *Global Change Biology* 23: 5309–5317. DOI: 10.1111/gcb.13796.

Recruitment from seeds is among the most vulnerable stage for plants as global temperatures change. While germination is the means by which the vast majority of the world's flora regenerate naturally, a framework for accurately predicting which species are at greatest risk of germination failure during environmental perturbation is lacking. Taking a physiological approach, we assess how one family, the Cactaceae, may respond to global temperature change based on the thermal buffering capacity of the germination phenotype. We selected 55 cactus species from the Americas, all geo-referenced seed collections, reflecting the broad environmental envelope of the family across 70° of latitude and 3700 m of altitude. We then generated empirical data of the thermal germination response from which we estimated the minimum (T_b), optimum (T_o) and ceiling (T_c) temperature for germination and the thermal time (θ₅₀)

for each species based on the linearity of germination rate with temperature. Species with the highest T_b and lowest T_c germinated fastest, and the interspecific sensitivity of the germination rate to temperature, as assessed through $\phi 50$, varied tenfold. A left-skewed asymmetry in the germination rate with temperature was relatively common but the unimodal pattern typical of crop species failed for nearly half of the species due to insensitivity to temperature change at T_0 . For 32 fully characterized species, seed thermal parameters correlated strongly with the mean temperature of the wettest quarter of the seed collection sites. By projecting the mean temperature of the wettest quarter under two climate change scenarios, we predict under the least conservative scenario (+3.7°C) that 25% of cactus species will have reduced germination performance, whilst the remainder will have an efficiency gain, by the end of the 21st century.

Predicting the global incidence of seed desiccation sensitivity.

Wyse*, S. V. & Dickie*, J. B. (2017). *Journal of Ecology* 105: 1082–1093. DOI: 10.1111/1365-2745.12725.

The ability of seeds to tolerate desiccation plays an important role in plant regeneration ecology. Globally, the majority of species produce desiccation-tolerant

(orthodox) seeds, while comparatively few produce desiccation-sensitive (recalcitrant) seeds that are unable to survive dehydration. The trait has important implications for species conservation, as desiccation-sensitive species cannot be conserved using traditional seed banking techniques. In addition, these species may be less resilient to the increases in droughts predicted for some regions under climate change scenarios.

The best available resource on seed desiccation tolerance is the Royal Botanic Gardens, Kew's Seed Information Database. This database contains seed desiccation-sensitivity data for over 18 000 taxa, approximately 3% of which have desiccation-sensitive seeds. However, this database is likely biased towards desiccation-tolerant species. Previous attempts to estimate the proportion of seed plants with desiccation-sensitive seeds have ranged from 7% to 50%. Here, we aimed to overcome sampling bias to derive a best estimate for the proportion of seed plants with desiccation-sensitive seeds, based on current data.

We used a recently developed method, based on taxonomic relatedness, to account for sampling bias and estimate the proportion of seed plants with desiccation-sensitive seeds. As a comparison, given that seed desiccation sensitivity is strongly related to habitat, we repeated our analyses using habitat as a basis.

The predictions from our taxonomy-based models ranged between estimates of 7.5% and 19.6% of the





world's seed-plant species with desiccation-sensitive seeds, depending on model type, while the habitat-based models suggested a value of approximately 8%. Our evidence suggests that, based on current data, the best estimate of the proportion of species with desiccation-sensitive seeds is likely to be approximately 8%. Tropical and subtropical moist broadleaf forests had the highest incidence of seed desiccation sensitivity, where an estimated 18.5% of the seed-plant flora possessed the trait.

Synthesis

Alongside our estimation of the numbers of species with desiccation-sensitive seeds, we provide data on taxa and habitats where this trait may be most prevalent. These findings can be used to support conservation planning, particularly with respect to providing decision support for in and ex situ conservation techniques.

Orchid prospecting: from the birth of the tetrad to the Google Era.

Bateman*, R. M. (2017). *Journal of the Hardy Orchid Society* 14 (3): 95–103.

No abstract available.

IOCC VI. The Sixth International Orchid Conservation Congress: Hong Kong, May 2016.

Fay*, M. F. (2016). *Orchid Conservation News* 3: 1–4.

No abstract available.

IUCN SSC Orchid Specialist Group.

Fay*, M. F. (2017). In: *2015 Annual Report of the Species Survival Commission and the Global Species Programme*.

No abstract available.

Using genetic data to inform conservation management – *Cypripedium calceolus*.

Fay*, M. F. (2017). In: Swartz, N. D. & Dixon, K. D. (eds). *Conservation methods for terrestrial orchids*. Plantation: J. Ross Publishing. pp.176–177.

No abstract available.

Discovery of a second population of the Critically Endangered Madagascan suicide palm *Tahina spectabilis*.

Gardiner*, L. M., Rabehevitra*, D., Letsara, R. & Shapcott, A. (2017). *Oryx* 51 (2): 205–206. DOI: 10.1017/S003060531700014X.

No abstract available.

Developing *ex situ* conservation collections for the native succulents of the British Virgin Islands.

Gdaniec, A. & Hamilton*, M. A. (2017). *CactusWorld* 35 (3): 149–158.

No abstract available.



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



Useful plants – medicines.

Allkin*, R., Patmore*, K., Black*, N., Booker, A., Canteiro*, C., Dauncey, E., Edwards*, S., Forest*, F., Giovannini*, P., Howes*, M.-J. R., Hudson*, A., Irving*, J., Leon*, C., Milliken*, W., Nic Lughadha*, E., Schippmann, U. & Simmonds*, M. S. J. (2017). *In: Willis*, K. J. (ed.) State of the World's Plants 2017*. Richmond: Royal Botanic Gardens, Kew, pp.22–29

At least 28,187 plant species are currently recorded as being of medicinal use. Fewer than 16% (4,478) of the species used in plant-based medicines are cited in a medicinal regulatory publication. It is clear that the international trade in medicinal plants is growing fast.

Segregation of hydroxycinnamic acid esters mediating sweetpotato weevil resistance in storage roots of sweetpotato.

Anyanga, M. O., Yada, B., Yencho, G. C., Ssemakula, G. N., Farman, D. I., Mwanga, R. O. M. & Stevenson*, P. C. (2017). *Frontiers in Plant Science* 8: DOI: 10.3389/fpls.2017.01011.

Resistance to sweetpotato weevils (*Cylas* spp.) has been identified in several sweetpotato (*Ipomoea batatas*) landraces from East Africa and shown to be conferred by hydroxycinnamic acids that occur on the surface of storage roots. The segregation of resistance in this crop is unknown and could be monitored using these chemical traits as markers for resistance in F1 offspring from breeding programs. For the first time in a segregating population, we quantified the plant chemicals that confer resistance and evaluated levels of insect colonization of the same progeny in field and laboratory studies. We used a bi-parental mapping population of 287 progenies from a cross between *I. batatas* 'New Kawogo,' a weevil resistant Ugandan landrace and *I. batatas* 'Beauregard' a North American orange-fleshed and weevil susceptible cultivar. The progenies were evaluated for resistance to sweetpotato weevil, *Cylas puncticollis* at three field locations that varied climatically and across two seasons to determine how environment and location influenced resistance. To augment our field open-choice resistance screening, each clone was also evaluated in a no choice experiment with weevils reared in the laboratory. Chemical analysis was used to determine whether differences in resistance to weevils were associated with plant compounds previously identified as conferring resistance. We established linkage between field and laboratory resistance to *Cylas* spp. and sweetpotato root chemistry. The data also showed that resistance in sweetpotato was mediated by root chemicals in most but not all cases. Multi-location trials especially from Serere data provided evidence

that the hydroxycinnamic acid esters are produced constitutively within the plants in different clonal genotypes and that the ecological interaction of these chemicals in sweetpotato with weevils confers resistance. Our data suggest that these chemical traits are controlled quantitatively and that ultimately a knowledge of the genetics of resistance will facilitate management of these traits, enhance our understanding of the mechanistic basis of resistance and speed the development of new sweetpotato varieties with resistance to sweetpotato weevil.

Frutales silvestres y promisorios de Pando (Wild and promising fruit trees of Pando, Bolivia).

Araujo-Murakami, A., Reyes, J.-F. & Milliken*, W. (2016). Bolivia: Herencia / Museo de Historia Natural Noel Kempff Mercado.

Una de evidencias más explícitas del amplio uso de la biodiversidad por los pueblos de la Amazonía son las frutas provistas por distintos árboles y palmeras. Han sido alimento desde tiempos inmemoriales y aún hoy representan una parte importante de la dieta familiar de las poblaciones indígenas y campesinas y, también, generan recursos económicos importantes a la economía local. Para el Departamento de Pando, por ejemplo, al igual que el resto de la Amazonía Norte de Bolivia, el fruto de la castaña es su principal producto de exportación y la base de su economía. Y, aunque existen en la región una gran cantidad de otras frutas con cualidades alimenticias, medicinales o para fabricación de cosméticos, este potencial es todavía poco utilizado en procesos productivos. Por otra parte, han sido la base de la conservación de la región y tienen la capacidad de seguir siéndolo porque son recursos renovables. Para alentar este proceso, ponemos a disposición del público el presente libro "Frutales silvestres y promisorios de Pando". En el libro se enlista y menciona 106 especies frutales silvestres y cultivados que crecen en Pando, de las cuales 84 son silvestres, además de 22 que son cultivadas en la región cuyo origen o distribución natural no llega a Bolivia. A cada una de las especies prioritarias se la ubica taxonómicamente y se describe la planta, su distribución, su hábitat natural. Además, se presenta datos del estado del cultivo, usos alimenticios y otros usos y se describe las técnicas de recolección y almacenamiento. También, se describe el cultivo y la gestión de la plantación. Finalmente, se describe el potencial económico de especies prioritarias. La información está organizada en tres secciones: En la primera se presenta información en detalle de 15 especies consideradas prioritarias para la vida del hombre amazónico y de gran potencial económico. En la segunda parte se presentan

16 especies con menor uso actual, pero que pueden llegar a ser importantes para la vida y economía de la región, con información más específica de los frutales. En la tercera sección se presenta información resumida de 13 especies introducidas de amplio uso en la Amazonía. No está demás mencionar que en Pando existen muchas otras especies silvestres con frutos comestibles que no están enlistadas en el presente documento. Creemos que esta información puede constituirse en un insumo importante para la planificación de actividades productivas y de seguridad alimentaria en base a especies frutales para Pando y para el resto de la región amazónica. Consideramos que, por la vocación forestal del departamento, los huertos frutales y el desarrollo de sistemas agroforestales que incorporan estas especies pueden ser la mejor forma de asegurar un manejo productivo responsable y sostenible, además de contribuir a la conservación de los bosques existentes pensando en las generaciones futuras. El presente libro ha sido posible gracias al apoyo financiero de la 'Iniciativa Darwin' (Darwin Initiative) y la 'fundación innocent' (innocent foundation) del Reino Unido. Fue desarrollado a través de la alianza entre tres instituciones: el Museo de Historia Natural Noel Kempff Mercado de la Universidad Autónoma Gabriel Rene Moreno, Herencia y el Real Jardín Botánico de Kew (Royal Botanic Gardens, Kew), a través del proyecto Bosques del Futuro.

Fundamental species traits explain provisioning services of tropical American palms.

Cámara-Leret*, R., Faurby, S., Macía, M. J., Balslev, H., Gödel, B., Svenning, J.-C., Kissling, W. D., Rønsted, N. & Saslis-Lagoudakis, C. H. (2017). *Nature Plants* 3: 16220. DOI: 10.1038/nplants.2016.220.

The well-being of the global human population rests on provisioning services delivered by 12% of the Earth's ~400,000 plant species. Plant utilization by humans is influenced by species traits, but it is not well understood which traits underpin different human needs. Here, we focus on palms (Arecaceae), one of the most economically important plant groups globally, and demonstrate that provisioning services related to basic needs, such as food and medicine, show a strong link to fundamental functional and geographic traits. We integrate data from 2,201 interviews on plant utilization from three biomes in South America—spanning 68 communities, 43 ethnic groups and 2,221 plant uses—with a dataset of 4 traits (leaf length, stem volume, fruit volume, geographic range size) and a species-level phylogeny. For all 208 palm species occurring in our study area, we test for relations between their traits and perceived value. We find that people preferentially use large, widespread



species rather than small, narrow-ranged species, and that different traits are linked to different uses. Further, plant size and geographic range size are stronger predictors of ecosystem service realization for palm services related to basic human needs than less-basic needs (for example, ritual). These findings suggest that reliance on plant size and availability may have prevented our optimal realization of wild-plant services, since ecologically rare yet functionally important (for example, chemically) clades may have been overlooked. Beyond expanding our understanding of how local people use biodiversity in mega-diverse regions, our trait- and phylogeny-based approach helps to understand the processes that underpin ecosystem service realization, a necessary step to meet societal needs in a changing world with a growing human population.

The Economic Botany Collection at Kew: Analysis of accessions data.

Cornish*, C., Driver, F. & Nesbitt*, M. (2017). *Mobile Museum Working Paper 1*. Royal Botanic Gardens, Kew & Royal Holloway, University of London.

This is the first of a series of Working Papers produced as part of the Mobile Museum Project (www.royalholloway.ac.uk/mobilemuseum).

Variation of theanine, phenolic, and methylxanthine compounds in 21 cultivars of *Camellia sinensis* harvested in different seasons.

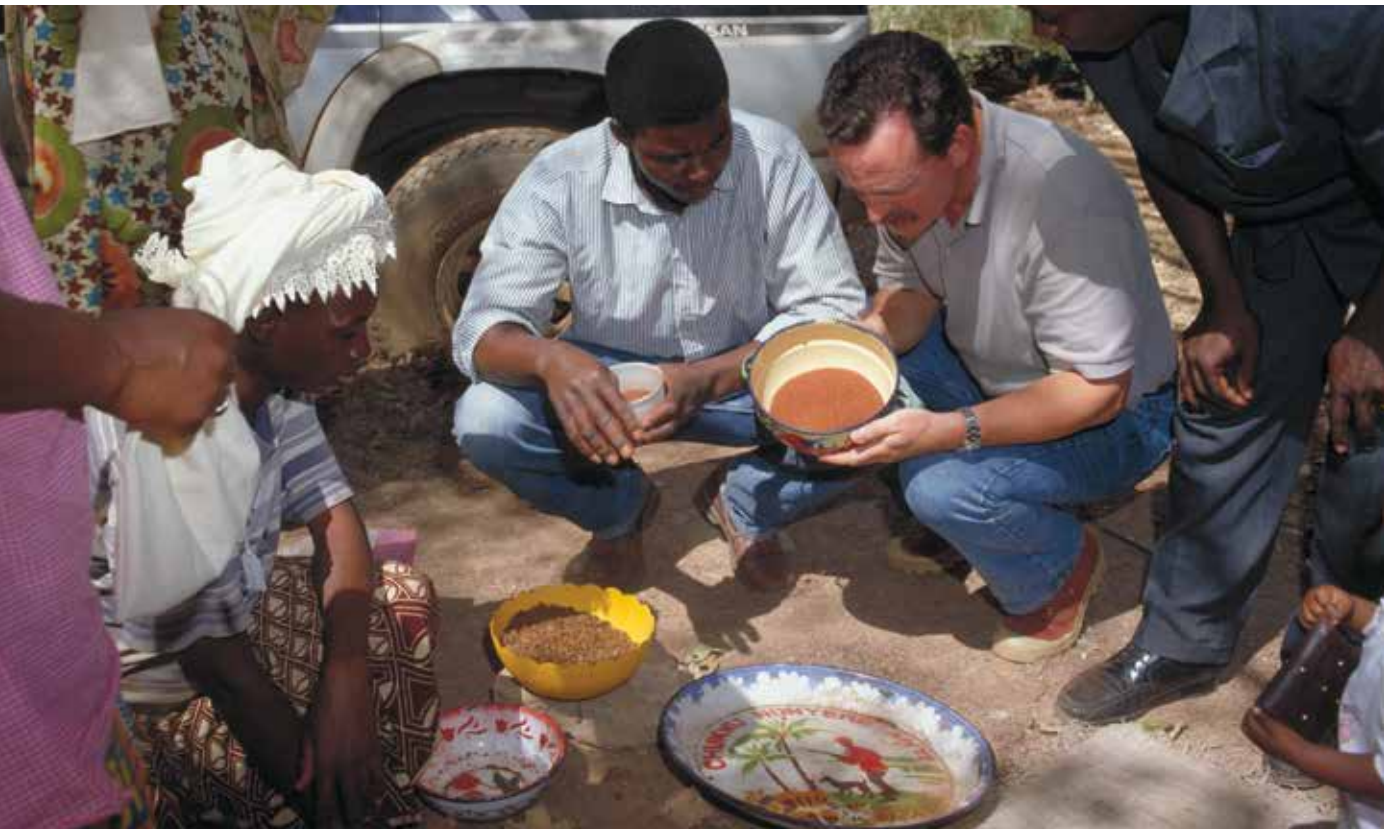
Fang*, R., Redfern, S. P., Kirkup*, D., Porter*, E. A., Kite*, G. C., Terry, L. A., Berry, M. J. & Simmonds*, M. S. J. (2017). *Food Chemistry* 220: 517–526. DOI: 10.1016/j.foodchem.2016.09.047.

This is the first study to use chemometric methods to differentiate among 21 cultivars of *Camellia sinensis* from China and between leaves harvested at different times of the year using 30 compounds implicated in the taste and quality of tea. Unique patterns of catechin derivatives were observed among cultivars and across harvest seasons. *C. sinensis* var. *pubilimba* (You 510) differed from the cultivars of *C. sinensis* var. *sinensis*, with higher levels of theobromine, (+)-catechin, gallic catechin, gallic catechin gallate and theasinensin B, and lower levels of (–)-epicatechin, (–)-epigallocatechin (EGC) and (–)-epigallocatechin gallate (EGCG), respectively. Three cultivars of *C. sinensis* var. *sinensis*, Fuyun 7, Qiancha 7 and Zijuan contained significantly more caffeoylquinic acids than others cultivars. A Linear Discriminant Analysis model based on the abundance of 12 compounds was able to discriminate amongst all 21 tea cultivars. Harvest time impacted the abundance of EGC, theanine and afzelechin gallate.

Anatomical changes to the wood of *Croton sonderianus* Muell. (Euphorbiaceae) when charred at different temperatures.

Gasson*, P., Cartwright, C. & Dias-Leme, C. L. (2017). *IAWA Journal* 38 (1): 117–123. DOI: 10.1163/22941932-20170161.

Wood retains most of its anatomical characteristics when charred, but charring temperature determines the appearance of the resulting charcoal and this depends largely on the proportions and distribution of the constituent vessels, fibres and parenchyma, as well as moisture content. This study describes the structural changes in the charcoal of the wood of *Croton sonderianus* Muell. Arg. at two temperatures, 400°C or 600°C. This species is an important source of charcoal in the caatinga of the northeast part of Brazil. The samples were heated for ten minutes to reach treatment temperature, charred for two hours at either 400°C or 600°C and then left to cool to ambient temperature for 30 to 60 minutes. Our observations showed that most of the changes occurred when charcoal was produced at 600°C, but the qualitative features necessary for identification were retained. At this temperature, cells lost their circular shape, became angular and occasionally amorphous, the middle lamella disappeared and the walls of adjacent cells coalesced, cell walls became thinner, and the prismatic crystals developed cracks and became porous. Our findings are compared with those for two previously studied *Mimosa* species which have an entirely different anatomy.





Medicinal plants used to treat snakebite in Central America: Review and assessment of scientific evidence.

Giovannini*, P & Howes*, M. J. R. (2017). *Journal of Ethnopharmacology* 199: 240–256. DOI: 10.1016/j.jep.2017.02.011

Ethnopharmacological relevance

Every year between 1.2 and 5.5 million people worldwide are victims of snakebites, with about 400,000 left permanently injured. In Central America an estimated 5500 snakebite cases are reported by health centres, but this is likely to be an underestimate due to unreported cases in rural regions. The aim of this study is to review the medicinal plants used traditionally to treat snakebites in seven Central American countries: Belize, Costa Rica, El Salvador, Guatemala, Honduras, Nicaragua and Panama.

Materials and methods

A literature search was performed on published primary data on medicinal plants of Central America and those specifically pertaining to use against snakebites. Plant use reports for traditional snakebite remedies identified in primary sources were extracted and entered in a database, with data analysed in terms of the most frequent numbers of use reports. The scientific evidence that might support the local uses of the most frequently reported species was also examined.

Results

A total of 260 independent plant use reports were recorded in the 34 sources included in this review, encompassing 208 species used to treat snakebite in Central America. Only nine species were reported in at least three studies: *Cissampelos pareira* L., *Piper amalago* L., *Aristolochia trilobata* L., *Sansevieria hyacinthoides* (L.) Druce, *Strychnos panamensis* Seem., *Dorstenia contrajerva* L., *Scoparia dulcis* L., *Hamelia patens* Jacq., and *Simaba cedron* Planch. Genera with the highest number of species used to treat snakebite were *Piper*, *Aristolochia*, *Hamelia*, *Ipomoea*, *Passiflora* and *Peperomia*. The extent of the scientific evidence available to understand any pharmacological basis for their use against snakebites varied between different plant species.

Conclusion

At least 208 plant species are traditionally used to treat snakebite in Central America but there is a lack of clinical research to evaluate their efficacy and safety. Available pharmacological data suggest different plant species may target different symptoms of snakebites, such as pain or anxiety, although more studies are needed to further evaluate the scientific basis for their use.

Impacts of nitrogen and phosphorus: from genomes to natural ecosystems and agriculture.

Guignard*, M. S., Leitch*, A. R., Acquisti, C., Eizaguirre, C., Elser, J. J., Hessen, D. O., Jeyasingh, P. D., Neiman, M., Richardson, A. E., Soltis, P. S., Soltis, D., Stevens, C. J., Trimmer, M., Weider, L. J., Woodward, G. & Leitch*, I. J. (2017). *Frontiers in Ecology and Evolution* 5: 70. DOI: 10.3389/fevo.2017.00070.

Nitrogen (N) and/or phosphorus (P) availability can limit growth of primary producers across most of the world's aquatic and terrestrial ecosystems. These constraints are commonly overcome in agriculture by applying fertilizers to improve yields. However, excessive anthropogenic N and P inputs impact natural environments and have far-reaching ecological and evolutionary consequences, from individual species up to entire ecosystems. The extent to which global N and P cycles have been perturbed over the past century can be seen as a global fertilization experiment with significant redistribution of nutrients across different ecosystems. Here we explore the effects of N and P availability on stoichiometry and genomic traits of organisms, which, in turn, can influence: (i) plant and animal abundances; (ii) trophic interactions and population dynamics; and (iii) ecosystem dynamics and productivity of agricultural crops. We articulate research priorities for a deeper understanding of how

bioavailable N and P move through the environment and exert their ultimate impacts on biodiversity and ecosystem services.

Effect of Chinese herbal medicine on Alzheimer's disease.

Howes*, M. J. R., Fang*, R. & Houghton, P. J. (2017). *International Review of Neurobiology* 135: Neurobiology of Chinese Herbal Medicine, Zeng B.-Y., Zhao K. (eds.): pp. 29–56. DOI: 10.1016/bs.irm.2017.02.003.

Alzheimer's disease (AD) is reaching epidemic proportions yet treatment strategies are limited and are restricted to providing symptomatic relief for the cognitive and behavioral and psychological symptoms of dementia (BPSD). Chinese herbal medicine (CHM) has been a valuable source of medicines for centuries and research has burgeoned in recent years to understand the scientific basis for their use. Some plants have been used in CHM for AD symptoms (e.g., *Polygala tenuifolia*), while others are CHMs for different conditions, but they show mechanistic effects relevant to AD (e.g., *Salvia miltiorrhiza*). Some CHMs (e.g., *Ginkgo biloba* extract, and huperzine A from *Huperzia serrata*) show pharmacological activities relevant to AD, and promising effects on cognitive functions in clinical trials. Other CHMs show effects relevant to BPSD (e.g., *Crocus sativus*). This chapter discusses available scientific evidence for CHM plants and formulae that have been used both traditionally for AD, and those that have been used traditionally but not specifically for AD symptoms, and encompasses chemical, pharmacological and clinical studies. The ethnopharmacological approach to understanding the use of CHMs for AD is also discussed.



Chemical variation and insecticidal activity of *Lippia javanica* (Burm. f.) Spreng. essential oil against *Sitophilus zeamais* Motschulsky.

Kamanula, J. F., Belmain, S. R., Hall, D. H., Farman, D. I., Goyder*, D. J., Mvumi, B. M., Masumbu, F. F. & Stevenson*, P. C. (2017). *Industrial Crops and Products*: 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.

The role of disease in bee foraging ecology.

Koch*, H., Brown, M. J. F. & Stevenson*, P. C. (2017). *Current Opinion in Insect Science* 21: 60–67. DOI: 10.1016/j.cois.2017.05.008.

Diseases have important but understudied effects on bee foraging ecology. Bees transmit and contract diseases on flowers, but floral traits including plant volatiles and inflorescence architecture may affect transmission. Diseases spill over from managed or invasive pollinators to native wild bee species, and impacts of emerging diseases are of particular concern, threatening pollinator populations and pollination services. Here we review how parasites can alter the foraging behaviour of bees by changing

floral preferences and impairing foraging efficiency. We also consider how changes to pollinator behaviours alter or reduce pollination services. The availability of diverse floral resources can, however, ameliorate bee diseases and their impacts through better nutrition and antimicrobial effects of plant compounds in pollen and nectar.

Do linden trees kill bees? Reviewing the causes of bee deaths on silver linden (*Tilia tomentosa*).

Koch*, H. & Stevenson*, P. C. (2017). *Biology Letters* 13 (9): DOI: 10.1098/rsbl.2017.0484.

For decades, linden trees (basswoods or lime trees), and particularly silver linden (*Tilia tomentosa*), have been linked to mass bee deaths. This phenomenon is often attributed to the purported occurrence of the carbohydrate mannose, which is toxic to bees, in *Tilia* nectar. In this review, however, we conclude that from existing literature there is no experimental evidence for toxicity to bees in linden nectar. Bee deaths on *Tilia* probably result from starvation, owing to insufficient nectar resources late in the tree's flowering period. We recommend ensuring sufficient alternative food sources in cities during late summer to reduce bee deaths on silver linden. Silver linden metabolites such as floral volatiles, pollen chemistry and nectar secondary compounds remain underexplored, particularly their toxic or behavioural effects on bees. Some evidence for the presence of caffeine in linden nectar may mean that linden trees can chemically deceive foraging bees to make sub-optimal foraging decisions, in some cases leading to their starvation.

Wild Orchids of ornamental importance.

Lan, S. R., Karasawa, K., Chen, S. C. & Cribb*, P. J. (2017). Beijing: Science Press.

Orchidaceae are the largest family of flowering plants, containing approximately 800 genera and 27000 species, of which not a few are world-famous for their charming flowers such as some species of *Phalaenopsis*, *Cymbidium*, *Dendrobium*, *Cattleya*, *Oncidium*, *Paphiopedilum*, *Pleione*, etc. In the present book, an attempt is made to include as many these wild species as possible in the hope that it will be a useful and convenient reference book for orchidologists, especially orchid breeders and growers. There are altogether 372 genera, 1833 species, 2 subspecies and 28 varieties included in this book. All the species selected here are briefly described in both Chinese (or Japanese) and English.

Forage quality declines with rising temperatures, with implications for livestock production and methane emissions.

Lee*, M. A., Davis*, A. P., Chagunda, M. G. G. & Manning, P. (2017). *Biogeosciences* 14: 1403–1417. DOI: 10.5194/bg-14-1403-2017.

Livestock numbers are increasing to supply the growing demand for meat-rich diets. The sustainability of this trend has been questioned, and future environmental changes, such as climate change, may cause some regions to become less suitable for livestock. Livestock and wild herbivores are strongly dependent on the nutritional chemistry of forage plants. Nutrition is positively linked to weight gains, milk production and reproductive success, and nutrition is also a key determinant of enteric methane production. In this meta-analysis, we assessed the effects of growing conditions on forage quality by compiling published measurements of grass nutritive value and combining these data with climatic, edaphic and management information. We found that forage nutritive value was reduced at higher temperatures and increased by nitrogen fertiliser addition, likely driven by a combination of changes to species identity and changes to physiology and phenology. These relationships were combined with multiple published empirical models to estimate forage- and temperature-driven changes to cattle enteric methane production. This suggested a previously undescribed positive climate change feedback, where elevated temperatures reduce grass nutritive value and correspondingly may increase methane production by 0.9% with a 1°C temperature rise and 4.5% with a 5°C rise (model average), thus



creating an additional climate forcing effect. Future methane production increases are expected to be largest in parts of North America, central and eastern Europe and Asia, with the geographical extent of hotspots increasing under a high emissions scenario. These estimates require refinement and a greater knowledge of the abundance, size, feeding regime and location of cattle, and the representation of heat stress should be included in future modelling work. However, our results indicate that the cultivation of more nutritious forage plants and reduced livestock farming in warming regions may reduce this additional source of pastoral greenhouse gas emissions.

A time-series of methane and carbon dioxide production from dairy cows during a period of dietary transition.

Lee*, M. A., Todd, A., Sutton, M. A., Chagunda, M. G. G., Roberts, D. J. & Rees, R. M. (2017). *Cogent Environmental Science* 3: 1385693. 1-14. DOI: 10.1080/23311843.2017.1385693.

Emissions from dairy farms are contributing to the increased concentrations of greenhouse gases which are linked to recent climate change. Altering diets has been proposed as a greenhouse gas mitigation strategy in dairy systems. The magnitude of mitigation and the time taken for cows to adapt to new diets has not been comprehensively quantified. Methane (CH₄) and carbon dioxide (CO₂) produced by dairy cows was measured for six weeks using the sulphur hexafluoride tracer technique following a change in diet; from barley straw and protein supplements to grazed grass. CH₄ and CO₂ production increased linearly as the animals adapted to their new diets, however, production did not reach an asymptote six weeks into the grazing period. This suggested that metabolic activity and greenhouse gas emissions may not have been at their maximum. There was substantial variation between individuals with high emitting cows producing four times more CH₄ than low producing cows. Cows which produced greater amounts of CH₄ consistently also produced greater CO₂. We demonstrate that feeding regime plays an important role in determining greenhouse gas emissions and we highlight that transition periods in greenhouse gas models and future experiments must be sufficiently large to allow for adaptation.

Chinese medicinal plants, herbal drugs and substitutes: an identification guide.

Leon*, C. & Lin, Y. L. (2017). Royal Botanic Gardens, Kew: Kew Publishing.

This is the first botanically authoritative and practical illustrated identification guide to Chinese medicinal



plants and drugs and their substitutes. It offers authoritative guidance on the identification of the herbal drugs themselves, and the plants from which they are sourced.

Over the past 15 years, the authors have been collecting plant specimens throughout China, using verified species to create typical TCM reference drugs, prepared according to traditional methods.

The herbal drugs included in this book are officially recognised from the Chinese *materia medica* (as defined in the Chinese Pharmacopoeia) and their selection has been based on those popular in international trade, as well as those recognised by the European Herbal and Traditional Medicine Practitioners Association, and those that are easily confused, substituted or adulterated with other plants.

The authors provide a wealth of information on 226 herbal drugs, each illustrated extensively with colour photographs. Plant descriptions are given for official species and substitutes, with details on the harvesting, source and natural range, conservation status, the number of wild Chinese species, and up to date taxonomy and nomenclature for all Latin scientific names. Accompanying this is the derivative drug morphology, showing crude and processed forms, along with drug common names, properties and uses, and toxicity rating. Guidance is given on when to use laboratory-based methods to improve identification robustness.

Resilience potential of the Ethiopian coffee sector under climate change.

Moat*, J., Williams*, J., Baena*, S., Wilkinson*, T., Gole, T. W., Challa, Z. K., Demissew, S. & Davis*, A. P. (2017). *Nature Plants* 3: 17081. DOI: 10.1038/nplants.2017.81.

Coffee farming provides livelihoods for around 15 million farmers in Ethiopia and generates a quarter of the country's export earnings. Against a backdrop of rapidly increasing temperatures and decreasing rainfall, there is an urgent need to understand the influence of climate change on coffee production. Using a modelling approach in combination with remote sensing, supported by rigorous ground-truthing, we project changes in suitability for coffee farming under various climate change scenarios, specifically by assessing the exposure of coffee farming to future climatic shifts. We show that 39–59% of the current growing area could experience climatic changes that are large enough to render them unsuitable for coffee farming, in the absence of significant interventions or major influencing factors. Conversely, relocation of coffee areas, in combination with forest conservation or re-establishment, could see at least a fourfold (>400%) increase in suitable coffee farming area. We identify key coffee-growing areas that are susceptible to climate change, as well as those that are climatically resilient.



The archaeobotany of Aşvan: environment & cultivation in eastern Anatolia from the Chalcolithic to the Medieval period.

Nesbitt*, M., Bates, J., Hillman, G. & Mitchell, S. (2017). Vol. Monograph 33. London: British Institute at Ankara.

This volume contains the final publication of the archaeobotanical remains recovered from four sites at the village of Aşvan in eastern Turkey, which were excavated between 1968 and 1973 as part of the archaeological rescue project in the Keban Dam region. An extensive programme of archaeobotanical research involved detailed study of the modern flora, the observation and recording of pre-mechanised agricultural practices and large-scale recovery of ancient botanical samples by water sieving. The report traces the evolution of cultivation in the region from the Chalcolithic to the Medieval period, charting the dominance of emmer and hulled barley in the Chalcolithic period, the emergence of free-threshing wheats in the Early Bronze Age and the introduction of irrigated summer crops, especially millet, by the Hellenistic period. Detailed attention is also given to the assemblage of weed seeds as proxy evidence for environmental conditions and climate change from around 4000 BC to the present day.

Pollen extracts and constituent sugars increase growth of a trypanosomatid parasite of bumble bees.

Palmer-Young, E. & Thursfield*, L. (2017). *PeerJ* 5: p.e3297. DOI: 10.7717/peerj.3297.

Phytochemicals produced by plants, including at flowers, function in protection against plant diseases, and have a long history of use against trypanosomatid infection. Floral nectar and pollen, the sole food sources for many species of insect pollinators, contain phytochemicals that have been shown to reduce trypanosomatid infection in bumble and honey bees when fed as isolated compounds. Nectar and pollen, however, consist of phytochemical mixtures, which can have greater antimicrobial activity than do single compounds. This study tested the hypothesis that pollen extracts would inhibit parasite growth. Extracts of six different pollens were tested for direct inhibitory activity against cell cultures of the bumble bee trypanosomatid gut parasite *Crithidia bombi*. Surprisingly, pollen extracts increased parasite growth rather than inhibiting it. Pollen extracts contained high concentrations of sugars, mainly the monosaccharides glucose and fructose. Experimental manipulations of growth media showed that supplemental monosaccharides (glucose and fructose) increased maximum cell density, while a common floral

phytochemical (caffeic acid) with inhibitory activity against other trypanosomatids had only weak inhibitory effects on *Crithidia bombi*. These results indicate that, although pollen is essential for bees and other pollinators, pollen may promote growth of intestinal parasites that are uninhibited by pollen phytochemicals and, as a result, can benefit from the nutrients that pollen provides.

Tropical ulcer plant treatments used by Papua New Guinea's Apsokok nomads.

Prescott*, T. A. K., Homot, P., Lundy, F. T., Fang*, R., Patrick, S., Cámara-Leret*, R. & Kiapranis, R. (2017). *Journal of Ethnopharmacology* 205: 240–245. DOI: 10.1016/j.jep.2017.05.001.

Ethnopharmacological Relevance

The tropical ulcer is a debilitating bacterial infection that is common in Papua New Guinea. Deploying healthcare infrastructure to remote and inaccessible rainforest locations is not practical, therefore local plants may be the best treatment option. Here we present an ethnobotanical survey of the tropical ulcer plant medicines used by the semi-nomadic Apsokok who roam the remote central mountains of Papua New Guinea's West New Britain Province. In vitro biological activity in assays relevant to tropical ulcer wound healing is also presented.

Materials and Methods

Focus groups and semi-structured interviews were used to acquire information on the uses of plants, vouchers of which were identified by comparison with authentic herbarium specimens. Antibacterial disc diffusion assays with *Staphylococcus aureus* and *Fusobacterium ulcerans*, MMP-9 enzyme inhibition and dermal fibroblast stimulation assays were carried out on plant saps and aqueous extracts of plant material. LC-MS was used to identify known plant metabolites.

Results

The ethnobotanical survey identified sixteen species that were used to treat tropical ulcers, all of which were applied topically. A subset of twelve species were investigated further in vitro. Four species produced zones of inhibition with *S. aureus*, all 12 species provided low level inhibition of MMP-9 and 8 species stimulated dermal fibroblast proliferation, although cytotoxicity occurred at higher concentrations. The extract of *Homalium foetidum* Benth. inhibited *S. aureus* and MMP-9 while at lower sub-cytotoxic concentrations stimulated fibroblast proliferation. Trans-3-O-p-coumaroylquinic acid cis-3-O-p-coumaroylquinic acid were detected in the aqueous extract of *H. foetidum*.

Conclusions

Topical application of plant saps to wounds results in very high localised concentrations of plant metabolites which is likely to result in inhibition of MMP proteases. *H. foetidum* is a candidate plant for tropical ulcer treatment in remote areas.

A mini HIP HOP assay uncovers a central role for copper and zinc in the antifungal mode of action of allicin.

Prescott*, T. A. K. & Panaretou, B. A. (2017). *Journal of Agricultural and Food Chemistry* 65 (18): 3659–3664. DOI: 10.1021/acs.jafc.7b00250.

Garlic contains the organosulfur compound allicin which exhibits potent antifungal activity. Here we demonstrate the use of a highly simplified yeast chemical genetic screen to characterize its mode of action. By screening 24 validated yeast gene deletion “signature” strains for which hypersensitivity is characteristic for common antifungal modes of action, yeast lacking the high affinity Cu²⁺ transporter Ctr1 was found to be hypersensitive to allicin. Focusing on transition metal related genes identified two more hypersensitive strains lacking the Cu²⁺ and Zn²⁺ transcription factors Mac1 and Zap1. Hypersensitivity in these strains was reversed by the addition of Cu²⁺ and Zn²⁺ ions, respectively. The results suggest the antifungal activity of allicin is mediated through restricted Cu²⁺ and Zn²⁺ uptake or inhibition of Cu²⁺ and Zn²⁺ metalloproteins. As certain antimicrobial modes of action are much more common than others, the approach taken here provides a useful way to identify them early on.



Leaf trichomes and foliar chemistry mediate defence against glasshouse thrips; *Heliothrips haemorrhoidalis* (Bouché) in *Rhododendron simsii*.

Scott-Brown*, A. S., Gregory, T., Farrell*, I. W. & Stevenson*, P. C. (2016). *Functional Plant Biology* 43 (12): 1170–1182. DOI: 10.1071/FP16045.

Herbivore defence mechanisms are a costly diversion of resources away from growth and reproduction. Thus time-limited and tissue specific expression in critical plant parts is more efficient as defined by optimal defence theory. Surprisingly little is known about *Rhododendron* herbivore defence but it may be mediated by combined chemical and physical mechanisms. *Rhododendron simsii* Planch. survives cyclic infestations of a leaf-feeding thrips, *Heliothrips haemorrhoidalis* (Bouché), which severely damage mature leaves but avoid terminal young leaves suggesting specific, localised defence expression. We examined correlations between the distribution of thrips and feeding damage with density of trichomes and the concentration of the diterpenoid, grayanotoxin I, a compound implicated in but not previously reported to mediate invertebrate defence in *Rhododendron*. Our data show that as leaves matured the number of thrips and area of feeding damage increased as trichome density and grayanotoxin I concentration decreased, this inverse correlation suggesting trichomes and grayanotoxin I mediate defence in younger leaf tissue. Grayanotoxin I was tested against *H. haemorrhoidalis* and was toxic to immature life stages and repellent to the adult thrips, reducing numbers of first instars emerging on leaves when applied at ecologically relevant concentrations. This

work demonstrates that the pattern of defensive traits in foliage of a species of *Rhododendron* is key to its ability to tolerate cyclic infestations of a generalist herbivore, effectively conserving vital tissues required for growth and reproduction.

The gardener's companion to medicinal plants.

Simmonds*, M. S. J., Howes*, M.-J. & Irving*, J. (2017). UK: Frances Lincoln.

The beautifully illustrated *Gardener's Companion to Medicinal Plants* is an A-Z of healing plants and home remedies, featuring more than 270 plants used for their medicinal properties, as well as 24 practical projects for homemade teas, oils, tinctures and creams with a tradition of safe use. Each plant is illustrated with a beautiful work of botanical art from Kew's archives.

Many of our most important drugs are derived from plants and many more are yet to be discovered: much research in this area is overseen by the Royal Botanic Gardens, Kew where the book's three authors are employed. This contemporary Herbal offers a fresh take on the 5,000-year-old tradition of recording plants with medicinal value and with life-changing benefits.

Plant conservation policies and international trade.

Smyth*, N., Dhanda*, S., Williams*, C., Cable*, S., Ralimanana*, H., Simpson*, R. & Clarke, G. (2017). In: Willis*, K. J. (ed.) *State of the World's Plants 2017*. Richmond: Royal Botanic Gardens, Kew, pp.78–85



2016 was an exciting year for conservation policy. Two of the major conventions that help to protect plant diversity – the Convention on Biological Diversity (CBD) and the Convention on International Trade in Endangered Species of Wild Fauna and Flora (CITES) – hosted conferences to advance global conservation aims, and 31,517 plant species are currently listed on the CITES appendices. It was also the year when the UN Sustainable Development Goals officially came into force.

Pesticidal plants in African agriculture: local uses and global perspectives.

Stevenson*, P. C. & Belmain, S. R. (2016). *Outlooks on Pest Management* 27 (5): 226-230. DOI: 10.1564/v27_oct_10.

In 2001 in this publication we drew attention to the wealth of potential in pesticidal plants in Africa. We reported from a regional focus on West Africa where we had been undertaking research identifying new plant sources of pesticides, verifying their efficacy and considering how we could apply our scientific knowledge to improving the way farmers used them. Here, 15 years on, we consider how this research and development domain has changed, what are the success stories and priorities for Africa and where is this sector heading. Plants cannot move so must defend themselves against herbivores where they stand. We occasionally encounter these defensive traits when we are stung by nettles or pricked by a cactus. However, most plants depend on non-physical chemical mechanisms of defence which are often subtle but highly effective survival strategies. Farmers across the world have for centuries exploited these biological activities and used plants that have particularly potent defence chemicals to control pests in stored food or in the field. In fact, the earliest commercial pesticides were of plant origin such as rotenone and nicotine but the dawn of industrial organic chemistry provided a suite of highly effective pest control agents that left plant chemistry far behind. Yet, as the negative environmental impacts of synthetic chemicals began to emerge in the 1960s and 70s, the pendulum swung back towards more natural pest management strategies during the 1980s and 90s. Scientists were again full of optimism that plants might provide the next generation of effective but environmentally benign pesticides. A huge amount of time and resource was invested to study plants for their potential as pesticides. The better studied was the Neem tree (*Azadirachta indica*) which produces tetratriterpenoid feeding repellents and development inhibitors including azadirachtin A and several analogues. While some plant products



have had limited commercial success globally these have largely been restricted to Neem (triterpenoids), Derris (rotenoids), Pyrethrum (pyrethrins) and various mixtures of essential oil products (e.g. 1, 8 cineole, α -pinene, verbenone). The optimism of the 80s and 90s unfortunately did not deliver a revolution in more natural pest control products, and a recent assessment of biological pesticides of any kind suggests they constitute less than 1% of all pest control products, with pesticidal plants being a small fraction of this.

Plant secondary metabolites in nectar: impacts on pollinators and ecological functions.

Stevenson*, P. C., Nicolson, S. W. & Wright, G. A. (2017). *Functional Ecology* 31: 65–75. DOI: 10.1111/1365-2435.12761.

The ecological function of secondary metabolites in plant defence against herbivores is well established, but their role in plant–pollinator interactions is less obvious. Nectar is the major reward for pollinators, so the occurrence of defence chemicals in the nectar of many species is unexpected. However, increasing evidence supports a variety of potential benefits for both plant and pollinator from these compounds.

Beneficial effects may include: (i) mediating specialization in plant–pollinator interactions, (ii) protecting nectar from robbery or larceny and (iii) microbial activity including preservation of nutrients in nectar from degradation and reduction in disease levels in pollinators.

Secondary metabolites in nectar can be toxic or repellent to flower visitors, but equally they can go undetected or even make nectar more apparent or attractive. These biological effects are concentration dependent, so must be considered at a range of ecologically relevant doses. For example, caffeine occurs in nectar and improves honeybee memory for odours associated with food rewards, which enhances pollen transfer at naturally occurring concentrations but is repellent to honeybees at higher concentrations.

This review synthesizes evidence from recent literature that supports selection for secondary metabolites in floral nectar as an adaptation that drives the co-evolution between plants and their pollinators. However, their presence in nectar could still simply be a consequence of their defensive role elsewhere in the plant (pleiotropy). We highlight the need for more studies demonstrating measurable benefits to the plant, the importance of exposure levels and effects on target species beyond the current emphasis on alkaloids and bees.

Macroscopic authentication of Chinese *materia medica* (CMM): A UK market study of seeds and fruits.

van der Valk, M. A., Leon*, C. J. & Nesbitt*, M. (2017). *Journal of Herbal Medicine*: DOI: 10.1016/j.hermed.2017.03.007.

This small-scale macroscopic and quantitative authentication study, the first of its kind in the UK and elsewhere, assesses the identity and purity (excluding pesticides and heavy metals) of a selection of Chinese *materia medica* (CMM) seeds and fruits on the UK market. 25 fruit and seed CMM were chosen based on their inclusion in the Chinese Pharmacopoeia (2010, referred hereafter as 'official species'), maximum dimension of 10 mm, and regular use in Traditional Chinese Medicine (TCM) practice in the UK according to UK practitioners. In 2012 samples were obtained



from six TCM wholesale traders and eight retail dispensaries in southeast England. Macroscopic identity and purity testing was undertaken drawing on expertise at the Royal Botanic Gardens, Kew and its collection of vouchered CMM reference drugs, herbarium specimens and published identification texts. Of the 25 CMM requested from suppliers, 23 were obtained, represented by 211 samples. 191 samples were identified as being sourced from the correct drug; 20 were identified as sourced from unofficial species. Of the 191 correct samples, 5 displayed major contamination by other plant material, stones, earth, etc. (defined as >5% of sample volume), and 12 had minor contamination (2–5%). 95% of samples derived from medicinally cultivated plants were sourced from an official species, 5% were contaminated; in contrast, 78% of wild-sourced CMM samples were sourced from an official species, and 14% showed contamination. These results aim to guide the further development of good practice in TCM herbal drug quality control, for which suggestions are provided.

Editorial: How can secretomics help unravel the secrets of plant-microbe interactions.

Vincent, D., Plummer, K. M., Solomon, P. S., Lebrun, M. H., Job, D. & Rafiqi*, M. (2016). *Frontiers in Plant Science* 7: 1777. DOI: 10.3389/fpls.2016.01777.

Secretomics describes the global study of proteins that are secreted by a cell, a tissue or an organism, and has recently emerged as a field for which interest is rapidly growing. The versatility of oomycetes, fungi, and bacteria allows them to associate with plants in many ways depending on whether they grow as a biotroph, hemibiotroph, necrotroph, or saprotroph. When interacting with a live organism, a microbe will invade its plant host and manipulate its metabolism either detrimentally if it is a pathogen or beneficially if it is a symbiont. Deciphering secretomes became a crucial biological question when an increasing body



of evidence indicated that secreted proteins were the main effectors initiating interactions, whether of pathogenic or symbiotic nature, between microbes and their plant hosts.

Plants, war and the natural capital of empire.

Wearn*, J. (2017). *The Linnean* 33 (1): 20–24.

Plants and their derivative products have frequently been integral to, and the sources of, conflict within the framework of imperial trade and international law.

The flora of the Somme battlefield: a botanical perspective on a post-conflict landscape.

Wearn*, J. A., Budden*, A. P., Veniard*, S. C. & Richardson, D. (2017). *First World War Studies* 8: 63–77.

The unmistakable devastation wrought on the battlefields of the First World War was epitomized in the Somme region of northern France in 1916. The Battle of the Somme became an infamous embodiment of death and destruction, characters which prevailed during subsequent decades. However, the process of healing – of people and landscape – has been central to the legacy of the Somme. Natural regeneration went hand-in-hand with revived agricultural livelihoods, pilgrimages to war cemeteries, and the introduction of commemorative planting to reinforce national identities and provide an atmosphere of tranquillity. The long overlooked wartime activities of Sir Arthur Hill, former Director of the Royal Botanic Gardens, Kew, provide a unique baseline for examining these changes. Hill purposefully recorded the wild flora immediately after the Battle and pioneered horticultural work with the Imperial War Graves Commission. We present here a scientific and cultural analysis of the post-conflict physical and experiential botanical transformation of the Somme. We identify three distinctive components – the wild, the managed and the planted – which now form a mosaic across this land, and place the Somme in the wider context of polemobotany and the study of conflict landscapes. Plants form the principal setting and also the main adornments for remembrance on the Somme: timeless purveyors of memory. Thus, the botanical legacy of the Somme remains potent a century on.

Climate change – which plants will be the winners?

Willis*, K., Carretero*, J., Enquist, B., Kuhn*, N., Tovar*, C. & Vandvik, V. (2017). In: Willis*, K. J. (ed.) *State of the World's Plants 2017*. Richmond: Royal Botanic Gardens, Kew. pp.42–49

Plants with thicker leaves, efficient water-use strategies, deeper roots and higher wood density are better adapted to cope with future climate change. Plant responses to climate change follow three main trajectories: move, adapt or go extinct.

The natural capital of city trees.

Willis*, K. J. & Petrokofsky, G. (2017). *Science* 356 (6336): 374–376. DOI: 10.1126/science.aam9724.

The term “natural capital” refers to elements of nature that, directly or indirectly, produce value for people. Determining the location and quality of natural capital assets, and the ecosystem services that they provide for human well-being, is now underway in many countries, not just in the countryside but also across cities. One example of such natural capital is provided by city trees, which can take up substantial amounts of carbon dioxide (1) and also cause local cooling, thereby ameliorating the urban heat island effect (2). City vegetation can also reduce pollution and improve human health. However, understanding the characteristics of particular species is critical, and planting the wrong species in the wrong places can cause unintended problems.

Bee nutrition. [Patent application].

Wright, G. A., Shafir, S., Nicolson, S. W. & Stevenson*, P. C. (2017). Patent number: WO 2017/085477 A1. UK.

The present invention relates to compositions, methods and products for providing nutrition to insects such as bees, e.g., honey bees. Certain embodiments of the present invention also relate to methods of providing nutrition to bees e.g., colonies of bees together with methods of preparing a composition for providing nutrition to bees.



Endophytic fungal diversity of *Fragaria vesca*, a crop wild relative of strawberry, along environmental gradients within a small geographical area.

Yokoya*, K., Postel*, S., Fang*, R. & Sarasan*, V. (2017). *PeerJ* 5: e2860. DOI: 10.7717/peerj.2860.

Background

Fungal endophytes are highly diverse ubiquitous asymptomatic microorganisms, some of which appear to be symbiotic. Depending on abiotic conditions and genotype of the plant, the diversity of endophytes may confer fitness benefits to plant communities.

Methods

We studied a crop wild relative (CWR) of strawberry, along environmental gradients with a view to understand the cultivable root-derived endophytic fungi that can be evaluated for promoting growth and tolerating stress in selected plant groups. The main objectives were to understand whether: (a) suboptimal soil types are drivers for fungal distribution and diversity; (b) high pH and poor nutrient availability lead to fungal-plant associations that help deliver fitness benefits; and (c) novel fungi can be identified for their use in improving plant growth, and alleviate stress in diverse crops.

Results

The study revealed that habitats with high pH and low nutrient availability have higher fungal diversity, with more rare fungi isolated from locations with chalky soil. Plants from location G were the healthiest even though soil from this location was the poorest in nutrients. Study of environmental gradients, especially extreme habitat types, may help understand the root zone fungal diversity of different functional classes. Two small in vitro pilot studies conducted with two

isolates showed that endophytic fungi from suboptimal habitats can promote plant growth and fitness benefits in selected plant groups.

Discussion

Targeting native plants and crop wild relatives for research offers opportunities to unearth diverse functional groups of root-derived endophytic fungi that are beneficial for crops.

Manual de Etnobotânica: Plantas, Artefatos e Conhecimentos Indígenas.

Cabalar, A., Stern da Fonseca Krueel, V., Martins, L., Milliken*, W. & Nesbitt*, M. (eds) (2017). São Paulo: Instituto Socioambiental.

No abstract available.

Home and away: discovering the gardeners of the Empire in the archive of the Royal Botanic Gardens, Kew.

Clarke*, L. J. (2016). *Local History News* 121: 10–11.

No abstract available.

Botany behind glass: The vegetable kingdom on display at Kew's Museum of Economic Botany.

Cornish*, C. (2017). In: Berkowitz, C. & Lightman, B. (eds). *Science Museums in Transition: Cultures of Display in Nineteenth-Century Britain and America*. Pittsburgh, PA: University of Pittsburgh Press, pp.188–213.

No abstract available.

Coffee farming and climate change in Ethiopia: impacts, forecasts, resilience and opportunities. Summary report 2017.

Moat*, J., Williams*, J., Baena*, S., Wilkinson*, T., Demissew, S., Challa, Z. K., Gole, T. W. & Davis*, A. P. (2017). In: Royal Botanic Gardens, Kew. The Strategic Climate Institutions Programme (SCIP), pp.37.

No abstract available.

Priority science for the preservation of priority crops.

Pritchard*, H. W. (2016). *Indian Journal of Plant Genetic Resources* 29 (3): 272–278.

No abstract available.





