3 FEBRUARY 2021 ISSUE 67 YEAR 2020 COVID-19

THE BEAN BAG

A NEWSLETTER TO PROMOTE COMMUNICATION AMONG RESEARCH SCIENTISTS CONCERNED WITH THE SYSTEMATICS OF LEGUMINOSAE/FABACEAE

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ON THE COVERS: CERCIS CANADENSIS (CERCIDOIDEAE) PHOTOS WARREN CARDINAL-MCTEAGUE

FROM THE EDITORS

The Bean Bag started in 1974 on the initiative of Charles (Bob) Gunn and Richard Cowan and the first printed issue was distributed 45 years ago in May 1975. The aim of the annual newsletter is to keep legume researchers informed about new publications, events and projects focused on the systematics of the family Leguminosae.

We warmly thank Brigitte Marazzi, previous editor of the Bean Bag, for all her hard work compiling the newsletter over the last five years, and especially for transforming it into a much more colourful and well-illustrated format. We also thank Gwilym Lewis at Kew for help with checking this issue and supporting the continued archiving of the Bean Bag. Finally, we thank the legume community and our many contributors for sharing their time and insights.

For recent issues see: The Bean Bag | Kew
Earlier issues (1975 to 2007) are available via the Biodiversity Heritage Library

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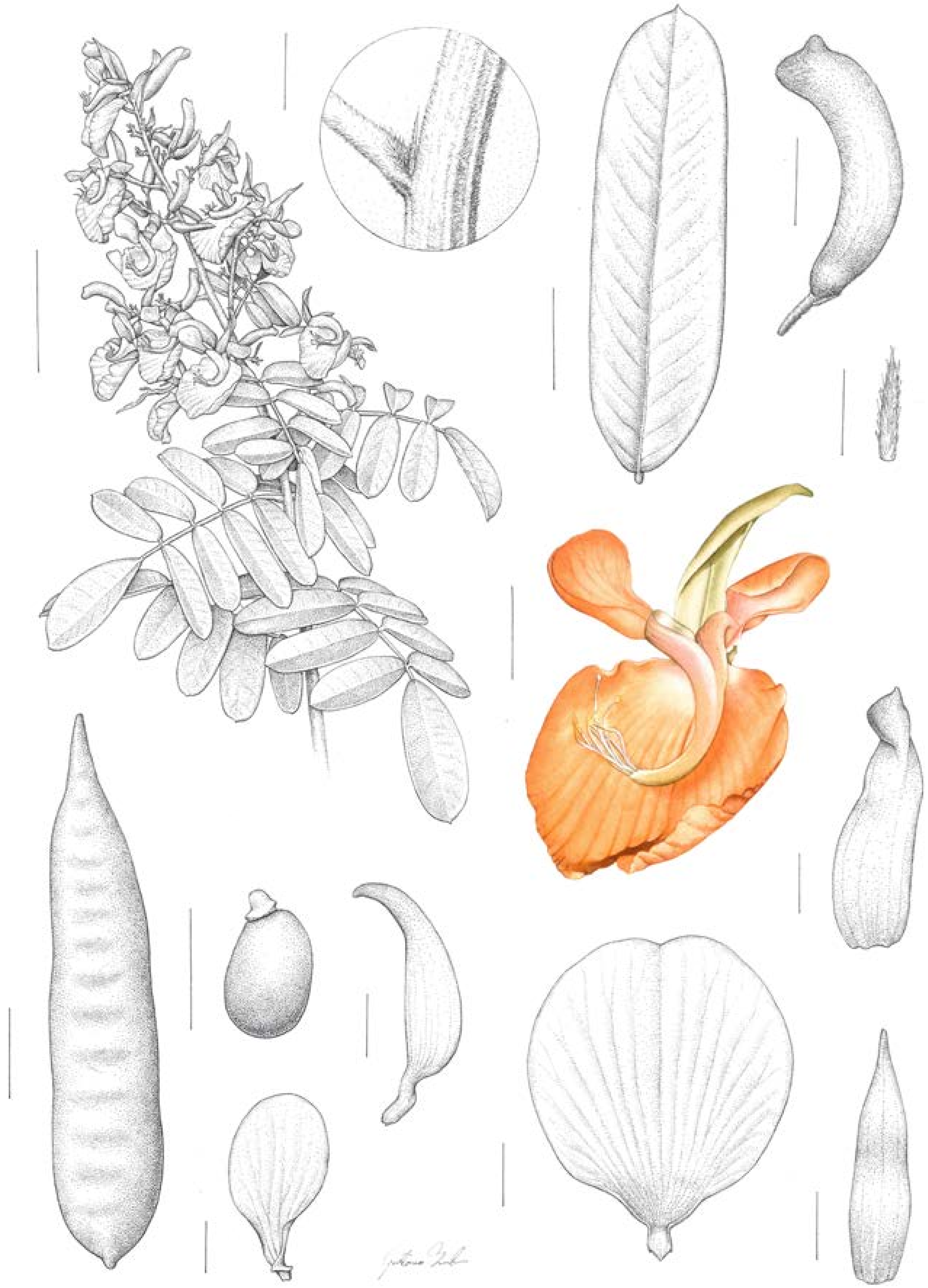
Left: Abarema cochliacarpos (Caesalpinioideae) Luciano de Queiroz 15538, fruit pods, photo Colin Hughes.
Right: This year's artist spotlight is Gustavo Surlo and his magnificent illustrations of Harpalyce (Papilionoideae). See São-Mateus et al. 2019 in New Legume Species Highlights for more detail. Nominate an artist for next year!

ARTIST SPOTLIGHT: GUSTAVO SURLO



LEGUME PHYLOGENY WORKING GROUP REPORTS

Intro by Colin Hughes

The **Legume Phylogeny Working Group**, LPWG was established in 2010 as an informal global consortium of legume systematists to foster collaborative research in legume systematics, building on several decades of data sharing and collaboration since the first International Legume Conference organised by Roger Polhill and colleagues in 1978.

While the name LPWG implies a specific focus on phylogenetics, in practice the LPWG spans a broader range of activities across legume systematics and evolution as a whole. LPWG activities have resulted in two major collaborative papers published under the LPWG umbrella:

- An overview paper in 2013 [LPWG. 2013. Legume phylogeny and classification in the 21st century: Progress, prospects and lessons for other species–rich clades. *TAXON* 62: 217-248. https://doi.org/10.12705/622.8]
- A major community-endorsed phylogenetically-based subfamily classification of the legume family in 2017 [LPWG. 2017. A new subfamily classification of the Leguminosae based on a taxonomically comprehensive phylogeny. *TAXON* 66: 44-77. https://doi.org/10.12705/661.3]

In May 2020, an informal pop-up meeting of a subset of the LPWG led to the establishment of four new working groups under the LPWG umbrella. These working groups are focused on **Taxonomy**, **Phylogenomics**, **Occurrence Data**, and **Functional Trait Data**, and have been established with a view to further stimulating and coordinating large-scale collaborative family-wide data assembly and analyses. Each working group has two coordinators and short reports on the aims and activities of each working group are presented here.

It is important to note that these working groups are open to wider participation by all! If you want to get involved in a specific working group, please contact the individual working group coordinators (contact details below).

TAXONOMY WORKING GROUP

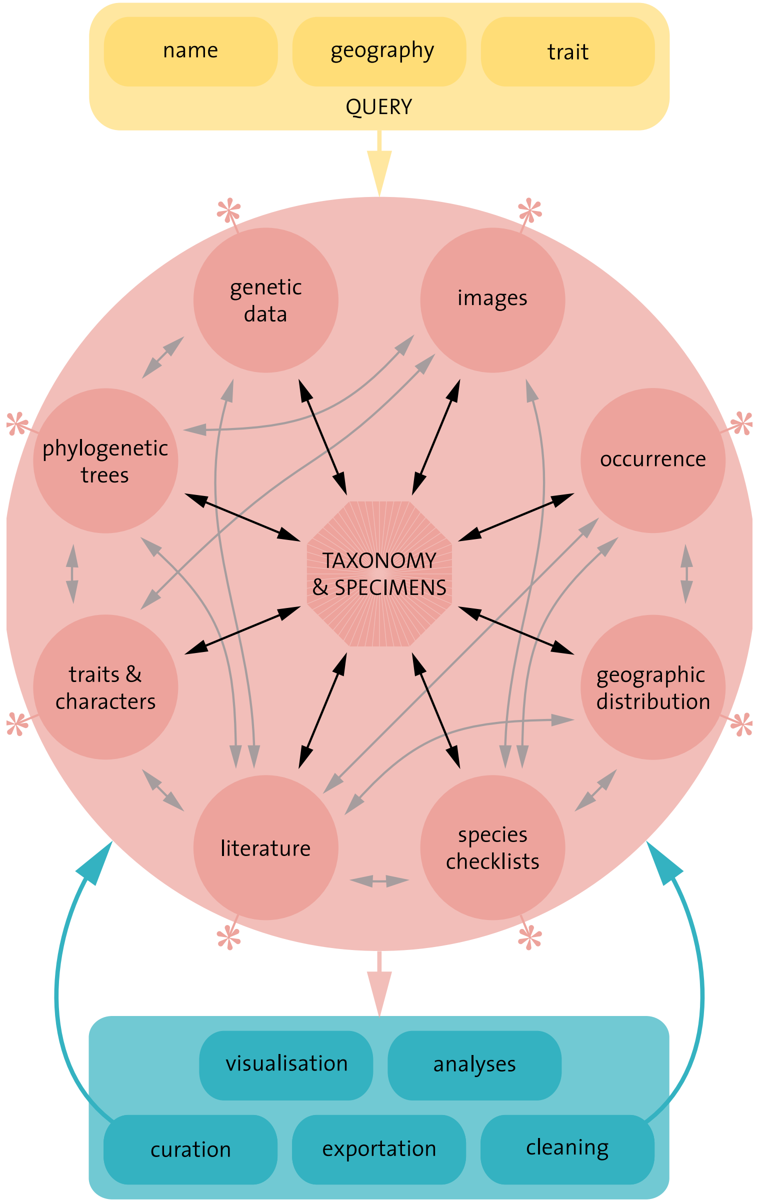
Coordinators:
Marianne le Roux (South African National Biodiversity Institute, SANBI, South Africa)
Anne Bruneau (Université de Montréal, Canada)

The **Legume Taxonomy Working Group** has the central goal of putting together a community-endorsed consensus list of legume species names and their synonyms. Because several online sources are now out of date, the legume community considered this initiative critical to underpin ongoing and future legume research. The group was established in May 2020 and its aim is to provide an accurate and up-to-date family classification that can be used for down-stream analyses of all kinds of applied and fundamental research questions, including conservation, agronomic and green infrastructure purposes. This up-to-date species list will also provide the critical backbone for other LPWG working groups focusing on assembling occurrence and functional trait data from public databases, literature and collections, for example. Ultimately, we would expect the LPWG-verified and endorsed species list to be adopted and used as the taxonomic backbone for Leguminosae for large international initiatives such as the Global Biodiversity Information Facility (GBIF), Catalogue of Life, World Flora Online, and several ongoing phylogenomic projects. This is important to avoid duplication of efforts by a small pool of taxonomic experts.

In collaboration with Rafaël Govaerts at Royal Botanic Gardens, Kew, the Taxonomy Working Group initiated the process using Kew's core checklist data, available for download on Kew's World Checklist of Vascular Plants (WCVP). This core checklist links to the International Plant Name Index (IPNI) and also underlies the Plants of the World Online website. The WCVP list includes all the Darwin Core fields that the legume community considers important for downstream analyses. To revise the list of legume species names, a network of 38 coordinators for the subfamilies (and tribes for Papilionoideae) were assigned the task of approaching other legume taxonomic experts for assistance in checking and editing the list of legume names. The revised lists are forwarded to Rafaël Govaerts who checks the proposed modifications and integrates the information in an updated legume species list. The Taxonomy Working Group has also established an arbitration committee whose role is to evaluate and arrive at a decision about conflicting taxonomies (often, whether or not to recognise certain genera), and which met for the first time in December 2020. The revised species list will acknowledge the input of contributors to the ratification of the legume taxonomy. The plan is to have a list of accepted names in draft format during the first half of 2021.

Down the line, the taxonomic list will be used to link to and synthesise other data types – traits, descriptions, higher level taxonomy, occurrence and specimen data, dynamic maps and images. One of the goals of the LPWG is to collate information on legumes so that it is easily accessible and useful to researchers and other users around the world. For this, the legume community is developing an online portal for the family which can encompass richer data sets from multiple partners using a sound species checklist and benefitting from knowledge held in "Legumes of the World Online". The current collaboration represents an important step toward achieving that goal.

The LPWG recently applied for a pilot portal via a new program at GBIF. This application was successful and the LPWG community, in coordination with the Canadensys GBIF node, will implement a thematic portal in the first half of 2021. This pilot will serve all legume occurrences currently in GBIF and will be underpinned by the consensus list of legume names and will also allow easy viewing of the legume taxonomy used. The portal will also have areas for describing the work of the four LPWG working groups. The portal is not expected to meet all LPWG needs, but will provide a first step for showcasing the work of the LPWG and more broadly the family Leguminosae.



If you would like to participate in this endeavour and share your taxonomic expertise, please contact us at: m.leroux@sanbi.org.za, anne.bruneau@umontreal.ca

Further reading:
Bruneau, A., Borges, L.M., Allkin, R., Egan, A.N., De la Estrella, M., Javadi, F., Klitgaard, B., Miller, J.T., Murphy, D.J., Sinou, C., Vatanparast, M. & Zhang, R. 2019. Towards a new online species-information system for legumes. *Australian Systematic Botany* 32: 495–518. https://doi.org/10.1071/SB19025

Left: Architectural overview of the plans for a Legume Systematics Portal, connecting data from external sources (*). From Bruneau, A. et al. 2019. Australian Systematic Botany, 32: 495-518.

PHYLOGENOMICS WORKING GROUP

Coordinators:
Felix Forest (Royal Botanic Gardens, Kew, U.K.)
Erik Koenen (University of Zurich, Switzerland)

The **Legume Phylogenomics Working Group** brings together different teams from across the legume research community that have been investigating phylogenetic relationships within the family at different taxonomic levels using genomic-scale data sets. The principal aim of the group is to compile a well-sampled robust generic-level phylogenetic tree for the family, to serve as the basis for the progressive reconstruction of a complete species-level phylogenetic tree for the entire family. This generic-level phylogenetic framework is crucial to improve the subfamilial classification of the family (i.e. delimitation of tribes) and test the monophyly of genera to help with re-delimitation of genera suspected to be non-monophyletic.

The group also aims to find ways to harmonize the different target enrichment (hybrid capture) gene sets and approaches that have been developed for the family. At least five different target enrichment probe sets have been developed for specific legume clades, including Detarioideae, Caesalpinioideae (incl. the mimosoid clade), Cercidoideae and Papilionoideae. In addition, the hybrid capture approach developed for the NitFix project led by Pamela and Doug Soltis (see separate report in this issue of the Bean Bag) is being applied to a large sample of more than 9,000 species across legumes. In addition, the Angiosperms353 universal bait set developed for the Plant and Fungal Trees of Life project at Royal Botanic Gardens, Kew is currently being used to sequence these genes for a sample of genera covering all major legume groups, with a particular focus on subfamily Papilionoideae and its early-diverging lineages. The Working Group maintains an overview of the various legume gene sets that are being sequenced and has assessed overlap amongst them. Because the overlap in genes targeted by these various approaches is minimal, there are limited possibilities of directly combining the different data sets.

Given the advanced state of the work undertaken by several groups who have designed the probe sets enumerated above, phylogenomics within legumes is advancing rapidly on several fronts, with well sampled studies emerging for all subfamilies. Given that the monophyly of each subfamily is well established, these parallel efforts will each provide valuable information on phylogenetic relationships within the family.

If you would like to discuss and share information about legume phylogenomics initiatives, please contact us at: f.forest@kew.org, erik.koenen@systbot.uzh.ch

OCCURRENCE DATA WORKING GROUP

Assembling a global, expert-verified species occurrence dataset for family Leguminosae

Coordinators:
Edeline Gagnon (Royal Botanic Garden, Edinburgh, U.K.)
Joe Miller (Global Biodiversity Information Facility, GBIF, Denmark)

The central goal of the **Legume Occurrence Working Group** is to produce an expert-verified, global occurrence dataset for the entire legume family. As legumes are economically and ecologically important, such a dataset would find many uses among ecologists, evolutionary biologists, conservationists, plant breeders, foresters and others. To ensure data reproducibility, we focus primarily on preserved specimens from herbaria, although other records that are verifiable are also being considered.

While it is now extremely easy to download data from global occurrence databases such as GBIF and use standard cleaning tools, custom-made R scripts and OpenRefine to edit the data, there are still a number of important bottlenecks to assembling high-quality occurrence data, including:

- Having an up-to-date and accurate list of accepted names and synonyms for all legumes;
- Verifying the taxonomic identity of occurrence records;
- Assessing whether the final set of occurrence records for any given species accurately represents the known geographic distribution.

Our strategy is to overcome these difficulties by:

- Basing our occurrence dataset on the checklist being generated by the Legume Taxonomy WG;
- Working with legume experts to assess the quality of the occurrence dataset;
- Encouraging collaboration with taxonomists and other botanists to clean, assess and contribute geo-referenced data through a semi-automated process of micro-publications.
- Encouraging return of cleaned occurrence records back to the original data providers so that the data improvement is sustained.

We expect different occurrence datasets will present different challenges (e.g. additional geo-referencing, use of different databases depending on geographic regions, how to identify non-native records) and will require different cleaning strategies. All data will be required to meet minimum standards based on specified guidelines and tools, while some users will clean and explore their data further if they wish. Each dataset would generate a micro-publication including the methods and tools they used, and an assessment of data quality and completeness. Furthermore, micro-publications, with associated DOIs would make the work citable providing recognition for this type of work.

Pending completion of the Legume Taxonomy WG checklist the Occurrence Working Group has:

- Compiled a list of current and on-going efforts to assemble and geo-reference occurrence record data. Our survey indicates that while considerable efforts have been made for certain subfamilies, significant challenges remain for amassing data for subfamily Papilionoideae, in which most legume species diversity is concentrated.
- Produced a series of R scripts for (i) retrieval of GBIF data based on a list of accepted names and synonyms; (ii) cleaning of the retrieved occurrence data, based on the framework of the script from Ringelberg et al. (2020), modified to add tools from the R Package "CoordinateCleaner" (Zizka et al. 2019), plus additional custom scripts provided by E. Gagnon and Y. Barros Souza. These scripts will be made available shortly through GitHub.

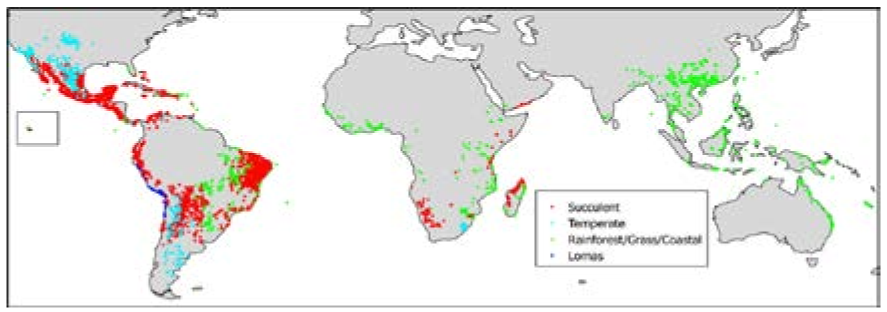
During 2021 we plan to organize a meeting to present and discuss the proposed workflow and R scripts for retrieval of data directly from GBIF and standard cleaning tools. In addition, updates are expected about new GBIF-hosted data cleaning tools and occurrence data indexing to an updated taxonomy that includes many recommendations from the legume taxonomic working group. We are also planning a brainstorming meeting to explore ideas for using the new expert-verified global legume occurrence data in legume biogeography. Further details about these meetings will be available shortly. Finally, once the species checklist is available, we plan to move forward with legume-wide data cleaning.

New community developed best practices document in georeferencing have been published by GBIF. This set of three guides provide theory, methods and advice on spatial interpretation of locations.

If you are interested in participating in our group, or have questions, please contact edeline.gagnon@gmail.com or jmiller@gbif.org. We are keen to hear from everyone working to expand and improve the quality of available legume occurrence data.

References:
Ringelberg, J.J., Zimmermann, N.E., Weeks, A., Lavin, M. & Hughes, CE. 2020. Biomes as evolutionary arenas: convergence and conservatism in the trans-continental Succulent Biome. *Global Ecology and Biogeography* 29: 1100-1113. https://doi.org/10.1111/geb.13089

Zizka, A., Silvestro, D., Andermann, T., et al. 2019. CoordinateCleaner: Standardized cleaning of occurrence records from biological collection databases. *Methods in Ecology and Evolution* 10: 744– 751. https://doi.org/10.1111/2041-210X.13152



Exemplar data set used to map the distribution of the Caesalpinia Group based on 17,260 quality-controlled occurrence records. From Gagnon, E. et al. 2019. New Phytologist, 222: 1994-2008.

FUNCTIONAL TRAIT WORKING GROUP

The mysterious world of legume functional traits

Coordinators:
Renske Onstein (German Centre for Integrative Biodiversity Research (iDiv), Germany)
Leonardo Borges (Universidade Federal de São Carlos, Brazil)

Even after generations of work by an army of legume workers, the myriad and beauty of legume morphology, structure and function are still a mystery. How and when did all those traits evolve? What factors lie behind their evolution? How do they dictate and influence how legumes interact with the world?

Driven by such questions, the **Legume Functional Trait Working Group** was founded. The working group aims to increase communication between researchers studying legume traits to facilitate collaboration and avoid redundant data collection efforts. We also want to promote sharing and integration of data and collection protocols.

So far, there are several on-going projects in the legume trait world. Some of us are interested in the ecology of traits (e.g. herbivore defense – K. Dexter et al.; drought adaptation – F. Velasquez et al.), while others focus on the (macro-)evolution of traits in certain lineages (e.g. pod and leaf traits in Mimosoids/*Albizia* – R. Onstein/E. Ruttimann et al.; whole plant morphology – L. Borges). We study a range of traits – from spines to leaves to roots to fruits – and use a range of methods to obtain trait data, such as (automatically) screening monographs and floras, fieldwork, or assessing herbarium specimens, including online specimens. One novel approach being explored by W. Cardinal-McTeague and A. Bruneau, is assessing reflectance/spectral emission from herbarium samples to associate this with other, more difficult-to-measure traits. When optimized, this method has the potential to quickly assemble massive amounts of trait data from herbarium collections.

To coordinate on-going and future trait sampling efforts, we collectively keep track of on-going projects, share already published trait and wider morphological data, and maintain a list of traits, character states and their definitions. We also established a shared folder for depositing legume monographs for trait mining and as a valuable source and overview of systematic work across legumes.

We welcome your input and ideas in the legume trait working group, or simply to receive your favourite monographs. Please get in touch if you would like to become part of our group, are interested in working with traits, have ongoing trait-related projects or future

Exemplar Legume Functional Traits. Clockwise from top left: ant associations involving extrafloral nectaries, domatia and beltian bodies, Vachellia cornigera; growth forms: a fire-adapted geoxyle with an underground lignotuber, Calliandra longipes; armature: Prosopis ferox; nodulation: nodules of Lupinus nubigenus; seed dispersal syndromes: fleshy arils of Pithecellobium lanceolatum; pollination syndromes: humming bird pollinated flowers of Erythrina lanata. All photos Colin Hughes.

plans, or simply to share a virtual cup of coffee and talk more about the mysterious world of legume traits. Our group is still growing, and we welcome anyone interested in legume (functional) traits to join our efforts. To get involved, please contact onsteinre@gmail.com or aquitemcaqui@gmail.com

ADVANCES IN LEGUME SYSTEMATICS 14: CLASSIFICATION OF CAESALPINIOIDEAE

Erik Koenen, Colin Hughes, Anne Bruneau, and Gwilym Lewis

We are planning to assemble and publish a special issue in a taxonomic journal (possibly PhytoKeys, but other options are being considered) devoted to the systematics of Caesalpinioideae, as part of the **Advances in Legume Systematics** (ALS) series. This special issue will feature:

1. A new phylogenomic framework sampling nearly all genera in the subfamily.
2. A new tribal classification for Caesalpinioideae, potentially published under the LPWG umbrella.
3. A particular focus on generic delimitation in the Mimosoid clade,
4. We invite contributions on all aspects of Caesalpinioideae taxonomy, but in particular contributions involving generic delimitation and nomenclatural changes in the Mimosoid clade.

If you are interested in contributing to ALS14, please send an email to erik.koenen@systbot.uzh.ch. We will then keep you informed and invite you to an online meeting to be organised in March 2021 to further discuss these plans. We look forward to hearing from you!

Left to right: Stryphnodendron rotundifolium, Balizia pedicillaris, Piptadenia flava (photos Colin Hughes) and Hydrochorea corymbosa (photo Erik Koenen).

REQUEST FOR LATHYRUS IMAGES

Greg Kenicer

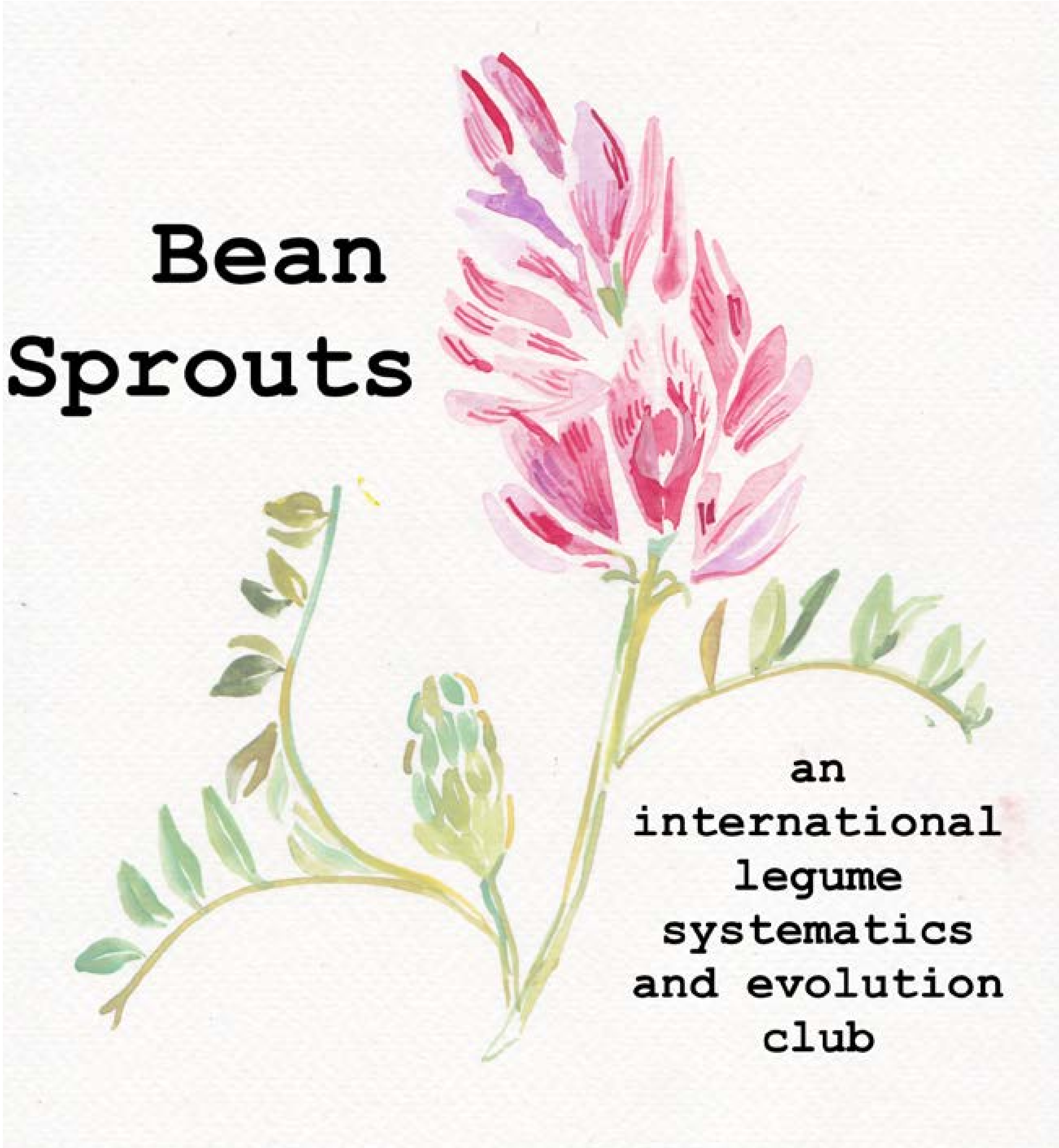
Greg Kenicer (Royal Botanic Gardens, Edinburgh) is looking for **images of *Lathyrus*** to illustrate a horticultural monograph of the genus. If you can help, by providing images of wild species – particularly those from Turkey and the wider Eastern Mediterranean and 'Near East', Russia, China and North America, he would be very grateful. All images will be fully credited to the photographer.

This is a full-colour book produced by the Royal Horticultural Society as part of their 'Complete Guides' series. Although *Lathyrus odoratus* is the main focus (written by Roger Parsons), it is also the first book to provide a comprehensive overview of the wider genus for the general public, so an excellent chance to show the diversity of this fascinating group. It includes short accounts for each species, including a full-colour image, which is where we need your help. Anything you can do to help would be greatly appreciated.

If you think you can provide images from your local area or fieldwork. please send them (e.g. on wetransfer or similar), with your preferred wording for credit to Greg on: gkenicer@rbge.ac.uk, before February the 15th.

Many thanks in advance, Greg

Left to right: Lathyrus aureus, L. multiceps, L. rotundifolius, L. sativus & L. tingitanus (photos Greg Kenicer).



Watercolour by Sascha Stannard..

Sophie Winitsky and Joseph Charboneau

Bean Sprouts is a new online, international legume systematics and evolution club for graduate students and early career scientists to connect, share research, discuss papers, and invite speakers centered around our favorite (the best) plant family! How often we meet will depend on how many people want to participate, so let us know if you're interested! We tentatively plan to have our next meeting over Zoom in late February.

Email Sophie Winitsky (winitskys@gmail.com) or Joseph Charboneau (jcharbon@email.arizona.edu) to be included!

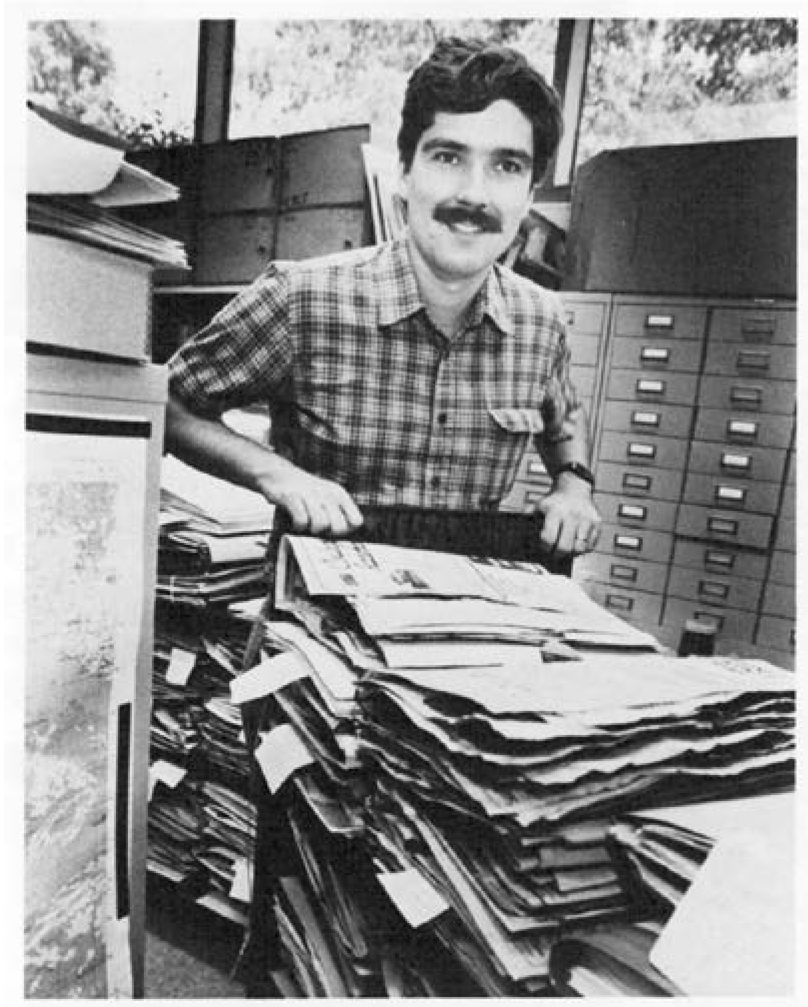
JAMES LEE ZARUCCHI PHD, FLS (1952-2019)†

Roger Polhill & Colleagues

Jim Zarucchi sadly died at the relatively young age of 67 on 21 July 2019 in St Louis, Missouri. In his first year at Harvard University he was inspired to take up systematic botany by the legendry economic botanist Richard Evans Schultes and as an undergraduate made the first of many expeditions to remote parts of Colombia. By the end of his life he had made 5,720 plant collections, mainly from that country, but also from Brazil, Ecuador, Madagascar and the United States. He graduated in 1974, continued to work under Schultes at Harvard as a teaching fellow and curator of the Economic Herbarium of Oakes Ames, obtaining his doctorate on Apocynaceae in 1982. He had a postdoctoral fellowship at Kew and the British Museum in 1981-1982, followed by a further postdoctoral fellowship at the Smithsonian in 1982-1983.

In 1984 he was enlisted by Peter Raven to establish a Neotropical Legume Project at the Missouri Botanical Garden. Under the auspices and patronage of the economic botanist Boris Krukoff, Peter Raven had an outreach programme to foster the budding discipline of chemosystematics at Kings College London and Kew. To provide a taxonomic framework to interpret the new findings Jim worked with Kew to foster the first International Legume Conference at Kew in 1978 and the subsequent volumes of Advances in Legume Systematics. The third International Legume Conference was conceived and edited by Charles Stirton, hosted by Jim at the Missouri Botanical Garden in 1986, and the proceedings, Advances in Legume Biology, efficiently seen through the press by Jim in 1989.

In December 1984, at the Missouri Botanical Garden, Peter Raven chaired the memorable inaugural meeting of the International Legume Database and Information Service (ILDIS). This was the brainchild of Frank Bisby from Southampton University in the UK who perceived the potential of personal computers, then only just beginning to become universal, to record and organise botanical information. Under the leadership of Frank Bisby, Jim Zarucchi, and Roger Polhill from Kew agreed to form the Directorate of ILDIS. It was agreed to compile the New World data in Tropicos, then quite newly established, as an information resource, and the Old World information in Alice that had been designed and maintained by Bob Allkin and Peter Winfield to record data in traditional floristic style with a hierarchy of accepted names and synonyms. Over the next three decades Jim conscientiously accumulated an enormous abount of information for Tropicos, but regrettably, due to an increased involvement in other projects, left no permanent record to match the comprehensive set of Old World Legume Checklists published by



Jim Zarucchi in 1984 in the herbarium in the Lehmann Building soon after he started his working in the MO herbarium. Photo Courtesy Missouri Botanical Garden.

Kew between 1989 and 2003. Jim was always a most hospitable host for meetings at Missouri.

Jim was promoted to Associate Curator in 1990 and played a major part in other Missouri projects, co-editing the Catalogue of the Flowering Plants and Gymnosperms of Peru, published in 1993, managing the Flora of China Checklist and advising on the botanical component of the Phytochemical Dictionary of the Leguminosae published in 1994. The Flora of North America Project was floundering when Jim took it over as Managing Editor and Editorial Director in 1996, going on from strength to strength under his skilled supervision to be the great work it is today. Jim was rewarded as the Anne L Lehmann Curator of North American Botany in 2006, an endowed position he held for the rest of his illustrious life. He is greatly missed by all that knew him as evidenced by the fuller obituaries published in the Annals of the Missouri Botanical Garden 104: 512-514 (2019) and Taxon 68: 1144-1145 (2019).

Further reading:
Ulloa Ulloa, C., Charron, T., Kuhl J. 2019. In Memoriam: James L. Zarucchi (1952–2019). *Annals of the Missouri Botanical Garden*, 104(3), 512-514. https://doi.org/10.3417/2019515

Funk, V. 2020. James Lee Zarucchi (1952–2019). *TAXON*, 68(5): 1143-1144. https://doi.org/10.1002/tax.12136

NEW LEGUME SPECIES HIGHLIGHTS 2020

Compiled by Colin Hughes

Six new species of *Chamaecrista* from the Diamantina Plateau, Brazil

Chamaecrista rupertiana, photo Matheus Martins Teixeira Cota

Cota et al.'s (2020) 82-page taxonomic account of the 64 species of *Chamaecrista* from the campos rupestres of the Diamantina Plateau, Minas Gerais, Brazil, adds six new species. These new species further augment the exceptionally high species diversity and endemicity of *Chamaecrista* in the campos rupestres and hint that more species remain to be described in this species-rich genus.

Two of these new species, *C. howardii* and *C. rupertiana* are named in honour of Howard Irwin and Rupert Barneby, who established the modern classification of subtribe Cassiineae and assembled the last major taxonomic account of the New World species.

Cota, M.M.T., Rando, J.G. and Mello-Silva, R. 2020. *Chamaecrista* (Leguminosae) of the Diamantina Plateau, Minas Gerais, Brazil, with six new species and taxonomic novelties. *Phytotaxa* 469: 1-82. https://doi.org/10.11646/phytotaxa.469.1.1

Dalea rubriflora – A new red-flowered species from Mexico

This is the first species in the genus *Dalea* which has permanently ruby red-flowers and is placed in a new Section *Rubriflorae*. *Dalea rubriflora* is known from a single collection from the state of Zacatecas in Mexico where it grows in oak forest at 2,590 m elevation.

Castillón, E.E., Martinez-Ramirez, J., Mares-Guerrero, A.A. and Ocampo, G. 2020. A new outstanding species and a new section of *Dalea* (Fabaceae: Papilionoideae) from central Mexico. *Phytotaxa* 454: 145-152. https://doi.org/10.11646/phytotaxa.454.2.6

Dalea rubriflora, photo Julio Martínez Ramírez

Two new species of *Harpalyce* from the Cerrado hotspot in Brazil

In a lavishly and comprehensively illustrated paper by São-Mateus et al, two new species of the poorly-known Papilionoid genus *Harpalyce* – *H. correntina* and *H. tombdorensis* are described from the Brazilian Cerrado. The resupinate flowers with the vexillary lip of the calyx strongly cucullate at its apex are characteristic of section *Brasilianae*, endemic to Brazil.

São-Mateus, W.M., Simon, M.F., de Queiroz, L.P., Jardim, J.G. and Cardoso, D.B. 2019. Two new species of *Harpalyce* (Leguminosae, Papilionoideae) from the Cerrado hotspot of biodiversity in Brazil. *Kew Bulletin* 74: 61. https://doi.org/10.1007/s12225-019-9845-y

Harpalyce correntina, photo Edwesley de Moura

Additions in *Indigofera*

With ca. 750 species, *Indigofera* is the third-largest legume genus, and as with all large pantropical genera, new species continue to steadily accrue. Here *I. centralis* is added to a growing tally of recent additions to the genus from Australia. Interestingly, *I. centralis* was first collected between 1877 and 1889 with a specimen lurking in the Melbourne herbarium and only brought to light based on new material collected 100 years later, vindicating the idea that many undescribed species are already in collections!

Wilson, P.G. and Rowe, R. 2020. A new species of *Indigofera* (Fabaceae: Faboideae) from Central Australia. *Telopea* 23: 113-117. http://dx.doi.org/10.7751/telopea14402

Indigofera centralis, photo Dave Albrecht

The diversity of *Indigofera* in the Sino-Himalayan region with > 100 species is also increasing with description of *I. yuanjiangensis*.

Zhao, X.L., Jiang, L.S. and Gao, X.F. 2020. *Indigofera yuanjiangensis* (Fabaceae: Papilionoideae), a new species from Yunnan, China. *Phytotaxa* 455: 235-239. https://doi.org/10.11646/phytotaxa.455.3.7

I. yuanjiangensis, photo Xin-Fen Gao

Mimosa carolina from the Brazilian Cerrado

Mimosa carolina, photo Marcelo Simon

Mimosa carolina, endemic to the northern fringes of the Brazilian Cerrado, adds to the formidable diversity of *Mimosa* species from the Cerrados and Campos Rupestres of Brazil, a major hotspot for the genus with > 200 species. In common with many *Mimosa* species from the fire-prone Cerrado, *M. carolina* is a geoxyle, resprouting from a substantial underground lignotuber or xylopodium and forming a large spreading mat of prostrate shoots.

Morales, M., Fortunato, R.H. and Simon, M.F. 2020. A new species of *Mimosa* L. ser. *Bipinnatae* DC. (Leguminosae) from the Cerrado: Taxonomic and phylogenetic insights. *Plants* 9: 934. https://doi.org/10.3390/plants9080934

Python vine from Guangxi Province in China: *Mucuna guangxiensis*

The pantropical/subtropical genus *Mucuna* has ca. 105 species with around 18 species in China and Japan. The new species described here, *Mucuna guangxiensis* forms a large woody twining liana (known locally as python vine) with large woody fruits up to 70 cm long and is only known from the type locality in Guangxi Province in China.

Jiang, K., Huang, Y. and Moura, T.M. 2020. *Mucuna guangxiensis*, a new species of *Mucuna* subg. *Macrocarpa* (Leguminosae-Papilionoideae) from China. *Phytotaxa* 433: 145-152. https://doi.org/10.11646/phytotaxa.433.2.5

Mucuna guangxiensis, photo Yun-Feng Huang

A new polyploid *Neptunia* from the Brazilian Caatinga

Santos-Silva et al's paper describing a new species of *Neptunia* (Caesalpinioideae: mimosoid clade) is a classical biosystematics study including cytological, anatomical and morphological data. *Neptunia windleriana* is endemic to Bahia state in Brazil growing in open Caatinga subject to seasonal flooding along the São Francisco River.

Santos-Silva, J.S., Carvalho, M.S., Santos, G.S., Braga, F.T., de Andrade, M.J.G. and de Freitas Mansano, V. 2020. *Neptunia windleriana*: A new polyploid species of *Neptunia* (Leguminosae) from Brazil recognized by anatomy, morphology and cytogenetics. *Systematic Botany* 45: 483-494. https://doi.org/10.1600/036364420X15935294613392

Neptunia windleriana, photo Juliana Santos Silva

A new wild *Phaseolus* bean species from Costa Rica

The discovery and description of this new species of Phaseolus from Costa Rica emphasizes that there are still many new species to be described even of wild relatives of important pulse crops like Phaseolus beans. In common with the majority of newly described species, *P. albicarminus* is a globally rare endemic, known from just three populations on the western flanks of the Talamanca range in Costa Rica.

Debouck, D.G., Chaves-Barrantes, N. and Araya-Villalobos, R. 2020. *Phaseolus albicarminus* (Leguminosae, Phaseoleae), a new wild bean species from the subhumid forests of southern central Costa Rica. *Phytotaxa* 449: 1-14. https://doi.org/10.11646/phytotaxa.449.1.1

Phaseolus albicarminus, photo Daniel Debouck

Two new prostrate subshrub *Stylosanthes* species from Bahia, Brazil

Stylosanthes, with ca. 65 species, is a notoriously difficult genus taxonomically and it is encouraging that new taxonomic work on the genus is underway in Brazil, where the majority of the species occur. This has resulted in two new species of prostrate subshrubs endemic to the Serra Geral and Chapada Diamantina in Bahia.

Ferreira, J.J.D.S., Gissi, D.S., Perez, A.P.F. and Silva, J.S. 2020. Two new species of *Stylosanthes* Sw. (Leguminosae—Papilionoideae) endemic to Bahia State, Brazil. *Phytotaxa* 456: 157-165. https://doi.org/10.11646/phytotaxa.456.2.3

Stylosanthes minima, photo Jamile Jorge Ferreira

Tachigali inca, a new species from the western Amazon

Tachigali inca, newly described this year by Huamantupa-Chuquimaco et al., is a 40 m tall tree in terra firme forests of the western Amazon of Brazil, Peru and Bolivia. It is characterized by unusual large cylindrical slightly ribbed ant domatia immersed in the leaf rachis. The presence of ants with strong formic acid is indicated by the common names Tachi (Brazil) and Tangarana (Peru).

Huamantupa-Chuquimaco, I., de Lima, H.C. and Cardoso, D.B. 2020. *Tachigali inca* Caesalpinioideae – Leguminosae, a new species of giant tree from Amazonian forests. *Webbia* 75: 243-250. https://doi.org/10.36253/jopt-9604

Tachigali inca, photo Isau Huamantupa-Chuqimaco

The epithet of the distinctive new species *T. cardiophylla* from the Kimberley sandstones of north-west Australia, is derived from the Greek *kardia* (heart) and *-phyllus* (-leaved) in reference to the emarginate apex of the heart-shaped terminal leaflets. Ryonen Butcher reports that she is in the process of describing 35 new *Tephrosia* taxa, mainly from western Australia and the Northern Territory, so there are many more species to come soon.

Tephrosia cardiophylla, photo Kevin Thiele

Butcher, R. 2017. *Tephrosia cardiophylla* (Fabaceae: Millettieae), a distinctive, new, conservation-listed species from Western Australia's Kimberley sandstones. *Nuytsia* 31: 47-51. https://florabase.dpaw.wa.gov.au/science/nuytsia/944.pdf

A total of the 36 new legume species described in 2020 is presented in the Bibliography.

FROM AMAZON TREE LEGUMES TO NITROGEN-FIXING MAIZE: WHAT'S THE CONNECTION?

Euan K. James, Marta Maluk, and Janet I. Sprent

The James Hutton Institute, Invergowrie, Dundee DD2 5DA, UK

A team at the James Hutton Institute, Dundee, Scotland, forms part of a research consortium led from the Crop Science Centre, part of the Department of Plant Sciences Sainsbury Laboratory at the University of Cambridge, which is aiming to transfer the ability to form Nitrogen (N)-fixing nodules to non-legumes, especially cereals (https://www.ensa.ac.uk/). Nodulation is a process through which legume plants form a symbiosis with bacteria that live in the roots of the plants and take N from the atmosphere to convert it into compounds that the plant can use for its growth. In cereal crops like maize, wheat and rice, there is no capacity for making root nodules, and so these crops are dependent on farmers applying large quantities of fertiliser to obtain their nitrogen. Fertilisers are expensive and are now recognised as highly damaging in terms of pollution from nitrates in drinking water, as well as producing high greenhouse gas emissions that contribute to global warming. A major aim in biotechnology is to transfer the root nodulating ability of legumes to cereal crops so that they are no longer dependent on expensive and polluting nitrate fertilisers. The **Engineering Nitrogen Symbiosis for Africa** (ENSA) research project is specifically targeting maize as an important crop in sub-Saharan Africa for smallholder farmers who cannot afford fertiliser. However, the transfer of nodulation ability to maize is very complicated, because many genes are involved.

The Hutton team are involved in the Evolution of Nodulation sub-project within ENSA. This sub-project aims to understand how legumes were able to evolve and develop the ability to form nodulating symbioses with soil bacteria called rhizobia. By better understanding how nodulation evolved in legumes it is hoped to gain insights into whether this trait can be transferred to cereals. For example, it is known that most land plants, including cereals and legumes can form root symbioses with arbuscular mycorrhizal fungi (AMF), and the genetic/developmental pathway underpinning this symbiosis is common to all land plants that interact with AMF; this same pathway has been adopted and adapted by legumes (and a number of other plant lineages within the Rosid clade) to form N-fixing nodules (Radhakrishnan et al. 2020). Therefore, in theory it should be possible to engineer the AMF developmental pathway in other plant groups, such as cereals, to make N-fixing nodules.

Figure 1. Location of the Rio Cuieiras legume sampling expedition Dec 2019.

Most, but not all, of the ca. 20,000 species of legumes are nodulated (Doyle 2016; Sprent et al. 2017). Nodulation is the "norm" in subfamily Papilionoideae (>97% nodulated), rare in non-mimosoid members of subfamily Caesalpinioideae sensu LPWG (2017) (c. 30% nodulated), but common in the mimosoid clade within this subfamily (>93% nodulated). Nodulation is absent in > 6,000 legume species, and has never been reliably reported in subfamilies Cercidoideae, Detarioideae, Dialioideae, and Duparquetioideae (Sprent et al. 2017). Recent work documenting the presence or absence of key genes for nodulation in fully-sequenced genomes of species within the N-fixing clade of the Rosids, including several legumes, suggested that nodulation was acquired once, but subsequently lost many times across this group, and that this explains the "patchy" occurrence of nodulation in the N-fixing clade sensu lato (Griesmann et al. 2018; Van Velzen et al. 2018). However, many questions remain about how and/or why nodulation has re-

Figure 2. Flooded forest, photo Euan James.

Figure 3. Digging for Jacqueshuberia nodules.

Figure 4. Nodules on Jacqueshuberia roots, photo D. Cardoso.

mained so widespread and stable in certain legume subfamilies/clades, but has been apparently so massively lost in others.

Against this background, the specific aims of the Hutton team within ENSA are to assemble an interactive database ILDON (International Legume Database of Nodulation) to catalogue all reliable reports of nodulation (both current and future) and to document the diversity of nodule structures across all legume genera and species using the latest legume taxonomy. The Hutton team is analysing wild and cultivated legumes to define precisely the nature of infection and nodule structure. They are specifically interested in identifying species that undertake "primitive" crack versus "advanced" root hair entry; centralised versus peripheral nodule vasculature; and "primitive" fixation threads versus "advanced" symbiosomes. Understanding the diversity and phylogenetic distribution of these nodule traits is fundamental for unlocking the potential for successful transfer of nodulation to non-fixing crops. An important aim is to identify legume genomes for sequencing that could be used to identify the genes underpinning these important nodulation traits.

As part of this work, in December 2019, a field expedition was conducted to the Brazilian Amazon to sample root nodules from legume trees. The Amazon region is globally one of the richest legume diversity hotspots and a centre for radiation of many legume genera, including a number of key "basal" genera in subfamilies Caesalpinioideae and Papilionoideae whose nodulation status and characteristics remain unknown. As such, the Amazon is a prime site for sampling taxa which can assist in our understanding of how nodulation evolved in legumes. The expedition concentrated around the Rio Cuieiras, a tributary of the Rio Negro (the northerly one of the 2 rivers that combine to make the Amazon "proper" at Manaus) (Fig. 1). December marks a period where increased precipitation and runoff from the Andes results in the Amazonian river level rising rapidly, so many of the forests were flooded or in the process of becoming flooded (Fig. 2).

Target legume genera and species were partly determined on the basis of enigmatic or incomplete reports of nodulation, but also on the availability of nodules on certain genera in the area covered by the expedition, which could only be determined by excavating their

root systems. The sampled nodules are now being analysed, including DNA fingerprinting of the legume species, investigating nodule anatomy, rhizobial isolation and genome sequencing of selected isolates to determine the evolutionary history of their symbiosis genes (*nod*, *nif*).

Highlights of the expedition included:

1. Absolute confirmation of nodulation by *Jacqueshuberia*, making it only the eighth non-mimosoid genus in subfamily Caesalpinioideae to be shown to be nodulated (Fig. 3, 4).
2. Collections of nodules from other non-mimosoid Caesalpinioideae genera, such as *Campsiandra*, *Moldenhawera*, and *Tachigali*.
3. Sampling of nodules from *Pentaclethra* macroloba an early-branching mimosoid.
4. Sampling of enormous nodules from several individuals of the profusely-nodulated, early-branching papilionoid genus *Swartzia* (Fig. 5, 6).

Figure 5. Digging for Swartzia nodules.

Figure 6. Swartzia polyphylla nodules, photo D. Cardoso.

We acknowledge the invaluable support and assistance of the Instituto Nacional de Pesquisas Amazônica (INPA), especially Charles Zartmann, without whom the expedition would not have been possible. In addition, we thank Domingos Cardoso (UFBA, Salvador, BA) and Haroldo de Lima (Jardim Botanico, Rio de Janeiro, RJ) for their botanical expertise, and Eduardo Gross (UESC, Ilheus, BA) for help with nodule sampling. The assistance and hospitality of communities in the Rio Cuieiras is also acknowledged. ENSA is sponsored through a grant to the University of Cambridge by the Bill & Melinda Gates Foundation and the UK government's Foreign, Commonwealth and Development Office (FCDO).

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A NEW RESOURCE FOR LEGUME DIVERSITY AND SYSTEMATICS: THE NIT-FIX PROJECT

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Legumes are famous for their symbiotic relationship with bacteria that fix nitrogen, but we still have much to learn about this globally important symbiosis. Understanding the incredible diversity of legume species and their relatives is one key to unlocking the mystery of the evolutionary origins and genetic basis of this critical innovation in plant and microbial evolution.

Nitrogen-fixing symbioses between plants like legumes and their relatives can give plants an advantage in nitrogen-poor soils, and may be associated with ecological shifts to extreme habitats. Deconstructing how this symbiosis works across a wide range of plant diversity could reduce fertilizer use, thereby reducing the high energy cost of production, limiting agricultural runoff, and securing the food supply in arid parts of the globe, while enriching our understanding of how symbioses have been critical planetary drivers of evolution and ecology.

We, along with colleagues at the University of Florida and the University of Wisconsin-Madison, have recently been awarded grants from the U.S. Department of Energy and the U.S. National Science Foundation to investigate the evolutionary origins of nitrogen-fixing symbioses and identify the genomic innovations that led to root nodule development. The results of these analyses will be applied to verifying the molecular mechanisms of nodulation and engineering nodulation in bioenergy crops (https://nitfix.org).

Any exploration of a trait's genetic basis and evolution relies on a robust phylogenetic hypothesis. Because of the explosive diversification of plants that acquired the nodular nitrogen-fixing symbiosis, all of which are members of the "the nitrogen-fixing clade" of angiosperms, building the phylogenetic framework needed to rigorously answer questions about this symbiosis requires unprecedented efforts to reconstruct relationships among legumes and other members of the nitrogen-fixing clade (non-legume Fabales, Rosales, Cucurbitales, and Fagales).

We have assembled phylogenomic data comprising hundreds of gene sequences for over

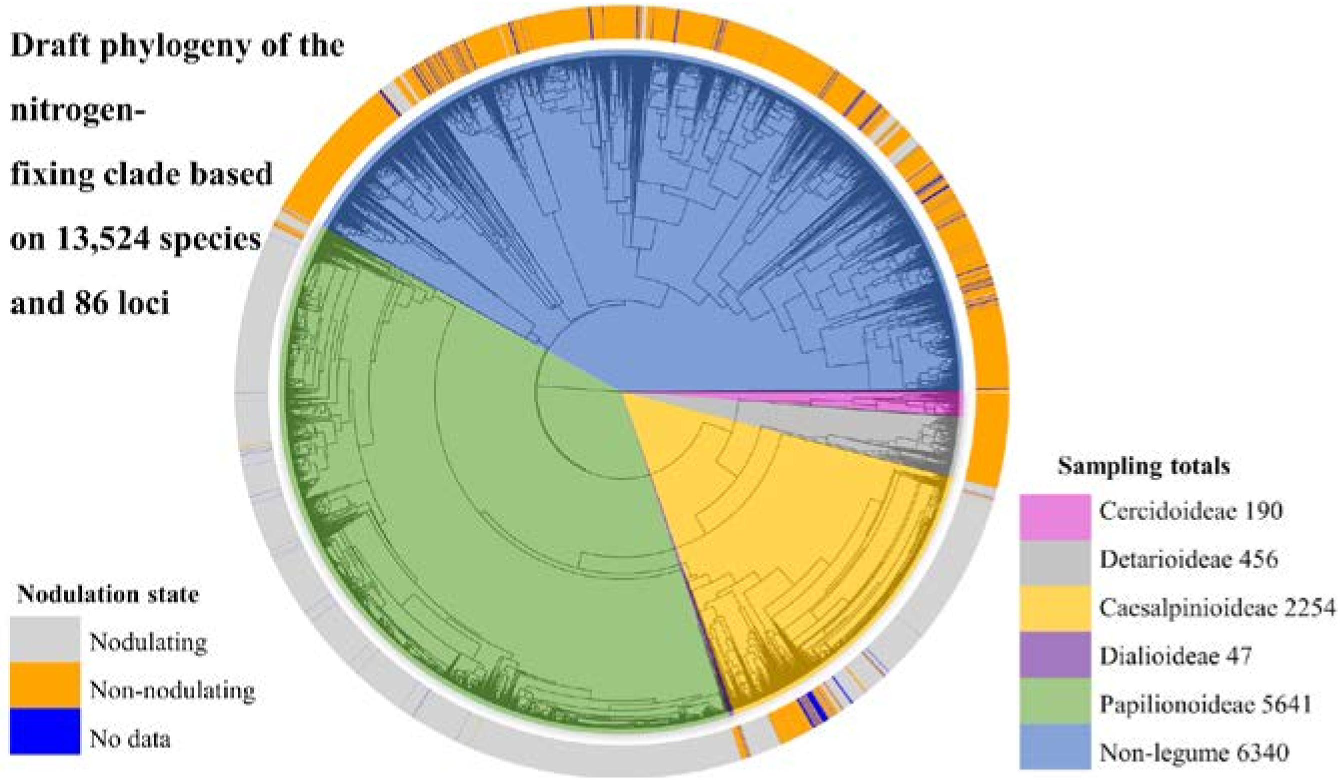

Figure 1. A draft phylogeny of the nitrogen-fixing clade based on currently assembled data and analysis. Relationships among clades may change based on on-going analyses. Genus-level nodulation states are plotted at the tree tips, and legume subfamily clades and numbers of species sampled per clade indicated with colors (the monospecific subfamily Duparquetioideae sample is not indicated).

13,000 species in the nitrogen-fixing clade as part of the wider "NitFix" project. We are using a subset of these gene sequences for phylogenetic analysis (Fig. 1). The rest of the gene set comprises functional genes related to nodulation that we are screening for association with nodulation.

Using plant specimens preserved in herbaria, we have sampled and sequenced close to 50% of the diversity of the nitrogen-fixing clade, including over 8,000 legume species, some of which have never been included in a molecular study. In collaboration with experts of the Legume Phylogeny Working Group, our evolutionary analyses (Fig. 1) are based on the most up-to-date legume taxonomy and genus-level nodulation-trait information available, both of which represent critical improvements upon earlier efforts to study the evolution of nodulation in the nitrogen-fixing clade.

Our dataset will form an integral resource for the study of the evolution of nodulation and will make the nodulating clade the most densely sampled model clade for comparative research in plants. We also hope that our dataset will be a valuable resource for the legume research community to investigate compelling questions related to legume systematics and evolution due to its increased sampling and resolution of many legume genera and its potential to robustly resolve deeper relationships within legume phylogeny.

For more information on this project, please visit https://nitfix.org or email hkates@ufl.edu or rfolk@biology.msstate.edu

NEW INSIGHTS INTO THE ROLE OF POLYPLOIDY IN LEGUME EVOLUTION

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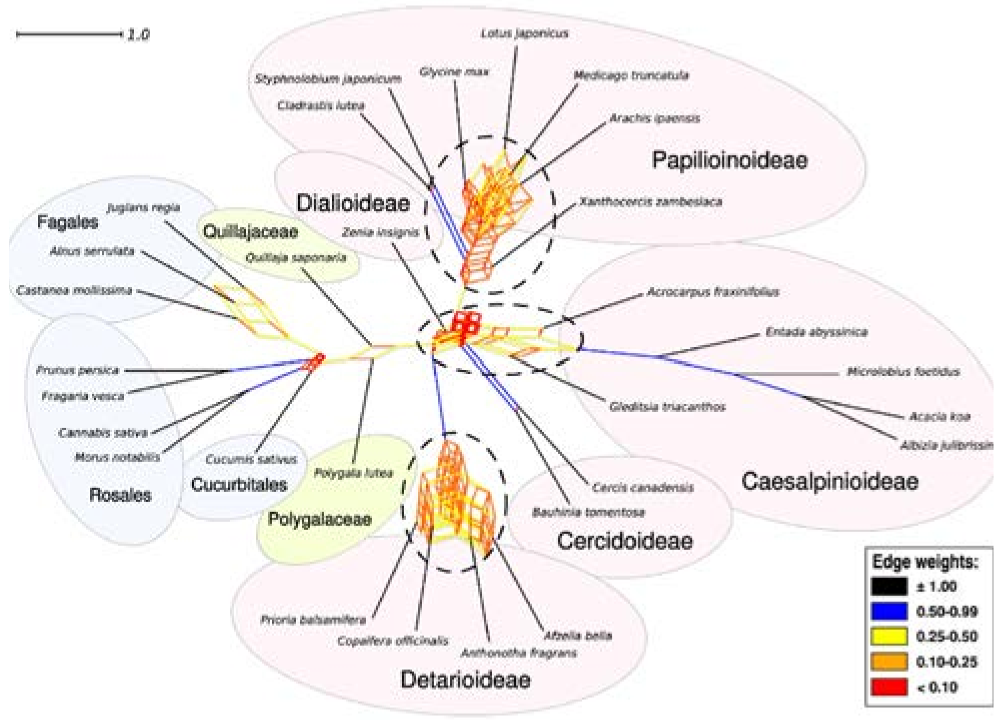
2020 produced a major advance in legume systematics, evolution, and comparative genomics in two papers by Koenen et al. (2020a, b). These studies have propelled legumes into the phylogenomics era, using thousands of genes from the nucleus as well as the chloroplast to provide a dated phylogeny for the family and to explore the implications for legume diversification and evolutionary biology. They are "instant classics"—thorough, detailed, insightful, provocative, scholarly works of the first magnitude—and it is impossible to do full justice to them in the space available here, so I will focus on just one consequential topic for which these papers provide revolutionary information for the family: polyploidy.

Discussions about polyploidy at all levels of legume evolution go back at least to Goldblatt's 1981 paper on "cytology and phylogeny" in Advances in Legume Systematics Part2. In the early 2000s, correlated divergence times of gene transcripts (Ks peaks) led to the hypothesis of ancient whole genome duplications (WGDs) in the genomes of *Medicago* and *Glycine* (Blanc and Wolf 2004; Schlueter et al. 2004), which an early phylogenomic analysis confirmed as being a shared event (Pfeil et al. 2005). A decade later, Cannon et al. (2015) showed that this WGD was present in the ancestor of subfamily Papilionoideae; surprisingly, they also found evidence for three additional independent WGD events: in *Copaifera* (Detarioideae), *Bauhinia* (Cercidoideae; but not in *Cercis*) and in all five Caesalpinioideae (sensu LPWG 2017) sampled. This work was based on gene and taxon sampling from the Thousand Plant Transcriptomes (1KP) project, whose capstone paper (Leebens-Mack et al. 2019) also identified these four legume events among the 244 green plant WGDs. More recently, Stai et al. (2019) hypothesized that Cercidoideae, other than *Cercis*, is derived from an allopolyploid ancestor formed by hybridization between an unknown diploid species and a diploid ancestor of modern *Cercis*.

With their much better taxon sampling and the use of several analytical strategies, Koenen et al. (2020b) explored the WGD issue thoroughly, and the first part of the title of their paper captures their conclusions: "The origin of legumes is a complex paleopolyploid phylogenomic tangle." In contrast to previous conclusions, their results best support

Figure 3 from Koenen et al. (2020b). Filtered supernetwork of the legumes showing tangles of gene tree relationships at the bases of the legumes, and subfamilies Detarioideae and Papilionoideae, that correspond to WGDs, as well as possible reticulation at the base of Caesalpinioideae.



three WGD events, with one each in the lineages leading to Papilionoideae and Detarioideae, respectively. The third event, like the papilionoid-specific WGD, occurred very early in legume history, during the rapid radiation of the six subfamilies near the Cretaceous-Paleogene Boundary (KPB; around 66 million years ago). This event may have occurred in the lineage leading to all legumes, or it may have involved hybridization between early ancestors of two extant legume lineages—an allopolyploid reticulate "tangle".

As Koenen et al. (2020b) appropriately note, more work is needed to address this important comparative genomics question, which impinges on many significant evolutionary issues. The results of Koenen et al. (2020a, b) imply that all anatomical, morphological, biochemical, physiological, and ecological characters are underlain by genes that belong to gene families whose membership and expression patterns are shaped by WGDs. Both auto- and allopolyploidy are known to generate evolutionary novelty (e.g., Levin 1983; Freeling and Thomas 2006; Doyle and Coate 2019), and hybridity in allopolyploids is associated with heterosis (Washburn and Birchler 2014). To take just one important legume trait, the symbiotic fixation of atmospheric nitrogen, it was suggested that polyploidy could have played a role in either the origin or the refinement of nodulation (Young et al. 2011; Li et al. 2013). Cannon et al. (2015), in reporting additional polyploidy events distributed across both nodulating and non-nodulating legumes, concluded that the relationship between polyploidy and nodulation was too complex for simple generalizations. As Koenen et al. (2020a) noted, there has been renewed debate about the number and placement of nodulation origin and loss in the "Nitrogen Fixing Nodulation Clade" of rosids in which legumes are embedded (van Velzen et al. 2019; Battenberg et al. 2018). Nodulation has been suggested to be responsible for the evolutionary success of legumes, though this, too, remains an open question (Afkhami et al. 2018). And the idea that polyploidy may have facilitated the survival of key plant lineages across the KPB (Fawcett et al. 2009) is an old idea, now refined with new insights for legumes by Koenen et al. (2020b).

How the phylogenetic distribution of nodulation and polyploidy fit separately or together in the context of legume diversification are big questions, and years of exciting work lie ahead. Koenen et al. (2020a, b) have provided an excellent foundation on which to build the next generation of legume systematics and evolutionary genomics.

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LEGUME BIOGEOGRAPHY ROUNDUP 2020

Legumes Shed New Light On the Assembly of Tropical Biomes

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Legumes are an ideal group for investigating questions in biogeography from macro to micro scales. The cosmopolitan distribution of the family across almost all major biomes and continents, the high diversity of legume species in many habitats, and their abundance in plant communities mean that legumes can provide a useful proxy for investigating patterns of flowering plant diversity more generally. This prominence of legumes in biogeography is reflected in several notable legume biogeography papers in 2020.

Here, we focus on some key questions in tropical biogeography, but for those with more temperate and subtropical floristic and biogeographic interests, we recommend that you read two papers by Duan et al. (2020) on papilionoid legumes - liquorice (*Glycyrrhiza*) and the Cladrastis clade. The *Cladrastis* paper deals with North America – East Asia disjunctions, with suggested migration routes including the boreotropics, North Atlantic and Bering Land Bridges. *Glycyrrhiza*'s remarkably wide distribution includes temperate South America and Australia, which are suggested to have been reached by long-distance dispersal.

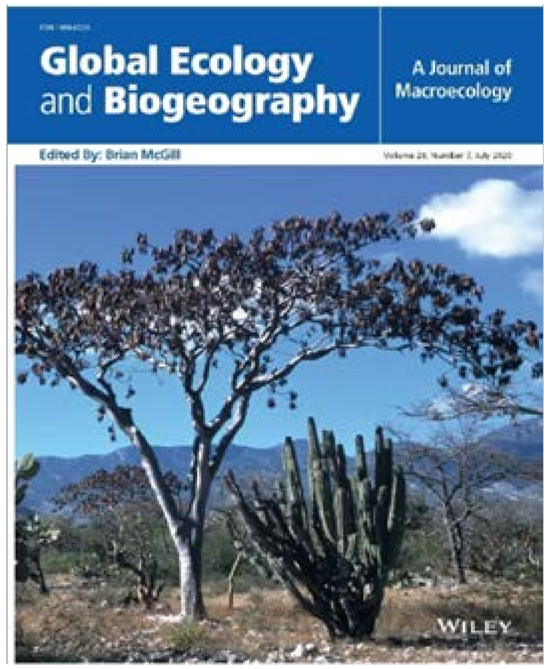
An important question in tropical biogeography is when and how the hyperdiversity of species in rainforests was assembled, and the longstanding debate as to whether rainforests are museums of ancient diversity that accumulated gradually since their early Ceno zoic origin, cradles of much more recent and rapid species diversification, or assemblages that result from high episodic species turnover combining both more ancient diversity and recent diversification. Legumes have been central to that debate, and three papers in 2020 provide intriguing new insights.

First, in a phylogenomic study of the Berlinia clade of subfamily Detarioideae, a lineage largely endemic to African rainforests and savannas, de la Estrella et al. (2020) densely sampled the genera *Anthonotha* + *Englerodendron* which are almost entirely restricted to African rain forests. What is striking about this study is the recency of the species divergences within the *Anthonotha* + *Englerodendron* clade. With crown ages of 2Mya for *Anthonotha* and 3.4Mya for *Englerodendron*, the 17 species in each genus diversified almost entirely during the Pleistocene. Another paper this year by Choo et al. (2020) on African and Madagascan detarioid legumes, whilst focusing mostly on issues of evolutionary switches amongst biomes, also infers the ages of African rainforest species of *Daniellia*. Their diversification started 10Mya, but much speciation is recent - starting in the late Pliocene and continuing into the Pleistocene. This new evidence from Africa mirrors the recency of several Amazonian rainforest clades, suggesting that recent species diversification in rainforests may be a global phenomenon.

Second, new insights into the processes underlying the generation of Amazonian rainforest tree diversity were presented by Schley et al. (2020) in a detailed phylogenetic and population genetic study of the detarioid genus *Brownea*. Schley et al (2020) presented some of the first evidence that reticulation or hybridisation between both older lineages and extant species has been important in the diversification of tropical rainforest trees. Although hybridisation is undoubtedly a major evolutionary force in temperate floras, a prevailing paradigm, promoted by influential figures in tropical ecology and evolution, including Peter Ashton (1969) and Alywn Gentry (1982), is that hybridisation is rare in tropical trees. One of Schley et al.'s most striking results is the rampant non-monophyly of several widespread species of *Brownea*, a feature predicted for rain forest species by Pennington & Lavin (2016), and which Schley et al. attribute to reticulation. Overall, they argued that their data suggest that *Brownea* forms a syngameon, i.e. a widespread species complex in which there is geneflow between sympatric congeneric species. What is clear from all this is that species diversification in rainforests is complex, intricate and still very poorly understood. See also the Kew Science News piece on this study: Taboo trysts between tropical trees.

At the other end of the lowland tropical rainfall gradient, legumes have also played a central role in defining the global distribution and understanding the historical assembly of seasonally dry tropical forests. Legumes are often the most species-rich and abundant lineage in these dry vegetation formations, though their most characteristic element is plants with stem-succulence, including cacti and the emblematic baobabs of Africa and Madagascar. It was studies of legume clades that first pointed towards the idea of a trans-continental Succulent Biome (Schrire et al., 2005; Lavin et al., 2004; Gagnon et al. 2019; Donoghue, 2019). In a recent paper, Ringelberg et al. (2020) characterized, modelled and mapped this global succulent biome in detail for the first time by using the distribution of stem succulent species as a proxy and assembled a set of legume (and other) phylogenies to demonstrate high levels of succulent biome phylogenetic conservatism across the transcontinental distribution of this biome. Once again, the prominence of legumes for addressing biogeographical questions comes to the fore.

Two co-occurring Brownea lineages (Brownea grandiceps (photo © Rowan Schley) and Brownea jaramil-loi (photo © Xavier Cornejo)) and their putative hybrid Brownea "rosada" (photo © J. L. Clark); Figure from Shley et al (2020).



Right: Typical tropical dry deciduous, grass-poor, fire-free, succulent-rich vegetation in the Tehuacán Valley in central Mexico, part of the trans-continental Succulent Biome which was mapped by Ringelberg et al. (2020). The prominent tree, laden with fruits and leafless during the dry season, is Conzattia multiflora (Leguminosae: Caesalpinioideae), photo Colin Hughes.

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LEGUME BIBLIOGRAPHY UNDER THE SPOTLIGHT

A Taxonomic Revision of Flemingia (Leguminosae: Papilionoideae) in India

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Finally a taxonomic revision of the genus *Flemingia* in India has been published. I started working on Indian *Flemingia* in 2014 under the guidance of Dr. M.M. Lekhak (SUK), Maharashtra, India as a part of my doctoral studies. During the work we collaborated with Prof. L.J.G. van der Maesen from the Naturalis Biodiversity Center, Leiden, the Netherlands. I collected 24 species and one variety of the 29 taxa reported in India and living material is being maintained in the Botanic Garden, Shivaji University, Kolhapur, with voucher specimens deposited in SUK. The present work is an outcome of the taxonomic study conducted over more than nine years. A revision of subg. *Rhynchosioides* had been published earlier (Gavade et al. 2019) and hence is not a part of the present publication.

From the abstract: Indian *Flemingia* species are grouped under five subgenera, namely *Chalaria*, *Flemingiastrum*, *Lepidocoma*, *Ostryodium* and *Rhynchosioides*. In the present work, we revised the taxonomy of the genus (excluding subg. *Rhynchosioides*) based on the study of live material and preserved specimens. We reported 21 species and one variety (22 taxa) in India, of which one variety is endemic, i.e. *F. praecox* var. *robusta*. All the taxa have been described, illustrated and their ecology discussed. In the process, twelve binomials (*F. angustifolia*, *F. blancoana*, *F. chappar*, *F. congesta*, *F. grahamiana*, *F. latifolia*, *F. macrophylla*, *F. nudiflora*, *F. paniculata*, *F. stricta*, *F. wallichii* and *F. wightiana*) and one trinomial (*F. praecox* var. *robusta*) are lectotypified. *Flemingia sericans* and *F. stricta* subsp. *pteropus* are proposed as new synonyms for *F. macrophylla* and *F. stricta*, respectively. *Flemingia parviflora*, an Australian species, is recorded for India for the first time. *Flemingia strobilifera* var. *nudiflora* is raised to species level and a new combination proposed, i.e. *F. nudiflora*. *Flemingia tiliacea* is relegated to the synonymy of *F. nudiflora*. A taxonomic key for the subgenera and species analysed is provided for easy identification. Additionally, distributional maps for the genus and species are presented. Line drawings are included for each species, and colour photographs embellish the paper.

Citation:
Gavade, S.K., van der Maesen, L.J.G., Lekhak, M.M. 2020. Taxonomic revision of the genus *Flemingia* (Leguminosae: Papilionoideae) in India. *Journal of Plant Taxonomy and Geography (Webbia)* 75: 141-218. https://doi.org/10.36253/jopt-8767

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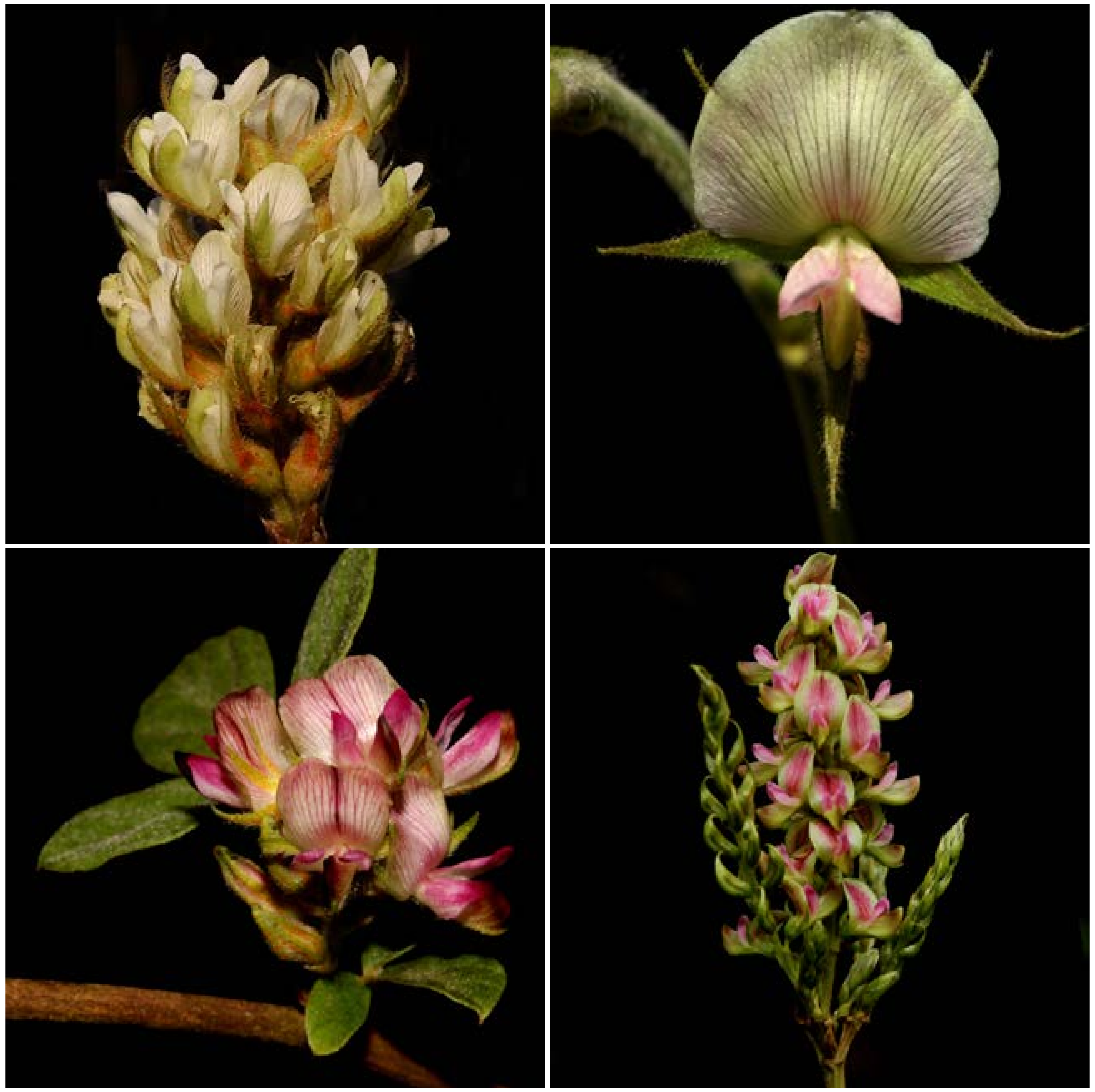

Clockwise from top left: Flemingia grahamiana, F. paniculata, F. procumbens & F. semialata, all photos, Dr. M.M. Lekhak.

LEGUME BIBLIOGRAPHY 2020

Compiled by Warren Cardinal-McTeague

Methodology – The Legume Bibliography 2020 was manually collated on 28-Oct-2020 and 05-Jan-2021 using keyword searches and screening of the first 10 pages of Google Scholar and on the websites of the most frequently encountered journals (Appendix 1). The keywords included "**Leguminosae**" or "**Fabaceae**" and publications were limited to the year 2020. Where available, *.bib or *.ris files were downloaded and imported into Mendeley Desktop v.1.19.4 and manually tagged under the headings provided below. Most legume-related research is presented here, with the exception of the >54 Pharmacology studies exploring health and anti-microbial properties of numerous legume extracts. The final list was then reviewed by Colin Hughes and any publications missed by these methods were manually added. Automated approaches and DOIs are being considered for the future. The complete bibliography is available for direct download in BibTeX (*.bib), Research Information Systems (*.ris), and EndNote XML (*.xml) format.

Results – A total of 300 publications were recovered for the Legume Bibliography 2020:

17 Anatomy & Morphology
6 Biogeography
29 Chloroplast Genomes
7 Development
60 Ecology
13 Floristics
10 Microbiology, Nodulation & Symbiosis
28 Molecular Biology, Genetics & Genomics
3 Paleobotany
3 Palynology
6 Physiology
18 Phylogenetics, Phylogenomics & Evolution
11 Phytochemistry
20 Population Genetics
36 Taxonomy
33 New Species

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Appendix 1: List of frequently encountered journals that were searched for keywords in addition to Google Scholar.

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ADDENDUM

BIBLIOGRAPHY 2020 ADDITIONS

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