Evolutionary relationships and taxonomy of Microtea (Microteaceae), a basal lineage in the core Caryophyllales

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Caryophyllales 2018

Instituto de Biología, UNAM
September 17-23

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WEDNESDAY

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General program

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MONDAY 17

MONDAY SEPTEMBER 17TH

9:00-11:25	**Registration and Poster hanging**
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13:00-14:25	**LUNCH BREAK**
14:30-15:25	*Key note talk:* **Héctor Hernández** A general appraisal of the diversity and distribution of the Cactaceae in Mexico
15:30-15:55	**Sabine von Mering** Caryophyllales.org – Assembling the database for the online dynamic monograph of all Caryophyllales species
16:00-16:30	**Anush Nersesyan** The Caryophyllaceae family in Armenia: taxonomy and conservation
16:30-16:55	**Nadja Korotkova** Cactaceae on Caryophyllales.org – an online taxonomic backbone for the family
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17:30-17:55	**Hossein Akhani**, Thomas Borsch, Maryam Malekmohammadi, Zeinab Matinzadeh, Alexander Rudov Living on the edge: Diversification of Caryophylles in SW Asia in extreme environments

KEY NOTE TALK

Prof. Dr. Héctor M. Hernández

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A general appraisal of the diversity and distribution of the Cactaceae in Mexico

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The study and interpretation of the diversity and geographical patterns of the Cactaceae bring us to a better understanding of this emblematic plant family in several fields of knowledge, such as evolutionary biology, biogeography, ecology, conservation biology, and natural resource management. This knowledge, however, remains for the most part incomplete and imprecise. Specifically, global maps built with updated, geo-referenced primary sources are still lacking for most of the species in the family. With about 50 genera and 560 species, Mexico harbors the richest assemblage of cacti in the world. The greatest concentration of members of the family occurs in the arid and semi-arid regions of the country, most notably the Chihuahuan Desert, the Sonoran Desert and the Tehuacan Valley. Additional areas with moderate levels of species diversity, especially columnar species belonging to the tribe Pachycereeae, occur in highly seasonal tropical deciduous forest areas, along the Pacific slope from northern Sinaloa to the Isthmus of Tehuantepec in Oaxaca, as well as in the dry coastal strip of Yucatán. In addition, terrestrial and epiphytic genera and species in the tribes Pachycereeae and Hylocereeae are fairly common in the more humid tropical ecosystems of south and south-eastern Mexico, and in Central America. Our studies primarily developed in the Chihuahuan Desert, have allowed us to visualize the general patterns of cactus diversity and endemism in this region. With 39 genera (43% endemic) and 329 species (70% endemic), the Chihuahuan Desert stands out as having the highest diversity of Cactaceae, both at the national and global levels. During the last two decades we have conducted several research projects aimed at improving the biogeographic knowledge of Mexican Cactaceae, with a strong emphasis on generating useful data for their conservation. Our long-term project *"Mapping the cacti of Mexico"* represents an effort aimed at understanding in detail the spatial patterns of diversity and endemism of Cactaceae in North America.

Caryophyllales.org – Assembling the database for the online dynamic monograph of all Caryophyllales species

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The generic checklist for the order Caryophyllales published in 2015 both in print and online (Hernández-Ledesma et al. 2015, Caryophyllales.org) provided a critically revised assemblage of 749 accepted genera for the order. This synopsis represented a first step towards the aim of creating a global synthesis of the species diversity in the angiosperm order Caryophyllales, integrating the work of numerous specialists from all around the world. In 2016/17, work on the second step – the species-level taxonomic backbone – began in a collaborative effort by experts from the Caryophyllales Network. Work on the species level treatments was started with a number of selected families such as Aizoaceae, Amaranthaceae, Cactaceae, Caryophyllaceae, Nepenthaceae, and Plumbaginaceae but also several of the small families of the order. These studies are fundamental as case studies to inform the establishment of a general workflow for such online monographs and to act as showcases for the numerous relevant results that can be obtained. While larger genera receive a lot of scientific attention, smaller taxa tend to be neglected and have few or no active experts at all (so-called 'orphan taxa'). On the other hand, active experts in most cases focus just on geographically restricted parts of larger genera. This result in quite different challenges for the task ahead: in larger genera all available data have to be integrated (and a consensus classification must be found). In small(er) groups, researchers have to start with assembling the little information available and motivating participation. Therefore, it will be important that further experts join our initiative as authors and editors. The talk will provide a summary about the changes made in the database and shown on-line in the portal Caryophyllales.org (generic checklist) compared to the 2015 print publication, give an overview on the ongoing work to achieve coverage at the species level, and highlight the next steps to be taken. It illustrates the challenges in terms of species numbers and names to be treated but it also shows that quick progress can be made in establishing a global online synthesis of Caryophyllales.

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The Caryophyllaceae family in Armenia: taxonomy and conservation

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The family Caryophyllaceae Juss. is represented in Armenia (S Caucasus) by 33 genera and 169 species from all the 3 subfamilies: Caryophylloideae Arn., Minuartioideae Beilschm., Illecebroideae Arn. Here grow 21 Caucasian endemics, 7 of which are endemics of Armenia: *Allochrusa takhtajanii* Gabrielian & Dittr., *Bufonia takhtajanii* Nersesian, *Dianthus grossheimii* Schischk., *D. takhtajanii* Nersesian, *D. zangezuricus* Nersesian, *Gypsophila takhtadzhanii* Schischk. ex Ikonn *Silene chustupica* Nersesian. Many taxa are affected by the anthropogenic pressure. 20 species of the Caryophyllaceae are included in the Red Data Book of Armenia (2010). During the last years, a series of new species were described and some new records for Armenia were published. A significant part of the species is still to be assessed for a new edition of the Red Data Book of Armenia. The main threats are restricted area of distribution, and habitat loss because of mining, illegal forest logging, expansion of arable lands, road construction, overgrazing and recreation activities. Taxonomic research, including phylogenetic studies and development of conservation measures for the genus *Dianthus* L. in the S Caucasus and particularly in Armenia, has been supported by the ongoing project "Developing Tools for Conserving the Plant Diversity of the South Caucasus" (funded by VolkswagenStiftung) for the last 7 years. The project enables to reveal new data on many Caucasian species of the genus. The data on *D. anatolicus* Boiss., *D. martuniensis* M. Kuzmina and *D. gabrielianae* Nersesian are valuable for assessment of the threats faced by the taxa in this region. The first phylogenetic results revealed that a polymorphic *Dianthus orientalis* Adam alliance is non-monophyletic. There are also indicators of hybridization processes in many investigated species (N. Korotkova, T. Borsch, A. Nersesyan, unpublished data). Phylogenetic studies are to be continued. An online taxonomic backbone for *Dianthus* is being elaborated for publishing through the Caryophyllales.org portal. Data input on the Caucasian *Dianthus* species into EDIT platform has started this year.

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Cactaceae on Caryophyllales.org – an online taxonomic backbone for the family

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I present the species-level taxonomic backbone for the Cactaceae in the Caryophyllales.org portal. In total, 1.570 species and 385 infraspecific taxa are accepted in 141 genera. Some 6.000 names are treated, including all basionyms of the accepted taxa, many homotypic synonyms, and also many heterotypic synonyms. I also present an overview of the phylogenetic knowledge in Cactaceae. Enormous progress has been made in the last decade and almost all Cactaceae genera have been included in phylogenetic analyses. Some have been studied in great detail, and resulting phylogeny-based synopses or monographic treatments have been published based on these studies. Examples include *Aylostera*, *Disocactus*, *Cephalocereus*, *Harrisia*, the Hylocereeae and *Pfeiffera*. This highly desirable approach to Cactaceae systematics is increasingly used, but such studies still remain an exception rather than the rule. For most other Cactaceae genera, there are phylogenetic studies delimiting their circumscription with varying support but no resulting taxonomic treatments at the species level. For many other genera, the phylogenetic results have remained inconclusive for various reasons, the most commonly one being insufficient taxon sampling and low node support. In such cases, the CITES Cactaceae checklist (Hunt 2016) was taken as the basis for the taxonomic backbone presented here, because this is the most up-to-date complete compilation of Cactaceae names in current use and because it also largely follows the new phylogeny-based generic concepts. The next goal will be to include all remaining c. 11.400 Cactaceae names from the World Flora Online taxonomic backbone (based on The Plant List v. 1.1). Furthermore, it will be essential to invite further experts on genera, tribes and subfamilies as contributors and editors. Thus the Cactaceae portal will be directly based on the works of scientists studying the family, making their results and contributions widely visible. In the long run, it has the potential to become the main source for phylogenetic and nomenclatural information for the family.

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Assembling an online synthesis of the Nepenthaceae

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The Caryophyllales Network strives to assemble an online dynamic synthesis of the order Caryophyllales, uniting the current knowledge about the phylogeny of the order with up-to-date information on the individual taxa contained. Concurrently, we try to resolve all scientific names that have been used in the order. Capturing taxonomic and nomenclatural data and the decision processes involved in the definition and circumscription of the taxa requires highly complex specialised software. The Caryophyllales Network uses the EDIT Platform for Cybertaxonomy for that purpose. In that context, and also in order to demonstrate possible workflows between the Network and the World Flora Online (WFO) initiative, we were looking for a model group to try out the necessary procedures, if possible already going beyond mere taxonomic backbone (checklist) data. We sought a relatively small family with clear monophyly also on the generic level, and with existing high-quality electronic open access data which could be used as a starting point. With most of the taxa in the monotypic Nepenthaceae occurring in the Malesiana area and thus already present in the EDIT Platform in highly structured form, that family appeared to be an ideal candidate. In the context of the online treatment of that family, we describe the steps taken to assemble the database, starting with the digitisation of the Flora Malesiana treatment by Cheek and Jebb (2001), the use of and interaction with other electronic sources, the assembly of additional information, the connection with the World Flora Online initiative, the preparation of a data paper, and the prospects for the maintenance and further development of the Caryophyllales database.

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Living on the edge: Diversification of Caryophylles in SW Asia in extreme environments

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SW Asia is located in the arid zone of the Old World where six major phytogeographical regions including the Irano-Turanian, Euro-Siberian, Mediterranean, Saharo-Sindian and Somalia-Masaein regions meet. The flora of this area is therefore influenced by both the Holarctic and the Paleotropic kingdoms. This area is of special interest not only because of the origin of ancient civilizations and origin of three main world religions, but also for the threats to its rich-biodiversity due to global warming, unsustainable development, desertification, water shortage, habitat degradation and existing political conflicts. SW and Central Asia are centres of diversity and origin of several lineages of the Caryophyllales. Within angiosperms, this order is the "hot spot" of highly specialized plant groups which inhabit saline, gypsum, sandy and desert soils. The families Caryophyllaceae, Chenopodiaceae, Plumbaginaceae, Polygonaceae and Tamaricaceae are highly diversified in this area from extreme desert conditions to highest peaks. The success of members of Caryophyllales in harsh environments is related to evolving highly specialized morpho-physiological traits including C4 photosynthesis, specialized of assimilating shoots (succulence, scaly leaves, aphylly, thornyness), structures to exudate, prevent the uptake, or demobilize toxic elements. Adaptations to high salinity employ a variety of mechanisms. In this presentation an overview of the existing extreme environmental conditions in SW Asia will be shown with their characteristic natural vegetation. Based on this, we highlight some recent advances in our understanding of the diversity and evolution of the Caryophyllales in SW Asia including C4 photosynthesis (in particular of single-cell functioning C4), gypsum, salt tolerant and sandy dune floras. Finally, we present results on phylogenetic relationships and hybridization in the genus *Tamarix* as a most successful C3 Caryophyllales genus that evolved in harsh environments of SW Asia. It is astonishing that as C3 plants, *Tamarix* species are the only plants that constitute forest on the edge of the hottest desert of the planet.

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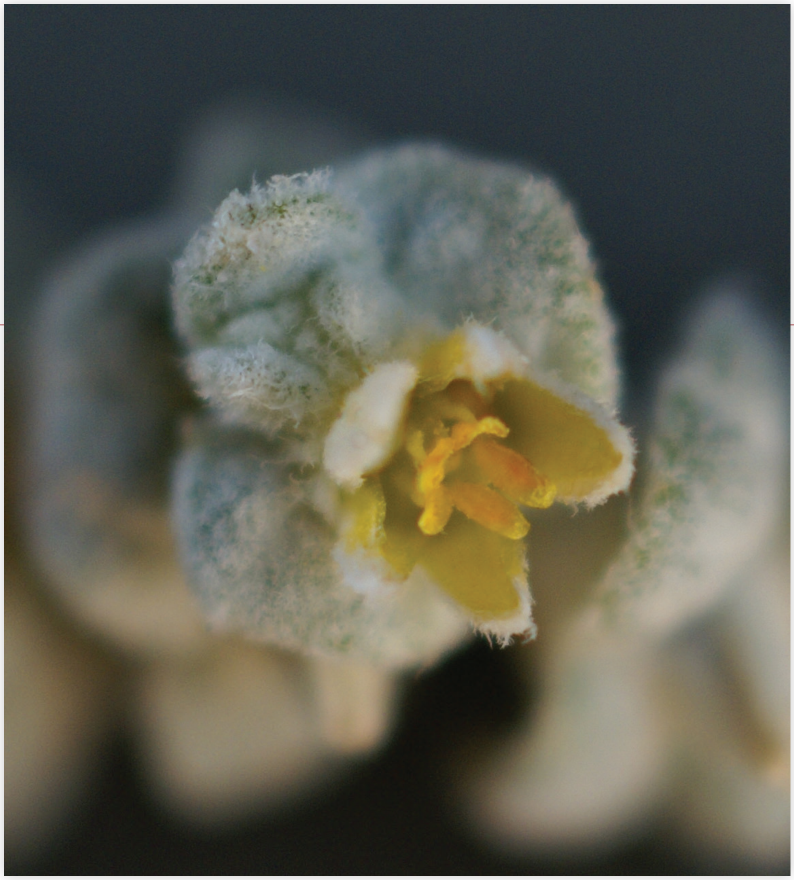


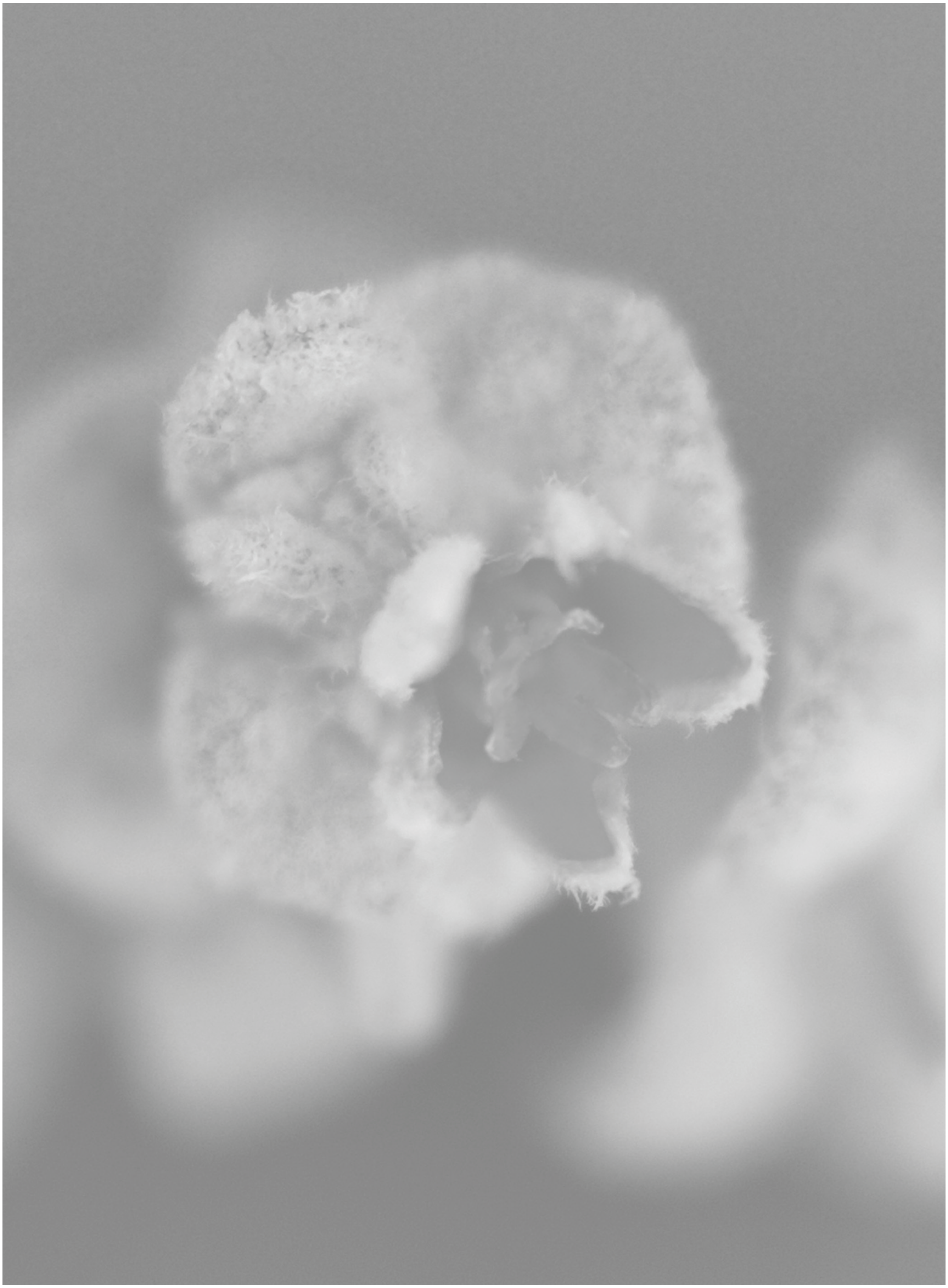
TUESDAY 18

TUESDAY SEPTEMBER 18TH

9:00-10:00	*Key note talk:* **Thomas Borsch** Towards a comprehensive picture on the evolution, species diversity and classification of the Amaranthaceae *s.str.*
10:00-10:25	**COFFEE BREAK & POSTER PRESENTATIONS**
10:30-10:55	**Alexander P. Sukhorukov,** Maya V. Nilova, Anastasiya A. Krinitsina, Maxim A. Zaika, Kelly A. Shepherd Molecular phylogenetic data and seed coat morphology resolve the generic position of some critical Chenopodioideae (Chenopodiaceae–Amaranthaceae) with reduced perianth segments
11:00-10:25	**Héctor Tapia,** Daniel Sánchez, Salvador Arias Utility of morphological data on phylogenetic combined analyses: two examples in the Cactaceae
11:30-11:55	**Isaura Rosas-Reinhold, Salvador Arias** Resolving the phylogenetic relationships and species circumscription in the genus *Aporocactus* (Cactaceae)
12:00-12:25	**Gilberto Ocampo** Phylogenetics, systematics, and an exploratory view of the phylogeographic patterns of Portulacaceae
12:30-12:55	**Diego F. Morales-Briones,** Ya Yang Exploring reticulation patterns in Amaranthaceae *s.l.*
13:00-14:25	**LUNCH BREAK**
14:30-14:55	**Israel L. Cunha Neto**, Marcelo R. Pace, Cyl Farney C. de Sá, Norman A. Douglas, Michael J. Moore, Michael H. Nee, Veronica Angyalossy A developmental and evolutionary perspective on the vascular system of Nyctaginaceae
15:00-15:25	**Ulises Rosas,** Itzel Santiago-Sandoval, Jesús González-Sánchez, Fernanda Chávez, Salvador Arias, Jerónimo Reyes-Santiago Natural variation and diversity of root architecture in *Mammillaria* species

TUESDAY SEPTEMBER 18TH

15:30-15:55	**Silvia Zumaya-Mendoza,** Silvia Aguilar-Rodríguez, Teresa Terrazas Wood anatomy of *Iresine* P. Browne (Amaranthaceae *s.l.*)
13:00-14:25	**COFFEE BREAK & POSTER PRESENTATIONS**
16:30-16:55	**Teresa Terrazas,** Agustín Maceda Wide-band tracheids in Cactaceae and their homology with other Caryophyllales
17:00-17:25	**Ivonne Sánchez-del Pino,** Erick Aguilera-Cauich Soil gypsum concentration affinity in populations of *Tidestromia* Standl. (Gomphrenoideae, Amaranthaceae) present in the Cuatrociénegas Basin, Coahuila, Mexico.
17:30-17:55	**Julieta Álvarez-Manjarrez,** Roberto Garibay-Orijel, Abraham Solís-Rodríguez The novel and unknown interactions of Caryophyllales: roots and mycorrhizal fungi



KEY NOTE TALK

Prof. Dr. Thomas Borsch

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Towards a comprehensive picture on the evolution, species diversity and classification of the Amaranthaceae *s.str.*

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The Amaranthaceae *s.str*. constitute a well-supported monophyletic family with some 850 species in about 80 genera. Most of the diversity is found in tropical and subtropical regions of the Americas, Africa and Australia, with a remarkable diversity of life forms including trees, woody lianas, scrubs, perennial and annual herbs occurring in wet tropical forests to arid desert vegetation. Since the first hypotheses on Amaranthaceae relationships (Müller & Borsch 2005, Ann. Missouri Bot. Gard. 92, 66-102) significant progress has been made by adding further sequence data and by increasing the taxon sampling to include well beyond half of the species in phylogenetic trees. The mostly New World Gomphrenoideae are the largest radiation (ca. 400 species), that started to diversify about 25 mya, whereas the largely African Achyranthoid clade is the second major radiation (c. 150 species), with the crown group starting to diversify about 22 mya (Di Vincenzo & al. 2018, Ann. Bot. 122, 69-85). Among Caryophyllales, the Amaranthaceae stand out by a number of characteristic morphological features, for which molecular data sets and trees permit an understanding of character evolution but also to test their possible effects as traits on species diversification. Among these are complex cymous inflorescence structures, parts of which (sterile flowers and bracteoles with hooks) evolved multiple times into adhesive appendages serving epizoochory within the Achyranthoid clade. The use of state dependent speciation and extinction models revealed a strong asymmetry in gaining these modified flowers, but no effect on species diversification rates. Pollen morphology is highly diverse in the family, and characterizes entities from species to major clades as can be shown on the example of the *Iresine* clade (Borsch & al., Taxon, in press) whereas other pollen characters evolved multiple times such as stellate pores in the Achyranthoid clade. The research on Amaranthacae provides a good example on how evolutionary approaches can be integrated to support the continuous discovery and description of species diversity in one of the major families of flowering plants. It is noteworthy how many new discoveries continue to be made by collecting in the field and exploring herbaria, and considering that the analysis of species limits in an evolutionary framework is just beginning.

Molecular phylogenetic data and seed coat morphology resolve the generic position of some critical Chenopodioideae (Chenopodiaceae–Amaranthaceae) with reduced perianth segments

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The former *Chenopodium* subgen. *blitum* and the genus *Monolepis* (Chenopodioideae) are characterized in part by a reduced (0–4) number of perianth segments. According to recent molecular phylogenetic studies these groups belong to the reinstated genera *Blitum* incl. *Monolepis* (tribe Anserineae) and *Oxybasis* (tribe Chenopodieae). However, key species such as *Chenopodium antarcticum*, *C. exsuccum*, *C. litwinowii*, *C. foliosum* subsp. *montanum*, and *Monolepis spathulata* were not included, and so their phylogenetic position within Chenopodioideae remained equivocal. These species were incorporated into an expanded phylogenetic study based on nrDNA (ITS region) and cpDNA (trnL-trnF and atpB-rbcL intergenic spacers and rbcL gene). Analyses confirm the placement of *Chenopodium antarcticum*, currently known as *Oxybasis antarctica*, *C. exsuccum*, *C. litwinowii* and *C. foliosum* subsp. *montanum* within *Blitum*. Two of the three accepted species of *Monolepis*, the type species *M. trifida* (= *M. nuttalliana*) and *M. asiatica*, were included in *Blitum* congruent with previous studies. The North American *M. spathulata* nested within (ITS and atpB-rbcL analyses) or sister (trnL-trnF intergenic spacer) to the tribe Dysphanieae. To date, few reliable morphological characters have been proposed that consistently distinguish *Blitum* (incl. two *Monolepis* species) from *Oxybasis*; however, two key differences are evident: (1) the presence of the long-petiolate rosulate leaves in *Blitum* vs their absence in *Oxybasis*, and (2) a seed coat structure with the outer wall of the testa cells lacking stalactites ('non-stalactite seed coat'), and an obvious protoplast in *Blitum* vs seed coat with the outer walls of the testa cells having stalactites ('stalactite seed coat') and reduced protoplast in *Oxybasis*. *Monolepis spathulata* also has stalactites in the outer cell walls of the testa and lack of rosulate leaves. These unique features in combination with the phylogenetic results, confirm that this species is unlike all other *Blitum*, and therefore the recent combination *Blitum spathulatum* is erroneous. Indeed, the morphological and molecular distinctiveness of *Monolepis spathulata* from all *Dysphanieae* suggest that it should be recognized as a new monotypic genus.

The study of AS, MV and AK was supported by the grant of Russian Foundation for Fundamental Research (project 18-04-00029).

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Utility of morphological data on phylogenetic combined analyses: two examples in the Cactaceae

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The development of novel phylogenetic techniques has allowed to analyze combined datasets improving consistently the topology, resolution and branch supports, but some issues require to be outlined yet. Two aspects must be recognized: 1) the employment of appropriate assumptions (parameters and models) and, 2) the accurate definition and scoring of characters and character states. The settings can be optimized before the running of a phylogenetic analysis, while the morphological data matrices admit a series of artifacts that cannot be identified prior to the analysis completion and eventually prevail obscure afterwards. Moreover, the effect of a singular character or a combination of characters has barely been tested for its contribution on tree topology, resolution, or branch supports. Several morphological characters that have been tested previously reveal a large amount of homoplasy, by means of parallel or convergent evolution, but also proceed from a vague understanding of how evolutionary processes affect related structures on related and unrelated taxa. In the Cactaceae there are more than a few examples of homoplastic characters, some of which even appear as the result of unsuspected events as hybridization and introgression. In the phylogenetic context, the value of morphological characters could be underestimated, but also has been treated vaguely as a source of information about evolution. We use data from two recent phylogenetic studies on the tribe Echinocereeae to account for the homoplasy contained in the different data types (molecular and morphological), either combined or individually. The genera examined here were *Echinocereus* and *Cephalocereus*, including representative species of related genera. The different phylogenetic methods employed yield partial explanations about the evolutionary process, but also reported different effects of the inclusion of different data types. We observe a high amount of homoplasy in the morphological matrix, compared with the molecular one, and confirm several characters as non-reliant for phylogenetic purposes. Some vegetative characters were found the most homoplasious ones, but they are not privative. Even the same character could be accounted as informative or homoplastic considering a different set of taxa or topology. Prior and posterior interpretation of characters are a concern to reach the understanding of evolutionary processes.

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Resolving the phylogenetic relationships and species circumscription in the genus *Aporocactus* (Cactaceae)

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Epiphytic cacti is a highly diverse group, mainly represented by more than five linages. One of them is the tribe Hylocereeae, which is distributed in Mexico and Central America. Recent molecular investigations have revealed that the Hylocereeae and other cacti with epiphytic habit evolved independently. The use of molecular markers has revealed that some morphological characters used to recognize species and genus are homoplastic, such as growth form, habit, and flower color. *Aporocactus* Lem. is one of these genera that had only been studied at the morphological level, and for this reason it was included in *Disocactus* Lindl. This is mainly because of the cylindrical stem, diurnal and colorful flowers, as well as ornithophilia as pollination syndrome. Recent studies with molecular markers have shown that this genus is not related to *Disocactus*, but we still don't know what the sister clades are. Another problem using morphological characters in this genus is the species delimitation. This is because the morphological variation in size and color of flowers has led some authors to recognize up to five species, while others recognize only two. Thus, we performed a phylogenetic analysis using 22 *Aporocactus* terminals, that correspond to five published names, in their natural distribution area, and employing four cpDNA molecular markers (trnL-trnF, psbA-trnH, rpl16 and trnQ-rps16). The analyses were made using Maximun Parsimony and Bayesian Inference methods. Two strongly supported phylogenies were obtained, allowing us to resolve that *Aporocactus* is a monophyletic group, independent from *Disocactus*, and conformed only by two species: *A. flagelliformis* with magenta flowers, distributed in Guanajuato, Hidalgo, Queretaro and Veracruz and *A. martianus* with red flowers localized in Oaxaca and Veracruz. Also, we resolved the *Aporocactus* position inside the Hylocereeae tribe, as sister genus of *Selenicereus* (including *Hylocereus*) and *Weberocereus*, showing that the flower color, the period of anthesis and pollination syndrome are homoplastic characters in this tribe, making it a complex group.

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Phylogenetics, systematics, and an exploratory view of the phylogeographic patterns of Portulacaceae

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Portulacaceae is a monogeneric family closely related to Anacampserotaceae, Cactaceae, and Talinaceae. *Portulaca* has more than 100 species distributed worldwide, although Africa and South America have an important number of endemic taxa. Here I discuss the diversification patterns of Portulacaceae and explore the phylogeographic patterns of *P. mexicana*, an endemic species from central Mexico. The evolutionary relationships within *Portulaca* were obtained using chloroplast and nuclear markers and served as the base for studying character diversification, as well as divergence times and historical biogeographical patterns. The phylogenetic analyses recovered *Portulaca* as monophyletic and showed the presence of two main groups: one with species found in Africa, Asia, and Australia, and another one with taxa from around the world. Some characters were estimated to be homoplastic; however, a few features were useful to characterize groups within the family. The age of Portulacaceae was estimated in 23 million years and the Southern Hemisphere was found to be the potential area of ancient distribution. These results will be considered to propose a new infrageneric classification, which will include two subgenera and six sections. On the other hand, a preliminary phylogeographic analysis using one chloroplast marker showed that there is a moderate level of genetic structure and gene flow among individuals of 12 *P. mexicana* populations; however, the phylogenetic analysis does not support the populations as monophyletic. Using a coalescence tree, the Mexican Plateau is recovered as the ancestral distribution area of the species, with multiple dispersal events to the Trans Mexican Volcanic Belt (TMVB), the southernmost limit of its distribution range. *Portulaca mexicana* may have originated 3.8 my ago, which may suggest that the TMVB represented an effective barrier against the specie´s dispersal to lower latitudes. These preliminary results may help to promote further studies to understand evolutionary patterns within *Portulaca* species.

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Exploring reticulation patterns in Amaranthaceae *s.l.*

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Amaranthaceae *s.l.* (including Chenopodiaceae) constitute the most diverse lineage (ca. 180 genera and 2500 species) of the Caryophyllales. Amaranthaceae *s.s.* and Chenopodiaceae have been united as Amaranthaceae *s.l.* based on the assumption that Chenopodiaceae is paraphyletic in relation to Amaranthaceae *s.s.* This paraphyly is product of the controversial position of the subfamilies Betaoideae and Polycnemoideae within the alliance. Earlier phylogenetic analyses based on ITS and limited chloroplast regions, in addition to morphological data, provide support for an affiliation of Betoideae with Chenopodiaceae. Like in Chenopodiaceae, Betoideae has sepaloid tepals in contrast to petaloid tepals in Amaranthaceae *s.s.* and Polycnemoiideae. The filaments of Chenopodiaceae and Betoideae are inserted on a hypogynous disc, a rim, or tepal bases but are not united into a filament tube like in Polycnemoideae and Amaranthaceae *s.s.* On the other hand, Polycnemoideae has been associated to Amaranthaceae *s.s.* Polycnemoideae shows petaloid tepals, filament tubes, 2-locular anthers like in Amaranthaceae *s.s.*, while in terms of habitat preferences it is more like many members of Chenopodiaceae, reason why Polycnemoideae has been considered as morphological intermediate between Chenopodiaceae and Amaranthaceae *s.s.* Furthermore, recent phylogenomic studies support the monophyly of the traditional Chenopodiaceae, including its sister relationship to Polycnemoideae and also the monophyly of the traditional Amaranthaceae *s.s.*, including its sister relationship to Betaoideae. Nevertheless, significant discordance has been detected regarding the position of Polycnemoideae and Betaoideae. Here we re-examine previously transcriptome and genome data as well as the plastome to explore the sources of conflict within Amaranthaceae *s.l.* We used a plurality of phylogenetic methods and found extensive conflict between and within gene trees and species trees regarding the positions of Polycnemoideae and Betaoideae. All phylogenetic analyses recovered the four clades as in recent studies, but species tree methods inferred different topologies for the relationships between these clades. Species network analyses revealed that Polycnemoideae and Betaoideae are likely the product of two independent hybridization events between ancestral lineages of Chenopodiaceae and Amaranthaceae *s.s.* Additionally, we established that these hybridization events represent the main sources of incongruence among the species trees.

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A developmental and evolutionary perspective on the vascular system of Nyctaginaceae

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Nyctaginaceae has a broad occurrence in the Americas, containing taxa with an outstanding diversity of habits, including shrubs, trees, herbs, lianas, and subshrubs. Nyctaginaceae are also unique since all their members have vascular cambial variants. In Nyctaginaceae, these variants are present not only in lianas, but also in herbs, shrubs and trees. However, the interpretation of the cambial variants occurring in Nyctaginaceae is controversial, since they are sometimes interpreted as successive cambia and sometimes as interxylary phloem. Moreover, while their ontogeny is still poorly understood, practically nothing is known on their diversity and phylogenetic distribution. Therefore, this research aims at integrating data on the ontogeny of the vascular system of Nyctaginaceae stems within a phylogenetic context, in order to understand its development, diversity, distribution, and evolution. For this purpose, we are broadly sampling taxa within the family, especially from plants growing in their natural populations. Standard methods in plant anatomy are being carried out to delimit anatomical characters and to precisely establish the origin and type of the cambial variants, which will then be mapped onto a well-supported phylogeny for the family. By doing this, it becomes possible to evaluate their pattern of evolution, and to assess whether the habit and habitat transitions that have occurred in this plant family are associated with the acquisition of new anatomical architectures. In Nyctaginaceae, we identified two types of steles, the eustele and the polycyclic eustele, which is characterized by the presence of medullary bundles. The polycyclic eustele is the ancestral character state for Nyctaginaceae, being distributed throughout the family except for the genera *Reichenbachia* and *Ramisia*. Successive cambia are ancestrally distributed in Nyctaginaceae, however, they were lost independently at least twice in lineages where interxylary phloem has evolved instead. Since cambial variants are pervasive in Nyctaginaceae, their evolution in the family cannot be linked to different habits. In fact, the ancestral habit for the family was inferred as being a shrub/scandent-shrub, already with the cambial variant and medullary bundles. Information on the development of the vascular system of Nyctaginaceae stems will be continuously gathered within this project in order to unravel its diversity and evolution.

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Natural variation and diversity of root architecture in *Mammillaria* species

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Plant roots display a wide variety of growth strategies allowing them to respond to the local microenvironments, and adapt to conditions of the macroenvironment, including the soil. Some of the mechanisms and environmental cues that control root development are known, but we still lack understanding on those that promote diversity in root architecture, and the variety of responses to the microenvironment. Here, we are investigating these phenomena in cacti species of the *Mammillaria* genus. By examining the root growth in a wide range of *Mammillaria* species and populations, we have characterized the natural variation and diversity of developmental dynamics in root architecture. We have observed that some *Mammillaria* species have a dominant root axis with low branching, resembling a primary root. Later in development, the dominance of the root main axis is lost and lateral roots proliferate. In other species, the main root is not recognizable because proliferation of lateral and adventitious roots starts early in development. Interestingly, we have observed similar patterns within populations of the *M. haageana*, indicating that natural variation in root dynamics and architecture among populations, is recapitulated between species with longer divergence times. Previous studies have shown that primary roots in Cactoideae species have determinate meristems, which fully differentiate days after germination. We observed that this is the case in *Mammillaria*, opening the question on the nature of the dominant root axis in species and populations of this clade. Closer inspection of dominant roots and lateral roots, indicates that both are composed of many segments of sympodial roots, which leave an easily recognizable scar with root hairs. This opens the question on what are the developmental programs that determine whether a dominant root branches since early in development, or behaves as a primary root, regardless of being composed of segments of sympodial roots, but inhibiting the emergence of lateral roots. Hence, we will propose hypotheses on the developmental control of sympodial root emergence, and the mechanisms that generate diversity and natural variation in root architecture in *Mammillaria*.

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Wood anatomy of *Iresine* P. Browne (Amaranthaceae *s.l.*)

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Iresine is an American genus of Amaranthaceae *s.l*. To understand its wood anatomy and correlation with habit and habitat a comparative study was carried out based on 25 species of *Iresine*. We present the most extensive wood anatomical survey of *Iresine* to date; species sampling represent the full diversity in growth habit and habitat. Our observations confirm wood descriptions for other Amaranthaceae having diffuse porosity, simple perforation plates, alternate intervessel pits, and nucleated fibers in all species of *Iresine*. Successive cambia is present in the species studied with two types recognized, in concentric rings and patches; being the last more common in shrubs. Species typically have heterogeneous multiseriate rays, except for *I. hebanthoides* and *I. rhizomatosa* where rays are absent. Rays could have meristematic centers as recorded in few other Amaranthaceae. Our extended study provides clear evidence that the multiseriate rays with meristematic centers is a common trait suggesting that the hydraulic conduction of water, phosphates and minerals is complex through an axial-radial flow in *Iresine*, particularly in *I. arbuscula* and *I. rzedowskii*. Not all quantitative wood characteristics followed the trends expected with habitat. The shrubs show the highest variation for vessel and fiber diameter. Discriminant analysis allowed separating species based on the combination of quantitative wood features. For example, species of the dry scrub, as *I. rotundifolia*, *I. schaffneri* and *I. stricta*, have narrower vessel diameters (< 35 µm) and thicker walls in vessels and fibers (? 4 µm). Those species growing in the dry scrub were separated from the species of more mesic environments, as *I. ajuscana* and *I. arbuscula*, which show wider vessel diameters (> 45 µm) and thinner walls in vessels (< 2.2 µm) and fibers (1.5 µm). Seven species have distinctive characters not shared with other species as *I. latifolia* with diffuse porosity and two or three pairs pith bundles, *I. rzedowskii* with thick periderm and *I. cassiniiformis* with a lignified pith.

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Wide-band tracheids in Cactaceae and their homology with other Caryophyllales

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In Cactaceae and other Caryophyllales a type of cells name wide-band tracheid, vascular tracheid or helical idioblast has been described. In the case of Cactaceae, they are mainly associated to secondary xylem and several authors have consider that wide-band tracheids favor water storage, avoid embolisms, and are the most common cell type in the wood of globose species. For some Opuntioideae, wide-band tracheids have been described to be present in both pith and secondary xylem. Here we explore the homology of wide-band tracheids following the development of vascular and fundamental tissues in seedlings and compare them with adult plants. Seedlings of ten species representing the three subfamilies (Pereskioideae, Opuntioideae and Cactoideae) of Cactaceae were prepared for light and fluorescence microscopy. All species have in their epicotyl collateral vascular bundles with 2-5 tracheary elements with annular to reticulate secondary cell walls. As fascicular vascular cambium differentiates, vessel elements and wide-band tracheids are the main cell types present in the secondary xylem in seven species of Cactoideae and *Opuntia streptacantha*. No wide-band tracheids were observed in *Pereskia lychnidiflora* and *Cylindropuntia imbricata*. Our observations confirm earlier descriptions that *P. lychnidiflora* does not develop wide-band tracheids. Furthermore, in *C. imbricata*, wide-band tracheids develop late but from pith parenchyma cells, thus they are not homologous to the other ones derived from vascular cambium. Optimization of wide-band tracheids in the most recent phylogeny of Caryophyllales will be discussed at the light of our findings on the ontogeny of vascular tissue.

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Soil gypsum concentration affinity in populations of *Tidestromia* Standl. (Gomphrenoideae, Amaranthaceae) present in the Cuatrociénegas Basin, Coahuila, Mexico

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The Cuatrociénegas Basin (CCB) has been recognized for its high species richness and the greatest quantity of endemic flora. The CCB is unique due to its white gypsum dunes and wetlands which have exclusive ecosystems. Four taxa of *Tidestromia* occur in the CCB: *T. suffruticosa* (Torrey) Standl. var. *suffruticosa*, found in rocky soils containing some gypsum; *T. suffruticosa* (Torr.) Standl. var. *coahuilana* I.M. Johnst., found in somewhat gypseous soils; *T. rhizomatosa* I.M. Johnst., described either as halophytic, gypsophile or gypsophile; and *T. lanuginosa* (Nutt.) Standl., found in diverse soil types. In this study, we aimed 1) to evaluate the concentration of gypsum in the soils where *Tidestromia* taxa grew in the CCB and 2) to determine if there was a correlation in the occurrence of *Tidestromia* species due to edaphic and ecological factors. Ecological information was noted for fifteen populations of *Tidestromia* along the CCB and soil samples were taken from thirty sites. Multivariate non-parametric analyses were performed to determine if there was a correlation between soil elements, ecological factors and the occurrence of *Tidestromia* taxa. Analyses indicated that gypsum was not a determinative parameter in the distribution of gypsophiles and gypsovags species of *Tidestromia* in CCB. No correlation was found between the edaphic conditions in the thirty sites tested and the presence of *Tidestromia*. Based on the fifteen *Tidestromia* populations studied, principal component analysis revealed that pH, $CaSO_4$, and Mg in PC1 (33%); and K and N in PC2 (22%) represented the edaphic variation. BEST analyses indicated a high correlation between plant canopy cover with the presence of gypsum and Nitrogen (Rho: 0.79). Among the four taxa of *Tidestromia* collected in the CCB, *T. rhizomatosa* grew in soils with high gypsum concentrations (29.3-35.2 meq/100g soil) whereas *T. suffruticosa* var. *coahuilana* (0.01 meq/100g soil) was less tolerant of gypsum.

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The novel and unknown interactions of Caryophyllales roots and mycorrhizal fungi

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Underground interactions are still a black box in ecological studies; these interactions can involve fungi, bacteria or other edaphic organisms. Mycorrhizal associations are present in 90% of the terrestrial plants and each year new interactions are discovered. Members of Caryophyllales have been reported as non-mycorrhizal; however there are several studies showing ectomycorrhizas in *Achatocarpus* (Achatocarpaceae), *Asteropeia* (Asteropeiaceae), *Guapira*, *Neea*, *Pisonia* (Nyctaginaceae) and *Coccoloba* (Polygonaceae). These families have mainly tropical distribution with the exception of Asteropeiaceae. All of them form ectomycorrhizas with diverse and endemic fungal species, as *Thelephora versatilis*. Our results in the Neotropical dry forest showed that Caryophyllales hosted unique fungal species and demonstrate that several families within the order produce ectomycorrhizas making necessary a full study of root associations within the order.

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WEDNESDAY 19

WEDNESDAY SEPTEMBER 19TH

9:00-10:00	*Key note talk:* **Mike Moore** A genome-wide perspective on Caryophyllales phylogeny and evolution
10:00-10:25	**COFFEE BREAK & POSTER PRESENTATIONS**
10:30-10:55	**Daniel M. Martínez-Quezada,** Salvador Arias, Teresa Terrazas The significance of stem structural characters in the phylogeny of the Hylocereeae
11:00-10:25	Erick Aguilera-Cauich, Karen Solís-Fernández, Ivonne Sánchez-del Pino, Rolando Cifuentes-Velásquez, Hilda Flores-Olvera, Rubén H. Andueza-Noh, **Ariadna Ibarra-Morales** Assessment of morphological diversity of *Amaranthus hybridus* L. and *A. cruentus* L. in the Mayan region
11:30-11:55	**Idelfonso Castañeda-Noa,** Susy Fuentes, Rosalina Berazaín-Iturralde, Thomas Borsch The Caribbean *Coccoloba*, phylogenetic and morphological patterns.
12:00-12:25	Karen Alejandra Alfaro-Escamilla, Rubén Andueza Noh, **Ivonne Sánchez-del Pino** Phylogeography of *Tidestromia lanuginosa* (Gomphrenoideae, Amaranthaceae) for the determination of taxonomic circumscription and evolution
12:30-12:55	**Alexander P. Sukhorukov,** Maya V. Nilova, Felipe Rosetto, Michael Moore, Norman A. Douglas Taxonomic evaluation of reproductive characters in Nyctaginaceae
13:00-14:25	**LUNCH BREAK**
14:30-14:55	**Patricia Hernández-Ledesma,** Julia Olivieri, Hilda Flores-Olvera, Helga Ochoterena, Norman A. Douglas, Michael Moore Evaluating the infrageneric classification of *Mirabilis* L. (Nyctaginaceae) in a phylogenetic context
15:00-15:25	**Sabine von Mering,** Daniel B. Montesinos-Tubée, Rosa Isela Meneses, Juan Manuel Acosta, Thomas Borsch Systematics and phylogeny of *Arenaria s.str.* (Caryophyllaceae) with special focus on Latin American species

WEDNESDAY SEPTEMBER 19TH

15:30-15:55	**Luisa Senna,** Ana Maria Giulietti An approach using exploratory statistics for the *Alternanthera brasiliana* complex
13:00-14:25	**COFFEE BREAK & POSTER PRESENTATIONS**
16:30-16:55	**Jeannine Marquardt,** Calvinna Caswara, Thomas Borsch Target enrichment of orthologous genes for epiphytic cacti to support the analysis of species level relationships and species limits
17:00-17:25	**Cornelia Klak,** Pavel Hanáček, Peter V. Bruyns Phylogeny, biogeography and age of the Aizooideae (Aizoaceae)
17:30-17:55	**Ya Yang,** Michael J. Moore, Samuel F. Brockington, Stephen A. Smith Functional phylogenomics of the Caryophyllales: transcriptomes, genomes, gene and genome duplication, biochemistry, and beyond.
18:00-18:25	**Closing remarks**

KEY NOTE TALK

Prof. Dr. Michael M. Moore

Professor of Biology
Oberline College
PhD, University Texas, Austin, 2005
Research interests on plant systematics and the origin and evolution of plant diversity

A genome-wide perspective on Caryophyllales phylogeny and evolution

Michael J. Moore (*1), Ya Yang (2), Joseph Walker (3), Tao Feng (4), Alfonso Timoneda (4), Ning Wang (3), Lucas Majure (5,6), Norman Douglas (1,7), Gang Yao (8), Jianjun Jin (8), Hongtao Li (8), Junbo Yang (8), Jessica Mikenas (1,9), Vera Hutchison (1), Caroline Edwards (1), Julia Olivieri (1,10), Venkata Shiva Mandala (1,11), Matthew Croley (1), Rebecca Mostow (1,12), Sonia Ahluwalia (3), Nathanae (l) Walker-Hale (13), Raúl Puente (5), Mark W. Chase (14), Maarten J. M. Christenhusz (15), Gudrun Kadereit (16), Maximilian Lauterbach (16), Urs Eggli (17), Hilda Flores-Olvera (18), Helga Ochoterena (18), Pamela S. Soltis (6), Douglas E. Soltis (6), Tingshuang Yi (8), Dezhu Li (8), Samuel F. Brockington (4), Stephen A. Smith (3)

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The Caryophyllales comprise approximately 6% of angiosperm species diversity (approximately 12,500 spp. in 40 families) and are found on all continents and in all terrestrial ecosystems, from tundra to tropical rainforests, but are particularly diverse and abundant in semiarid, saline, and temperate environments. In conjunction with this ecological variation, the clade exhibits extreme life history diversity, ranging from tropical trees, temperate annual herbs, and long-lived succulent cacti to a diverse array of carnivorous plants, including sundews and epiphytic pitcher plants. This remarkable diversity has fostered a long history of research, making Caryophyllales one of the best-characterized major angiosperm clades with respect to morphology, ecophysiology, and life history. For example, the Caryophyllales exhibit repeated origins of such fundamental morphological and ecophysiological traits as a differentiated perianth, betalain and anthocyanin pigmentation, C4 and CAM photosynthesis, and leaf and stem succulence. Hence, resolving the backbone phylogeny of Caryophyllales and its constituent families with confidence would provide the necessary framework for future comparative evolutionary analyses of these and other key traits. Recent multigene phylogenetic analyses have helped to clarify the backbone relationships among many Caryophyllales lineages, but the core Caryophyllales in particular contain several relatively ancient and apparently rapid radiations that have so far proved difficult to resolve (e.g. early Centrospermae, early Portulacineae, and early phytolaccoids). To resolve these relationships, we employed transcriptome and plastome sequencing to generate large data sets for over 150 key Caryophyllales taxa. Phylogenetic analyses of these data have helped to resolve the backbone relationships of Caryophyllales while simultaneously revealing high levels of gene tree incongruence at certain key nodes. These data further yield important insights into aspects of the diversification and molecular evolution of the clade.

The significance of stem structural characters in the phylogeny of the Hylocereeae

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The Hylocereeae is a monophyletic group in which eight genera are recognized based on molecular data; however, genera relationships remain partially resolved. In this study combined analyses of molecular and structural characters for Hylocereeae were carried out, with the aim of recognizing if there are structural synapomorphies that support the genera and if the relationships between them are resolved. We studied seventy species of the eight genera of Hylocereeae, as well five of the Echinocereeae as outgroup. The samples were prepared for light and scanning electron microscopy. Thirty-five morpho-anatomical characters were incorporated into a matrix with the molecular characters of four chloroplast DNA regions. Phylogenetic analyses were conducted using maximum parsimony and maximum likelihood; bootstrap was used to calculate the support of the branches. The maximum likelihood analysis resulted in a more robust phylogenetic hypothesis, unlike the maximum parsimony analysis that failed to recover the genera with high bootstrap values. Four of the genera have at least one structural synapomorphy (*Acanthocereus*, terrestrial plants with arched branches and large prismatic crystals in the epidermis, *Aporocactus*, cortical bundles with secondary growth and a delay in the wood fiber differentiation; *Epiphyllum*, less than 2 ?m cuticle; *Kimnachia*, druses in the cortical cells). The remaining genera can be recognized by unique combination of characters. The relationship between *Epiphyllum*, *Kimnachia* and *Pseudorhipsalis* is supported by the lignification of cortical cells and the differential secondary growth. The cortical and vascular characters are as important taxonomically as the epidermal traits, a condition that had not been reported for another group within Cactaceae.

Notes ....

Assessment of morphological diversity of *Amaranthus hybridus* L. and *A. cruentus* L. in the Mayan region

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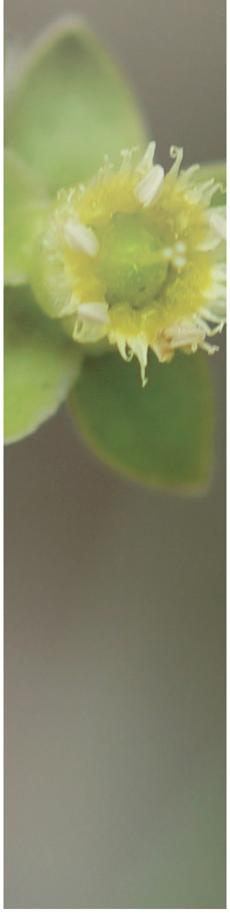
Amaranthus L. (Amaranthaceae) is a cosmopolitan genus that includes economically important species. Wild and cultivated amaranths have been utilized by different civilizations throughout history ornamentally and as important sources of food, medicine and forage. There are three main cultivated grain amaranths in the world (*A. caudatus* L., *A. cruentus* L. and *A. hypochondriacus* L.), and the domestication center of *A. cruentus* has been proposed to be located in southern Mexico or Guatemala. Despite being a proposed region of domestication, *Amaranthus* diversity in the Mayan region has been inadequately studied. Two *Amaranthus* species, *A. cruentus* and *A. hybridus*, which are part of the "*A. hybridus* species complex" and occur in the Mayan region, were studied using multivariate statistical methods. Fifty-seven herbarium specimens, 20 specimens of *A. cruentus* and 37 specimens of *A. hybridus* were evaluated in this study. Twenty-two pistillate floral characters were measured, and a multivariate morphometric analysis was performed using each specimen as an operational taxonomic unit. The principal component analysis revealed variation of 64.5% for *A. cruentus*, 52.1% for *A. hybridus*, and 54.2% for *A. cruentus* and *A. hybridus* data matrix combined. Morphological characters including outer and inner sepals, utricle and bracts exhibited variation within and between species and proved to be important diagnostic characters for species identification and taxa circumscription. Multidimensional nonmetric scaling (MDS) analysis of the morphological characterization of *A. cruentus*, *A. hybridus* and the species combined demonstrated high levels of diversity. Previous morphometric studies of *A. cruentus* and *A. hybridus* from America were compared with our sampling to test morphological traits and we found our material highly morphological different. The high morphological diversity observed in *A. cruentus* and *A. hybridus* could be associated to natural processes of diversification and hybridization. The regional differences between species suggested differing diversification processes, and evidence of a potential second center of domestication for *A. cruentus*.



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The Caribbean *Coccoloba,* phylogenetic and morphological patterns

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Coccoloba has ca. 120 Neotropical species with high levels of endemism reported for the Caribbean. With the goal to understand the origin and diversification of the diversity of this genus in the Caribbean, we are following up a two-tailed approach: First, all the material from the Caribbean islands (from herbaria, own fieldwork) and information from the literature was critically reviewed and has resulted in a checklist of ca. 60 species for this region, so far largely based on comparative morphology. Second, an overall phylogeny is being reconstructed for the whole genus, with a particularly dense representation of the Caribbean members. The sampling currently comprises 108 species and represents the four sections of *Coccoloba*. A matrix of 21 morphological characters was generated, considering also those characters that were used as diagnostic for taxonomy for the sections. Sequences of three plastid (trnLF, matK-trnK and rpl16) and one nuclear marker (ITS) were generated. Phylogenetic reconstruction indicates a Caribbean clade, with signal mostly coming from morphological characters. Also, a subclade is resolved supporting the section *Rhigia* Wright ex Griseb. Whereas genetic distances within *Coccoloba* are generally very low, the rpl16 intron includes a large and at species-level highly variable stem-loop region. One interesting result is that molecular data depict one clade mostly with species from Mesoamerica and South America which also encloses *Coccoloba venosa* with good support, which is a species distributed in the Caribbean but apparently very distantly related with the other taxa in this region.

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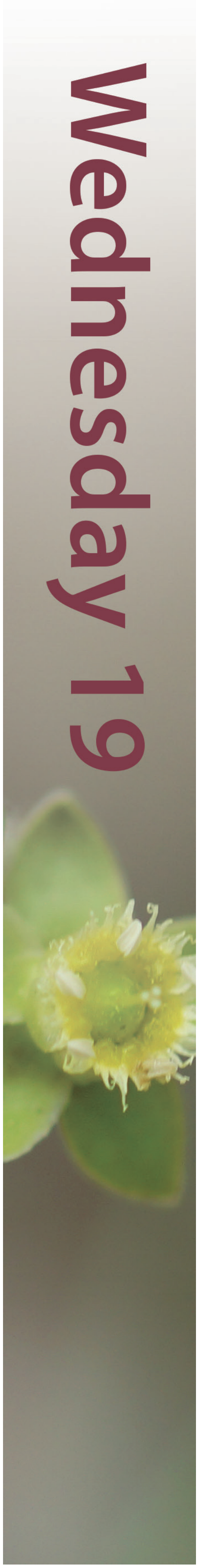

Phylogeography of *Tidestromia lanuginosa* (Gomphrenoideae, Amaranthaceae) for the determination of taxonomic circumscription and evolution

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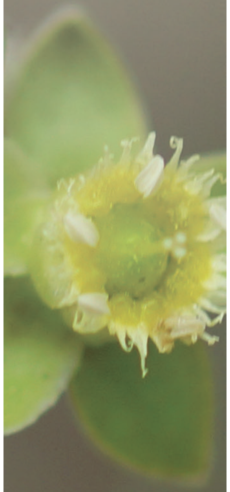
Of the eight species in the genus *Tidestromia*, *T. lanuginosa* (Nutt) Standl. (Gomphrenoideae, Amaranthaceae) is recognized as the most widespread and adaptable to different edaphic conditions. Recent studies have reported high levels of morphological and intraspecific anatomical variation within *T. lanuginosa* demonstrating the need for research focused on genetic and phylogenetic variation at the intraspecific level. Our main goals were 1) to understand the genetic diversity and evolutionary history of *T. lanuginosa*, 2) to circumscribe *T. lanuginosa*, and 3) to document its conservation status and the possible endemicity of specific forms of *T. lanuginosa* in Mexican deserts. Two molecular markers of chloroplast, the intergenic region psbJ-petA and the intron and spacer trnL-trnF were amplified in a sample of 122 individuals, from 26 populations of *T. lanuginosa*, which were collected in the Mexican states of Chihuahua, Coahuila, Nuevo León, San Luis Potosí and Tamaulipas. The data were analyzed based on phylogeographic analyses using MEGA7, DnaSP, BARRIER, SAMOVA and BAPS software. The results suggested the existence of four groups for *Tidestromia lanuginosa* (T1A, T1B, T2 and T3) separated by edaphic, climatic and orographic barriers. This study supports the recognition of two new species and two intraspecific taxa. The resultant groups of *T. lanuginosa* revealed high values of genetic diversity and little genetic flow among groups, supporting speciation events. Based on the findings of this study, we propose the Chihuahuan desert as a conservation center for *T. lanuginosa* as its ancestral haplotype originates from this region and three of the four groups identified in this study distributes in there.



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Taxonomic evaluation of reproductive characters in Nyctaginaceae

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Nyctaginaceae is one of the most diverse families in the core Caryophyllales, comprising approximately 400 species. A persistent accessory fruit, the anthocarp, deriving from a uniseriate perianth and covering the fruit, is of special interest, because it has never been investigated in detail across the family. 150 species from 27 genera were included in this analysis. The representatives of earlier branching lineages of the family (tribes Leucastereae and Boldoeae) have an anthocarp without a distinct distal petaloid limb, or the anthocarp teeth are dark coloured like in Reichenbachia. The anthocarp in Boldoeae and *Reichenbachia* (Leucastereae) remains herbaceous until dissemination, with a simplified anatomical structure consisting of several-layered, thin-walled cells. Although the anthocarps of the rest of Leucastereae (*Andradea*, *Ramisia* and *Leucaster*) are morphologically distinct, their anatomical topography does not have drastic differences from the structure of *Reichenbachia*. Anatomically, the anthocarp is more complicated and diverse in remaining clades of the family, with simultaneous simplification of the fruit and seed covers (pericarp and seed coat, respectively). In Colignonieae, the calyx-like anthocarp is anatomically differentiated into thin-walled parenchyma and sclerenchyma sheath, similar to the remaining tribes of the family. The Colignonieae, Pisonieae, and Bougainvilleeae all possess an anthocarp that at flowering stage is green or yellowish outside and diversely colored and petaloid (white, lilac, or yellow) on the inner surface. Pisonieae is the first tribe in the Nyctaginaceae with an anthocarp that has been drastically changed its shape, colour and consistency compared with basal tribes. The prominent limb, equaling or exceeding the anthocarp-forming perianth portion, is remarkable in *Bougainvillea* (Bougainvilleeae) and all Nyctagineae; in the latter, it reaches 17 cm in some *Acleisanthes* and Mirabilis. The emergence of the large and diversely coloured limb in Nyctagineae is connected with pollination by different *Hymenoptera* and *Lepidoptera*. The tribe Nyctagineae is also remarkable for the independent emergence of the mucilage, which has evolved several times.

The study of AS and MN was carried out with the support of grants from the Russian Science Foundation (carpological research: 14-50-00029).

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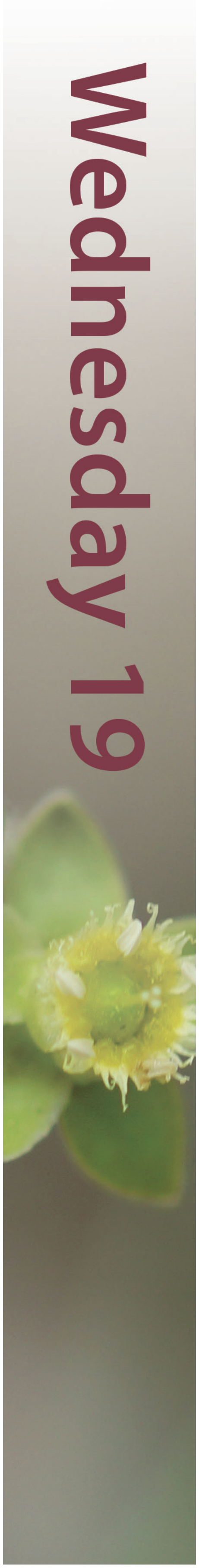

Evaluating the infrageneric classification of *Mirabilis* L. (Nyctaginaceae) in a phylogenetic context

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Mirabilis, a large genus within Nyctaginaceae, with 50-60 American and one Asiatic species, includes herbs, suffrutices and subshrubs with involucres of accrescent bracts, often connate, which surround one or more flowers. The current classification for the genus, from the nineteen century by Heimerl and later modified by Le Duc, is based on morphology and includes six sections: *Quamoclidion*, *Mirabilis*, *Oxybaphus*, *Oxybaphoides* and the monotypic *Mirabilopsis*, and *Watsoniella*. These sections were characterized by the involucre morphology, number of flowers per involucre, perianth form, number of stamens per flower and several characters of the anthocarp. The monophyly of the genus has been tested with a poor sampling lacking thorough representation of the infrageneric groups. In order to evaluate the classification of the genus in a phylogenetic context, we performed a parsimony and maximum likelihood analysis based on morphological and molecular data comprising partial matK, ndhF and ycf1 plastid genes and the nuclear ITS for 49 terminals of *Mirabilis*, representing five of the six sections. The preliminary results show that *Mirabilis* is monophyletic, supported by the cymose arrangement of inflorescences as a sinapomorphy, but the sections are paraphyletic. Based on the cladogram we propose a novel infrageneric classification for the genus.

Notes

Systematics and phylogeny of *Arenaria s.str.* (Caryophyllaceae) with special focus on Latin American species

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The circumscription of the genus *Arenaria* (sandworts) has long been debated and changed several times in the past. Recent molecular phylogenetic studies have shown that the genus in its old and wider circumscription was polyphyletic resulting in the segregation of several former subgenera as distinct genera (e.g. *Eremogone*, *Odontostemma*, *Shivparvatia*). *Arenaria s.str*. comprises about 100-135 species of small annual or perennial herbs distributed mostly in temperate and colder regions of the Northern hemisphere (Holarctic) but extending to southern South America. Many *Arenaria* species are found in dry and sandy habitats or on high mountains. While many Eurasian *Arenaria* species were included in a recent study by Sadeghian et al. (2015), little attention has been paid to the Central and South American species of the subgenera *Leiosperma* and *Dicranilla*. This group also includes a number of specialized cushion plants adapted to high altitude habitats. Since species numbers and limits are uncertain, a broad sampling is aimed for, including accessions covering geographic distribution and morphological variability. Sequence data for three molecular markers (matK-trnK, trnL-trnF, and ITS) have been generated so far and the data set will be expanded to include the regions matK-trnK-psbA, trnL-trnF, and rpl16 as standard chloroplast marker. Preliminary results of our phylogenetic analyses show that a Neotropical clade including all the Andean *Arenaria* taxa is emerging, and indicating that subgenera *Leiosperma* and *Dicranilla* are probably not natural groups in the current circumscription. Within this project the EDIT Platform for Cybertaxonomy is used as a tool to assemble a dynamic and integrative monography of *Arenaria* and relatives presenting the status quo of our knowledge about the genus.

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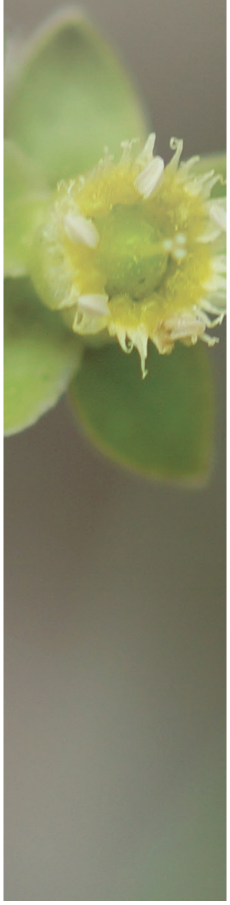

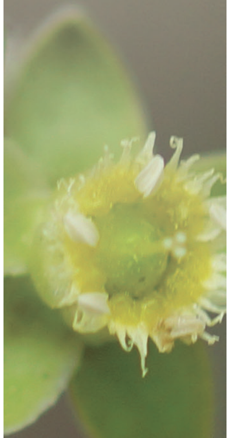

An approach using exploratory statistics for the *Alternanthera brasiliana* complex

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The Brazilian species complex includes *A. brasiliana* (L.) Kuntze, *A. ramosissima* (Mart.) Chodat, *A. bahiensis* Pedersen, *A. villosa* Kunth, and *A. flavescens* Kunth. The five species have been confused with *A. brasiliana* and display characters borrowed from those of Kuntze's diagnosis for its varieties. We analyzed 410 specimens identified in Brazilian herbariums as *A. brasiliana*. Exploratory statistical analysis was used to define discrete mutually exclusive morphological (phenetic) groups, followed by a cluster analysis, using the highest cutoff point, for the reconstruction of taxonomic units. Construction of more detailed taxon boundaries for the Brasilian species complex allowed for the separation of *A. brasiliana*, *A. bahiensis*, *A. flavescens*, and *A. villosa*, the synonymization of *A. ramosissima* with *A. brasiliana*, and the finding that two species, *A. praelonga* and *A. pubiflora*, might have been victims of erroneous determinations.

Notes ....

Target enrichment of orthologous genes for epiphytic cacti to support the analysis of species level relationships and species limits

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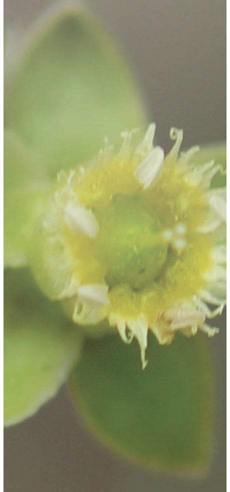
Cactaceae present a divers plant group of up to 1900 species. Most recent phylogenetic studies applied chloroplast markers to infer phylogenetic relationships. Cactaceae are also one of the angiosperm lineages in which the ITS region of the nuclear ribosomal DNA does not show concerted evolution (Harpke & Peterson 2006, Mol. Phylogen. Evol. 41:579-93) – hence, phylogenetic trees based on nuclear genomic regions are still largely absent to date or limited to analyses of single loci (such as PHY-C) in single genera. However, speciation in Cactaceae might be frequently influenced by hybridisation, polyploidisation and incomplete lineage sorting (e.g. Copetti & al. 2017, PNAS: 201706367; Yang & al. 2017, BioRxiv:143529), which can only be explored by nuclear markers. In addition, there are many Cactaceae clades with high speciation rates, requiring information from many variable nuclear loci in order to resolve relationships and delimit species. In this study, we focus on epiphytic cacti (tribe Hylocereeae, 80 taxa), for which a species-level plastid phylogenetic framework was recently published (Korotkova, Borsch & Arias 2017, Phytotaxa 327:1-46). Since target enrichment of nuclear genes already proved successful for the Portullugo clade (Moore & al. 2018, Syst. Biol. 67:367-83), we aim to design baits for orthologous gene regions (incl. exons/introns) from transcriptome RNAseq and genome data. Our investigation contributes to the project "Plant collections in Botanic Gardens – living resources for integrative evolutionary research (Evo-BoGa)" with the overall goals to robustly assess model plant groups' diversity in living collections, to use these collections for fundamental research of evolution, taxonomy and ex situ conservation, and to develop integrated curatorial workflows for specimens and associated data. We used SMRT sequencing of total RNA from *Epiphyllum pumilum* to obtain full-length isoforms to complete other cacti RNA/WGS data (*Carnegia gigantea*, *Lophora williamsii*, *Opuntia* cochenillifera, *Pereskia grandifolia*, *Echinocereus pectinatus*, *Hylocereus polyrhizus*, *Leuenbergeria bleo*). Identification of orthologous genes from few distantly related taxa is challenging, therefore, we present the comparison of different pipelines to infer orthologs and to design baits (e.g. Yang & Smith 2014, MBE, 31(11):3081-92; Faircloth 2017, Meth. Ecol. Evol., 8(9):1103-12).

The project is funded by the German Ministry for Research and Education (BMBF).



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Phylogeny, biogeography and age of the Aizooideae (Aizoaceae)

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The Aizooideae is an early-diverging lineage within the Aizoaceae. It is most diverse in southern Africa, but also has endemic species in Australasia, Eurasia and South America. We derived a phylogenetic hypothesis from Bayesian and Maximum Likelihood analyses of plastid DNA-and ITS sequences. We find that one of the seven genera, the *fynbos*-endemic *Acrosanthes*, does not belong to the Aizooideae, but is an ancient sister-lineage to the subfamilies Mesembryanthemoideae & Ruschioideae. Based on its morphological distinctness and phylogenetic placement we propose a new subfamily, the Acrosanthoideae Klak, for *Acrosanthes*. *Galenia* and *Plinthus* are embedded inside *Aizoon* and we place all three under an enlarged *Aizoon*. For the Aizooideae, we explored their possible age by means of relaxed Bayesian dating and used Bayesian Binary MCMC reconstruction of ancestral areas to investigate their area of origin. Early diversification occurred in southern Africa in the Eocene-Oligocene, with a split into a mainly African lineage and an Eurasian-Australasian-African-South American lineage. These subsequently radiated in the early Miocene. For *Tetragonia*, colonisation of Australasia via long-distance dispersal from Eurasia gave rise to the Australasian lineage from which there were subsequent dispersals to South America and Southern Africa. Despite the relatively old age of the Aizooideae, more than half the species have radiated since the Pleiocene, coinciding with the large and rapid diversification of the Ruschioideae. Our reconstruction of ancestral character-states indicates that the expanding keels giving rise to hygrochastic fruits originated only once, i.e. after the split of the Sesuvioideae from the remainder of the Aizoaceae and that they were subsequently lost many times. Variously winged and spiky fruits, adapted to dispersal by wind and animals, have evolved independently in the Aizooideae and the Sesuvioideae. There is then a greater diversity of dispersal systems in the earlier lineages than in the Mesembryanthemoideae and Ruschioideae, where dispersal is mainly achieved by rain.

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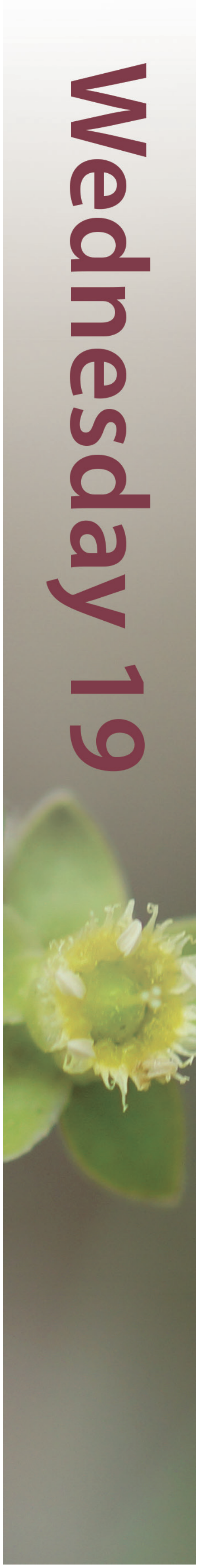

Functional phylogenomics of the Caryophyllales: transcriptomes, genomes, gene and genome duplication, biochemistry, and beyond

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Modern transcriptomic and genomic techniques offer the ability to explore the patterns and drivers of plant diversification on a scale never before possible. Using a dataset of genomes and transcriptomes from over 300 species across the Caryophyllales we found evidence for at least 30 ancient genome duplication events. From this enormous dataset of >15,000 genes per species, we discovered that many gene duplication events were associated with key adaptive trait changes, such as evolution of betalain pigmentation. Our work integrates not only new molecular phylogenomic and computational methods, including several developed for this study, but also field- and collection-based research to connect niche shifts to their genetic and genomic bases.

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POSTER SESSIONS

MONDAY 17- WEDNESDAY 19

Presented at the coffee breaks

Multivariate morphometric and geometric analyses of *Gymnopodium floribundun* Rolfe (Polygonaceae)

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Gymnopodium floribundum is a shrub or a small tree inhabiting in the tropical dry forests of Mesoamerica. Two varieties *G. floribundum* var. *floribundum* and *G. floribundum* var. *antigonoides* were recognized based on the shape, size and the degree of indument of the leaf-blades, inflorescences and flowers, but such characters exhibit a wide range of variation on its distributional area. We carry out a morphometric study to evaluate the variability of morphologic characters of nine populations of *G. floribundum* and to find patterns between morphology and geographic areas. The data matrix consisted of 224 individuals and 32 characters. To analyze the morphometric data a multivariate approach was employed and implemented in the R and for the geometric ones both the tpsDig2 v. 2.18 and CVAGen programs were used. The results suggest that the presence of three phenetic groups that correspond to three geographic regions: Belize, the Pacific Coastal Plain and the Yucatan Peninsula. The distances between the floral fascicles, length and width of the outer and inner perianth segments are diagnostic characters to differentiate the populations studied. The phenetic groups found would correspond pro parte to the varieties recognized by Standley and Steyermark in 1946. However, they would have to be confirmed by molecular characters and by using phylogenetic and phylogeographic approaches.

Notes

Are there leaf anatomical features unique to gypsophile Caryophyllales in the Chihuahuan Desert?

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Caryophyllales is notable for the number of taxa tolerant to high salt concentrations, and some families scattered through this clade include gypsophiles that are able to handle sulfur. Although many studies have focused on the leaf anatomy of halophytes, only a few have been done for gypsophiles, which are exposed to water and nutrient scarcity due to the high gypsum content of more than 5% in their habitat. The Chihuahuan Desert (CD) houses one of the richest floristic diversity on gypsum soils, including 59 species of Caryophyllales, most of which are endemic to this ecosystem. We proposed to explore if there are leaf morphoanatomical features unique to gypsophile Caryophyllales of the Chihuahuan Desert. Leaves of 48 species belonging to 25 genera representing 21 families and 14 orders across angiosperm were fixed in the field using FAA. The sampling covers gypsophiles, gipsovags and gypsophobes, including 10 species of three Caryophyllales families: Amaranthaceae, Caryophyllaceae and Nyctaginaceae. Permanent anatomical slides were made for the 48 species, and 35 morphoanatomical characters and 103 character states were used to describe them. A wide foliar anatomical variation with of epidermis, mesophyll, and venation was found. A comparison of these characters among the 48 studied species shows no features that can be associated to gypsophile Caryophyllales. The morphological and anatomical characteristics observed among the CD sampled species seem to be correlated to nutrient-poor soils, high levels of light intensity, temperature, and transpiration, and high photosynthetic efficiency rather than to gypsum. This is the case, for example, of leaves size (leptophylly and nanophylly), with entire margin, epidermal cells with straight anticlinal walls, sunked stomata or at the same level as the adjacent epidermal cells and isolateral mesophyll. The Caryophyllales species show no difference in this respect and cannot be differentiated from the rest of the species by particular characters or character state combinations.

Notes ....

Pollen characters and DNA sequence data converge on a monophyletic genus Iresine P. Browne (Amaranthaceae, Caryophyllales) and help to elucidate its species diversity

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Iresine is a neotropical genus of the Amaranthaceae with most of the species diversity in Mexico and Mesoamerica. It has suffered a complex classification history with considerably diverging views on the genus concept. We have carried out a molecular phylogenetic analysis of Iresine and allied genera and a dense sampling of species. Trees depict a clade of *Iresine* with Irenella and *Woehleria* deeply nested. This clade is sister to the remainder of Gomphrenoideae including *Hebanthe* and *Trommsdorffia = Pedersenia*). One of two maximally supported subclades of *Iresine* comprises mostly species restricted to the Mexican highlands and adjacent areas, whereas the other subclade is composed of more widespread Mexican-Mesoamerican taxa. Pollen grains of Iresine and relatives were examined using high resolution SEM, which yielded a matrix of 15 pollen characters. Ancestral character state reconstruction shows dodecahedral grains (in *I. angustifolia* and *I. nigra*) to have evolved within the *Iresine* clade, not involving the complete suite of character shifts associated with metareticulate pollen but just an increase of aperture diameter and a slight decrease of mesoporia width. To the contrary, four character state transformations occurred in the common ancestor of core Gomphrenoideae that led to metareticulate pollen (shifts to a distal orientation of punctae and microspines, to a sunken position of apertures relative to the distal part of mesoporia resulting in narrow mesoporia higher then wide, and a reduction in the diameter of mesoporia). The *Iresine* clade is characterized by pollen with well-separated ektexinous aperture membrane bodies, rounded or triangular, and gradually tapering into a single spine. For this genus, 35 species are accepted. We provide a taxonomic backbone that summarizes our work during the past 15 years. The current state of knowledge on the taxon-concepts at species level is highlighted in three categories reflecting progress in analyzing species delimitation: A - Species level taxon probably is monophyletic in the present circumscription; B - Species limits not yet studied in more detail; C - Current data suggest that the taxon concept does not reflect a natural entity, and species limits require further study.

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Phylogenetic relationships in *Mammillaria* series *Supertextae* (Cactaceae) based on two chloroplast markers

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The taxonomy of *Mammillaria* has historically been troublesome due to morphological variability, with which three infrageneric categories have been proposed: subgenera, section and series. Supetextae is one of the 16 series proposed for the genus, is composed of seven to nine species that are distributed mainly in southern Mexico and Central America. Phylogenetic relationships within the series and between species of *Mammillaria* have not been resolved. Therefore, to address this topic, we used chloroplast DNA sequence data from the intron rpl16 and the intergenic spacer psbA-trnH. We obtained from GenBank the two markers for 91 species of *Mammillaria* and six species as external group. Within the series *Supertextae* nine species are included, as well as five subspecies of *M. haageana* and two of *M. albilanata*. An analysis was carried out using Bayesian inference and maximum likelihood. Our results show that subgenera and section are not resolved as monolithic groups as noted in previous works. On the other hand, the series *Supertextae* formed a well-supported monophyletic group and resolved as a sister group of the series *Polyacanthae*. The relationships within *Supertextae* show that two clades were formed by an inversion in rpl16.

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Phylogenetic relationships in *Peniocereus* (Cactaceae, Echinocereeae), based on five markers of cpDNA

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The phylogenetic relationship of the genus *Peniocereus* with other members of the tribe Echinocereeae is controversial and its sister group is unresolved in previous molecular phylogenies. This study aimed to corroborate the monophyly of *Peniocereus* and its relationship with *Nyctocereus*, and to reconstruct the ancestral states for nine morphological characters and the ancestral distribution areas. Five molecular markers of chloroplast DNA (rpl16, petL-psbE, psbA-trnH, trnL-trnF, and rpl32-trnL) and a broad outgroup represented by all genera of the subtribes Pachycereinae and Echinocereinae were used in Maximum Parsimony and Bayesian Inference phylogenetic analyses. The results strongly supported monophyly of *Peniocereus*, which comprises *P. greggii*, *P. johnstonii*, *P. lazaro-cardenasii*, *P. marianus*, *P. striatus*, *P. viperinus*, and *P. zopilotensis*. The genus is sister to the *Pachycereus* group (*Backebergia*, *Carnegiea*, *Lophocereus*, *Marshallocereus*, *Nyctocereus*, *Pachycereus*, and *Pterocereus*). The scandent branches, slender stems, and tabular papillose epidermis likely are synapomorphies of *Peniocereus*, and is inferred the Sonoran Desert as their ancestral distribution area.

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The Caryophyllaceae of Oaxaca, Mexico: diversity and distribution

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Oaxaca is the richest state of Mexico in vascular plants with ca. 10 000 species. The available literature shows contrasting estimations on the number of taxa of Caryophyllaceae in the state. Due to the lack of a taxonomic treatment for the flora of Mexico and specifically for this state, a thorough study to assess the Caryophyllaceae diversity in Oaxaca is desirable. The aims of this study are to update the Caryophyllaceae species inventory in Oaxaca, to know their distribution, and to provide identification keys and descriptions for the genera and species. In order to accomplish these aims specimens of ENCB, FCME, MEXU, SERBO, and OAX were reviewed and identified and field trips were made to collect botanical material. WINCLADA was used to generate a matrix of morphological characters to obtain standardized descriptions and identification keys. Finally, distribution maps were made with QGIS 2.6.1. Oaxaca hosts 12 genera and 30 species of Caryophyllaceae being *Drymaria* (9) and *Stellaria* (5) the most diverse; three species are endemic to the state. *Arenaria lanuginosa*, *A. lycopodioides*, *Cerastium nutans*, *Drymaria glandulosa* and *Stellaria ovata* have a wide distribution along Oaxaca, while other species are restricted to some localities. It is still necessary to research which of these species with restricted distribution are local endemics or which have narrow distributions as an artifact due to the lack of intense exploration in some parts of Oaxaca, especially in the periphery of the state, as well as in the Southwest, and East. Most species, but especially *Drymaria villosa*, *Silene laciniata* and *Triplateia moehringioides* are distributed in *Pinus*, *Quercus* and pine-oak forests, but some species are present in cloud or dry forests, or secondary vegetation.

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Genome and transcriptome mining in Cactaceae: A exploratory approach

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Nuclear genes have had limited utility due to lack of available genomic resources for non-model plants. The utility of nuclear genes in Cactaceae has been limited because multiple copies have been found in the explored regions and the lack of genomic resources. To avoid multiple copies, searches targeting single-copy genes can be made on genomes or transcriptomes of the interest group or related species. The aim of this study is to identify nuclear single-copy genes potentially useful for phylogenetic analysis in Cactaceae. To find a substantial number of these genes, we searched the genomes of two Asterids and three Caryophyllales species in the comparative genomic platform PLAZA 4.0 dicots, which were the available closer related taxa to Cactaceae. For reference the model plant *Arabidopsis thaliana* was also included in the search. We use the search engine to identify 313 genes present in one to three copies in the selected species. Then we develop an R script to only select gene families with one copy, resulted in 133 potential single-copy genes and further filter to keep 28 with intron of sizes ranging 800-1000 bp. The selected genes were then blasted in five Cactaceae genomes and found matches for five genes. These five genes were mined and assembled for three available Cactaceae transcriptomes from the oneKP platform. Primers for Sanger sequencing will be design for five potentially single-copy intron-rich regions to be amplified in *Mammillaria*, *Opuntia*, and *Pilosocereus* species.

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Contributions of the IEB herbarium and the "Flora del Bajío y de Regiones Adyacentes" to the study of the Caryophyllales in Mexico

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The IEB herbarium, founded in 1985, with a collection of ca. of 260 000 specimens of vascular plants, is considered the fourth in importance in Mexico, representing the most important collection from de Bajío Region including Guanajuato, Querétaro and northern Michoacán, although it also contains specimens from others regions of the country. The IEB holds ca. of 10 300 specimens of Caryophyllales representing 21 families, 180 genera and ca. 875 species, corresponding to ca. 64% of the species present in Mexico. Cactaceae with 59 genera and 347 species is the most well represented family in the herbarium, while *Iresine* (Amaranthaceae) is the most collected genus. The highest numbers of species are in Querétaro (247), Oaxaca (219) and Michoacán (217). The type specimen collection has 23 primary types (8 holotypes, 15 isotypes), the best represented families are Cactaceae (13) and Portulacaceae (5). Within the "Flora del Bajío y de Regiones Adyacentes" project, 13 of 17 Caryophyllales families registered in the region have their respective taxonomic treatments, representing a total of 47 genera and 107 species, of which 22 are endemic to Mexico. Until now nine names have been lectotypified. Cactaceae, Amaranthaceae and Chenopodiaceae that are diverse in Mexico, still do not have a taxonomic treatment, so it is expected that the diversity data of the Caryophyllales in the region should greatly increase. The IEB along with the "Flora del Bajío y de Regiones Adyacentes" are a reference for the knowledge of the Caryophyllales of Mexico

Notes

Relationships and character evolution within the “raphide” clade (Caryophyllales)

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The “raphide” clade within the Caryophyllales is characterized by the presence of intercellular raphide crystals that includes Agdestidaceae, Aizoaceae, Gisekiaceae, Nyctaginaceae, Phytolaccaceae and Sarcobataceae. The clade it is a well-supported lineage recovered by several molecular phylogenetic analyses, that have recently allowed the recognition of Petiveriaceae, traditionally included within Phytolaccaceae. However, the review of these studies shows that the internal relationships within the clade are only partially resolved, with Gisekiaceae and Aizoaceae recovered as first branches within the clade, either as sisters or as a grade, whereas Phytolaccaceae have been recovered as sister of a clade including Petiveriaceae and Nyctaginaceae and Agdestidaceae+Sarcobataceae for which the internal relationships are not resolved. With the aim of better understanding the phylogenetic relationships within the raphide clade, and to illuminate patters of morphological evolution we generated a set of rapidly evolving plastid sequence data, and analyzed this with maximum parsimony (MP), maximum likelihood (ML) and Bayesian (BA) methods. In addition, we carried out analyses using combined matrices ofmolecular and morphological characters to test for additional morphological support and to trace character state transformation of morphological characters. Our results confirm the raphide clade as monophyletic support by the presence of raphides as a synapomorphy, which are slightly modified to styloids in Petiveriaceae. Gisekiaceae and Aizoaceae were recovered as successive sisters to the remaining taxa, whereas Agdestidaceae+Sarcobataceae form a clade with Phytolaccaceae, which again is sister to Nyctaginaceae+Petiveriaceae. Within this last one, Petiveriaceae in addition with the styloids is supported by have 4-merous floral parts. Nyctaginaceae are supported by two synapomorphies, the type of fruit (anthocarp) and the gamotepalous flowers. On the other hand, although some treatments still classify Agdestidaceae within Phytolaccaceae, our results confirm its close relationship with Sarcobataceae, but no morphological characters were found support the latter relationship.

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An annotated checklist of Plumbaginaceae (Caryophyllales)

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This project aims to provide the most complete and up to date dataset for Plumbaginaceae which is developed in the framework of the Global Caryophyllales Initiative (Arias et al. 2016, Taxon 65(2): 427–428). Generic delimitations in the species level treatment are based on Caryophyllales genera (Hernández-Ledesma et al. 2015, Willdenowia 45(3):281–383) which were updated based on the studies of the first author or recently published research. The name data were mostly provided by an excerpt from the World Flora Online taxonomic backbone, which in turn is based on The Plant List version 1.1. The list were enriched with data from Tropicos, then imported as names into the EDIT Platform for Cybertaxonomy and subsequently assessed to their taxonomic status (correct, synonym, invalid name, etc.). As of August 15, 2018, ca. 85 % of the total of almost 3,000 names imported for Plumbaginaceae were evaluated to that end. The dataset includes species name, standardized author name (according to the International Plant Names Index), synonyms and the URL link to the protologue of the taxon if available online. For some species type information is given. Plumbaginaceae includes two accepted subfamilies (Limonioideae and Plumbaginoideae) and 28 accepted genera. *Afrolimon* is considered a synonym of *Limonium* (Malekmohammadi et al. 2017, Taxon 66(5): 1128–1146). The Plumbaginaceae dataset includes 1058 accepted species and 113 infraspecies names. *Limonium*, *Acantholimon* and *Armeria* are the most species rich genera in the family with 592, 292 and 99 accepted species names, respectively. In addition, 397 names were considered as unresolved, most of these are species of Statice (226 names), which have not been assigned to their correct genus (much of *Armeria* and *Limonium* have been called *Statice* in the past - Greuter et al. 2000, Regnum Vegetabile 138: 268). The majority of the *Statice* species were transferred legitimately to *Limonium* or other genera of Plumbaginaceae by Kuntze (1891, Revisio generum plantarum, 2: 393–397) but some are still unresolved. The hope is expressed that the present inventory may be of use for future studies that will help to fill the present gaps.

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Pollen morphology of the tribe Hylocereeae (Cactaceae)

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The tribe Hylocereeae (Cactaceae) includes 6 genera and 63 species of shrubby root-climbing plants distributed in the Neotropics. The generic and infrageneric classification in taxa of the tribe has been controversial and none of the genera of Hylocereeae has resulted monophyletic in phylogenetic studies published to date. Moreover results of the most recent phylogenetic research based on six plastid DNA markers changed the circumscription of the tribe and of a number of genera. Within this group, the pitahayas or dragon fruit (*Hylocereus undatus*, *H. polyrhizus*, *H. megalanthus*) stand out with attractive fruits of growing commercial interest, cultivated in Mexico since prehispanic times. These species have been recognized in *Hylocereus* and *Selenicereus*, two genera with ambiguous circumscriptions, with a remarkable morphological variation. Here we identify whether diagnostic pollen characters for the tribe Hylocereeae support current classification, with emphasis in *Hylocereus* and *Selenicereus*. Pollen grains of representative taxa of recognized genera in the tribe were acetolysed and examined under light and scanning electron microscopy. Our results indicate that pollen attributes can be used to characterize genera and that for the tribe, pollen grains are zonotricolpate oblate-spheroidal, with an average size of 100 µm and perforate exine with spinules of variable size.

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Evolutionary relationships and taxonomy of *Microtea* (Microteaceae), a basal lineage in the core Caryophyllales

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The basal position of the small American genus *Microtea* within the core Caryophyllales was suggested only recently in accordance with molecular phylogeny. However, the specific relationships within the genus were not traced. The results of our phylogenetic analysis based on the matK chloroplast gene suggest the monophyly of *Microtea* including *Ancistrocarpus* and other related genera. *Microtea* is divided into two major sister clades: clade A consisting of *M. glochidiata*, *M. maypurensis* and *M. tenuifolia*, and clade B uniting *M. debilis*, *M. sulcicaulis*, *M. scabrida*, *M. celosioides*, and *M. papillosa*. The nrDNA dataset (ITS), although containing only a limited number of accessions, shows the same species number in clade A, and the remaining species studied (*M. debilis*, *M. scabrida* and *M. celosioides*) form clade B. Subgeneric status is assigned to clades A and B corresponding with the names *Microtea* subgen. *Ancistrocarpus* subgen. nov. and *Microtea* subgen. *Microtea*, respectively. The diagnostic characters at the subgeneric level are as follows: length of pedicels, number of flowers at each node, number of stamens and styles. A multivariate analysis of 13 distinguishing morphological characters provides the information additional to the non-random emergence of taxonomically significant traits at the subgeneric level. The pericarp and seed ultrasculpture and anatomy are similar in all species. The species share the reticulate pericarp surface (regardless of presence or absence of finger-shaped outgrowths on its surface) and rugose or slightly alveolate seed sculpture. From a morphological point of view, we accept 10 *Microtea* species. A checklist includes a new diagnostic key, morphological descriptions and distribution patterns of each species. *Galenia celosioides* is the oldest legitimate name available for the plants previously known as *Microtea paniculata*. Many names were lectotypified. *Microtea sulcicaulis* is reported for the first time as native to Bolivia, and *M. maypurensis* is reported from Indonesia (Java), where it is found as an alien plant with an unclear invasion status.

The study of APS, MV and MK was supported by the grant of Russian Science Foundation (project 14-50-00029).

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Seedling development in the HEA clade (Cacteae)

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The HEA clade within Cacteae is integrated by five species of *Astrophytum*, two species of *Echinocactus* (excluding *E. grusonii* = *Kroenleinia grusonii*) and three species of *Homalocephala*. Recent phylogenetic studies in the HEA clade have demonstrated that the group is morphologically and molecularly well supported. In order to determinate the seedling development patterns present in the clade, we compared seedling morphology and growth types for two years in four species of *Astrophytum*, the three species of *Homalocephala*, and the two species of *Echinocactus*. Seedlings were growth under the same environmental conditions, photographed under a light microscope and preserved in ethanol at 75% during several periods in the first two years of age. Our observations helped to determinate four types of seedling development in the HEA clade. One type is characteristic of *E. platyacanthus*, *A. myriostigma*, *A. ornatum* and *A. capricorne*; the second type is characteristic of the three species of *Homalocephala*, *H. texensis*, *H. parryi* and *H. polycephalus* and the other two types correspond to the *E. horizonthalonius* and the *A. asterias* types. Our results suggest that seedlings derived from campilotropous embryos possessing conspicuous and acute cotyledons and 5 to 12 spines per areole, such as in *Homalocephala*, are plesiomorphic and that seedling develop from anatropous and orthotropous embryos, with rounded or obtuse cotyledons and 1 to 4 spines, such as in *Astrophytum* and *Echinocactus*, are derived. Seedlings in the HEA clade rapidly become ribbed while in *K. grusonii* and in some members of *Ferocactus*, the seedlings at the same age are tuberculated. These results support the exclusion of *K. grusonnii* of the HEA clade. This research is the first study dealing with seedling development in a phylogenetic context in the Cacteae.

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Workshops

Thursday 20	
9:00-10:00	**WORKSHOP 1** **Walter G. Berendsohn, Sabine von Mering, Thomas Borsch** ***Caryophyllales editorial workflows:*** Criteria and different qualities of species level treatments; mechanisms for updates of taxonomic groups already made available, including aspects of versioning, data-publications, citation practices, changes in authorship; quality control mechanisms, and role(s) of editors and access for editors to data, among other aspects.
10:00-10:30	COFFEE BREAK
10:30-13:00	**WORKSHOP 1**
13:00-14:30	LUNCH BREAK
14:30-16:00	**WORKSHOPS 1**
16:00-16:30	COFFEE BREAK
16:30-18:00	**WORKSHOPS 1**

Workshops

Friday 20	
9:00-10:00	**WORKSHOP 2** Michael M. Moore, Ya Yang, Diego F. Morales-Briones ***Practical considerations for plant phylogenomics***
10:00-10:30	COFFEE BREAK
10:30-13:00	**WORKSHOP 2**
13:00-14:30	LUNCH BREAK
14:30-16:00	**WORKSHOPS 2**
16:00-16:30	COFFEE BREAK
16:30-18:00	**WORKSHOPS 2**

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This list includes participants that sent a registration form and that confirmed their participation by paying the registration fee at the moment of publication of this volume. The contact information given here is based on the information provided by each participant in the registration form.

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How to get to the Instituto de Biología, UNAM (IB-UNAM)

There will be free transportation to/from the Caryophyllales 2018 venue reaching two destinations.

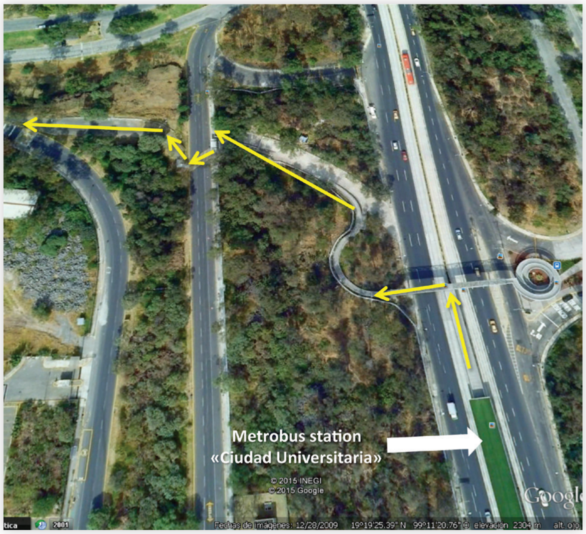
1-For those staying at the host hotel (Radisson Paraiso Perisur) a little bus will be waiting right outside the hotel lobby.

2-For those who chose to stay in another hotel, there will also be free transportation from the metro station "Universidad" , end stop of the green line No. 3 (Metro CU, inside the campus) to the Caryophyllales 2018 venue (Instituto de Biología) and back to the metro. There will be a special area reserved for those attending the meeting, which will be properly indicated. The stop looks like this, but it will be indicated with a Caryophyllales 2018 sign.

Transportation from Metro CU and the host hotel to the Caryophyllales 2018 venue (Instituto de Biología) will departure at 8:30 AM every day. Please be on time!

Transportation from the Caryophyllales 2018 venue (Instituto de Biología) to Metro CU and to the host hotel will be as follows: Monday 18:30 / Tuesday 18:30 / Wednesday 19:00 / Thursday 18: 30 / Friday 18: 30.

In case you miss the official transportation of the event, it is relatively easy to get to IB-UNAM using the subway system. Take the green line (No. 3) to the end stop "Universidad". As you exit the subway stop from the west side you will enter the University Campus (CU- standing for "Ciudad Universitaria"). The University has free transportation within the campus. It is a very big campus, so you need to take the correct bus or you will end up kilometers away from IB-UNAM. Route 4, will take you to the IB-UNAM, you should ask for the "Jardín Botánico" (Botanical Garden) stop. The Botanical Garden belongs to the Instituto de Biología and we also recommend you to visit it while you are at The Caryophyllales 2018 conference. For more information about the university campus please consult the web page http://www.unam.mx; more specifically, for location information within the campus, consult: http://www.mapa.unam.mx



It is also possible to get to the Caryophyllales 2018 venue by using “Metrobus” line 1 and walking for less than 15 minutes. Get off the Metrobus at the station Ciudad Universitaria. Get up the ramp and at its end take the left side. Use the way down and keep walking through the path until you reach a street. Cross the street and get up the stairs that are just in front. Cross a second street and continue waking strait until against the flow of cars. You will pass the Instituto de Investigaciones Biomédicas and the Instituto de Ecología. The nest institute is IB-UNAM. Enter the gate and continue walking strait towards the Botanical Garden. Once you are there you will find indications on how to get to the Caryophyllales 2018 venue.

Visit the National Herbarium of Mexico (MEXU)

We kindly invite you to visit the National Herbarium of Mexico (MEXU), located at the Instituto de Biología, National University of Mexico (IB-UNAM), in Mexico City, which holds the largest collection of dried plants in Latin America (more than 1,500,000 specimens) mainly from Mexico.

Although the largest collection at MEXU is the one of seed plants, it also hosts collections of algae, fungi, bryophytes, lichens, fruits and seeds, pollen and wood.

MEXU has a vigorous collecting activity and a very dynamic exchange programme with about 160 herbaria around the World. Its exchange and loan programme implies a movement of around 30,000 specimens a year. Every year, MEXU incorporates about 37,000 specimens in the collections. Because of this growth rate, the number of visitors and the broad collaboration with other institutions, MEXU is one of the most active herbaria of the world. Researchers associated with MEXU investigate a wide range of topics, from floristics to systematics and phylogenetic research, including structural data (i.e, palynology, anatomy, morphology) and molecular data (mainly DNA sequences, but also phytochemistry).

Visitors information

MEXU is open from Monday to Friday, 9:00 to 17:00 h, during regular labor days according to the UNAM calendar.

Users must register at the main entrance of the Instituto de Biología, where they will get an institutional identification number that they need to wear at all times while they are inside the institute. The guard will notify a technician, who will help the visitors to consult the collections.

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