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ISSUE 68

YEAR 2021

# THE BEAN BAG

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

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ON THE COVER: *HARPALYCE GREUTERI* (PAPILIONOIDEAE: BRONGNIARTIEAE) PHOTO BY PEDRO GONZÁLEZ

# WELCOME NOTE

## Issue 68: 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 47 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.

Bean Bag Number 68 is another bumper issue reporting on diverse aspects of another vibrant and busy year of global legume systematics research. One of the exciting developments during 2021 was the launch of a new [Legume Data Portal](#), which also posts news items of interest to the legume research community. You can read more about the Portal in this issue of the Bean Bag.

We thank Anne Bruneau for compiling reports from the Legume Phylogeny Working Group (LPWG) meeting in September 2021, which are reproduced here in edited form. Thanks also to Gwilym Lewis at Kew for help with checking this issue and facilitating the archiving of the Bean Bag in the Kew Research Repository, which was completed in 2021. Finally, thanks to you, the legume community as a whole, and our many contributors for sharing their time and insights.

For recent BB issues see the [Legume Data Portal](#)  
Earlier issues of the BB (1975 to 2021) are available via the [Kew Research Repository](#)

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Facebook: <https://www.facebook.com/groups/1484192248560637/>

## Editors:

**Colin Hughes**, University of Zürich, Switzerland

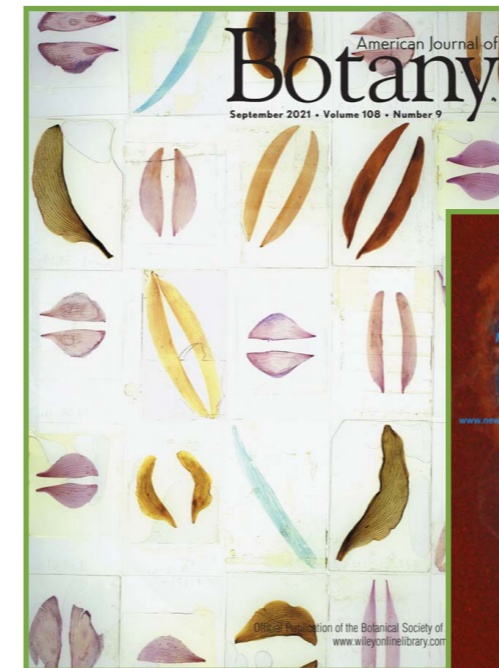
**Warren Cardinal-McTeague**, University of British Columbia, Canada (starting July 2022)



Fruits and seeds of  
*Brodriguesia santosii* R.S. Cowan,  
Detarioideae

Photo by Colin Hughes

# LEGUME COVER STORIES



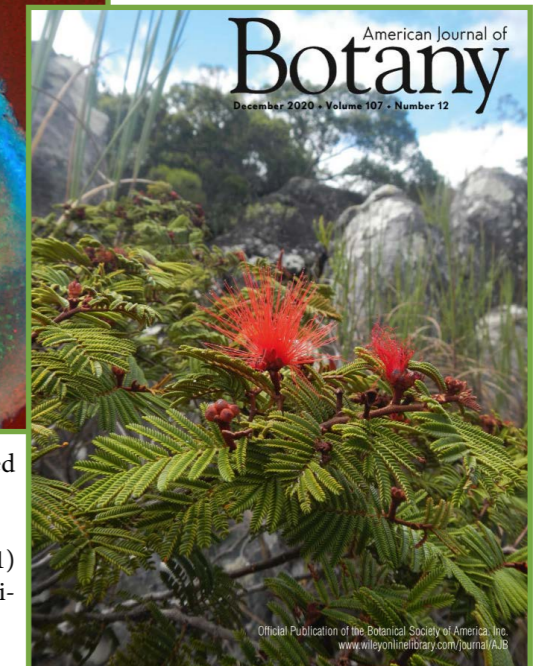
Cover image: Variation in the shape of the standard, keel, and wing petals in the pantropical genus *Erythrina* L., Gonzalo Bilbao.

Bilbao G, Bruneau A, Joly S (2021) Judge it by its shape: A pollinator-blind approach reveals convergence in petal shape and infers pollination modes in the genus *Erythrina*. *American Journal of Botany*, **108**: 1716-1730.



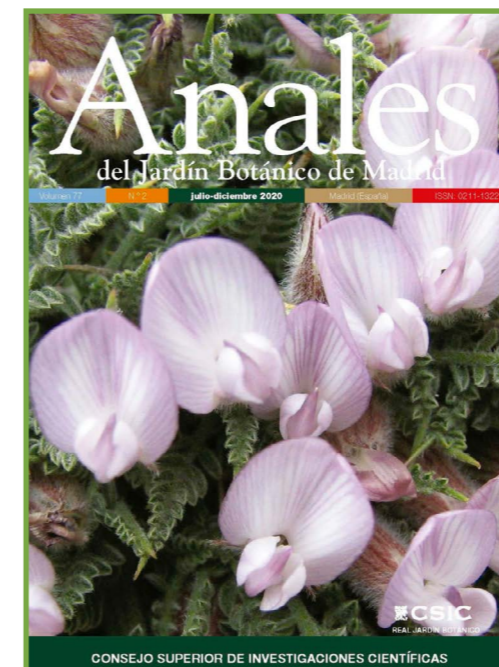
Cover image: Cross section of a root nodule of *Medicago truncatula* colonized by its nitrogen-fixing symbiont, *Sinorhizobium meliloti*, Ulrike Mathesius.

Mens C, Hastwell AH, Su H, Gresshoff PM, Mathesius U, Ferguson BJ (2021) Characterisation of *Medicago truncatula* CLE34 and CLE35 in nitrate and rhizobia regulation of nodulation. *New Phytologist*, **229**: 2525-2534.



Cover image: *Calliandra fuscipila* Harms, a shrub endemic to the campos rupestres of the Chapada Diamantina in northeast Brazil, Erik Koenen.

Koenen EJ, Kidner C, de Souza ÉR, Simon MF, Iganci JR, Nicholls JA, Brown GK, de Queiroz LP, Luckow M, Lewis GP, Pennington RT, Hughes CE (2020). Hybrid capture of 964 nuclear genes resolves evolutionary relationships in the mimosoid legumes and reveals the polytomous origins of a large pantropical radiation. *American Journal of Botany*, **107**: 1710-1735.



Cover image: *Astragalus wiesneri* Maassoumi & Pahlevani, a rare species in alpine habitats in the southern Zagros Mountains of Iran, Amir H. Pahlevani.

Pahlevani AH, Maassoumi AA, Osaloo SK (2020) What is *Astragalus wiesneri*? Disentangling a new species from its relatives in section *Anthylloidei*. *Anales del Jardín Botánico de Madrid*, **77**: e103.

# ARTIST SPOTLIGHT

## MARIANNE HAZLEWOOD

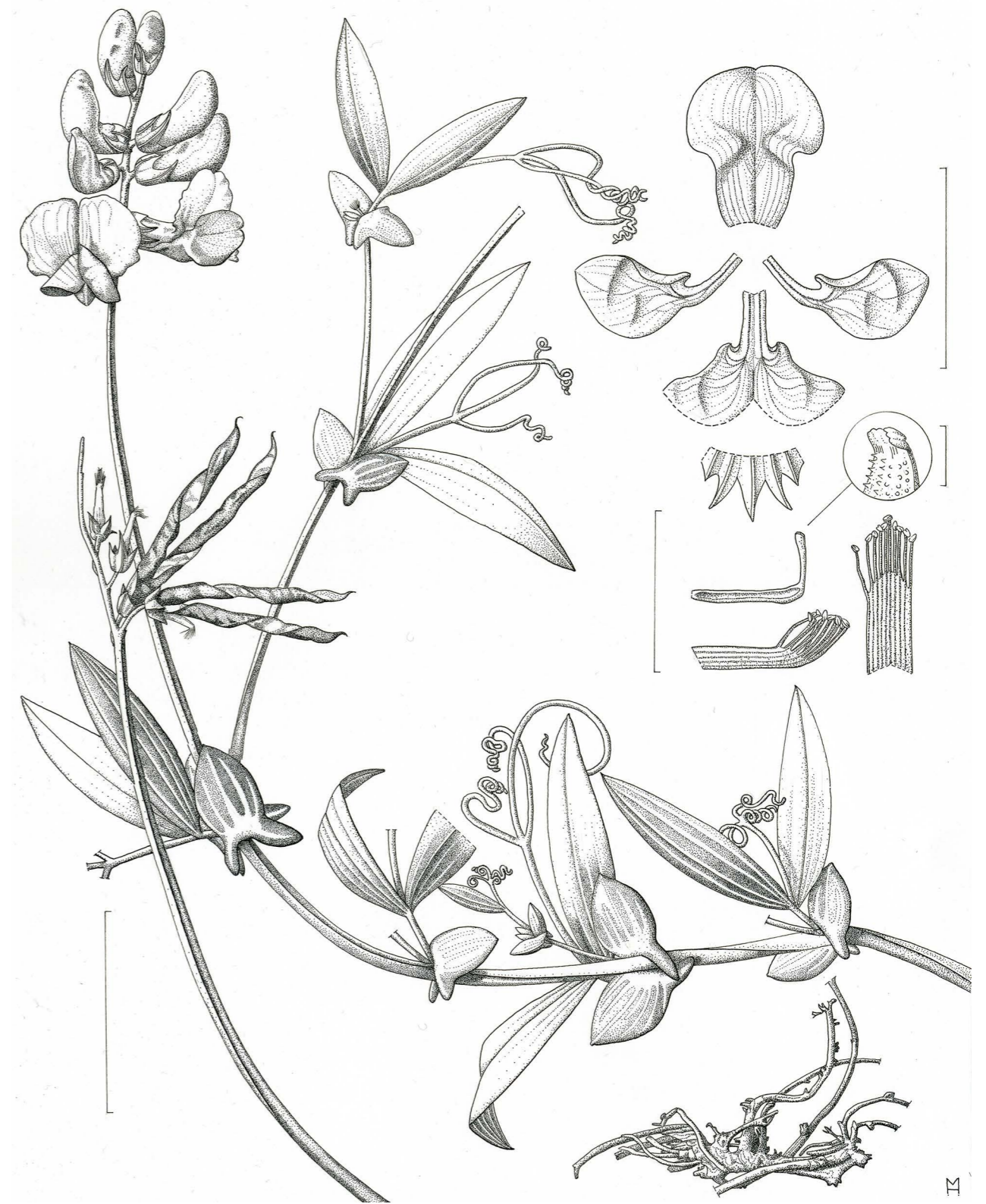


*Marianne Hazlewood* Dip BI is an RBGE (Royal Botanic Garden Edinburgh) graduate and RHS (Royal Horticultural Society) & BISCOT (Botanical Image Scotia) Gold award-winning and exhibiting botanical illustrator. She creates modern botanical illustrations in various media including watercolour, Japanese ink paste, screen print, digital graphics and pen-and-ink. Each medium offers a different refinement on a close observational process.

She has continued her connection with RBGE where she is currently a tutor on the Online Diploma in Botanical Illustration course. She loves working with the students and assisting them with their introduction to botanical illustration. She is a Visual Arts Scotland award winner and had a solo exhibition with Open Eye Gallery in October 2020 in Edinburgh. She has also displayed with the Society of Scottish Artists and regularly shows as a solo artist at the annual Pittenweem Arts Festival. Her illustrations have been featured in various botanical society group exhibitions & botanical publications. Her work is also in the RBGE Florilegium and the NHS (National Health Service) Lothian Art Collection. She is interested in connecting and working with botanists, horticulturalists, environmental scientists and other artists, and enjoys taking on commission work.

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<https://www.facebook.com/Marianne.E.Hazlewood/>

*Pisum sativum* L., Papilionoideae, by Marianne Hazlewood, 2021  
 [= *Lathyrus oleraceus* Lam.]



*Lathyrus magellanicus* Lam., Papilionoideae, by Marianne Hazlewood, 2015

# THE LEGUME PHYLOGENY WORKING GROUP

*Meeting Summarized by Anne Bruneau  
Edited by Colin Hughes*

A *Legume Phylogeny Working Group* (LPWG) virtual meeting was held on September 30<sup>th</sup>, 2021 to update the community on progress with the LPWG Working Groups, discuss new research initiatives and announce upcoming publications and events. 105 participants from 27 countries attended the meeting. The meeting was organised and introduced by Anne Bruneau (Université de Montréal). It was encouraging to see many veteran legume systematists alongside many young new legume researchers who were attending the meeting for the first time.



The LPWG was founded in 2010 with the objective of fostering collaboration and facilitating sharing of material and ideas amongst legume systematics researchers. Subsequent to the online meeting organised by Colin Hughes (University of Zürich) and Manuel de la Estrella (Universidad de Córdoba) in May 2020, five working groups - *Taxonomy, Occurrence Data, Traits, Phylogenomics* and *Open Tree of Life* - were established to advance research collaboration in these five areas which were considered of particular importance to understand the systematics and evolution of legumes. Updates and progress reports from each working group are presented below with the aim of encouraging other researchers to collaborate and contribute.

Anyone who is interested in collaborating with one or other of the Working Groups and projects is encouraged to contact the relevant working group coordinators.

# TAXONOMY WORKING GROUP

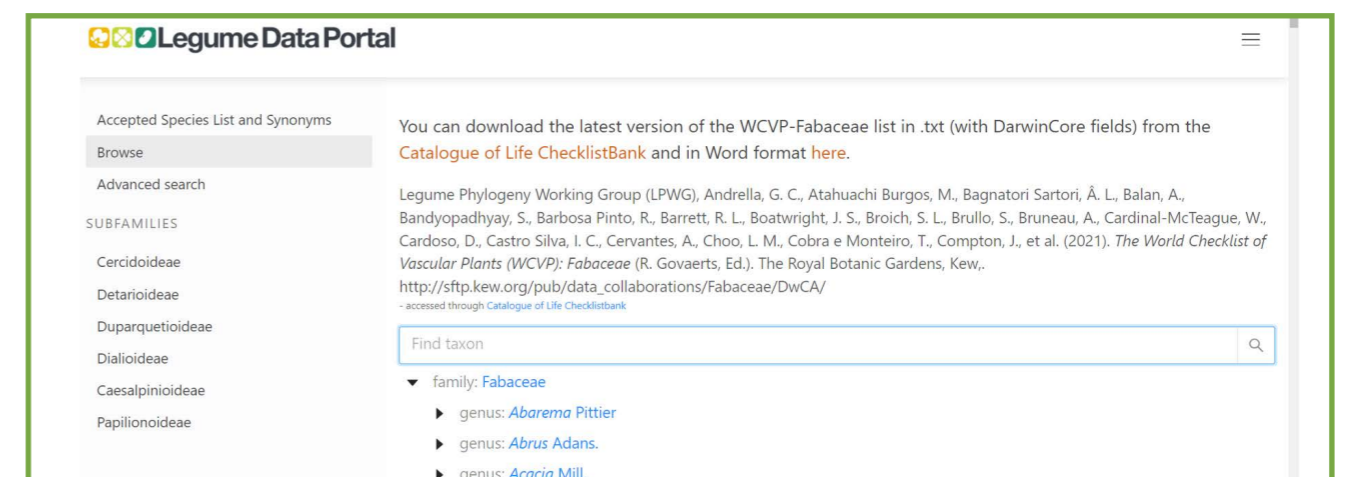
*A first updated version of the legume checklist published in 2021*

Coordinators:

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

The *Legume Taxonomy Working Group* was established in May 2020 and tasked to create an updated, community-endorsed legume species checklist. It is envisioned that this checklist will enable more effective collaboration undertaken by the broader legume research community and will serve as the primary source of taxonomic name information for legumes for other online platforms such as the Global Biodiversity Information Facility (GBIF) and Catalogue of Life (CoL). The Legume Taxonomy Working Group was chosen as the World Flora Online's (WFO) Taxon Expert Network (TEN) and will provide the taxonomic backbone for the Leguminosae within the WFO taxonomic backbone.

A network of 80 legume taxonomists, including 38 subfamily and tribe coordinators, from 24 countries collaborated with Rafaël Govaerts at the Royal Botanic Gardens, Kew, to update the legume checklist. In total, 6,167 corrections were captured and about 2,011 names added to the checklist. In June 2021, the first updated version of the checklist was published on the CoL's ChecklistBank (<https://data.catalogueoflife.org/dataset/2304/about>) and incorporated into the GBIF taxonomic backbone in December 2021. The checklist also feeds through to the new Legume Data Portal (<https://www.legumedata.org/>) where the checklist data are searchable (<https://www.legumedata.org/taxonomy/browse>).



A screenshot of the legume checklist search page on the Legume Data Portal.

Excellent progress has been made with updating the checklist especially for subfamilies Cercidoideae and Dialioideae which are fully checked, and Detarioideae of which 87% of the checking has been completed. About 45% of the Papilionoideae have been reviewed to date. Tribes Abreae, Amorpheae, Crotalariae, Dalbergieae, Desmodieae, Diocleae, Viciae, Galegeae, Genisteae, Millettieae, Phaseoleae, Robineae, Sophoreae and Trifolieae are still in progress. Because most people working on Caesalpinioideae are currently devoting their efforts to compiling *Advances in Legume Systematics Part 14* which will present a new generic and tribal/clade-based classification of Caesalpinioideae to be published in 2022, only about 3% of the genera in this subfamily have so far been checked. Once ALS14 is published, efforts will be directed to updating the Caesalpinioideae names in the checklist.

If you are interested in joining us in updating and maintaining the legume checklist, please contact Marianne le Roux ([m.leroux@sanbi.org.za](mailto:m.leroux@sanbi.org.za))

## OCCURRENCE DATA WORKING GROUP

Coordinators:

**Edeline Gagnon**, Technical University Munich, Germany

**Jens Ringelberg**, University of Zürich, Switzerland

**Joe Miller**, Global Biodiversity Information Facility (GBIF), Denmark

*The Occurrence Data Working Group* initially decided to wait for the accepted species checklist from the Legume Taxonomic Work Group and for the launch of the Legume Data Portal before deciding on the best approach to produce an expert-verified global occurrence dataset for the entire family. Now that the first version of Legume Checklist has been published (see previous report), the Working Group has been discussing an agreed set of automated filters for “cleaning” data that could be combined with an expert-curated occurrence dataset, and which could then be available for community use via the Legume Data Portal.

At the LPWG meeting in September, three short talks were presented: i) Charlotte Hagelstam-Renshaw (Université de Montréal, Canada) outlined the methods she is using to assemble occurrence data for subfamily Cercidoideae as part of her MSc; ii) Moabe Fernandes, Newton Postdoctoral fellow (University of Exeter, UK), presented his on-going work focused on assembling and cleaning occurrence data for all legumes in the Americas, with the goal of assessing phylogenetic and biodiversity hotspots for conservation. Moabe stressed the importance of finding ways to validate taxonomic identities of records as key to improving data quality; iii) Domingos Cardoso (Universidade Federal de Bahia, Brazil), presented “cleanHerb”, a new R package he has developed to easily standardize herbarium record data from biodiversity databases.

Joe Miller stressed that a longer-term goal for GBIF is to store and make these filtered “clean” data available for reuse with attribution. This is a difficult task but GBIF is making progress. A simple step researchers can do, is to keep track of the GBIF-IDs when they work with GBIF data; if modifications are made to the GBIF occurrence data, he suggested that researchers track why and how decisions are made so that the data can eventually be reused.

## TRAITS WORKING GROUP

Coordinators:

**Leonardo Borges**, Universidade Federal de São Carlos, Brazil

**Renske Onstein**, German Centre for Integrative Biodiversity Research (iDiv), Germany

*The Traits Working Group* continues to serve as a hub to connect researchers working on different aspects of legume morphology, with particular focus on compiling plant functional trait data. The main goals of the Working Group are to foster collaboration and to avoid redundant data collection.

Ongoing trait projects and research groups, a list of legume traits and definitions, and monographs used to extract trait data, are accessible in this google drive: <https://drive.google.com/drive/folders/1Eifg9x5S9ffoXP9A4myDHnKPd2Wm01y6>

If you work on a project including legume traits, Dr. Onstein suggests accessing the google drive and adding some information on your research project to the “research groups” spreadsheet. Taxonomic monographs provide a rich source of morphological and trait data and the working group is assembling a repository of legume monographs to facilitate the easier harvesting of data. If you have any pdfs of monographs, please deposit them in the “Monographs” folder.

One specific ongoing project is the creation of a functional trait dataset for all mimosoids. Those interested in including their trait data in this database, should e-mail Renske Onstein ([onsteinre@gmail.com](mailto:onsteinre@gmail.com)).

To receive updates and be part of this Working Group, please add your email address to the “Legume Traits WG” document located in the google drive.

At the LPWG meeting in September, four students presented aspects of their research on morphology and functional traits. **Francisco Velásquez Puentes** (iDiv) presented his project on the role of functional traits in biome evolution in the neotropics. **Rachel Souza Ferreira** (iDiv) presented her project on functional traits across mimosoids. **Yago Barros-**

**Souza** (Universidade Federal de São Carlos) presented his PhD work on the association between phylogenetic diversity and trait disparity in Brazilian vegetation. **Monique Maianne Silva** (Universidade Federal de São Carlos) presented her work on the evolution of floral morphological diversity in *Mimosa*.

## PHYLOGENOMICS WORKING GROUP

Coordinators:

**Félix Forest**, Royal Botanic Gardens Kew, UK

**Erik Koenen**, Université Libre de Bruxelles, Belgium

**At least eight** legume phylogenomics projects are underway, as summarized below:

1. Detarioideae. (M. de la Estralla, D.I. Ojeda, O. Hardy, F. Forest et al.) using a Detarioid-specific bait set for 250 species (one species per genus) plus the Angiosperms353 probes, with a particular focus on the *Berlinia* (D.I. Ojeda, A. Boom, S. Abeele, M. de la Estrella, O. Hardy et al.), *Saraca* (L.M. Choo, M. de la Estrella et al) and *Eperua* (E. Fortes, V. Mansano, J. Doyle, et al.) clades.

2. Caesalpinioideae. 422 taxa, including 146 of the 151 genera of subfamily Caesalpinioideae have been sequenced using the Mimobaits bait set of 997 genes. The first results for c. 120 taxa have been published (Koenen et al. 2020). The full 422-taxon tree is in preparation for publication. This new backbone phylogeny will be used as the basis for the new tribal / clade-based classification of the subfamily (ALS14 Part 2), for establishing a new generic system for the subfamily (ALS14 Part 1), for investigating phylogenetic turnover and biogeography, and for trait evolution studies. The project is led by Erik Koenen, Jens Ringelberg, Colin Hughes, et al., University of Zürich, Switzerland.

3. Phylogeny of *Albizia* s.s. and evolutionary origins of savanna species using selected exons from the *Mimobaits* probes to produce a new sectional classification, and trait and niche evolution studies in relation to historical assembly of African savannas. Led by E. Koenen, C. Lehmann and O. Hardy.

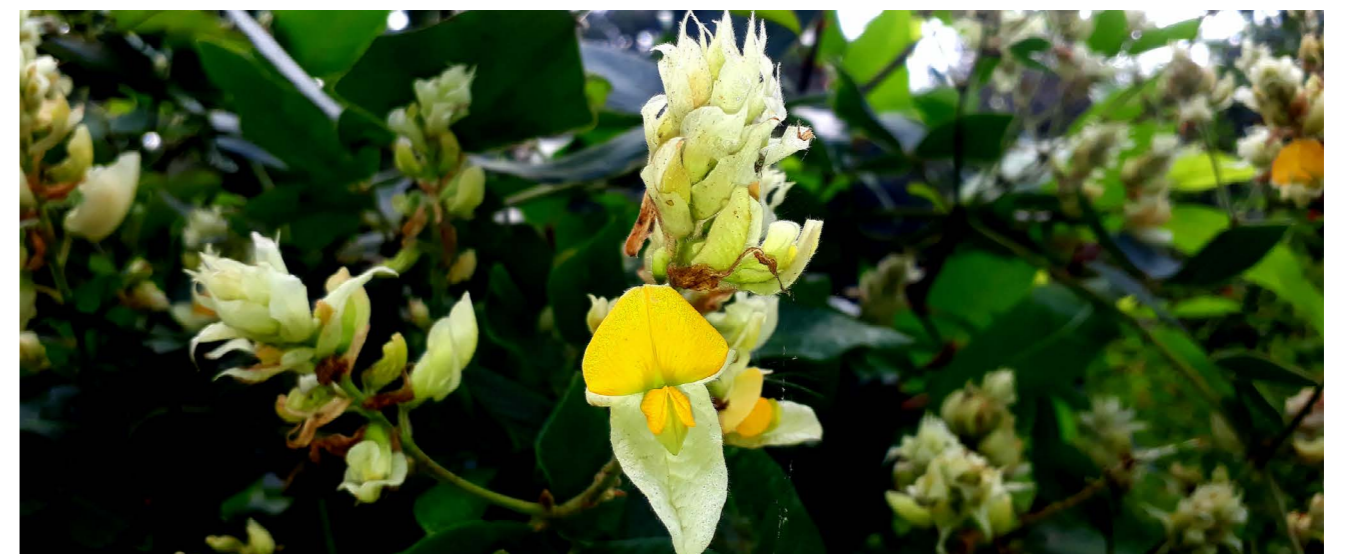
4. Phylogenomics and cytonuclear coevolution of Papilionoideae. The aims here are to 1) generate a fully resolved and well supported phylogeny of the major clades of papilionoids using multiple genes from all three genomes, 2) examine coevolution of nuclear, mitochondrial and plastid genes, and 3) determine if changes in nuclear encoded DNA repair, replication and recombination genes are correlated with mitochondrial and plastid genome complexity. Led by R.K. Jansen, T.A. Ruhlman and M.F Wojciechowski, with I.-S. Choi, C. Lee, D. Cardoso, L.P. de Queiroz, and H.C. de Lima.

5. Phylogenomics of subfamilies Cercidoideae and Dialioideae using Angiosperms353 + 86 genes of known function to resolve phylogenetic relationships, and study trait evolution, biogeography, whole genome duplication events, the fate of duplicated genes, root nodulation gene evolution, correlation between functional genes and trait evolution across biomes, and delineate species complexes. Led by A. Bruneau, W. Cardinal-McTeague, S. Cannon, C. Hagelstam Renshaw, L. Bourgeois-Racette.

6. Phylogenomics projects from the Ting-Shuang Yi lab, include three main topics: 1) Phylogeny of Leguminosae with 695 accessions including plastomes, mitochondrial and nuclear genes of ~74 tribal-level clades and more than 480 genera to build a solid backbone phylogeny for legumes; 2) plastome evolution: investigating the full history of plastome rearrangements, and the frequency of parallel inversions in different lineages/clades; 3) whole genome sequencing: plans include seven sequenced species covering all six subfamilies by PacBio/HiFi + HiC + RNAseq and a collaborative plan to sequence the genomes of representatives of all tribes.

7. Development of a bait set for legumes targeting 507 loci, tested on 25 taxa from across legumes and selected outgroup taxa (Vatanparast et al. 2018). The main aims are target-enrichment phylogenomics to improve the resolution of legume lineages at generic, tribal, and subfamily levels and a generic level phylogenomic backbone of phaseoloid legumes. Led by M. Vatanparast and A.N. Egan.

8. The legume project under the umbrella of the Plant and Fungal Trees of Life (PAFTOL) project at Kew has so far produced sequence data for 450 genera using the Angiosperms353 probes, most of which will be included in the angiosperm tree of life 2.0 released in December 2021 on the Kew Tree of Life Explorer (<https://treeoflife.kew.org/>) (109 genera already available from release 1.0). These genera will also be included in the PAFTOL “big angiosperm tree” paper in preparation. These collaborative efforts involve E. Koenen, F. Forest, G. Lewis, T. Pennington, R. Barrett, A. Bruneau, W. Cardinal-McTeague, D. Cardoso, J. Clugston, A. Egan, M. de la Estrella, B. Klitgaard, T. McLay, D. Murphy, M. Renner, R. Schley, M. Vatanparast, M. Wojciechowski and the PAFTOL team.



*Paracalyx scariosus* (Roxb.) Ali, Papilionoideae, photo by Sandip K. Gavade.

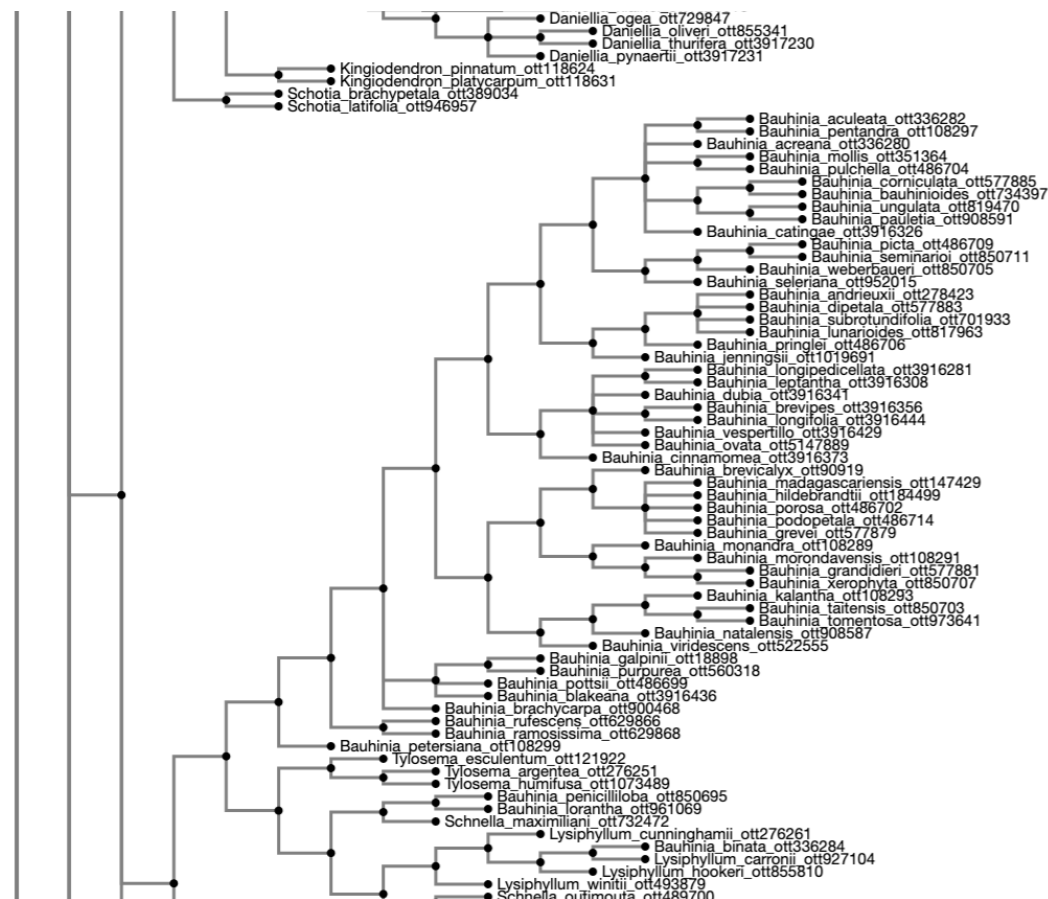
# OPEN TREE OF LIFE - LEGUME NODE

Coordinators:

**Vanessa Terra**, Universidade Federal de Uberlândia, Brazil

**Joe Miller**, Global Biodiversity Information Facility (GBIF), Denmark

*Open Tree of Life* (OToL) is a project to construct a comprehensive, dynamic and digitally-available tree of life by synthesizing published phylogenetic trees. Until a fully sampled single phylogenetic analysis is available for the legumes, the OToL can provide the best phylogenetic estimates for the family. Currently only about 30% of the legume species have been integrated into the OToL. The goal of the working group is to curate the Leguminosae/Fabaceae OToL tree with the latest phylogenies to create a resource for the legume community. Because it is very easy to import a phylogeny from Treebase (<https://www.treebase.org/treebase-web/home.html>) into OToL for further curation, legume systematists are encouraged to deposit their published trees in Treebase, where they can then be used to improve the OToL synthetic tree. Please see the legume portal (<https://www.legumedata.org/working-groups/OToL>) for more information.



Section of the 4,835 terminal Legume OToL (v. Dec 2019; phylogenies only), rendered on phylo.io

# ACACIA PHYLOGENOMICS & GENOMES

**Daniel Murphy**, Royal Botanic Gardens Victoria, Australia

*Dr. Dan Murphy* would like to draw attention to other legume researchers that two projects investigating the phylogenomics and genomics of *Acacia* are being led by a team of researchers based at the Royal Botanic Gardens Victoria in Melbourne, Australia, with support from the **Genomics for Australian Plants** (GAP) Initiative and in collaboration with *Acacia* researchers from other research institutions.



*Acacia pycnantha*, Australia's Floral Emblem, at Phillip Island, Victoria, Australia, photo by Dan Murphy.

A new project, started in 2022, will generate a backbone phylogeny of Australia's largest flowering plant genus, *Acacia*, including close mimosoid legume relatives as outgroups. A selection of species representing all major evolutionary lineages of *Acacia*, previously discovered in molecular phylogenies and morphological classification, is initially being sampled for a phylogenomic dataset using the Angiosperm353 baitset, and is expected to contribute to the ultimate aim of a new formal classification of the genus. A second project, to publish a draft genome for *Acacia pycnantha* (Australia's official floral emblem), is currently being finalised for publication (the mitome and plastome sequences and structural diversity were published here: <https://doi.org/10.46471/gigabyte.36>).

Both of these projects are intended to generate publicly accessible, genome-level reference datasets for *Acacia* research (e.g., in conservation genetics, invasive species biology, ecological studies and agro-forestry) as well as a co-ordinated approach to *Acacia* systematics research, and contribute to our understanding of the evolution of this major lineage of the Australasian flora.

**Full project descriptions are available here:**

[Acacia phylogenomics project](#)

[Acacia pycnantha reference genome](#)



# ADVANCES IN LEGUME SYSTEMATICS 14: CAESALPINIOIDEAE

Colin Hughes, University of Zürich, Switzerland

Luciano Paganucci de Queiroz, Universidade Estadual de Feira de Santana, Brazil

Gwilym Lewis, Royal Botanic Gardens Kew, UK

*The Advances in Legume Systematics* (ALS) series has been a highly successful and productive vehicle for publishing work on legume classification over many years, with 13 published volumes. Now we are assembling Part 14 which will focus on the classification of subfamily Caesalpinioideae (sensu LPWG, 2017).

The idea for ALS14 stems from the need for a new phylogenetically-based generic and tribal/clade-based classification of subfamily Caesalpinioideae which comprises c. 152 genera and c. 4,600 species. This need for a new classification has been apparent from numerous phylogenetic studies over the last two decades and has been spurred on by new work by Erik Koenen and Jens Ringelberg in Zürich to build a new phylogenomic backbone for the subfamily based on the *Mimobaits* gene set of 997 nuclear genes. This new backbone samples 146 of the 152 genera, and 422 taxa in total and has revealed extensive generic non-monophyly, especially in the Mimosoid clade where c. 25% of the genera are non-monophyletic.

ALS14 will be published in two parts. In Part 1 (edited by Colin Hughes, Luciano de Queiroz and Gwilym Lewis), the new backbone phylogeny documenting this non-monophyly will be presented alongside a series of papers that deal with generic delimitation issues, especially in Mimosoids and will contribute to aligning genera with clades. Part 2 (edited by Anne Bruneau and Luciano de Queiroz) will present a new phylogenetically-based tribal/clade-based classification of Caesalpinioideae plus a detailed synopsis of genera.

ALS14 will be published as a Special Issue of the Open Access plant taxonomy journal *PhytoKeys* ([https://phytokeys.pensoft.net/special\\_issues](https://phytokeys.pensoft.net/special_issues)). Sixteen papers have been submitted for ALS14 Part 1 and we are anticipating a set of 17 papers in total and these will be published in 2022. **For Part 2**, a large set of authors have been invited to contribute generic accounts for particular tribes, clades and grades and the **deadline there is 31<sup>st</sup> May 2022**.

If anyone who would like to contribute to ALS14 Part 2 and is not already involved, please let us know! We thank all the authors for jumping in to make ALS14 happen. We are optimistic that we can put together a useful and interesting volume. [colin.hughes@systbot.uzh.ch](mailto:colin.hughes@systbot.uzh.ch)



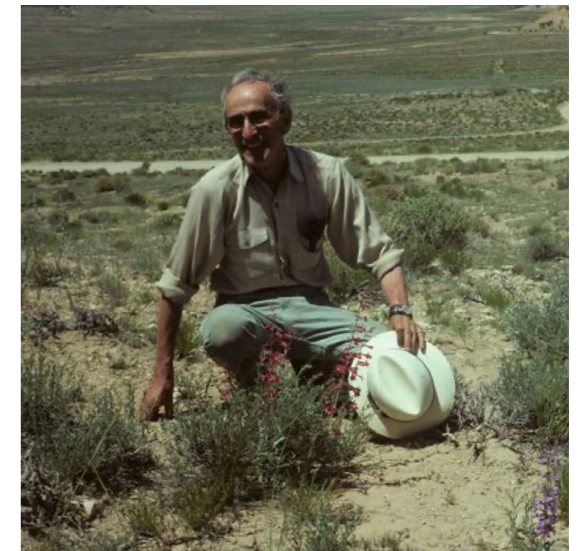
*Hydrochorea corymbosa* (Rich.) Barneby & J.W.Grimes, Caesalpinioideae, photo by Erik Koenen

# THE RUPERT BARNEBY AWARD OF THE NEW YORK BOTANICAL GARDEN

Benjamin M. Torke, New York Botanical Garden, USA

## FUNDING OPPORTUNITY

*The Rupert Barneby Award*, named in honor of the late New York Botanical Garden (NYBG) scientist and renowned legume expert, consists of US\$2000 granted annually to assist researchers to visit the New York Botanical Garden to study the rich herbarium collection of Leguminosae. Graduate students and early career professionals with research in systematics and/or legume diversity are given special consideration. **Projects that will result in the improved curation of the collection are desirable.**



Dr. Rupert Barneby

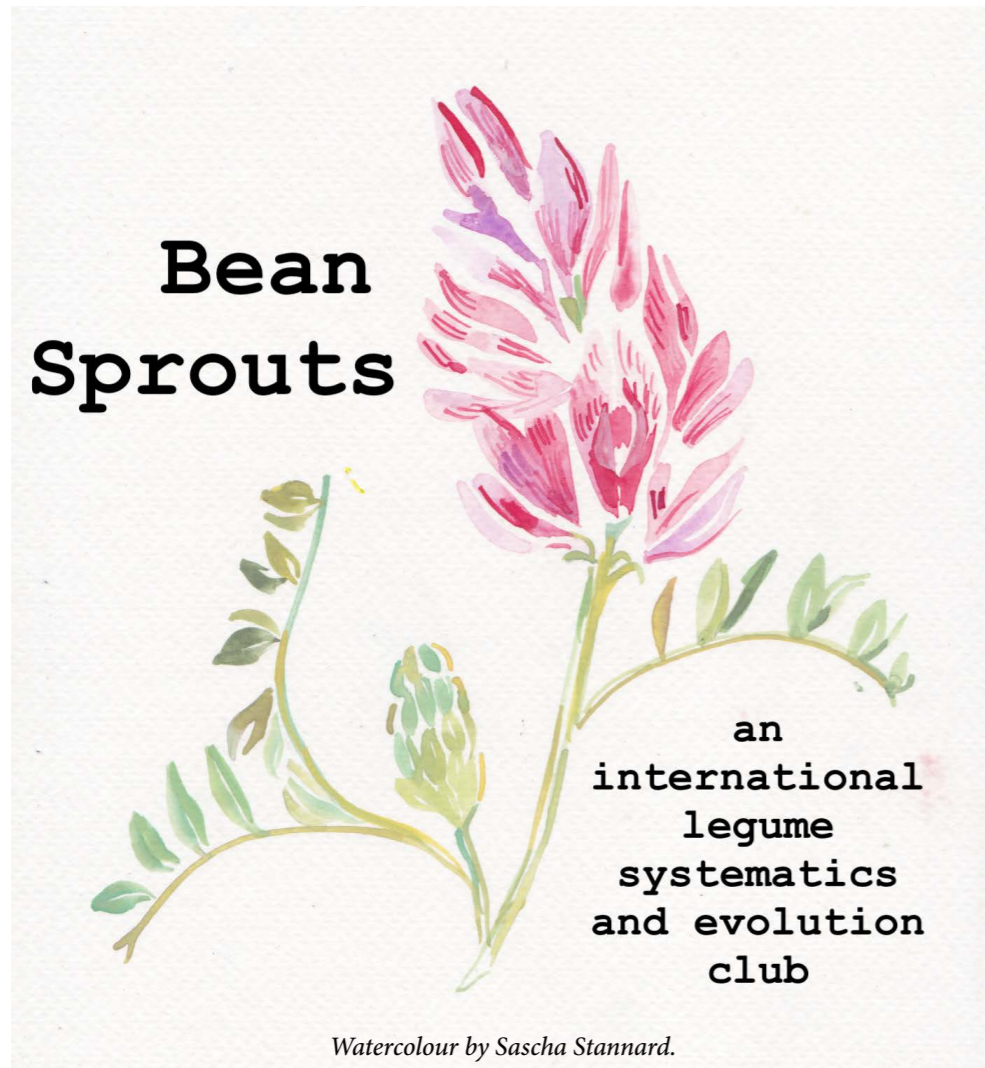
Anyone interested in applying for the award should submit their: 1) curriculum vitae; 2) a proposal describing the project for which the award is sought; 3) contact information for two individuals who can vouch for the qualifications of the applicant. **The proposal should address specifically the activities to be performed at NYBG** and should consist of: 1) title page with proposal title, applicant's name, address, and e-mail address; 2) body of the proposal of no more than two pages, including justification, objectives, and research plan; 3) literature cited; 4) travel budget.

The application should be addressed to **Dr. Benjamin M. Torke**, Institute of Systematic Botany, New York Botanical Garden, 1900 Southern Blvd., Bronx, NY 10458-5126, USA, and received no later than **March 1, 2022**.

Submission by e-mail is preferred (send to: [btorke@nybg.org](mailto:btorke@nybg.org)). Announcement of the recipient will be made before the end of March. Travel to NYBG should be planned for some period between July 1, 2022 and June 30, 2023. Recipients are asked to give a presentation at NYBG about their research.

# BEAN SPROUTS, AN INTERNATIONAL LEGUME SYSTEMATICS AND EVOLUTION CLUB

Sophie Winitsky, Montana State University, USA  
Joseph Charboneau, University of Arizona, USA



*Bean Sprouts* is a new online, international legume systematics and evolution club where graduate students, early career scientists, and the broader community can connect, share research, and invite speakers, centered around our favorite (the best) plant family!

We meet as a *Journal Club* to discuss recent papers and are hoping to start a *Virtual Legume Seminar Series* to explore current research around the world. Please let us know if you're interested in participating!

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

# FORTHCOMING: INTERNATIONAL LEGUME CONFERENCE, ILC8

Marcelo Simon, Empresa Brasileira de Pesquisa Agropecuária (EMBRAPA), Brazil  
Tania Moura, Instituto Federal Goiano, Brazil

*You may recall* from the closing moments of the ILC7 in Sendai 2018 that Brazil was chosen to host the next International Legume Conference. The Brazilian legume community initially planned the ILC8 to take place in 2022, but due to the pandemic situation and severe sanitary crisis that struck Brazil (and most of the world) in the last two years, our plans had to be put on standby. We considered having an online conference, but after discussing this option we decided that it would be better to postpone the event. Therefore, we opted for having the ILC8 as a conventional/in person conference and our intention is to deliver it in **July 2023**. Nevertheless, we will only pick a definitive date when we are sure that it will be safe for everyone to travel and meet.

The Brazilian legume community is very motivated to host the ILC8, which will take place in the colonial town of *Pirenópolis in central Brazil*. We are looking forward to warmly welcoming all of you to Brazil. In due time, you are going to hear from us again.

**Marcelo F. Simon**  
President of the 8th International Legume Conference

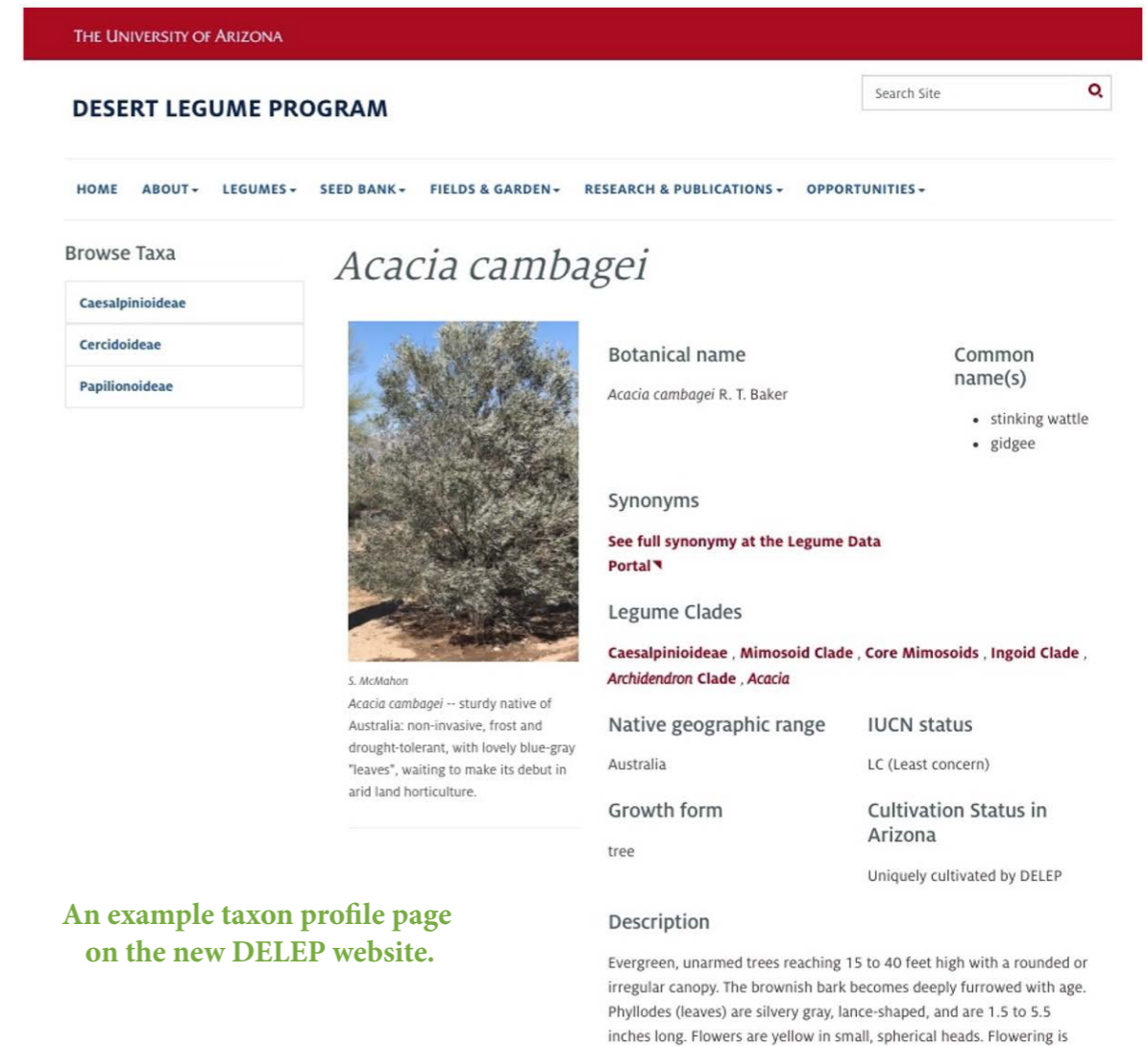
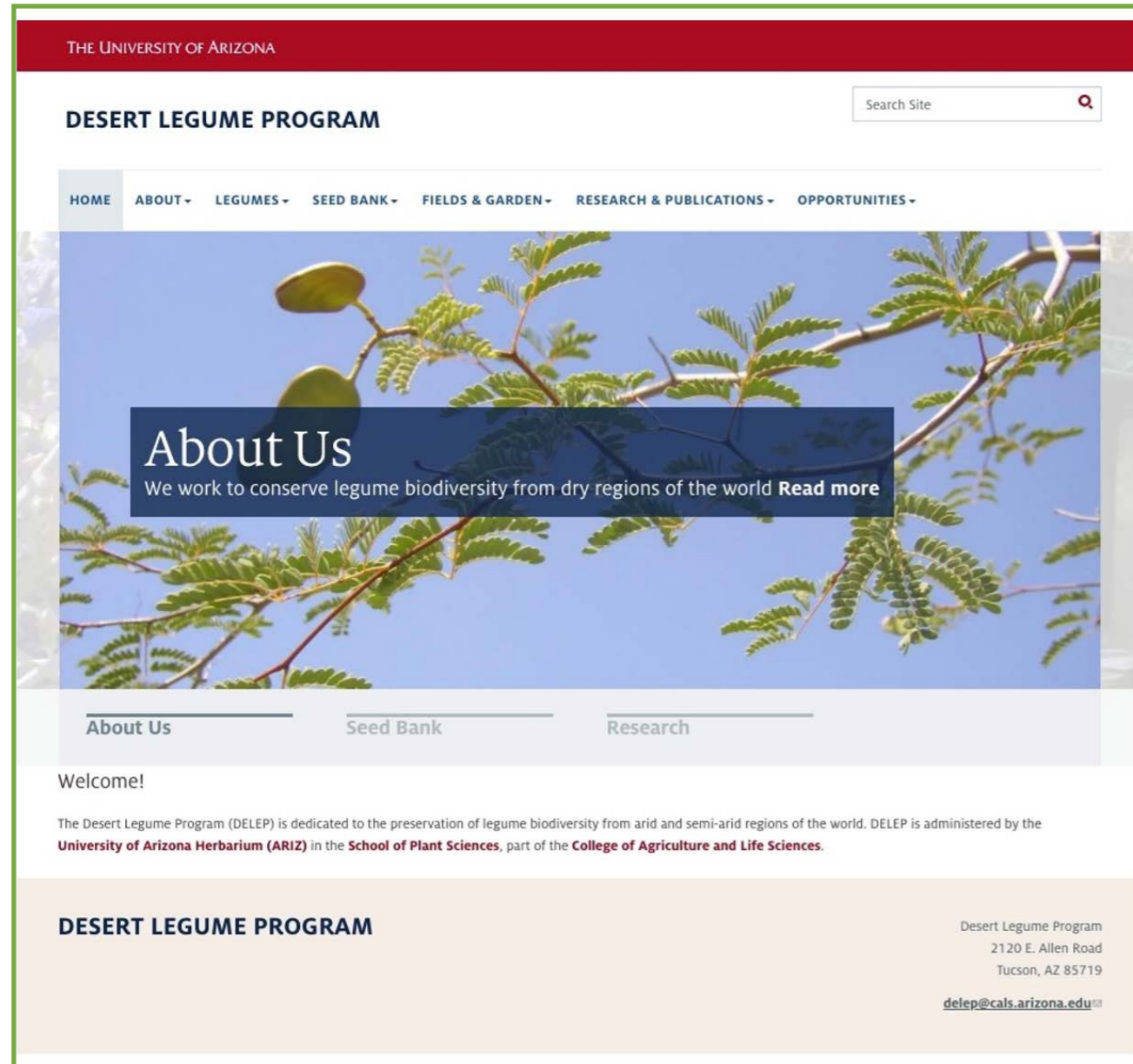


Town of Pirenópolis, Goiás, in central Brazil.

# UPDATED ONLINE RESOURCES FROM THE DESERT LEGUME PROGRAM

Joseph Charboneau, Matthew Johnson, Michelle McMahon  
University of Arizona Desert Legume Program

Since 1988, the *Desert Legume Program* (DELEP) has worked to preserve legume biodiversity from arid and semi-arid regions of the world through our seed bank and the living accessions in our evaluation fields. We are proud to announce updated resources on our seed accessions and living holdings now available on our new website (<https://cals.arizona.edu/desertlegumeprogram>).



An example taxon profile page on the new DELEP website.

While our Index Seminum has always provided a list of seed accessions available for request, our new website provides information on the seed bank holdings dynamically. Visitors can view expanded information on the origin of seed accessions and links to herbarium vouchers in the University of Arizona Herbarium. We are building taxon profile pages starting with the taxa represented in our demonstration garden, which has been funded by a grant from the Stanley Smith Horticultural Trust and other sources. These profile pages include information on the physical characteristics, habitat, and uses of the taxon and list all available seed accessions and living accessions at DELEP as well. Taxa are also listed by subfamily and clades at various depths, so users can easily find seed accessions by their phylogenetic relationships to a taxon of interest.

The site is built with the University of Arizona's QuickStart build of Drupal and custom Drupal data structures. We continue to add content and welcome comments, questions, or general inquiries regarding arid land legumes at [delep@cals.arizona.edu](mailto:delep@cals.arizona.edu). We anticipate that the site will provide richer context for researchers interested in accessing our collections, which include over 4,000 seed accessions from 67 countries representing more than 1,400 species. Seed requests can be submitted directly to DELEP by email or through USDA-GRIN (researchers outside of the US should submit their requests through USDA-GRIN to receive a phytosanitary certificate).

# FLORA DO BRASIL 2020: WHERE DOES THE LEGUMINOSAE FIT IN THE MEGADIVERSE BRAZILIAN FLORA?

Marli Pires Morim<sup>1</sup>, Fabiana Filardi<sup>1</sup>, Domingos Cardoso<sup>2</sup>,  
Haroldo Cavalcante de Lima<sup>1</sup> & Luciano Paganucci de Queiroz<sup>3</sup>

<sup>1</sup>Instituto de Pesquisas Jardim Botânico do Rio de Janeiro, Brazil

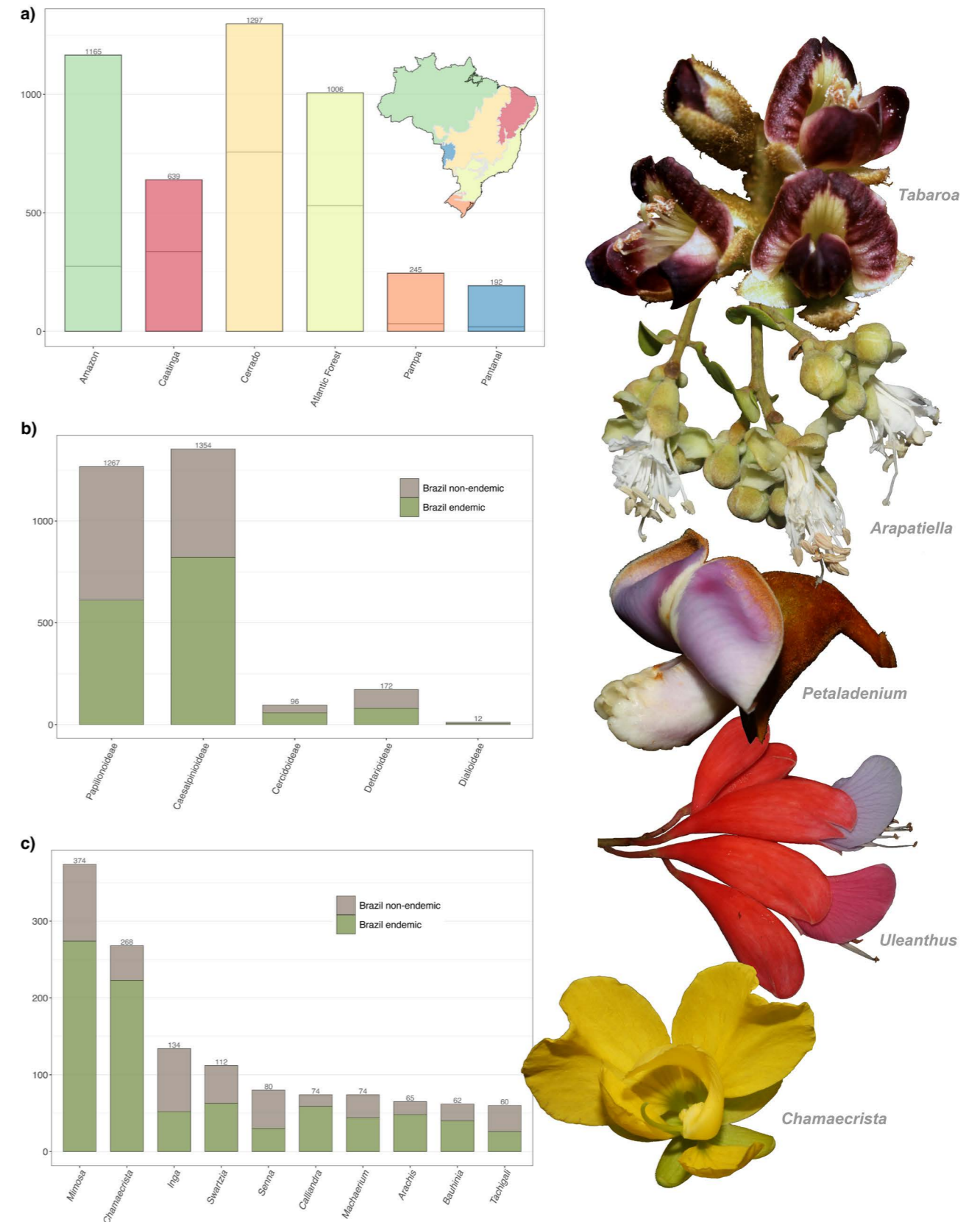
<sup>2</sup>Universidade Federal da Bahia, Brazil

<sup>3</sup>Universidade Estadual de Feira de Santana, Brazil

*The Flora do Brasil 2020 project* was started in 2008 by a collaborative network of Brazilian and international taxonomists, coordinated by the Rio de Janeiro Botanical Garden (JBRJ) and a scientific committee. The aim was to meet the 2010 – 2020 targets established by the Global Strategy for Plant Conservation (GSPC), under the umbrella and guidelines of the Convention on Biological Diversity (CBD). The initial phase, which became known as “List of Brazil” aimed to develop a working species checklist, with data on nomenclature (accepted names vs. synonyms) and geographic distribution for all species of plants, algae, and fungi occurring in Brazil. After successfully reaching the GSPC Target 1 in 2010, the elaboration of illustrated taxonomic online accounts for families and genera was established as the next objective to be achieved by the end of 2020. In both phases, from updating the species checklist to publication of the monographs of virtually all families that make up the extraordinary diversity of the Brazilian flora, the work was carried out on a fully online platform, where data were exclusively entered by taxonomic experts in the different plant groups\*\*.

By the end of the Flora do Brasil 2020 project (<http://floradobrasil.jbrj.gov.br/>), 979 scientists, more than twice as many as during the first phase (“Lista do Brasil”), had committed to preparing monographs (BFG, 2021). This massive effort resulted in dissemination of data on nomenclature, life forms and geographic distributions for all 46,975 native species of algae (4,972 species), bryophytes (1,584), ferns and lycophytes (1,380), angiosperms (32,696), gymnosperms (23) and fungi (6,320), as well as completion of taxonomic accounts for almost all families and genera of land plants. The project revealed that 55% of the land plant species are endemic to Brazil which is home to about 10% of all land plant species ever described on the planet.

The Leguminosae stand out in the megadiverse Brazilian Flora as the family with the highest species richness and remarkable levels of endemism, with 220 genera/18 endemic and 2,901 species/1,576 endemic from across all the legume subfamilies,



**Figure 1.** Taxonomic diversity and endemism of Leguminosae in the Flora of Brazil. (a) Species diversity across the main Brazilian phytogeographic domains; the lower parts of the histogram below the lines represent the proportion of endemic species in each domain. (b) Species diversity and endemism for each legume subfamily. (c) The ten most species-rich genera. Flower images show representatives of a recently described monotypic endemic genus from the Caatinga (*Tabaroa*), a small endemic genus from the Atlantic Forest (*Arapatiella*), two monotypic Amazonian genera that had long remained poorly known (*Petaladenium* and *Uleanthus*), and one of the most species-rich legume genera in Brazil (*Chamaecrista*).

except Duparquetioideae (**Fig. 1b**). The ten most diverse genera are *Mimosa* (374 species), *Chamaecrista* (268), *Inga* (134), *Swartzia* (112), *Senna* (80), *Calliandra* (74), *Machaerium* (74), *Arachis* (65), *Bauhinia* (62) and *Tachigali* (60), which together comprise 45% of the total species diversity of Brazilian legumes (**Fig. 1c**).

The Brazilian species of Leguminosae vary greatly in terms of growth forms, from giant trees and canopy lianas to tiny herbs across all different ecosystems within the main Brazilian phytogeographic domains. The Cerrado is home to the largest number of species (1,297 species), followed by the Amazon (1,165), Atlantic Forest (1,006), Caatinga (639), Pampa (245) and Pantanal (192) (**Fig. 1a**). The Atlantic Forest and Caatinga concentrate the largest number of endemic legume genera, with nine genera occurring exclusively in one or both of these phytogeographic domains. Most endemic genera are monotypic, for example, *Arapatiella*, *Blanchetiodendron*, *Paubrasilia* (Atlantic Forest), *Tabaroa* (Caatinga), *Androcalymma*, *Petaladenium*, *Uleanthus* (Amazon), and *Sellocharis* (Pampa) (**Fig. 1**).

The results obtained for Leguminosae in the context of the Flora do Brasil 2020 stem from the inputs and collaboration of 102 taxonomists (86% Brazilian and 14% international). Of the 220 genera that naturally occur in Brazil, 210 had their taxonomic accounts completed for the Flora do Brasil 2020, all of which can be accessed online at: (<https://reflora.jbrj.gov.br/reflora/floradobrasil/FB115>) or downloaded as PDF files from within the main publication called “*Coleção Flora do Brasil 2020*” (<http://dspace.jbrj.gov.br/jspui/handle/doc/126>). Although the complete account of all Leguminosae has not quite been finished yet, on the project page there is a comprehensive morphological description of the family, and identification keys for its subfamilies according to the newest phylogenetic classification (LPWG, 2017) and for all the genera with native, naturalized or cultivated species in Brazil. For each genus, field or herbarium images and information about its origin, distribution in the country, morphological features and key for species identification are provided.

The last decade has seen great advances in our knowledge of the diversity of the flora of Brazil, and the Leguminosae is no exception in this regard. However, biodiversity in many regions of the country is still poorly known, especially in the Amazon and Cerrado. Many legume species remain under-collected, phylogenetically enigmatic or still to be described and revealed to science. The “Flora do Brasil Online” project is continuing. The broad and fruitful collaborative network of legume taxonomists is continuing their joint efforts to finalize and continue updating all monographs. In addition to filling taxonomic knowledge gaps in the Brazilian flora, concerted efforts with the Legume Phylogeny Working Group (LPWG) and the recently launched Legume Data Portal (<https://www.legumedata.org>) will undoubtedly be important to meet the challenges of placing all Brazilian legumes in a robust molecular phylogeny of the family and understanding their patterns of geographic distribution in a global context.

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#### Footnote\*\*

For more details about the historical background and results of the Flora do Brasil 2020 project, visit the website <http://dspace.jbrj.gov.br/jspui/handle/doc/118>. To download any taxonomic account in PDF format, including the many that are already finished for the legume genera, access <http://dspace.jbrj.gov.br/jspui/handle/doc/126>. Furthermore, the data assembled on richness and occurrences of Brazilian plant and fungi species are available for download at: [http://ipt.jbrj.gov.br/jbrj/resource?r=lista\\_especies\\_flora\\_brasil](http://ipt.jbrj.gov.br/jbrj/resource?r=lista_especies_flora_brasil), while the morphological data obtained from the taxonomic accounts have also been integrated into the World Flora Online project (<http://www.worldfloraonline.org/>).



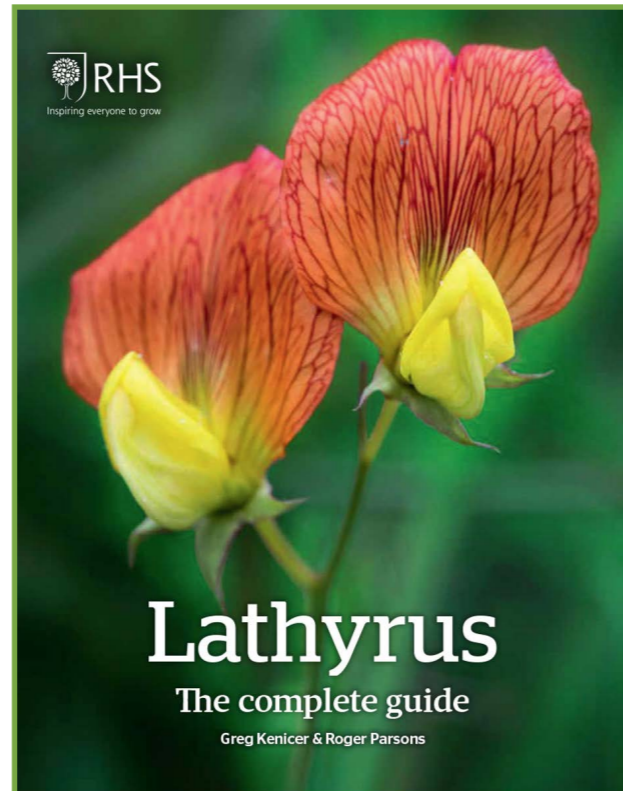
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# LATHYRUS: A HORTICULTURAL MONOGRAPH

Reviewed by Colin Hughes, University of Zürich, Switzerland

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The genus *Lathyrus*, the archetypal pea of the pea family, has a new taxonomic monograph published in 2021. This is the fifth in the acclaimed series of Royal Horticultural Society (U.K.) *Horticultural Monographs*, and the second focusing on a legume genus, with a previous volume on *Wisteria*. As a horticultural monograph, it presents a fusion of botanical and science-based horticultural knowledge in a single volume. This fusion has been melded by the partnership of **Greg Kenicer**, a taxonomist based at the Royal Botanic Garden, Edinburgh, and **Roger Parsons** a horticulturalist and plantsman who has dedicated his life to growing, selecting, and curating varieties of one species of *Lathyrus*, the sweet pea, *Lathyrus odoratus*.



In addition to a taxonomic account of the 150 wild species of *Lathyrus*, 95 of them illustrated with photographs, the monograph also includes a detailed account of the numerous cultivated varieties of this one species, *L. odoratus*, one of the most treasured garden plants of temperate regions. Sweet peas are grown for their prolific, delightfully scented flowers produced in pastel, as well as more vibrant colours, from pure white to every possible shade of pink, lavender, purple, maroon, crimson and red. 1200 named horticultural varieties are listed in this book, their names resembling a colour chart for paints – *Apricot Queen*, *Beaujolaïs*, *Blue Danube*, *Bouquet Pink*, *Little Red Riding Hood*, *Orange Dragon*, *Pink Cupid*, *Purple Prince*, *White Supreme*, *White Gem*, and many more. 550 cultivars are illustrated with photographs, presenting a lavish and ravishing display of the diversity of flower colours, dispositions and petal shapes which vary in all manner of subtle ways only identifiable by a handful of sweet pea experts. Harnessing this diversity has been the product of decades of selection, breeding and propagation.

This work has been carried out by a small set of dedicated growers, plantsmen, seedsmen,

and hobbyists, many of them sweet pea aficionados and fanatics. They established a veritable sweet pea cottage industry which blossomed initially in the U.K. fuelled by the quintessentially British gardening traditions of flower shows, competitions, National Plant Collections, specialist plant nurseries and the National Sweet Pea Society. This passion for sweet peas and selecting new varieties later spread to North America, Australia, New Zealand, Chile, and Japan. All this history and diversity is amply documented in this monograph.

With this strong focus on flowers and their extravagant colour variation, it would be easy to overlook the many other striking aspects of *Lathyrus* diversity. The leaves, stipules and tendrils of *Lathyrus* species are also extremely labile, including varieties where the leaflets have been replaced by tendrils forming aphyllous leaves that are completely tendrillous and support the plant in a tangled mass, while in *L. aphaca* where leaflets are also absent and reduced to tendrils, the expanded sagittate stipules take over the photosynthetic function. The diversity of habitats and environments where wild *Lathyrus* species occur is equally impressive and amply documented in this monograph with detailed notes on habitats and distributions.

Even with such a large chunk of this monograph devoted to just this one species, *L. odoratus*, there is, nevertheless, still plenty of space assigned to documenting the history and domestication of the other economically important species, including *L. sativus*, the grass pea, an important Neolithic food plant from the Middle East, *L. cicera*, the red-flowered chickling vetch, another food plant used in early times, and *L. tuberosus* which has edible tubers. None of these of course match the garden pea in terms of economic importance. While the garden pea has generally been known by the name *Pisum sativum*, it is now clear that the genera *Pisum* and *Vavilovia* are phylogenetically nested within *Lathyrus*<sup>1</sup>, and the authors of the *Lathyrus* monograph have bitten the bullet to treat these two genera as synonyms of *Lathyrus*. Thus, *Pisum sativum* is now *Lathyrus oleraceus*, a change that may be hard to swallow for breeders, geneticists and agronomists working with peas and the associated vast literature on *Pisum* that stretches back to Gregor Mendel's pioneering experiments. Time will tell if this new synonymy becomes widely accepted or not.

This is a magnificent monograph, richly filled with keys, descriptions, notes and photographs, and an excellent template for other legume genera of horticultural importance.

<sup>1</sup>Schaefer H, Hechenleitner P, Santos-Guerra A, de Sequeira MM, Pennington RT, Kenicer G, Carine MA (2012). Systematics, biogeography, and character evolution of the legume tribe Fabeae with special focus on the middle-Atlantic island lineages. *BMC Evolutionary Biology*, 12: 250. <https://doi.org/10.1186/1471-2148-12-250>



**Roger Parsons** owns a *Lathyrus* nursery, Roger Parsons Sweet Peas, in the U.K., where he holds a National Plant Collection of the genus. He is the author of *Sweet Peas: An Essential Guide* (2011) and was Chairman of the U.K. National Sweet Pea Society from 2017 to 2020.

**Greg Kenicer** works at Royal Botanic Garden Edinburgh (RBGE) and is a specialist in wild *Lathyrus* diversity. He did a PhD on the South American species and, with international collaborators, has studied the biogeography, evolution, and taxonomy of *Lathyrus*. He also curates a second National Plant Collection of the genus held at RBGE.

<https://www.summerfieldbooks.com/product/lathyrus-the-complete-guide/>

## LEGUME DATA PORTAL

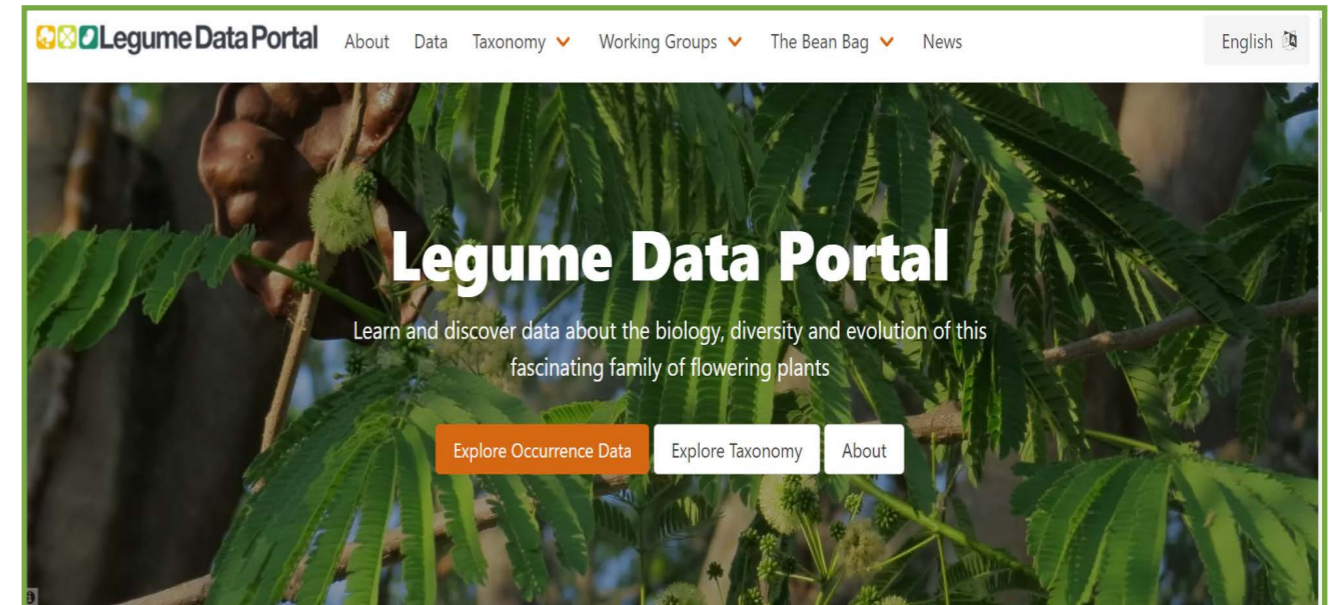
Carole Sinou<sup>1</sup>, Joe Miller<sup>2</sup> & Anne Bruneau<sup>1</sup>

<sup>1</sup>Université de Montréal, Canada

<sup>2</sup>Global Biodiversity Information Facility (GBIF), Denmark

In November 2020, the *Global Biodiversity Information Facility* (GBIF) launched a program to host tailored data portals for GBIF nodes in their community. The portals were designed primarily for GBIF country nodes and regions to showcase occurrence data for particular geographical areas. The LPWG was chosen as one of only two taxon-focused projects with the objective of presenting data about Leguminosae. GBIF provides the informatics infrastructure and expertise, while the legume community is responsible for the content. GBIF is interested in encouraging dialogue with expert communities in order to improve data quality and increase visibility and use of GBIF mediated data, which come from herbaria. In its initial phase, the portal has three major types of information for our community: the latest taxonomic information; distribution data from GBIF; and a platform for community communication. The Legume Data Portal was developed under the umbrella of *Canadensys* ([www.canadensys.net](http://www.canadensys.net)), which is an associate participant node of GBIF and publishes data from Canadian collections and initiatives.

The need for scientists to exchange, share and organise data has resulted in a proliferation of taxonomic and biodiversity research data portals in the past decades. These cyberinfrastructures have had a major impact and helped to revitalise taxonomy by allowing quick access to bibliographic information, biological and nomenclatural data, and specimen information. A pioneering example is the *International Legume Database and Information Service* (ILDIS), which was established in 1985, and led the way in developing methods and thinking with regard to taxonomic data management more generally. However, due to lack of resources, lack of institutional support and community

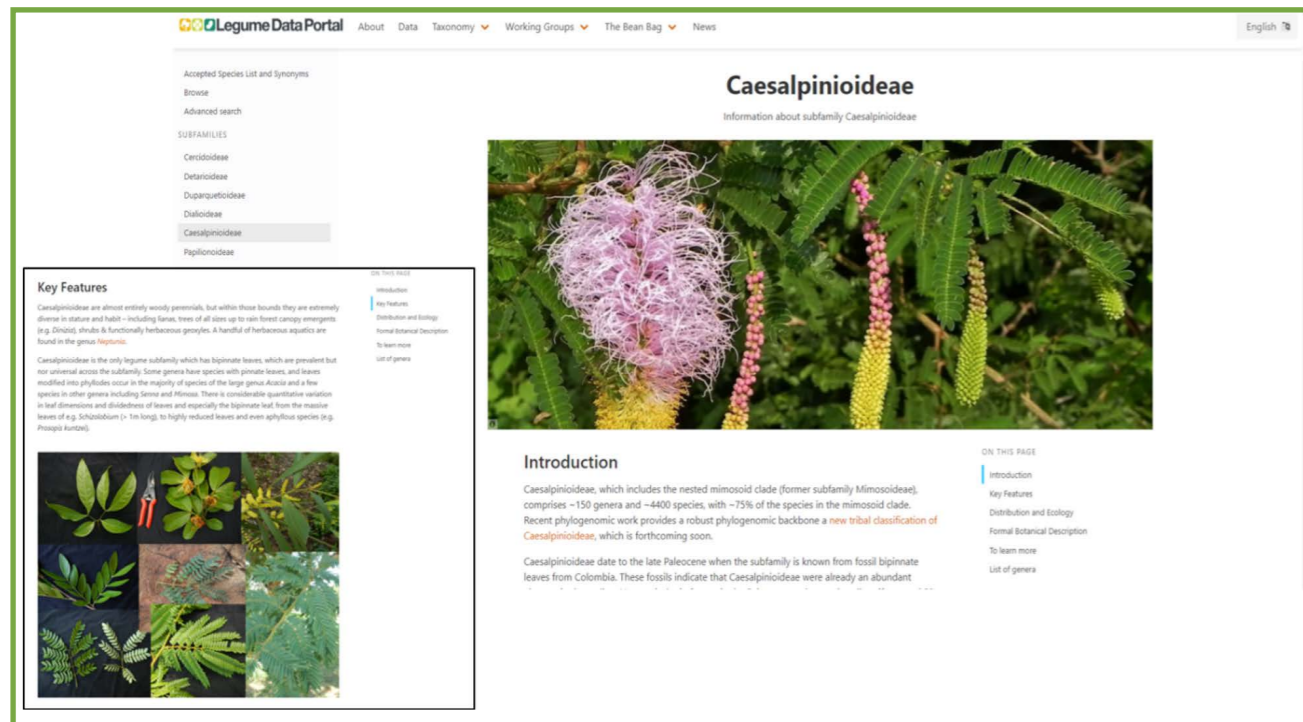


involvement, as well as evolving software protocols, increased data complexity, and the need for distributed data curation, ILDIS had not been curated by the community for over ten years. In a 2019 paper in *Advances in Legume Systematics Part 13*, [Bruneau et al.](#) proposed the establishment of a new Web portal to facilitate access to scientifically validated data about legumes, stemming from several years of discussions within the LPWG and a workshop held during the International Legume Conference in Japan in 2018. The collaboration with GBIF has provided the LPWG with a framework for helping to curate global data resources and working together to report data quality issues to data providers, leading to enhanced quality data on legumes.

The new Legume Data Portal was officially launched on September 30<sup>th</sup> 2021 at the virtual LPWG meeting. The portal currently provides an overview of the legume family and each of the subfamilies and a summary of the work and objectives of the LPWG and its five working groups.

The new verified legume species checklist generated by the Taxonomy Working Group is available to browse, search and download from the Legume Data Portal (<https://www.legumedata.org/taxonomy/species-list>). For each genus there are links to the relevant pages on GBIF and the *World Checklist of Vascular Plants* (WCVP). The LPWG Taxonomy Working Group is currently exploring available tools for curating the species checklist with the aim of encouraging community engagement in maintaining an accurate and up-to-date species checklist. This new verified checklist is now the primary taxonomic backbone for the nearly 22 million legume occurrence records served through GBIF and the Legume Data Portal. An accurate legume checklist is important for research. It is also expected to become the primary source of scientific names for other global online platforms that serve biodiversity data (e.g., World Flora Online). In the future, we would like to provide further information about legumes, including links to trait, genomic and phylogenetic data, and curated images of legume species.

The Legume Data Portal also showcases legume occurrence data, including specimens



Example of subfamily description for Caesalpinioideae

and citizen science records, currently available on GBIF (<https://www.legumedata.org/data?view=MAP>). A series of filters have been applied to these data to automatically clean obvious distribution errors, but users can apply additional filters as required. Users can download data for downstream analyses and obtain a DOI for citing the dataset from GBIF. The Legume Occurrences Working group aims to provide tools and scripts for cleaning occurrence data and sharing cleaned occurrence datasets for the family.

GBIF maintains all scientific names it receives linked to specimens from herbaria all over the world, including many names that are not available or aligned with the new LPWG taxonomy. These occurrence data points, even though they are shared with GBIF, remain underutilized and don't represent our current knowledge of legume species distributions. GBIF will provide the LPWG with a list of all legume names currently used in herbaria that share data with GBIF with the hope that in due course all data can be reconciled with the LPWG taxonomy. In turn GBIF can quantify the value added by taxonomy on the quality of GBIF occurrence data which we hope will convince funding bodies of the value of taxonomy. Overall, the goal is to improve data quality for better science. GBIF is using the legume portal as an important test case.

Finally, a section of the Legume Data Portal is dedicated to the Bean Bag, with access to recent issues and a link to all back issues, and on the Portal home page you can see legume news items and announcements from the community. Legume news items and feedback about the portal should be sent to: [legumephylogenywg@gmail.com](mailto:legumephylogenywg@gmail.com).

The Legume Data Portal aims to encourage international collaboration and exchange amongst scientists and students, and provide a platform to share data and expertise on the systematics and evolution of the Leguminosae with a broad community of users. Please take a look, and please contribute!



GBIF map view showing the distribution of occurrences for the mimosoid legume genus *Senegalia* on the Legume Data Portal. The user can click on an occurrence point and directly obtain the specimen data for the records that populate that locality.

## LEGUME GENOME SEQUENCING CONSORTIUM

Shifeng Cheng<sup>1</sup>, Ashley N. Egan<sup>2</sup>, Warren Cardinal-McTeague<sup>3</sup>,  
Gane Ka-Shu Wong<sup>4</sup> & Jeffrey J. Doyle<sup>5</sup>

<sup>1</sup>Chinese Academy of Agricultural Sciences, China

<sup>2</sup>Utah Valley University, USA

<sup>3</sup>University of British Columbia, Canada

<sup>4</sup>University of Alberta, Canada

<sup>5</sup>Cornell University, USA

**With the development of** genomic sequencing technologies and bioinformatics, the ability to “sequence everything” for an entire genus or even for an entire family, is becoming a reality. Such endeavors enable super-pangenome or extensive comparative evolutionary analyses through dense taxonomic sampling. These advances open new ways to explore diversity in a broad comparative context, leveraging whole-genome sequences to dissect traits of interest in the context of phylogenomics, in order to gain a deeper and more holistic view of the evolution of legumes. We are launching the “**Legume Genome Sequencing Consortium**”, which aims to generate deep genome sequences of representative species



from all major lineages of legumes. This will include broad sampling of representatives of almost all the 770 legume genera, and all major (and many orphan) legume crops and their global diversity panels, as well as trait-based phylogenomics and multi-omics studies. The consortium aims to build an open, inclusive, interactive, and collaborative platform for the community in order to make an impact. We list four of the main components and the existing subprojects that are already under way. Each of these has potential for collaboration with the LPWG and the wider legume community. The fifth section invites brainstorming to propose additional complementary sub-projects, to maximize the value of this initiative and ensure that the consortium is fully inclusive, and creative across the legume community.

### 1. “Legume Nodulation and NFN Clade Phylogenomics v2.0” Project

In this subproject, two parts will be highlighted, aiming to sequence and assemble up to 300 high-quality chromosome-level genomes by combining long-read technologies like PacBio/ONT, Illumina or MGI short-read technologies, and linked read technologies like stLFR or HiC, etc. The first part is to sequence genomes from different legume lineages and or representatives of Fabales lineages which have lost the ability to nodulate (including from subfamilies Cercidoideae, Detarioideae, Duparquetioideae, Dialioideae, some Caesalpinioideae, and some Papilionoideae). Species of particular interest will be covered like *Nissolia* from Dalbergieae, the ADA clade and Swartzieae from Papilionoids, and many taxa phylogenetically encompassing the clade that includes *Chamaecrista* and mimosoids in the Caesalpinioideae.

The second part is outside the legumes to sequence and assemble the genomes of “comparison pairs” of nodulating and non-nodulating taxa representing the other nine nodulating families across the four orders in the *N<sub>2</sub>-Fixing root Nodule* (NFN) clade of angiosperms, which mostly come from the actinorhizal plants. This is a continuation of the v1.0 effort in the *EvoNod* consortium, launched in 2015 (<https://www.science.org/doi/10.1126/science.aat1743>). Specifically, the second part will include: 1) outgroups outside the NFN clade (e.g., Malpighiales, and other orders closely related to the NFN clade); 2) actinorhizal nodulators (about 230 species out of 24 genera) and their closely-related non-nodulator relatives, which include *Comptonia*, *Morella*, *Myrica*, *Alnus/Betula*, *Casuarina*, *Allocasuarina*, *Ceuthostoma*, and *Gymnostoma* from Fagales; the two subfamilies *Datisca* and *Coriaria* from Cucurbitales; *Dryas*, *Purshia*, *Chamaebatia*, *Cercocarpus*, *Elaeagnus*, *Hippophae*, *Shepherdia*, *Trevoa*, *Retanilla*, *Ochetophila*, *Colletia*, *Discaria*, *Kentrothamnus*, *Ceanothus* and *Parasponia* (associated with rhizobia) from Rosales.

### 2. Super-Pangenomics of Legume Crops

This effort is aligned with the *Global Grain Genomics Research Program* (G3RP consortium: <https://g3rp.com/>) (Cereal + Legume crops). The aim here is to sequence and assemble reference genomes for all known legume crops (grain legumes and other economically important root or tuber crops) and their wild relatives, and to assemble population-based global diversity panels. 100+ new/orphan (economically important) genomes can be sequenced, including various beans, pulses, or other herbaceous legumes.

Collaborative possibilities include: 1) building *de novo* chromosome-level reference-quality genomes for pan-genomic and phylogenomic studies; 2) building population-based global diversity panels and performing whole-genome re-sequencing to build variation maps across numerous accessions of crop species to elucidate crop legume evolution and domestication; 3) collecting germplasm (seeds or other propagules), and further growing the living plants for multi-omics efforts to assemble additional physiological and phenotype data.

### 3. Legume ENCODE and Gene Mapping Project

This Consortium is seeking to collaborate with the LPWG community to develop and combine genomics, phenomics and deep learning particularly in legume model systems to better understand traits and evolution, and the breeding potentials in agriculture: 1) Legume Functional Genomics: building an atlas of gene expression, gene epigenetics and regulation in a multi-omics framework, extending the existing or emerging legume model systems in a legume version of the ‘*ENCODE*’ project (see pENCODE: <https://pubmed.ncbi.nlm.nih.gov/25149370/>, or <https://www.encodeproject.org/>); 2) Gene mapping across the evolutionary tree: mapping or projecting genes, traits and variations of interest across lineages in a phylogenetic context both at the macro-evolutionary and the population levels. This requires a community effort to share, integrate and further develop existing legume datasets from genetics, genomics, and traits, to physiology, ecology, and phenotypes, enabling a joint linkage association study for trait dissection; 3) Deep Learning and legume genomics-based pre-breeding: building a database with a search engine, to integrate genomics and phenomics data for the existing legume model systems, and deploying deep learning with genomics for basic research and pre-breeding. The *Pisum sativum* [= *Lathyrus oleraceus*] (the Mendel pea) diversity panel and model system is already established and provides a good starting point together with several other model systems: *Glycine*, *Lotus*, and *Medicago*.

### 4. Legume Full-Coverage Phylogenomics

Two aspects will be covered: 1) Sequence and assemble 1-2 representative genomes for each of the c. 770 genera of Leguminosae, creating a new comparative framework of “*One Thousand Legume Genomes*”, and putting the genes/pathway/traits and any evolutionary innovations of interest into this context; 2) Explore legume diversity via collecting RNA-seq samples (transcriptomes) from seeds, flowers and roots/nodules, for each of the sequenced genome/species in Point 1. For more details about these plans, see: <https://academic.oup.com/gigascience/article/7/3/giy013/4880447>. Funding for sequencing is available and LPWG collaboration is being sought for this initiative from people with specific projects/clades that they could supply material of.

### 5. Question-Driven and Trait-Based Phylogenomics

The aim here is to encourage any ideas that fully utilize these state-of-the-art technologies, like multi-omics, single-cell or spatially-resolved transcriptome, molecular functional genomics and phenotyping technologies and to explore, stimulate and develop additional ideas and question-driven and trait-based collaborative subprojects.

We are calling for LPWG involvement in developing and structuring this exciting new initiative to maximize its value and ensure that it meet the needs of the entire global legume community. Please contact the **Interim Steering Group** if you are passionate, visionary, and motivated to volunteer to serve on the Steering Group, or if you already have particular species, germplasm, expertise, sampling plan, traits or genes of interest, or legume genome sequencing projects that you would like to be included in the context of this initiative. The main tasks and responsibilities of the Steering Group are to provide research direction, set priorities and evaluate research proposals, lobby funding agencies and publicize project progress, coordinate action points and optimize the overall timeline. More brainstorming is needed to get the ball rolling. The sequencing technologies, genomics and bioinformatics are now routinely applied in the **Agricultural Genomics Institute at Shenzhen, Chinese Academy of Agricultural Sciences** (AGIS, CAAS) and the **China National GeneBank** (CNGB, Shenzhen), the data and analyses will be shared in a timely manner and made publicly available to all participants in the consortium, following the Human Genome Project spirit (“Needed by All, Owned by All, Done by All, and Shared by All”). Seed and plant tissue samples need to be vouchered in recognized herbaria, shared and exchanged via a standard material transfer agreement.

To facilitate planning of these initiatives, Ashley N. Egan (Utah Valley University) has updated the previous list [see Egan & Vatanparast (2019) *Australian Systematic Botany* 32: 459-483 (<https://www.publish.csiro.au/SB/SB19019>)] of legume species whose genomes are either fully sequenced or currently being sequenced, whose phylogenetic distribution is illustrated on the following page.

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- Ashley N. Egan**, Utah Valley University, USA. [aegan@uvu.edu](mailto:aegan@uvu.edu)
- Warren Cardinal-McTeague**, University of British Columbia, Canada.
- Bruno Nevado**, Universidade de Lisboa, Portugal. [bruno@fc.ul.pt](mailto:bruno@fc.ul.pt)
- Firouzeh Javadi**, Kyushu University, Japan. [javadisf@yahoo.com](mailto:javadisf@yahoo.com)
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*Chamaecrista desvauxii* (Collad.) Killip, Caesalpinioideae, photo by Colin Hughes.

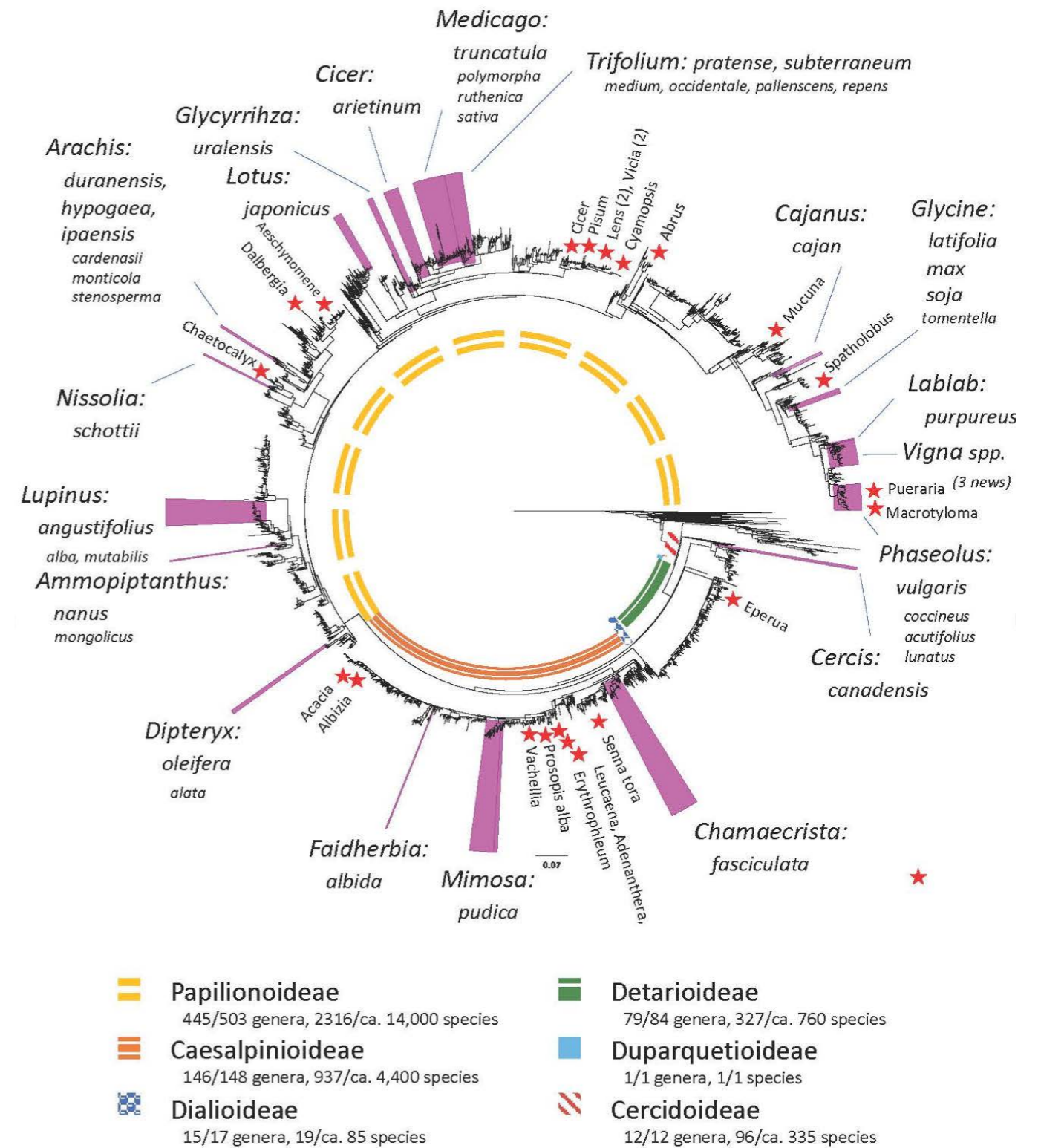


Figure modified from Egan and Vatanparast (2019) with stars and smaller font indicating new additions.

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# NEW LEGUME SPECIES HIGHLIGHTS 2021

Compiled by Colin Hughes, University of Zürich, Switzerland

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**New legume species** continue to be described at a steady pace from all continents across the globe. Even in well-studied genera which contain important pulse crops, new species continue to be discovered including the species of *Arachis* and *Cicer* described in 2021 which are highlighted here as potentially important crop wild relatives of peanut and chickpea. As might be expected, it is mainly the globally rare species that remain to be discovered in the field and many of the new species highlighted here are narrowly restricted endemics that are threatened or in some cases, critically endangered. It is also notable that newly described species are very often in species-rich genera from areas of high species diversity for those genera. The species highlighted here provide a flavour of the new discoveries of 2021. A full list of taxonomic papers is in the 2021 Legume Bibliography at the end of this issue of the Bean Bag.

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## Two new *Adesmia* species from southern Brazil

*Adesmia miottoae* Cobra, Iganci & Fort.-Perez is a prostrate perennial herb, endemic to the highland grasslands of SE Santa Catarina and NE Rio Grande do Sul in S Brazil. The species epithet honours Professor Silvia Terezinha Sfoglia Miotto for her contribution to studies of *Adesmia* and other legumes, especially in Rio Grande do Sul, Brazil. In addition, the same authors describe a second new species, *Adesmia subtropicalis* Cobra, endemic to Rio Grande do Sul and named with reference to its occurrence in transition areas between Pampa (temperate) and Mata Atlantica (tropical).



*Adesmia miottoae* and *A. subtropicalis* (Photos: Thiago Cobra e Monteiro)

Monteiro, T.C.e., Iganci, J.R.V., Seixas, D.P., Rodrigues, T.M. and Fortuna-Perez, A.P., 2021. A New Species of *Adesmia* (Leguminosae, Papilionoideae, Dalbergieae) from Southern Brazil, with Notes on Leaf Anatomy. *Phytotaxa*, 521(1), pp.48-56. <https://doi.org/10.11646/phytotaxa.525.1.5>

Monteiro, T.C.e., Iganci, J.R.V., Miotto, S.T. and Fortuna-Perez, A.P., 2021. *Adesmia subtropicalis* (Leguminosae, Papilionoideae, Dalbergieae), a new endangered species from the Brazilian Pampas. *Phytotaxa*, 521(3), pp.219-226. <https://doi.org/10.11646/phytotaxa.521.3.7>

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## *Arachis inflata*, a peanut with inflated fruits



*Arachis inflata* (Photos: habit, Guillermo Seijo; fruits, Margoth Atahuachi)

Seijo, G.J., Atahuachi, M., Simpson, C.E. and Krapovickas, A., 2021. *Arachis inflata*. *Bonplandia*, 30(2), pp.169-174. <https://doi.org/10.30972/bon.3024942>

Despite thorough exploration and characterisation of species and diversity of the crop legume genus *Arachis*, there are still many field collecting gaps. Recent fieldwork in eastern Bolivia has revealed an interesting and very unusual new species that has been named *Arachis inflata* Seijo, Atahuachi, C. E. Simpson & Krapov. The specific epithet, *inflata*, refers to its fruits which have conspicuous air chambers in the pericarp, giving a bullate external appearance, a fruit type that is unique in the genus *Arachis*.

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## A critically-endangered *Otholobium* from the western Cape, South Africa

Like many new plant species discoveries, *Otholobium outrampsii* C.H. Stirton & du Preez is a narrowly distributed endemic, known from just a single locality in the western Cape of South Africa. Based on field surveys it is judged to be Critically Endangered. The specific epithet honours the members of the Outramps Group of the Custodians of Rare and Endangered Wildflowers (CREW) Programme, who champion the protection of the rare and threatened plants of the southern Cape.



*Otholobium outrampsii* (Photos: Brian du Preez)

Stirton, C.H. and du Preez, B., 2021. *Otholobium outrampsii* (Psoraleae, Fabaceae)-a new species from the Western Cape, South Africa. *Bothalia-African Biodiversity & Conservation*, 51(2), pp.1-5. <https://doi.org/10.38201/btha.abc.v51.i2.5>

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## A critically endangered new species of *Antheroporum* from northern Thailand

*Antheroporum* is a small Papilionoid genus of c. five species in tribe Millettieae ranging from China to Indo-China and Thailand, characterised by unusually long petal claws. Like many new field discoveries, *Antheroporum puudjaae* Mattapha & Tetsana is known only from the type locality, is apparently narrowly endemic in limestone mountains in northern Thailand and is categorized as Critically Endangered. The species was named in honour of Pachok Puudjaa, a long-time collector of plants for the Flora of Thailand project.

Mattapha, S. and Tetsana, N., 2021. *Antheroporum puudjaae* (Millettieae: Fabaceae), a new species from Thailand. *Thai Forest Bulletin (Botany)*, 49(1), pp.130-134. <https://doi.org/10.20531/tfb.2021.49.1.16>

*Antheroporum puudjaae*  
(Photos: Sawai Mattapha)



## The hyper-diverse genus *Astragalus* just keeps on growing

It is perhaps no surprise that *Astragalus*, the largest genus of flowering plants with > 3000 species, is still growing. A steady stream of new species continues to be discovered and described in this hyper-diverse genus.

Here, two of the recently described species are highlighted: *Astragalus taledensis* P. Yan & Huan Zhang, an unusual and distinctive species narrowly endemic in NE Xinjiang Province, China distinguished by its simple leaves and prostrate stems, and *Astragalus wiesneri* Maassoumi & Pahlevani, a rare species, known only from the type locality in alpine habitats at 3500 – 3850 m elevation in the S Zagros Mountains of Iran.



*Astragalus taledensis* (Photos: Huan Zhang)

*Astragalus wiesneri* (Photos: Amir H. Pahlevani)

Zhang, H., Ren, S. and Yan, P., 2021. *Astragalus taledensis*, a new species of Leguminosae from Xinjiang, China. *Phytotaxa*, 524(3), pp.199-204. <https://doi.org/10.11646/phytotaxa.524.3.4>

Pahlevani, A.H., Maassoumi, A.A. and Osaloo, S.K., 2020. What is *Astragalus wiesneri*? Disentangling a new species from its relatives in section *Anthyloidei*. *Anales del Jardín Botánico de Madrid*, 77(2), p. 6. Real Jardín Botánico. <https://doi.org/10.3989/ajbm.2573>



*Campylotropis luquanensis* (Photo: Bo Xu)

## A new species of *Campylotropis* from SW China

*Campylotropis* of tribe Desmodieae, subfamily Papilionoideae comprises ca. 37 species centred in SW China which harbours 32 species, of which 20 are endemic, mostly in Yunnan and Sichuan Provinces. An additional species, *Campylotropis luquanensis* Bo Xu & L.S. Jiang, from that region has recently been described.

Jiang, L.S. and Xu, B., 2021. *Campylotropis luquanensis* (Fabaceae: Papilionoideae), a new species from Southwest China. *Phytotaxa*, 524(2), pp.114-118. <https://doi.org/10.11646/phytotaxa.524.2.6>

## *Cicer turcicum*, a new close wild relative of chickpea from Anatolia

The discovery of a new annual wild species in the genus *Cicer* is especially exciting because, as a crop wild relative, it has important potential for genetic improvement of the domesticated pulse crop, chickpea, *Cicer arietinum* L., or for de-novo domestication in its own right. *Cicer turcicum* Toker, J. Berger & Göktürk is a narrowly restricted endemic, known from just a single population in SE Anatolia in Turkey, quite distant from any other *Cicer* species. *Cicer turcicum* is an annual plant, closely related to *C. arietinum* and shows enhanced heat tolerance and resistance to bruchid seed beetles compared to chickpea.



*Cicer turcicum* (Photos: Cengiz Toker)

Toker, C., Berger, J., Eker, T., Sari, D., Sari, H., Göktürk, R.S., Kahraman, A., Aydın, B. and von Wettberg, E.J., 2021. *Cicer turcicum*: A new *Cicer* species and its potential to improve Chickpea. *Frontiers in Plant Science*, 12, p.587. <https://doi.org/10.3389/fpls.2021.662891>

## *Harpalyce greuteri*: A new serpentine endemic from NE Cuba



*Harpalyce greuteri*  
(Photo: Pedro González)

Cuba harbours 14 of the 34 species of *Harpalyce*, most of them serpentine endemics growing in xeromorphic, thorny or sub-thorny thickets. *Harpalyce greuteri* R. Rankin & P. A. González newly described in 2021 adds yet another serpentine endemic to this impressive tally of Cuban endemics. While the red standard petal colour is not unusual in *Harpalyce*, this new species differs from other red-flowered species in having an unusual black keel and partially black wing petals.

Featured on the cover of Issue 68.

Rodríguez, R.R. and Gutiérrez, P.A.G., 2021. *Harpalyce greuteri* (Leguminosae: Brongniartieae), a new species from eastern Cuba, with a synopsis of and key to the Cuban species of the genus. *Willdenowia*, 51(2), pp.209-219. <https://doi.org/10.3372/wi.51.51204>

## *Mimosa* – The census continues

Documentation of the high diversity of *Mimosa* species in the Brazilian cerrado and campos rupestres continues with the addition of *Mimosa pseudoracemosa* T.P. Mendes, Marc. F. Simon & M.J. Silva. In common with many fire-resistant mimosas, *M. pseudoracemosa* is a geoxyle with the leaves arising directly from the underground xylopodium. The species is probably restricted to the Chapada dos Veadeiros National Park, in northern Goiás State, Brazil.

Mendes, T.P., Simon, M.F., Perez, A.P.F. and Da Silva, M.J., 2021. Novelty in *Mimosa* sect. *Mimosa* ser. *Mimosa* subser. *Polycephalae*: A new species, new status, and new synonyms. *Phytotaxa*, 505(2), pp.121-138. <https://doi.org/10.11646/phytotaxa.505.2.1>



*Mimosa pseudoracemosa*  
(Photos: Moises Mendoza)

## *Lespedeza danxiaensis*, narrowly endemic on the summit of Mount Danxia, in Guangdong

*Lespedeza danxiaensis* Q. Fan, W.Y. Zhao & K.W. Jiang was discovered during field work in 2020. It is only known from ca. 100 individuals from the summit area of Mount Danxia in the Danxiashan National Nature Reserve in Guangdong Province, China and is readily distinguished by its unusual leathery leaflets.



Zhao, W.Y., Jiang, K.W., Chen, Z.X., Tian, B. and Fan, Q., 2021. *Lespedeza danxiaensis* (Fabaceae), a new species from Guangdong, China, based on molecular and morphological data. *PhytoKeys*, 185, p.43. <https://doi.org/10.3897/phytokeys.185.72788>

## A new *Hedysarum* from Uzbekistan



*Hedysarum sunhangii* (Photos: Inom Juramurodov)

Juramurodov, I., Tojibaev, K., Nikitina, E., Makhmudjanov, D., Yusupov, Z., Deng, T. and Dehkanov, D., 2021. *Hedysarum sunhangii* (Fabaceae, Hedysareae), a new species from Pamir-Alay (Babatag Ridge-Uzbekistan). *Phytotaxa*, 524(1), pp.1-13. <https://doi.org/10.11646/phytotaxa.524.1.1>

Of the c. 160 species of *Hedysarum*, more than half are distributed in central Asia with especially high levels of endemism in the Tien Shan Mountains and the SW Pamir-Alay in Uzbekistan where this new species is narrowly endemic. *Hedysarum sunhangii* Juram. & Tojibaev is named in honour of the Chinese botanist, Prof. Hang Sun, who promoted botanical collaboration between Uzbekistan and China.

## *Polhillia stirtoniana*

Legume workers will be delighted to see this new species, *Polhillia stirtoniana* du Preez named in honour of Charles Stirton for his work on Cape legumes and for his assistance in the formation of the Overberg Renosterveld Conservation Trust and establishment of the Haarwegskloof Private Nature Reserve and research centre in South Africa. The binomial is even more apt given that the genus *Polhillia* was established by Charles Stirton in honour of the eminent legume systematist Roger Polhill. This species, alongside two others newly described, was published as part of an excellently detailed and abundantly illustrated taxonomic monograph of *Polhillia* that brings the number of species in the genus to 11.



*Polhillia stirtoniana* (Photos: Brian du Preez)

du Preez, B., Dreyer, L.L., Stirton, C.H. and Muasya, A.M., 2021. A monograph of the genus *Polhillia* (Genisteeae: Fabaceae). *South African Journal of Botany*, 138, pp.156-183. <https://doi.org/10.1016/j.sajb.2020.12.022>

## A new *Indigofera* from the Cape biodiversity hotspot



*Indigofera wenholdiae* (Photos: Brian du Preez)

du Preez, B., Dreyer, L.L., Stirton, C.H., Muasya, A.M. and Schrire, B.D., 2021. *Indigofera wenholdiae* (Indigoferaeae, Fabaceae), a new species from the Western Cape Province, South Africa. *PhytoKeys* 182: 107–112. <https://doi.org/10.3897/phytokeys.182.72170>

Several legume genera form large species radiations in the Fynbos vegetation of the Cape Flora of South Africa, including a large endemic clade of the genus *Indigofera* with ca. 90 species. *Indigofera wenholdiae* du Preez & Schrire is the first of several new species that are being described for this clade.

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## BIBLIOGRAPHY SPOTLIGHT

### *A Look Inside the Stems of the Charismatic Genus Wisteria*

Rosa Nejapa, Universidad Nacional Autónoma de México (UNAM), México

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**Wisteria is a well-known** charismatic genus of lianas naturally occurring in temperate zones of eastern Asia and the eastern USA (however, it is now cultivated across the world given its ornamental value). Previous researchers studied anatomical stem features in genus *Wisteria*, especially in *W. sinensis* because of the presence of successive cambia. However, there is a controversy around the origin of successive cambia since different origins have been proposed for *W. sinensis*.

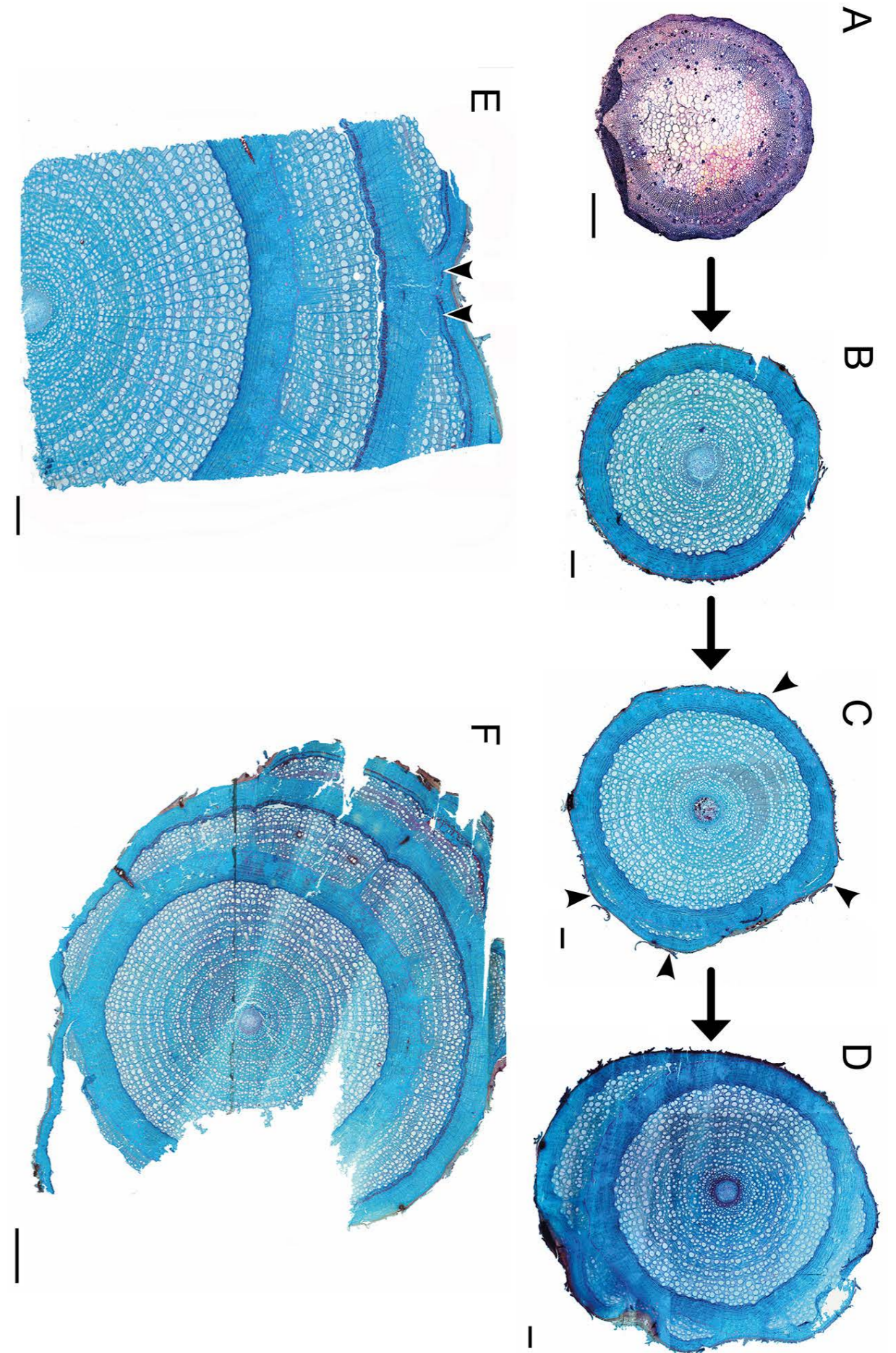
For my bachelor's thesis, under guidance of Dr. Marcelo R. Pace (Instituto de Biología, UNAM, México) and in collaboration with Dr. Pablo A. Cabanillas (Cátedra de Dendrología, Facultad de Ciencias Agrarias y Forestales, UNLP, Argentina), we collected ornamental material from *W. sinensis* in Argentina and the USA, taking advantage of the wide distribution of this cultivated species.

In addition, thanks to loans from the Forestry and Forest Products Research Institute (TWTw) wood collection from Tsukuba, Japan, we obtained stems derived from natural populations of *W. brachybotrys* and *W. floribunda*. The work carried out helped us to clarify the origin and development of the successive cambia and to check whether this cambial variant could be a synapomorphy of the genus.

In this study, we demonstrate that three species of *Wisteria* develop successive cambia in their stems. Through ontogeny carried out with samples cut from apical portions to the thick portions of the stems, we identified that the successive development of cambia was linked to the topological position of the pericyclic fibres, which is a distinct cambial variant for the genus.

#### Full reference:

Nejapa R, Cabanillas PA, Pace MR (2021) Cortical origin of the successive cambia in the stems of the charismatic temperate lianescent genus *Wisteria* (Fabaceae) and its systematic importance. *Botanical Journal of the Linnean Society*: boab091, <https://doi.org/10.1093/botlinnean/boab091>



Adapted from Fig. 2 of Nejapa et al. (2021). Transverse sections of the ontogeny of *Wisteria sinensis* stems. From the onset of secondary growth (A) to stems with two successive cambia (E and F).

# LEGUME BIBLIOGRAPHY 2021

Warren Cardinal-McTeague, University of British Columbia, Canada

**Methodology** – *The Legume Bibliography 2021* was manually compiled using keyword searches and date filtering on the websites of journals that frequently publish legume research (see below). The search terms were limited to “**Leguminosae**” and “**Fabaceae**”, and they were searched independently. In most cases, \*.ris files were able to be downloaded and imported into Mendeley Desktop v.1.19.8, where they were tagged under the headings provided. Most legume-related publications are presented here, with the exception of the numerous (>50) Pharmacology studies exploring health and anti-microbial properties of legume extracts. The final list was reviewed by Colin Hughes and Gwilym Lewis and any overlooked publications were manually added.

List of searched journals and publishers (updated annually, if one is missed please send a message to the editors). **Journals:** American Journal of Botany; Annales Botanici Fennici; Annals in Botany; Annals of the Missouri Botanical Garden; Australian Journal of Botany; AoB Plants; Biologia; Biotropica; BMC Ecology and Evolution; BMC Genomics; BMC Plant Biology; Boletim do Museu Integrado de Roraima; Botanical Journal of the Linnean Society; Botany; Brittonia; Caldasia; Candollea; Diversity; Ecography; Ecology; Ecology and Evolution; Flora; Frontiers in Plant Science; Grana; Hoehnea; International Journal of Plant Science; Journal of Applied Ecology; Journal of Biogeography; Journal of Ecology; Journal of Japanese Botany; Journal of Plant Taxonomy and Geography (Webbia); Journal of Systematics and Evolution; Journal of the Botanical Research Institute of Texas; Kew Bulletin; Mitochondrial DNA Part B; Molecular Ecology; Molecular Phylogenetics and Evolution; Nature; Neodiversity; New Phytologist; New Zealand Journal of Botany; Nordic Journal of Botany; Novon; Nuytsia; Pacific Science; Palynology; PeerJ; PhytoKeys; Phytologia; Phytotaxa; Planta; Plant Diversity; Plant Ecology and Evolution; Plant Species Biology; Plant Systematics and Evolution; Plants; Rodriguésia; South African Journal of Botany; Systematic Biology; Systematic Botany; Taxon; Telopea; Trees. **Publishers:** Bio Med Central; Elsevier; BioOne; Scielo; Taylor and Francis; University of Chicago Press; Wiley.

**Notes** – **1.** Books and Chapters are not included in the bibliography. Please submit an announcement for new legume books to be highlighted in the Bean Bag Newsletter. **2.** Pre-prints and early-view publications are not included in the bibliography, with the exception of a few journals that consider digital releases the date of effective publication (those articles may still be paginated into volumes in the following year). **3.** We recognize there are spelling errors in many of the article titles, including species and authorities. We present them verbatim as a matter of record.

**Acknowledgements** – Many thanks to our colleagues who provided their citations, some of which are recovered by these search methods. Please include \*.ris files with your submissions, when possible.

**Results** – A total of **351** new publications were recovered for the 2021 Bibliography:

## Bibliography Index

Anatomy & Morphology = 15

Biogeography = 4

Chloroplast Genomes = 43

Development = 4

Ecology = 33

Floristics = 11

Genetics, Genomics, & Molecular Biology = 32

Microbiology, Nodulation, & Symbiosis = 14

Paleobotany = 4

Palynology = 2

Phylogenetics, Phylogenomics, Systematics, & Evolution = 20

Physiology = 27

Phytochemistry = 10

Phytogeography = 10

Population Genetics & Genomics = 18

Taxonomy = 50

New Species = 54

## ANATOMY & MORPHOLOGY - 15

Aboulela M, El-Karemy ZAR, Hosni HA, Saleh S, Faried A (2021) Taxonomic implications of seed morphology and storage proteins in three tribes of the subfamily Papilionoideae (Fabaceae) in Egypt. *Phytotaxa* **484**, 75–95. doi:<https://doi.org/10.11646/phytotaxa.484.1.3>.

Andrade GC, Silva LC (2021) A new morphological marker of the effects of acid rain in the tropics on the stem of *Libidibia ferrea* var. *leiostachya* (Leguminosae–Caesalpinioideae). *Australian Journal of Botany* **69**, 491–499. doi:<https://doi.org/10.1071/BT21027>.

Aydin H, Sari D, Sari H, Eker T, Aykurt C, Toker C (2021) Phylogenetic relationships among *Pisum* L. species from Asia Minor inferred from pollen and seed coat morphology. *Grana* **60**, 347–355. doi:<https://doi.org/10.1080/00173134.2021.1912820>.

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