



THE EVOLUTION OF
COMPOSITAE
IN A GLOBAL CONTEXT



XII CONGRESO
LATINOAMERICANO
DE BOTÁNICA

21-28 Octubre 2018 | Quito - Ecuador



ASOCIACIÓN
BOTÁNICA
ECUATORIANA



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About the symposium

Compositae or Asteraceae (or comps) are the most diverse flowering plant family, with over 1,700 genera and 24,000-30,000 species. Members of the family inhabit every continent except Antarctica and they include 1 of every 10 flowering plants in the world. Besides its overwhelming diversity, the Compositae also play a key role in major ecosystems around the world, and are an important source of food, oil, industrial products, ornamentals and medicines. Given the importance of the family, much effort has been placed on getting together an international team of collaborators focused on studying the Compositae.

Latin America is of particular importance in the study of the evolution and diversification of the family, not only because of its major presence on the continent, but also because there is still so much that we don't know about the evolutionary processes that took place in the region.

The symposium "Evolution of Compositae in a global context" was proposed to the XII Latin American Botanical Congress organizing committee, with the main objective of getting together people actively working on the Compositae, so they could share their findings and further promote future collaborations between them while implementing new techniques and approaches that could help us know better this wonderful plant family.

All this information, gathered collectively, and freely shared among the large community of researchers will boost our efforts in the conservation of biodiversity and sustainability of the ecosystems and enhance the economic importance of the family for the benefit of humankind.

Organizing Committee

Itziar Arnelas
Mauricio Bonifacino
Vicki Funk
Gustavo Heiden

Cover photo

Chuquiraga jussieui, an incredible species typical of the Paramo vegetation in Ecuador is the plant chosen by the XII Latin American Botanical Congress to serve as its logo. The species belong to the earliest diverging lineage of the Compositae, the Barnadesioideae, a subfamily endemic of Latin America

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COMPOSITAE PHYLOGENOMICS

Jennifer R. Mandel, Rebecca B. Dikow, Carolina M. Siniscalchi, Ramhari Thapa, Linda Watson & Vicki A. Funk

Compositae phylogenomics

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Key words: Asteraceae, Genomics, Hyb-Seq, Phylogeny.

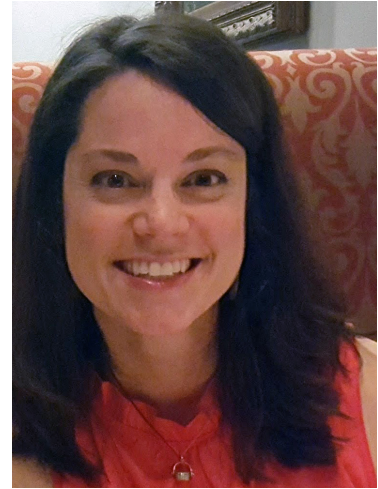
Compositae comprise more than 25,000 species of artichokes, dandelions and daisies, and represent 10% of all flowering plant species on Earth. Prior to the use of phylogenomics, many evolutionary relationships were not well-resolved which has hindered advances in our understanding of the family's origin and historical biogeography. Using the Hyb-Seq method, we sequenced hundreds of low-copy number nuclear markers plus partial plastomes for 250 species representing all major lineages within the family. Using these data, we generated robust phylogenetic trees using concatenated and coalescence-based analyses that represent nearly all subfamilies and tribes. In general, the topologies within tribes remain stable in both the nuclear and plastid trees, however relationships among subfamilies differ from existing classifications. Specifically, our nuclear data do not support the monophyly of Subfamilies Carduoideae and Cichorioideae, however phylogenies generated from plastid data provide weak support for their monophyly. The discordance between the

nuclear and plastid phylogenies suggests that reticulation may have occurred in the history of these lineages. We are using fossil data as time calibration points to estimate the age of the family and the origins of its major lineages. While it has traditionally been assumed that the family diverged from its South American sister family, Calyceraceae, 50-40 MYA, more recent molecular phylogenetic dating studies have estimated the age of the family to be as old as 85-72 MYA, and another study estimated the family's age to 69 MYA. These estimates were either based solely upon plastid phylogenies or nuclear loci with limited taxon sampling, we thus provide results from a comprehensive nuclear phylogeny both including and excluding the Antarctic fossil pollen. Our new phylogenetic reconstruction will provide unprecedented insight into the evolution and historical biogeography of the family including bolstering our understanding into the biogeographic origins, migrations, and diversifications of major lineages within Compositae.

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Dr. Jennifer Mandel is an Assistant Professor of Biology at the University of Memphis. Her lab studies evolutionary and ecological genetics in a variety of plant species conducting studies in the field, the greenhouse, and the lab. Major questions involve understanding mechanisms that drive and maintain biodiversity. Current projects in the lab include the application of targeted gene sequencing for phylogenomic applications especially in Compositae, population genetics of crop-wild relatives, and the study of heteroplasmy and paternal leakage of organellar genes and genomes. She received her PhD from Vanderbilt University, Nashville, Tennessee, USA in 2008 and completed a post-doc in Plant Biology at the University of Georgia, Athens, Georgia, USA before joining the Biological Sciences Department at the University of Memphis in 2014.

Cover photo

Members of Compositae are the most frequently grown garden plants. This brightly colored member belongs to the genus Gazania (Arctotideae) or "Treasure Flowers" and is native to South Africa widely cultivated for its showy corollas.



**SYSTEMATIC INSIGHTS INTO BARNADESIOIDEAE:
WHAT PHYLOGENOMICS CAN SAY ABOUT THE
EARLY EVOLUTION OF ASTERACEAE**

Paola de Lima Ferreira, Romina Batista, Tobias Adermann, Milton Groppo, Alexandre Antonelli & Christine Bacon

Systematic insights into Barnadesioideae: what phylogenomics can say about the early evolution of Asteraceae

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Key words: Compositae, Molecular Phylogeny, Neotropics, Next-Generation Sequencing, Taxonomy.

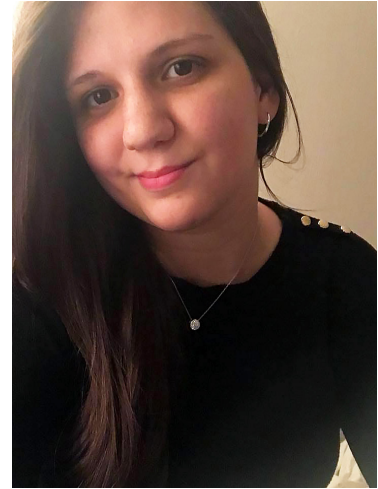
Phylogenetic hypotheses based on phylogenomics data has allowed the dream of many biologists to reconstruct the tree of life which was difficult in previously recalcitrant clades. Besides, molecular hypotheses have clarified the phylogenetic relationships within large angiosperms families such as the Asteraceae. However, reconstructing the evolutionary history in Asteraceae has been considered a hard task due to the lack of resolution and support using the traditional Sanger sequencing method trees. The main goal of the present work was to propose a phylogenetic hypothesis based on the target enrichment method for a special branch of Asteraceae, the subfamily Barnadesioideae. This subfamily comprises nine genera and nearly 85 species restricted to South America, from Venezuela to Argentina, which most of the species distributed along the Andes. A phylogenetic framework combined with biogeographic and morphological data will provide insights into the early evolution of

Asteraceae. Using high throughput sequencing, we generated nuclear data for 49 of 85 extant Barnadesioideae species using 9,689 baits targeting 1061 orthologous genes. Moreover, we used the raw data to recover almost the entire plastome, capturing a total of 114 genes. Phylogenetic hypotheses were estimated using maximum likelihood and bayesian analyses independently for nuclear, chloroplast DNA, and combining data sets. Our results showed well-supported phylogeny that resolves the relationships along the backbone of the Barnadesioideae. The phylogenetic framework generated in the study has been fundamental to infer biogeographical reconstructions of the group and to better understand the evolutionary history of Barnadesioideae, as well as shed light on the whole Asteraceae relationships.

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MSc Paola de Lima Ferreira is a Ph.D. student at the University of São Paulo, Department of Biology, Brazil. She is interested in evolutionary studies in different Angiosperm families, but specially in Asteraceae. During her carrier, she has focused her studies on the early evolution of Asteraceae, with emphasis on systematics, taxonomy, morphology and historical biogeography of the subfamily Barnadesioideae.

Cover photo

Chuiraga spinosa subsp. *humanpinta* C.Ezcurra. This evergreen shrub genus is ecologically important and constitutes part of the traditional medicine in Peru and Ecuador.



**LEVERAGING PHYLOGENOMICS TO IMPROVE
RESOLUTION OF THE EVOLUTIONARY
HISTORY OF *MOQUINIASTRUM* AND THE TRIBE
TO WHICH IT BELONGS, GOCHNATIEAE
(COMPOSITAE)**

Morgan Gostel & Vicki A. Funk

Leveraging phylogenomics to improve resolution of the evolutionary history of *Moquiniastrum* and the tribe to which it belongs, Gochnatieae (Compositae)

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Key words: High-Throughput Sequencing, Microfluidic PCR, Neotropics, Target Enrichment.

Moquiniastrum (Gochnatieae) is a genus comprising 21 species near the base of the Compositae. Distributed throughout much of South America, this genus is characterized by diverse morphologies, habits, and a slightly disjunct distribution in Argentina, Bolivia, Brazil, Paraguay, Peru, Uruguay, and Venezuela. Recent molecular phylogenetic studies that have sampled heavily from this genus suggest that current molecular markers are insufficient to accurately reconstruct the evolutionary history of this genus and its phylogenetic position relative to other genera in the Gochnatieae. We have evaluated a set of nearly 300 molecular markers for their phylogenetic utility at the species and genus level for this enigmatic group of taxa and present the results here. Through analysis of these loci, we have improved the resolution of phylogenetic relationships in these taxa among genera in the Gochnatieae and species of *Moquiniastrum*. Our results shed light on the evolution and radiation of an interesting

group in the Compositae throughout diverse habitats in South America. Based on our results, we suggest a combined approach to future phylogenomic studies utilizing both microfluidic PCR-based library prep and *in-situ* hybridization to maximize sequencing depth from limited budgets.

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Morgan Gostel's research combines traditional taxonomy and phylogenomics to understand the diversification of lineages in Compositae across landscapes. More specifically, his research focuses on radiations in dry forests throughout the neo- and paleotropics, using comparative morphology, high-throughput sequencing approaches, and biogeography to understand the process of evolution in these harsh environments and key innovations that have led to widespread radiations. Morgan was previously a GGI-Buck Postdoctoral Fellow at the National Museum of Natural History at the Smithsonian Institution. He received Bachelors and Masters degrees in Biology from Virginia Commonwealth University and his Ph.D. in Environmental Science and Policy from George Mason University. Morgan is a Research Botanist at the Botanical Research Institute of Texas (BRIT) and Director of the Global Genome Initiative for Gardens (GGI-Gardens).

Cover photo

Flowering capitulescence of Moquiniastrum polymorphum (Less.) G.Sancho from northern Uruguay, a widespread species in Gochnatieae that is distributed throughout southern Brazil, northeastern Argentina, Paraguay, and Uruguay

A close-up photograph of a cluster of purple flowers, likely from the Cardueae subtribe. The flowers have a complex structure with numerous small, star-shaped florets and prominent, dark purple stamens. The background is a soft, out-of-focus green, suggesting a natural habitat. The overall appearance is that of a thistle or similar member of the Asteraceae family.

**A NEW SUBTRIBAL CLASSIFICATION OF
CARDUEAE: A HAPPY PAIRING OF
NEXT-GENERATION-SEQUENCING AND
MORPHOLOGY**

Alfonso Susanna & The Cardueae Radiations group (in alphabetical order: Juan Antonio Calleja, Mercè Galbany-Casals, Núria Garcia-Jacas, Sonia Herrando-Moraira, Javier López-Alvarado, Jordi López-Pujol, Jian-Quan Liu, Jennifer Mandel, Llorenç Sáez, Alexander Sennikov & Roser Vilatersana)

A new subtribal classification of Cardueae (Compositae): a happy pairing of next-generation-sequencing and morphology.

Alfonso Susanna^{1*} and The Cardueae Radiations group (in alphabetical order: Juan Antonio Calleja², Mercè Galbany-Casals², Núria García-Jacas¹, Sonia Herrando-Moraira¹, Javier López-Alvarado², Jordi López-Pujol¹, Jian-Quan Liu³, Jennifer Mandel⁴, Llorenç Sáez², Alexander Sennikov^{5,6} & Roser Vilatersana¹)

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Key words: Carlininae, Cardopatiinae, Echinopsinae, Xerantheminae, Berardiinae, Stahelininae, Onopordinae, Carduinae, Arctiinae, Saussureinae, Centaureinae.

Classification of tribe Cardueae in natural subtribes has always been a challenge. Four of the classical subtribes are well-defined, natural entities as repeatedly confirmed by molecular data: the three basalmost ones—Cardopatiinae, Echinopsinae and Carlininae—and the terminal Centaureinae. This classification was unsatisfactory because it resulted in a deeply paraphyletic central subtribe, the Carduinae. Some natural groups within Carduinae were painstakingly delineated on morphological basis and the help of DNA sequences: The Xeranthemum group, the Onopordum group, the Cynara group, the Carduus-Cirsium group, the Arctium-Cousina group and the Saussurea-Jurinea group, together with two remarkable isolates: Berardia and Staehelina. However, the lack of support for some critical branches in our previous phylogenies refrained us from suggesting anything more than informal groups. The advent of next-generation-sequencing technology has changed dramatically the availability of molecular markers. We have applied the target-enrichment approach

developed for Compositae targeting 1061 conserved orthology loci to a set of 82 species. From the targets, 866 loci were recovered, which were concatenated in a supermatrix composed by 577,263 base-pairs. From off-target reads, we also recovered 85 plastid coding genes and created a second supermatrix with 75 species and 64,080 base-pairs. The phylogenetic analysis of the nuclear dataset has fully resolved all the nodes of the tree with very high support. The analysis of the plastid dataset shows some incongruences with the nuclear data that we will shortly discuss. On the basis of these results, we are proposing a new classification based on the previous informal groups, with the only minor retouch of merging together the Cynara and Carduus groups. The resulting classification of the tribe recognizes eleven subtribes, namely Carlininae, Cardopatiinae, Echinopsinae, Xerantheminae (re-instated), Berardiinae (new), Stahelininae (new), Onopordinae (new), Carduinae (redefined), Arctiinae (new), Saussureinae (new) and Centaureinae.

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Alfonso Susanna works on tribe Cardueae since 1981. Together with Núria Garcia-Jacas, he pioneered the molecular studies in the tribe and compiled the latest revisions of the Cardueae. He has carried important field collections in Middle Asia, North Africa and the Mediterranean Region, always focusing on the Cardueae. Alfonso presented his PhD in 1982 in the Autonomous University of Madrid. He is currently senior scientists at the Botanic Institute of Barcelona.

Cover photo

Staehelina petiolata in Greece. This genus is the type of the new subtribe *Staehelininae*



**PHYLOGENOMICS IN CICHORIEAE (COMPOSITAE)
WITH A FOCUS ON LACTUCINAE AND
SCORZONERINAE**

Katy Elizabeth Jones, Jennifer Mandel, Paul Johnston, Edward Schilling & Norbert Kilian

Phylogenomics in Cichorieae (Compositae) with a focus on Lactucinae and Scorzonnerinae

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Key words: Allopolyploidy, Compositae, Hyb-seq, Lactucinae, Scorzonnerinae, Systematics.

The tribe Cichorieae is one of the largest of the 12 tribes in the family Compositae. Members of this tribe can usually be recognised by the combination of having latex and capitula with ligulate flowers only. Cichorieae include over 90 genera with some 1500 species and further +8000 apomictics species in three genera. Using phylogenomic analyses (Hyb-seq Conserved Orthologous Set; Mandel et al. 2014) we are sampling broadly across the tribe to address a number of issues related to its circumscription, including the position of *Gundelia* with an unusual capitulum morphology and the relationships among early diverging lineages. Lactucinae and Scorzonnerinae subtribes are distantly related with respect to one another within the Cichorieae tribe, and Scorzonnerinae represents an early diverging lineage. Within these two subtribes none of the genera are monophyletic based on current circumscriptions, therefore deeper sampling within these two subtribes was conducted in order to investigate inter-

generic relationships. We also present the power of phylogenomic analyses at shallower taxonomic levels to shed light on the hybrid origin of an allopolyploid complex within the subtribe Lactucinae.

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My PhD focused on the systematics and biogeography of the Macaronesian endemic genus *Pericallis* (Asteraceae) at the Natural History Museum London. Now, I am a Postdoctoral researcher at the Botanic Garden and Botanic Museum Berlin and I work on the systematics and evolution within the Cichorieae tribe (Asteraceae). Using phylogenomic approaches I investigate the relationships within this tribe and aim to unravel the hybrid origin of an allopolyploid lineage within the lettuce genus (*Lactuca*).

Cover photo

Lactuca tatarica growing in the Botanic Garden Berlin (photo by Norbert Kilian). This Eurasian species is closely related to a native North American species (*L. oblongifolia*) and is likely associated with the hybrid origin of the allopolyploid lineage within *Lactuca*.



PHYLOGENOMICS OF *CHRESTA* AND RELATIONSHIPS WITHIN VERNONIEAE

Carolina M. Siniscalchi, Benoit Loeuille, Jennifer R. Mandel & José R. Pirani

Phylogenomics of *Chresta* and relationships within Vernonieae (Compositae)

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Key words: Caatinga, Cerrado, Chrestinae, Phylogeny, Target Capture.

Chresta has 18 species distributed in the Brazilian Cerrado and Caatinga, presenting striking morphological and ecological traits, which seem to constitute a turning point within some lineages in Vernonieae, as *Chresta* presents a combination of characters like secondary heads, common in Lychnophorinae, with pollen type C, usually found in some Vernoniinae. Previous phylogenetic studies on the genus sampled few species and did not provide enough resolution and support to define its sister group neither for a proper assessment of this morphological diversity in an evolutionary framework. In this study, we used recently developed HybSeq methods in order to resolve the relationships within *Chresta* species and to define its sister group and its position within Vernonieae. We used ~700 nuclear markers obtained from 60 terminals of *Chresta* and related taxa in Vernonieae aiming to get fully resolved and well-supported trees. *Chresta* is strongly supported as a monophyletic genus, and its sister group is consistently recovered as a clade formed by North, Central

and South American genera of Vernoniinae, while the relative position of *Chresta* in relation to Lychnophorinae and Lepidaploinae remains doubtful, probably due to insufficient sampling within these subtribes. Most clades obtained within *Chresta* are also strongly supported, and this allowed us to discuss the evolution of their morphological features in relation to ecological and environmental requirements.

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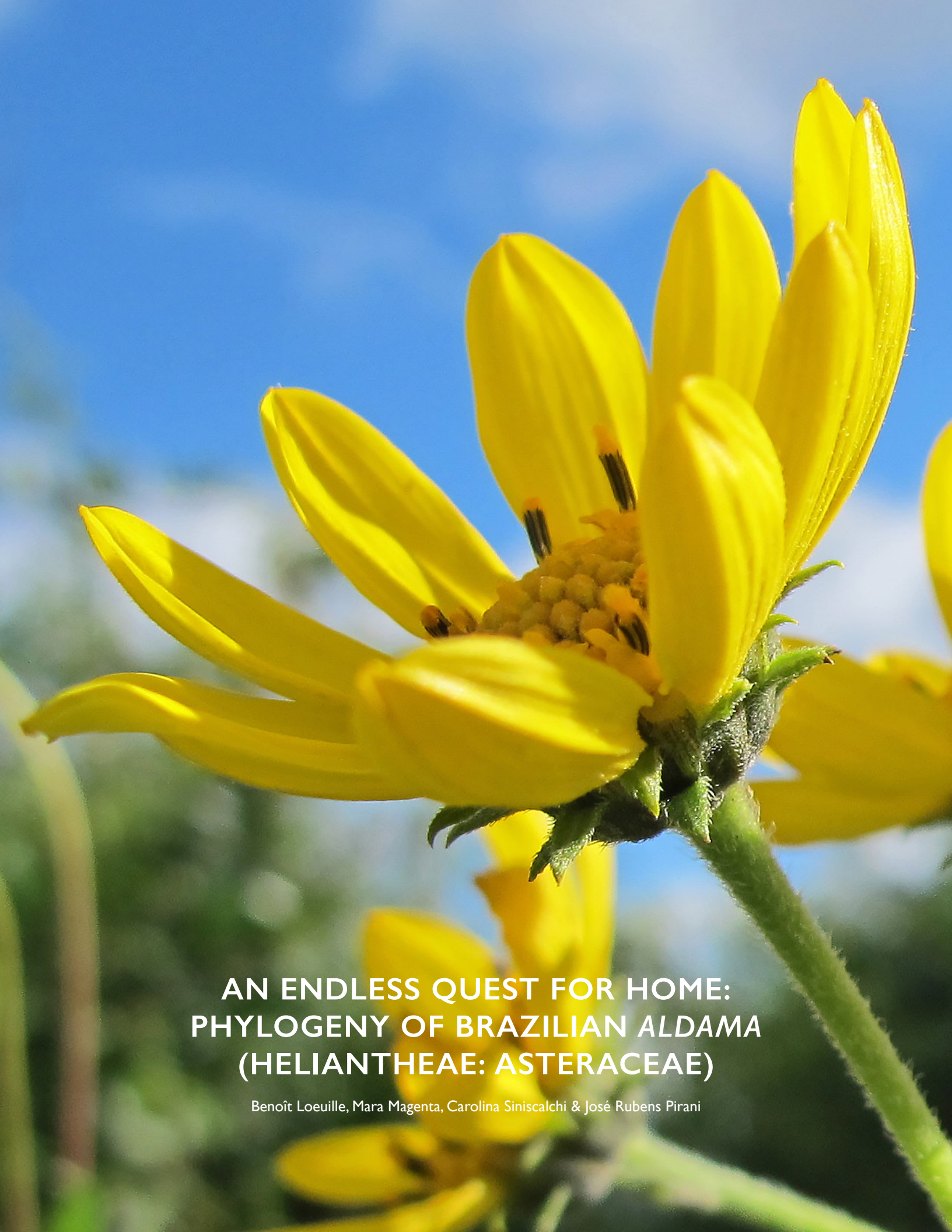
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I have been studying plant systematics and taxonomy since 2009, when I started my undergraduate research at the Plant Systematics Laboratory at Universidade de São Paulo, Brazil, where I have been since then. I started my career studying Leguminosae taxonomy and floristics. In 2012, I obtained my M.Sc. and started my Ph.D. research in 2014, this time with the Compositae. In my thesis I studied the systematics and evolution of genus *Chresta* (Vernonieae). I used phylogenomic methods to obtain a phylogeny of the genus, to better study its relation within tribe Vernonieae and its morphological evolution. Also, I used this genomic data to develop new microsatellite markers to study population genetics in some rupicolous species of *Chresta*. This part of my research was conducted at the Mandel Lab at the University of Memphis, TN, USA. I also conducted a taxonomic reevaluation of the genus, with the description of four new species. I graduated in January 2018 and in September 2018 I will start a postdoctoral fellowship at the University of Memphis.

Cover photo

Chresta sphaerocephala, the type species of the genus, is frequently found in several environments in Brazil, especially in the Cerrado. Like all species from the genus, it presents secondary heads, which probably help attract more pollinators and protect reproductive structures against herbivory.



**AN ENDLESS QUEST FOR HOME:
PHYLOGENY OF BRAZILIAN ALDAMA
(HELIANTHEAE: ASTERACEAE)**

Benoît Loeuille, Mara Magenta, Carolina Siniscalchi & José Rubens Pirani

An endless quest for home: phylogeny of Brazilian *Aldama* (Heliantheae: Asteraceae)

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Key words: Asterids, Compositae, Plastome, Systematics, *Viguiera*.

In the last decades, several molecular phylogenetic and taxonomic studies have shown the need to reevaluate the traditional circumscription of the large American genus *Viguiera* (Heliantheae: Helianthinae), with ca. 150 spp. The genus is currently restricted to two species from Mexico with pubescent stamen filaments since most species formerly treated as *Viguiera* have been transferred to *Aldama* (including *Rhysolepis*), despite forming a paraphyletic assemblage. The Brazilian species have been poorly sampled in previous studies and their belonging to *Aldama* remains controversial on morphological and phylogenetic grounds. In order to understand the evolutionary relationships of the Brazilian *Aldama* species with Andean and Central American *Aldama* species and other derived Helianthinae genera, we carried out a plastome phylogeny based on 27 (out of 30) Brazilian species and 12 outgroups. Parsimony and maximum likelihood analyses recovered highly similar topologies. The genus *Aldama*, as currently circumscribed,

is paraphyletic, as its type species is more closely related to *Pappobolus* and *Tithonia* than to South American *Aldama* species. A strongly supported large clade with all South American *Aldama* species emerged in our analysis. A putative morphological synapomorphy for this clade is the presence of campanulate-tubular disk florets (vs. tubular florets in the related clades). The relationships inside this clade are not fully understood due to the low nucleotide variation of the plastome (3.3%). Andean species of *Aldama* from Argentina and Chile are nested among Brazilian species. Two internal clades came out with strong biogeographical patterns: one including most of Brazilian species occurring in Cerrado Province and the other with one species from Pampean and *Araucaria* forest biogeographic Provinces. In conclusion, the genus *Aldama* is paraphyletic, Brazilian species emerged in a well-defined clade with other South American species and their quest for home has not yet ended.

Benoît Loeuille

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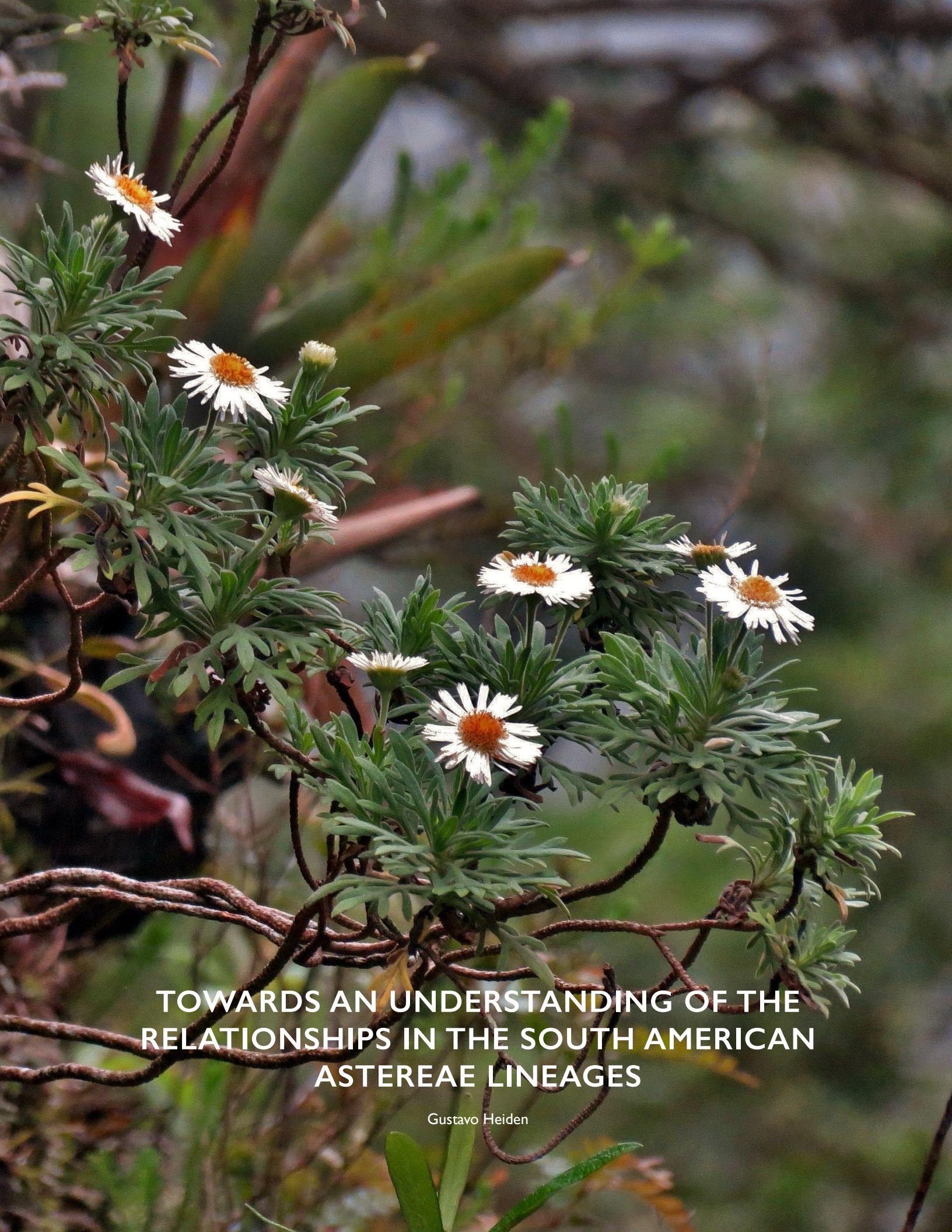
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I study the evolution of morphological, anatomical and phytochemical diversity of Neotropical Asteraceae in a phylogenetic context, focusing in the systematics of the tribes Vernonieae and Heliantheae. My main approach in research is to overcome the growing gap between the results of molecular phylogeny and those of traditional (morphological) taxonomy, using several sources of evidence (morphological, molecular, phytochemical, etc.) in the reconstruction process of phylogenetic trees and recognizing only taxa defined by morphological or phytochemical synapomorphies. My secondary research lines include taxonomic, phylogenetic, and floristic studies of the Gnaphalieae, Vernonieae, and Heliantheae tribes. I also work in theory of Systematics (Three-items analysis), History and Philosophy of Science (related to classification and homology) and Ancient Botany history (translation of Theophrastus). I am currently an Assistant Professor at the Federal University of Pernambuco (Brazil), Botany Department. I obtained my Pharm.D. at University of Lille 2 (France), M.S. at University of Paris 6 (France) and Ph.D. at University of São Paulo (Brazil).

Cover photo

Aldama anchusifolia (DC.) E.E.Schill. & Panero is a common species in southern South America (Argentina, Brazil, Paraguay and Uruguay).



**TOWARDS AN UNDERSTANDING OF THE
RELATIONSHIPS IN THE SOUTH AMERICAN
ASTEREAEE LINEAGES**

Gustavo Heiden

Towards an understanding of the relationships in the South American Astereae (Compositae) lineages

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Key words: Asteraceae, Baccharidinae, Compositae, Hinterhuberinae, Podocominae.

The tribe Astereae (Compositae/ Asteraceae) is monophyletic and mostly characterized by the ecaudate and ecalcarate anther bases, a disc floret style with two distinct marginal stigmatic lines and deltate to triangular or lanceolate style appendages that are glabrous adaxially and with sweeping hairs abaxially. The tribe has a worldwide distribution and is the second largest in the Compositae with 14 subtribes, 222 genera, and ca. 3100 species: 31 genera and ca. 740 species occur in South America. Recent phylogenetic studies placed part of the South American Astereae in the Paleo South American clade, while the remaining representatives of the tribe occurring in South America have unknown relationships and most of its subtribes could not be confirmed as monophyletic. With the aim of elucidating the relationships of the South American lineages, *ETS* and *ITS* sequences of 745 Astereae species, plus *Anthemis arvensis* (Anthemidae) as outgroup, were analysed with Bayesian approaches. Based on these analyses, *Pteronia*, *Novenia*, and *Oritrophium*, previously

placed within the Paleo South American clade, grouped together (PP=1) and emerged as the sister clade (PP=1) of a group of genera from New Zealand (PP=1) + a more restricted Paleo South American clade (PP=1). The subtribes Bellidinae (PP=1) and Grangeinae (PP=1) were nested in a polytomy that also contained a clade with the Australasian lineages, the remaining South American lineages, and the North American clade. The results corroborate that *Archibaccharis* is sister to *Plagiocheilus* (PP=1) and should be removed from Baccharidinae and Grangeinae respectively. Subtribes Podocominae s.s. (PP=1) and Baccharidinae s.s. (PP=1) were confirmed as monophyletic groups, whereas Baccharidinae emerged as sister (PP=0.9) to the North American clade (PP=1). Finally, the subtribe Hinterhuberinae is polyphyletic and needs a thorough phylogenetic study to redefine its limits.

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Gustavo Heiden is a Botanist interested in systematics, biogeography, evolution, conservation and applied uses of the plants, specially South American Subtropical and Temperate flora. Major research interests include systematics and evolution of Compositae; genetic resources and pre-breeding of crop wild relatives; sustainable management and use of the palm landscapes from Southern Brazil; and curation and exploration of herbaria data. Gustavo obtained his Bachelor and Licenciante degree in Biology from Universidade Federal de Pelotas, Master in Botany from Jardim Botânico do Rio de Janeiro, and PhD from Universidade de São Paulo. He currently works as researcher at Embrapa Clima Temperado, Pelotas, Brazil.

Cover photo

Hysterionica pinnatiloba, a South Brazilian narrow endemic daisy, which belongs to the North American clade of Astereae, living on the edges of canyons in the Atlantic Rainforest biome.



**KNOWING *BACCHARIS* L. (ASTEREAЕ,
COMPOSITAE) SPECIES IN SOUTHERN ECUADOR,
DELIMITATION ON MORPHOLOGICAL AND
PRELIMINARY MOLECULAR DATA**

Itziar Arnelas, & Valeria Alejandrina Salinas-Tinizaray

Knowing *Baccharis* L. (Astereae, Compositae) species in Southern Ecuador, delimitation on morphological and preliminary molecular data

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Key words: Andes, Hybridization, Phylogeny, Taxonomy.

Baccharis L. is one of the most diversified genera within Astereae (Compositae). The genus is characterized by its general tufted indumentum trichomes and dioecy. Due to the complexity of the species of the genus in Andes of south Ecuador, we present a preliminary morphological and molecular study of this genus in this area. We sampled 21 taxa in 31 population in Loja and Zamora-Chinchipec provinces. Preliminary phylogenetic trees were constructed using *ITS* and *CF* sequences (16 taxa); and multivariate analyses (21 taxa) were used to infer how morphological characters are or not in agreement with preliminary molecular results. Our results provide how morphology could explain the genetic relationships obtained for several species. This is the case of alate species *B. reticulata* and *B. genistelloides*, both commonly confused but morphologically well differentiated by its types of trichomes, involucral size and bract involucral shape. No intermixed individuals of both species have recovered in our phylogenetic nuclear trees. We corroborate

the morphological and genetic proximity of *B. quitensis* and *B. trinervis* var. *rhexioides* suggested by other authors. *B. decussata* subsp. *decussata*, which is commonly confused with *B. trinervis* var. *rhexioides*, is molecular and morphological clearly segregated from the second. The morphological and genetic proximity of *B. sinuata* and *B. cf. lloensis* was obtained. All sampled individuals of *B. pedunculata* are molecularly and morphologically circumscribed. Combining morphological and molecular data, we corroborate the morphological identity of several species commonly confused Andes of south Ecuador. The incongruences between nuclear and chloroplast tree suggest that hybridization might have played an important role in the evolution of the genus in this area.

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Dr. Itziar Arnelas Seco (Spain) is interested in taxonomy research involving biodiversity studies focusing on naming, describing and classifying different genus of vascular plants of Compositae. Much interest of her research is related to incorporating phylogenetic and population genetic information in taxonomy research through using molecular markers. She is working in tribe Astereae (Compositae) in Ecuador; but even she is involved in different families (Poaceae, *Festuca*; Polygonaceae, *Coccoloba*) in order to advance in the knowledge of tropical flora from the country. She obtained her PhD in University of Cordoba (Spain) in the context of Flora Iberica project. She is professor of Botany at Universidad Tecnica Particular de Loja (UTPL, Ecuador).

Cover photo

Baccharis alpina Kunth from National Park of Cajas (Azuay, Ecuador), growing in highly conserved paramos in humid environments.



**FLORAS IN THE XXI CENTURY: INVENTORYING
DIVERSITY IN A TIME OF NEXT GENERATION
SEQUENCING AND HABITAT DESTRUCTION,
THE EXAMPLE OF URUGUAYAN COMPOSITAE**

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Eugenia Pedrero, Cristina Trujillo, Federico Gadea, Andrés Rossado

Floras in the XXI century: inventorying diversity in a time of next generation sequencing and habitat destruction, the example of Uruguayan Compositae

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Key words: Asteraceae, Conservation, Flora, Uruguay.

Floristic studies are fundamental cornerstones upon which subsequent layers of enquiry and analysis of plant diversity are based on. As new paradigms arise and new methods to better understand diversity are proposed the scientific community and the funding sources constantly push funds away from alpha taxonomy, paradoxically an area without which the other approaches wouldn't exist. Uruguay remains still devoid of a flora. Partial attempts at different groups with variable degree of information occur but a unified and consistent treatment is still missing. Uruguay occurs in a transition zone where many species meet their distribution limits and are from a conservation perspective of the uttermost importance. The country has ca. 2500 native species and almost 500 adventitious ones. Uruguay's tradition in cattle grazing is witnessing an important shift in land usage that is impacting heavily on the flora. Tree plantations and extensive agriculture are claiming areas that had been somewhat protected by extensive cattle grazing. In addition,

several invasive species are gaining momentum. In this scenario, a flora is desperately needed. The Compositae with ca. 450 species is the most diverse family in Uruguay and except for the grasses it is also, ecologically the most predominant. An ongoing project taking on producing the floristic treatment for the family, involves a thorough analysis of the taxa, preparing descriptions from scratch, precisely defining terminology, and illustrating the taxa with high definition images. The information will be presented online using Scratchpads and Lucid keys. Further, usage of apps like iNaturalist inviting a general audience to observe nature is adding an extra layer to understand distribution filling the gaps of standard collection based methods. Paramount to all these efforts is the need to keep well curated plant collections, a worldwide challenge as administrators seem to fail understanding their importance and the need for their existence.

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Dr. Mauricio Bonifacino is interested in many aspects of Compositae research. He is currently mostly working on floras, specially with the Flora of Uruguay project, but he has also an interest in systematics and taxonomy of several groups mostly in the Astereae. His work and that of his students uses traditional morphological techniques, fieldwork, combined also with molecular methods. Mauricio obtained his Ing. Agr. from the Universidad de la República, in Uruguay, and his PhD in La Plata University, Argentina. He is a professor of Botany and Plant Systematics at Universidad de la República in Montevideo.

Cover photo

Schlechtendalia luzulifolia, a grass looking Barnadesieae, one of the distinctive Compositae species from Uruguay.



**BIG DATA: THE FUTURE OF COLLECTIONS BASED
RESEARCH IN THE COMPOSITAE (ASTERACEAE)**

Vicki A. Funk & Robert (Bort) Edward

Big data: the future of collections based research in the Compositae (Asteraceae)

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Key words: Herbarium.

Herbarium collections have always been critical in the development of our understanding of evolution. Morphological studies, conservation efforts and next generation sequencing all depend on collections. They provide identifications, distribution data, material for anatomy studies, leaf material for DNA work, vouchers for everything from pollen to chromosome counts and molecular work. We have now entered the age of “BIG Data” (Fig. 1). We know about the power of many genes to elucidate phylogenies, but, what is possible with other types of BIG data? How will it affect our attempts to understand evolution within the family? One project covers all North American Compositae (~2500 species): funded by the Powell Center (USGS) and iDigBio (NSF). The environment [including climate, topography and substrate properties such as geochemistry, texture, water retention] plays a large role in driving the diversity and distribution of species and communities. Interactions include adaptive radiations, key innovations, parallel evolution to adaptive peaks, and more.

Signatures of such processes should be visible in species' morphologies when correlated with environmental data in a phylogenetic context. To date, research identifying larger patterns has not been possible because of a lack of data. The USGS/NSF project involves the aggregation of hundreds of thousands of collecting localities cleaned and set up as a framework upon which to integrate spatial environmental and geophysical data and phylogenetics and huge morphological matrices to investigate the diversification and distribution of species in response to the environment. This project focuses on: What drives speciation and what constitutes extreme environments? How do regional floras compare with one another? What areas lack adequate sampling of biological, environmental, geochemical, and soil data? Are there regionally significant environmental variables that correlate with species diversity? Can we model diversity changes across gradients? And when placed in phylogenetic context can we explore evolutionary patterns in environmental tolerances.

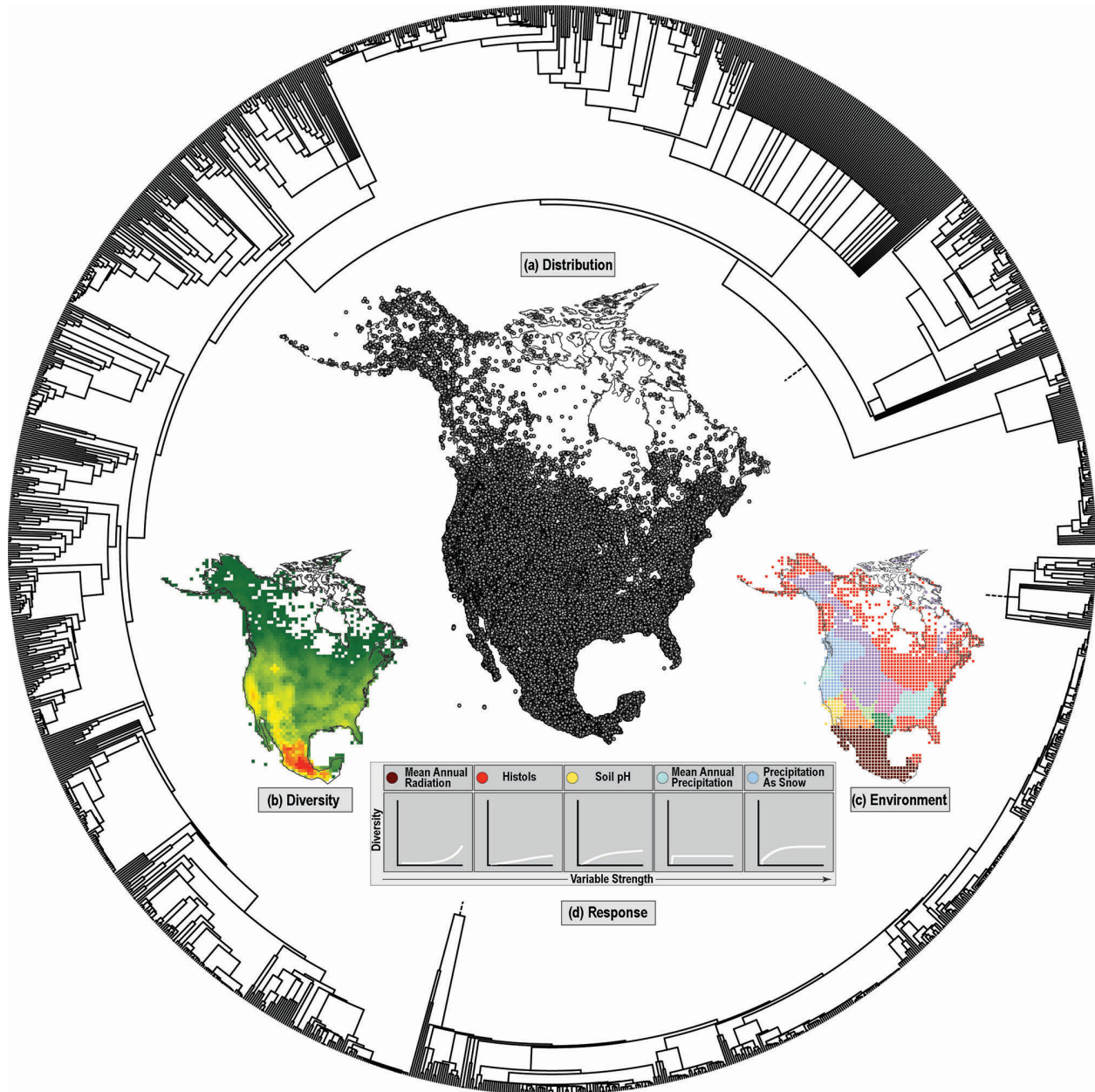


Figure 1. Using Big Data to answer large-scale questions about the role of the environment in driving species diversity: Locality records for North American radiations of Compositae (Asteraceae) (a), are used to calculate diversity metrics (b), and are combined with soil, geochemistry, climate, and topological data (c), to determine regionally significant environmental variables that correlate with this diversity. How diversity changes across gradients in variable strength can also be modeled (d), and placed in a phylogenetic context to explore evolutionary patterns in environmental tolerances.

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Vicki A. Funk currently works in the Department of Botany at the National Museum of Natural History. Major research interests include: Compositae (flowering plant family Asteraceae), systematics, phylogeny, biogeography, biodiversity, character evolution, evolutionary patterns & processes, phylogenomics, and the Compositae of the Andes, Guiana Shield, Madagascar, Pacific Oceania, Rocky Mts, South Africa, South America, Tibet. She obtained her PhD from Ohio State University and completed a postdoc at New York Botanical Garden before starting as a Research Botanist at the Smithsonian Institution in 1981. Currently she is a Senior Research Scientist.

Cover photo

Xenophyllum lycopodioides (S.F. Blake) V.A. Funk, was described from an area that is now in Tacna, Peru [then Chile]. It grows at about 5000m in elevation and has been collected by VF in southern Peru, northern Chile and nearby Bolivia. It grows in bare areas with sandy or other loose types of soil. A distinct and easily recognizable species it is characterized by fleshy triangular leaves and dark purple involucre bracts.

