species that occupy this rain forest understory environment. No species examined to date that exhibit splash seed dispersal have been identified from environments other than those described here.

Splash seed dispersal species might not only be correlated with wet understory environments, but are possibly more successful in these habitats as a result of this novel seed dispersal mechanism. Kvist (1991) commented on the occurrence of *Pearcea*, known to exhibit splash seed dispersal, in these environments where vascular plant diversity is exceedingly low. Such environments are also typical for other genera of gesneriads exhibiting splash seed dispersal including *Napeanthus* Gardn., *Monopyle* Moritz ex Benth., *Diastema*, *Gasteranthus*. Kvist (1991) speculated that the Gesneriaceae might well be the most represented flowering plant family for this particular habitat. It has been suggested as well that the understory genera are more advanced (Kvist 1991, Kvist & Skog 1996), though the understanding of this fruiting morphology being a switch from wind to animal dispersal may now be replaced with an increased understanding of water ballistics and splash cup morphology. It is possible that splash seed dispersal facilitates or even increases the chances that seeds are deposited in more available microenvironments thereby increasing the chance of survival here. While entirely speculation at this point, this hypothesis warrants further investigation.

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PHYLOGENETICS AND TAXONOMY

PT1 SOLTIS, DOUGLAS E.

Angiosperms – an overview

Over the past two decades there has been remarkable progress in resolving angiosperm phylogeny and patterns of evolution. Analyses of large, primarily plastid molecular data sets have revealed new insights into numerous historically contentious problems of deep-level angiosperm phylogeny, including relationships among ''basal angiosperms'' (not members of either the eudicot or monocot clades), among clades of *Mesangiospermae*, and among major clades of eudicots. The same large data sets also have provided evidence for numerous rapid radiations throughout the evolution of angiosperms. We recently completed phylogenetic analyses on 640 species representing 330 families (a data set of 25,260 aligned base pairs from 17 genes representing all three plant genomes, i.e., nucleus, chloroplast, and mitochondrion). These analyses resulted in a very well-resolved topology for angiosperms. Many important questions of deep-level relationships in the non-monocot angiosperms have now been resolved. Such trees enable us to take a broad phylogenetic perspective on character evolution, community assembly, and conservation. Our analyses further confirm that with large amounts of sequence data, most deep-level relationships within the angiosperms can be resolved. We anticipate that this well-resolved angiosperm tree will be of broad utility for many areas of biology, including physiology, ecology, paleobiology, and genomics. Furthermore, by clarifying the backbone of angiosperm phylogeny, we have provided a framework for more comprehensive efforts for an in-depth assessment of angiosperm phylogeny and systematics (e.g., sampling nearly all 15,000 angiosperm genera).

PT2 WEBER, ANTON

Research in Gesneriaceae: looking back and forward (my forty years observing gesneriads and gesneriologists)

A retrospective view is presented regarding the development and step-wise advancement of research in Gesneriaceae. It covers its inception in the eighteenth and early nineteenth century, but focuses on the last 40 years, when I was directly involved in Gesneriaceae research, and I was able to observe the world-wide research progress and the respective researchers involved. This 40-year period spans classical taxonomy, the availability of new technologies (e.g., SEM) and genetic and molecular methods. Looking into the future is presenting a mixed view: molecular systematics will boom over the next ten to twenty (maybe thirty) years, and with the prospect of more rapid and efficient molecular techniques and more powerful software, major issues of classification and phylogenetic and evolutionary relationships of Gesneriaceae may become completely resolved. This is my optimistic view. Subsequently, after this period – as far as Gesneriaceae are concerned – the significance of molecular systematics will probably decrease and lose its dominance it currently respects. Alongside this decline, there will likely be a return to and flourishing of basic biological (=field) research, provided that gesneriads and their habitats – and researchers – are still in existence.

PT3 CLARK, JOHN L.

Shuaria, an arborescent new genus in the tribe Beslerieae

A new neotropical genus, *Shuaria*, with a single species, *S. ecuadorica,* is described from the Cordillera del Cóndor and Amazonian regions of southeastern Ecuador and is placed in the tribe Beslerieae. The placement of *Shuaria* in the tribe Beslerieae is strongly supported by molecular sequence data generated from the nrDNA internal transcribed spacer region (ITS), and the cpDNA *trnL* intron, *trnL-trnF* intergenic spacer region. Sequence data were generated for 33 species representing most of the generic diversity from the tribes Beslerieae and Napeantheae. *Shuaria* is characterized by the following unique combination of relatively uncommon characters in the Gesneriaceae: arborescent habit; opposite leaf arrangement sometimes interrupted by alternate leaves; lepidote trichomes on vegetative and floral structures; small white flowers with a dorsal gibbosity at the base of the corolla tube; and a bivalved septicidally dehiscent capsule. *Shuaria* is restricted to the Ecuadorian provinces of Pastaza, Morona-Santiago, and Zamora-Chinchipe in lowland Amazonian tropical wet forest and in lower montane cloud forest on the western slopes of the Cordillera del Cóndor.

PT4 RAMÍREZ-ROA, ANGÉLICA

The neotropical genus *Moussonia*

Moussonia, a neotropical genus of the tribe Gloxinieae, includes 14 woody species distributed from Mexico to Panama, mainly in humid mountain forest. Traditionally the species were recognized by the tubular and red corollas and the annular nectary. However, due to the revision of some other characters, mainly leaf form, indument, inflorescence and calyx, around 24 species have been now recognized, some of them, previously included as synonyms of *M. elegans*. As a result most species of *Moussonia*, as well as *Achimenes* and *Solenophora*, are in Mexico.

PT5 CHAUTEMS, ALAIN • PERRET, MATHIEU

Taxonomical novelties and morphological diversity in the genus *Sinningia*: towards a reorganization of tribe Sinningieae

The Brazilian genus *Sinningia* displays plants varying from a few cm to shrubs of over 2 m. Some 10 new species were recently recognized, increasing the morphologic diversity of this genus. The basic pattern is represented by a perennial tuber producing shoots flowering once a year and subsequently going dormant for a few months. One of the new species develops perennial shoots above the basal tuber that are continuously growing and producing flowers several times a year. Another one gives rise to separate vegetative and fertile shoots that are strongly reduced in size and structure. A fruit structure unique for the Sinningieae was also found, consisting of a fleshy fruit dehiscing by two apical valves (2 slits) with one of the slits continuing to the base of hypanthium, instead of the usual dry capsule. The long-overlooked *S. polyantha* thrives in the transition zone between beach and coastal forest vegetation in southern Brazil with its tuber completely buried in sand, in contrast with the usual rocky outcrop habitat, or less-frequent forest habitat with plants growing either in humus-rich soil in humid forest or as epiphytes. Phylogenetic analyses, based on seven nuclear and plastid markers, indicate that tribe Sinningieae is composed of six main clades. The newly recognized species were placed in this phylogenetic framework. Most of these clades exhibit a large morphological diversity. However, a few morphological synapomorphies can be identified (e.g., hypanthium and nectary structure) and a reorganization of tribe Sinningieae is proposed with eight lineages recognized at generic level.

PT6 MORA, M. MARCELA • CLARK, JOHN L.

A molecular phylogeny of *Paradrymonia*: Insights for a new classification of a polyphyletic genus

Paradrymonia is a genus of facultative epiphytic herbs with 38 currently recognized species. It occurs throughout the Neotropics except for SE Brazil and the Caribbean with centers of diversity in Colombia and Ecuador. Species relationships within the genus and closely related genera were evaluated using molecular data from the nuclear ribosomal internal and external transcribed spacer regions (ITS and ETS), and the chloroplast trnH-psbA intergenic spacer region. Analyses utilizing parsimony, maximum likelihood and Bayesian inference methods were used to assess phylogenetic relationships among 22 species of *Paradrymonia* and closely related genera. A preliminary analysis strongly supports that *Paradrymonia*, as currently circumscribed, is polyphyletic and includes taxa in three different clades. A strongly supported clade containing the type species of *Paradrymonia* includes *Chrysothemis pulchella* and *C. friedrichsthaliana* and ten species of *Nautilocalyx*. Another clade including *Paradrymonia longifolia* and *P. anisophylla* nest within a paraphyletic *Drymonia*. Morphological characters such as bearded anthers, rosette habit, and corolla tube angulation are discussed as potential characters for circumscribing a new classification of generic boundaries.

PT7 CLAVIJO, LAURA • TEOH, VIEW-HUNE • PRITCHARD, ROSS • CLARK, JOHN R. • CLARK, JOHN L.

Multigene phylogeny of the Neotropical genus *Drymonia* (tribe Episcieae)

The genus *Drymonia*, with 73 currently valid species and as many as 20 or more undescribed species, is one of the most morphologically variable and largest genera within the Tribe Episcieae and the Neotropical Gesneriaceae. The genus ranges from Mexico and the Caribbean south through French Guiana, Brazil, and Bolivia. The center of diversity for the genus is in Colombia and adjacent Ecuador. The circumscription of *Drymonia* has been difficult due to morphological variation in corolla shapes among species and the apparent convergence of hypocyrtoid or pouched corollas within the genus and closely related genera. Recent phylogenetic studies suggest that *Drymonia* is not monophyletic due to the presence of species nesting in *Drymonia* from *Paradrymonia* and *Nautilocalyx*. In order to understand the generic boundaries and to identify major evolutionary lineages in the genus, a preliminary phylogeny for *Drymonia* is presented based on nuclear and chloroplast markers.

PT8 SMITH, JAMES F. • CLARK, JOHN L. • AMAYA-MARQUEZ, MARISOL

A preliminary new classification system for the species of *Columnea*

Columnea is the largest genus in terms of number of species in the New World Gesneriaceae.

Classification of *Columnea* as one genus or as separate genera has been controversial. Wiehler recognized a classification system based on vegetative, fruit, and floral characters and opted to divide *Columnea* into four genera: *Columnea*, *Trichantha*, *Dalbergaria*, and *Pentadenia*. He added a fifth genus to the complex by describing two species in the genus *Bucinellina*. This classification was not widely accepted and Wiehler's genera were considered sections within the genus *Columnea*. *Pentadenia* was split into two sections: *Pentadenia* with robust herbs and large ventricose corollas, and *Stygnanthe* with creeping herbaceous plants and narrow corollas. *Bucinellina* was never formally placed, but was considered close to the species of section *Ortholoma* (Wiehler's *Trichantha*). Molecular work since 1994 that sampled more than a single species of *Columnea* has always resolved the genus as monophyletic. Unfortunately, sporadic and uneven sampling, as well as limited data prevented a good test of the classification system within the genus. Recent phylogenetic analyses of 35 species and sequences of ITS and six rapidly evolving chloroplast regions have provided new information about the subdivision of *Columnea*. Based on that we propose a preliminary classification system that recognizes seven sections. The clades that represent the new sections are all strongly supported based on parsimony and Bayesian analyses. Sections *Columnea* and *Collandra* are largely unchanged, consisting of the species Wiehler named as genera (*Columnea* and *Dalbergaria*). Sections *Pentadenia* and *Ortholoma* are split into two sections each, and some of the species of *Ortholoma* are likely to be moved to *Stygnanthe*. *Bucinellina paramicola* nests within one of the *Ortholoma* sections based on our molecular data.

PT9 MÖLLER, MICHAEL • WEBER, ANTON

Phylogenetic relationships and high levels of polyphyly among Old World didymocarpoid Gesneriaceae genera

The ''Didymocarpoid Gesneriaceae'' (traditional Cyrtandroideae excl. Epithemateae) include >1800 species in 81 genera, distributed in Europe (3 genera), Africa & Madagascar (8), and Asia & Malesia (70). In their current circumscriptions, fewer than 32 genera are monotypic. Here results of molecular phylogenetic studies of all but a handful of genera are presented, based on nuclear ribosomal ITS and chloroplast *trn*LF intron-spacer sequences, and maximum parsimony and Bayesian inferences. There is a strong geographic pattern to the groups found, with the European and African + Madagascan representatives forming distinct groups embedded among the Asiatic genera. Genera of the basalmost lineages are largely confined to the Asiatic mainland, while the numerous ''advanced'' genera have also spread into the Malesian archipelago. Remarkably, all Asian & Malesian genera with twisted fruits fall in one clade although it also includes some taxa with straight fruits. About a quarter of the genera form strongly supported monophyletic clades, but generic relationships among these are tenuous. Many genera appear to be non-monophyletic, and some are highly polyphyletic, such as *Briggsia*, *Chirita*, *Henckelia* and *Raphiocarpus*. Based on our findings several systematic changes involving generic delimitations are necessary.

PT10 BRAMLEY, GEMMA L.C. • ATKINS, HANNAH J.

The taxonomy of *Cyrtandra*: how much do we know already and where do we go from here?

Cyrtandra is the largest genus in the Gesneriaceae, containing at least 600 species. Its distribution stretches east from the Nicobar Islands, across Malesia to the Philippines, Taiwan, southern Ryukyu Islands, northern Queensland and the Loyalty Islands, to the high islands of the Pacific and Hawaii. Taxonomic approaches to the genus have largely been in the form of regional revisions; there is no recent comprehensive treatment. One of the major focus areas for taxonomic work has been Borneo, but even here we have no integrated knowledge of *Cyrtandra* species because of piecemeal publication of species descriptions; as a result many specimens lie unidentified in herbaria. To assess how much we know about *Cyrtandra*, we need to bring this knowledge together to create a web-based *Cyrtandra* resource. Once we have assimilated all published information including current names (Skog & Boggan, 2007. http://botany.si.edu/Gesneriaceae/Checklist), distributions, identification keys and theories of related groups of species, we will be in a position to use this resource to facilitate our efforts to complete the picture. It is likely that future taxonomic work will be focused on the *Cyrtandra* of New Guinea and Sulawesi, two of the areas about which we have the least information. Targeted fieldwork to collect herbarium specimens and samples for phylogenetic anaylsis will partner taxonomic work and will complement current work on *Cyrtandra* of the Pacific and Hawaii (e.g., Clark et al. 2009. Mol. Phyl. Evol. 53: 982-994). The development of an infrageneric classification by furthering previous molecular phylogenetic studies will enhance taxonomic efforts.

PT11 CLARK, JOHN R. • WAGNER, WARREN L. • ROALSON, ERIC H.

On the origin and diversification of the monophyletic Pacific clade in the genus

Cyrtandra: recent insights from sampling along the southeast Asia-Pacific interface

With approximately 600 species, *Cyrtandra* is the largest genus in Gesneriaceae and occupies the greatest range for any genus in the family, extending throughout southeast Asia and into the Pacific. The Pacific clade, representing approximately half of all known species of *Cyrtandra*, are resultant from a single introduction to the islands. This introduction occurred approximately 20 MYBP with more recent radiations taking place in Samoa, Hawaii, the Society and Marquesas Islands. Resolving the affinities between these closely related lineages has provided a framework for new taxonomic studies. This presentation focuses on a phylogenetically based taxonomic study in Pacific *Cyrtandra* and outlines our strategy for tackling this unwieldy genus. Recent results to increase sampling during an expedition to the Solomon Islands are also discussed. We use maximum likelihood and Bayesian phylogenetic methods to analyze plastid and nuclear ribosomal sequence data for these and other samples. (also presented as a poster, P5).

PT12 WAGNER, WARREN L. • CLARK, JOHN R. • ROALSON, ERIC H.

Hawaiian *Cyrtandra*: A promiscuous lineage

Cyrtandra is one of the most difficult to understand genera in the Hawaiian flora. It has been revised five times since 1883. Particularly problematic is the question of what constitutes a "species" in *Cyrtandra* with the number of species recognized differing dramatically from 29 to 418 species! Differences in species number estimates are partly reflective of new discoveries over time, but significantly they are associated with vastly different interpretations of morphological variation observed. Work by Wagner & Herbst in the 1980s for a flora of Hawaiian Islands resulted in identification of 54 species, united by cohesive character suites and geography with numerous rare individuals with intermediate morphology in areas of sympatry. Unlike many other lineages in the Hawaiian Islands, *Cyrtandra* has minimally radiated into a variety of ecological situations and thus in areas of geographical overlap there are cases of sympatry. This discovery resulted in a revised interpretation of the rare individuals as hybrids rather than species. In our current revisionary work we recognize 59 species and 87 hybrid combinations. Limited study of hybridization using molecular data supports the hypothesis, but much more extensive work is currently underway (Roalson et al.) to address questions of species limits and the impact of hybridization on *Cyrtandra* diversification. We have sampled broadly across Hawaiian *Cyrtandra* for molecular phylogenetic analysis. Hawaiian species formerly were grouped into 2 subgenera and 5-6 sections. It was believed until recently that they resulted from 2 to as many as 6 independent colonizations from the Fijian region. Molecular phylogenetic studies by Cronk et al. (2005) suggested Hawaiian species originated from Taiwan and were of a single origin. More recently, Clark et al. (2008, 2009) corroborated the monophyly of the Hawaiian clade but their ancestral range reconstruction studies supported a Fijian origin for the clade as historically proposed.

PT13 WEBER, ANTON

A new formal classification of Gesneriaceae: an attempt to square the circle

By the application of molecular methods, enormous progress has been made in the past 15 years as to the recognition of relationships within the Gesneriaceae. Like in many other angiosperm groups, the molecular results show that traditional concepts have to be abandoned or modified to a large extent. To date, no new formal classification of Gesneriaceae has been proposed. Such a classification faces considerable problems, both in principle and practical respects. Nonetheless, an attempt is made and a subdivision of the family into subfamilies (2), tribes (5) and subtribes (more than a dozen) is proposed for discussion.

BIOGEOGRAPHY

B1 PERRET, MATHIEU • FEUILLET, CHRISTIAN

Diversification and systematics of the Gesneriaceae in Brazil: insights from a supermatrix approach

Brazil includes some 210 species of Gesneriaceae of which 62% are endemic to this country. Origin and causes of this diversity are, however, largely unknown and systematics of these Brazilian taxa still requires revisions. To address these issues, we reconstructed phylogenetic relationships among Gesnerioideae using several molecular markers assembled in a single matrix and a comprehensive sampling for the taxa that have a center of species richness and endemism in Brazil such as *Nematanthus*, *Codonanthe*, *Sinningia*, *Mandirola*, *Goyazia* and *Sphearorrhiza*. Using this phylogenetic tree, we could determine that Gesneriaceae diversity in Brazil mainly results from four independent radiations: two occurring in the Atlantic forest biome (Sinningieae and *Codonanthe-Nematanthus*) and two others in Central Brazil (*Mandirola* and *Sphaerorrhiza*). The lowland northern South America was identified as the ancestral area for the epiphytic clade *Codonanthe-Nematanthus*, whereas an Andean origin was found for the saxicolous/terrestrial clade

Mandirola. Within these lineages, flower diversification was largely associated with the evolution of different pollination systems and/or specific pollen placement on a same pollinator (e.g., through floral resupination). We showed that large homoplasy associated with flower diversification has caused considerable taxonomic confusion and we propose a new generic circumscription for the clade *Codonanthe-Nematanthus.* These preliminary results indicate that large phylogenetic analyses in Gesnerioideae are both feasible and useful to resolve systematic and evolutionary issues. We suggest that extending this effort to obtain a comprehensive phylogenetic framework for the Gesnerioideae is now possible and urge research groups to define a common strategy for taxa sampling and DNA marker selection.

B2 KOKUBUGATA, GORO • HIRAYAMA, YUMIKO • PENG, CHING-I • YOKOTA, MASATSUGU • MÖLLER, MICHAEL

Taxonomic reconsideration and phytogeographic relationships of *Lysionotus pauciflorus* sensu lato in Japan and Taiwan

Comparison of leaf morphological variation and phylogenetic relationships, based on nrITS and partial trnC-D cpDNA sequences, were conducted on samples of *Lysionotus pauciflorus* sensu lato collected from China, Japan, and Taiwan. The morphometric analysis showed that leaves of plants from Japan proper and those from Taiwan proper are not significantly distinguishable by their leaf ratio. The phylogenetic analysis strongly supported a monophyly of *L. pauciflorus* sensu lato samples, with Japanese and Taiwanese samples falling in a clade separate from Chinese samples. In the Japan-Taiwan clade, plants from Japan proper formed a sister clade to those from Okinawa Island (Japan) and Taiwan. The present results suggest that: 1) the *L. pauciflorus* s.l. samples from China, Japan, and Taiwan must be treated as a single species; 2) *L. pauciflorus* s.l. originated in China; 3) a single dispersal event, migration via a land-bridge during low sea-levels in a Pleistocene glacial maximum, from China to Taiwan + Japan can be proposed; 4) three oversea dispersal events, likely through anemochory, to Japan proper, across the Tokara gap, to Okinawa islands crossing the Kerama gap, and from Taiwan to Lanyu Island are indicated. This study gives further insight into the biogeographical dynamics between the Ryukyus and surrounding areas.

B3 CLARK, JOHN R.

Gesneriaceae biogeography: the integral role of geography in the taxonomy and systematics of gesneriads

It has been known for decades that the changing geography of our planet plays a central role in lineage diversification. It is only recently, however, that methodologies have become available to begin testing hypotheses on organismal ancestral range histories. In this presentation, the Gesneriaceae is discussed and the biogeographic history of the family is considered in light of new model-based methods. The *Cyrtandra samoensis* complex of species is highlighted and factors affecting its diversity are considered. Species within this and related clades evolved rapidly within the last 20 million years and numerous lineages have been spawned. Hybridization is thought to occur when recently divergent lineages become sympatric. Results from recent ancestral range and phylogenetic reconstructions of the genus are presented. It is argued that studying the origin and distribution of lineages within complex groups such as *Cyrtandra* is required to develop a satisfactory classification scheme.

FLORISTICS

F1 RAMÍREZ-ROA, ANGÉLICA • SKOG, LAURENCE E.

The Mexican Gesneriads

Mexico has around 100 species of gesneriads and almost 50% of them are endemics indicative of a relatively recent range expansion into North America. The genera *Achimenes*, *Columnea*, *Moussonia* and *Solenophora* are the best represented and have most of the endemic species. The largest number of genera, species and endemics are present in the states of Chiapas and Oaxaca, areas with the most humid forests. In the Mexican flora, the best represented gesneriads are the terrestrial herbs. Mexico is a center of origin and distribution of the family, the latter existing at least since the Lower Oligocene.

F2 CLARK, JOHN L. • SKOG, LAURENCE E. • MATOS, JESUS

The Gesneriaceae Flora of Cuba Project

The Flora of Cuba is an ambitious project that aims to produce family-level treatments of all vascular plants in Cuba. The project is coordinated by Cubans through the Ministry of Education (MES) and the Ministry of Education, Technology, and Environment (CITMA). As of February 2010 there were 16 volumes published covering 83 families. An out-of-date treatment on the Gesneriaceae of Cuba was published by Conrad Morton in 1957, but many of his names and species concepts were synonymzed by Skog in 1976. Four expeditions to Cuba were conducted between 2006 and 2008. Many poorly known species were photographed and documented with voucher specimens.

The circumscription of some wide-spread Caribbean species is reexamined based on recent fieldwork work in Cuba. Results pertaining to the rediscovery of poorly known species will be presented.

F3 FEUILLET, CHRISTIAN • SKOG, LAURENCE E.

The Gesneriaceae of the Guiana Shield and their distribution

After the publication of the Gesneriaceae for the Flora of the Venezuelan Guayana and the Flora of the Guianas, the data are combined with those from Brazilian collections. The distribution of the Guianan Gesneriaceae in the Guiana Shield is presented. Overall distribution in Tropical America in general is discussed and the geographical affinities of the Guianan gesneriad flora evaluated.

F4 YI-GANG, WEI • FANG, WEN • MÖLLER, MICHAEL

Gesneriaceae of South China

We published a monograph introducing Gesneriaceae species from South China, the center of diversity of Old World taxa. Here, more than 350 species of Gesneriaceae are known. Among the authors, we conducted hundreds of field trips over 16 years, and obtained extensive first-hand data on their situation in the field. We introduced some species into cultivation after carefully studying their ecological requirements. This book sums up this work that started in 1993, and covers more than 85% of the species in this family in southern China and 65% of the species in this family in China. Of these, some are new species and one a new genus, *Litostigma* Y.G.Wei, F.Wen & M.Möller, that forms an important link between basal and advanced lineages of subfamily Didymocarpoideae. This demonstrates that the botanically significant karst region in Southern China still holds surprises and will undoubtedly yield more systematic jewels in the future. Regarding the contents of the book, each species is illustrated with color pictures, described in detail, including additional information (e.g., chromosome numbers where available), comparison to similar species, information on their current status in the field and threats, a proposed IUCN status, and information on horticultural aspects. This work combines classical taxonomy with input from modern molecular phylogenetic work where appropriate. The Guangxi Institute of Botany, Chinese Academy of Sciences, is one of the most important academic research centers for Gesneriaceae in China, and desires to introduce Chinese representatives of this plant family to a wider audience through this book.

F5 MIDDLETON, DAVID J. • KIEW, RUTH

The challenge to revise the Southeast Asian Gesneriaceae

There are a number of large Flora projects currently underway in Southeast Asia: Flora of Thailand; Flore du Cambodge, du Laos et du Vietnam; Flora Malesiana and the Flora of Peninsular Malaysia. Of these Flora projects, active research is currently underway to complete the accounts of the Gesneriaceae for the Flora of Thailand and the Flora of Peninsular Malaysia in the near future. These projects are actively engaging with molecular phylogenetic research to ensure that a stable nomenclatural framework will be used in the Flora accounts. In Thailand there are about 26 genera and 170-180 species; in Peninsular Malaysia about 24 genera and more than 200 species. New taxa are frequently being discovered in these regions, particularly from underexplored areas, such as limestone sites in Thailand. The diversity of taxa and the progress on these accounts will be presented. The much more difficult task of revising the Gesneriaceae for the Flore du Cambodge, du Laos et du Vietnam and for Flora Malesiana will also be discussed, particularly in relation to collecting patterns in Southeast Asia and the enormous size of the task ahead.

F6 BARRIE, FRED • SKOG, LAURENCE E.

Flora Mesoamericana

Flora Mesoamericana is a collaborative effort between the Missouri Botanical Garden, the Instituto de Biología of the National Autonomous University of Mexico (UNAM), the Natural History Museum, London, and numerous specialists world-wide. The Flora describes the known vascular plants growing in the most southeastern states of Mexico (including the Yucatán Peninsula) and all the Central American republics. The project publishes its results in an Internet version (W3FM), as well as in printed volumes. The utility of the website is illustrated using the Gesneriaceae, and details about the distribution and diversity of gesneriads in the region are discussed.

DR1 ERTELT, JONATHAN

Observations on splash dispersal among Neotropical Gesneriaceae

The concept of a splash cup morphological structure serving as a dispersal mechanism was first written up with regard to several fungi and primitive non-vascular plant genera in the early 1950s. Since then the understanding of this type of structure has greatly increased. It is now recognized that there are fruits that employ this splashing activity for seed dispersal in at least 15 angiosperm families. Within the Gesneriaceae, Weber has detailed the understanding of this type of fruiting structure in several Old World genera and has noted it for a few Neotropical genera as well. This exploration undertakes to examine this fruiting structure as present in representatives of at least 11 genera in three tribes of the Neotropical Gesneriaceae.

DR2 WANG, CHUN-NENG • CHANG, JEN-YU

Developmental genetics of pseudovivipary in *Titanotrichum oldhamii*

Pseudovivipary refers to plants that all or some flowers of an inflorescence are converted into asexual bulbils. Although pseudovivipary is taxonomically widespread, its developmental genetic mechanism remains poorly understood. *Titanotrichum* is a monotypic genus of Gesneriaceae that is featured by producing asexual bulbils on its inflorescence. Toward the end of flowering season, the determinate floral meristem can revert to indeterminate bulbil inflorescences. Bulbil meristems then initiate at the axils of bulbil inflorescences branches which repeatedly divide themselves and eventually give rise to numerous bulbil primordia. The reversion of floral meristem to bulbil inflorescence implied that the floral meristem identity and stem cell maintenance genes such as ToFLO (LEAFY homolog), ToCEN (TFL homolog) and ToROA (WUSCHELL homolog) are likely to be involved in this floral transition process. The expression patterns of these genes were compared before and during the floral transition by RT-PCR and RNA in-situ hybridization. ToROA expression is not altered throughout the transition while ToFLO is gradually downregulated during the transition. ToCEN is expressed in the inflorescence top but not in the floral meristem before the floral transition. However, during the floral transition, ToCEN starts to express in floral meristems that are switching to bulbil inflorescence meristems. This indicates that ToCEN is probably involved in floral reversion to bulbil inflorescence process. Further functional studies by overexpression of ToCEN in *Arabidopsis* wild type and TFL mutants shall shed a light on what ToCEN's role is in psudovivipary.

DR3 ERTELT, JONATHAN

Notes and observations on root-shoot reproduction of clonal populations of herbaceous streamside Gesneriaceae

Meristematic activity is well documented within the Gesneriaceae. The anatomical development of secondary shoots from sub-surface roots resulting in clonal populations evidenced in other angiosperm groups has not been described. Anatomical studies as well as horticultural and habitat observations demonstrate the existence of this growth mechanism in three genera from three Neotropical tribes. The species examined are therefore clearly different in several key characters, but all are streamside growers in humid rain forest. The anatomical aspects of this growth habit are demonstrated and discussed along with possible ramifications of the streamside habitat.

DR4 ZAITLIN, DAVID

Sinningia speciosa in the Genomics Era

Over the last several years, I have been fortunate to be able to work with *Sinningia speciosa*, the ancestor of the cultivated Florist's Gloxinia. I recently discovered that the genome of *S. speciosa* is quite small for a flowering plant, approximately twice that of the model plant *Arabidopsis thaliana* (~300 million base pairs; Mbp). The nine other species of *Sinningia* included in the study also had small genomes that ranged from 250 Mbp in *S. harleyi* to 375 Mbp in *S. macrophylla*. A particularly significant finding was that genome size is not uniform within *S. speciosa*; reproducible variation of up to 20% was detected between wild populations sampled from across the species' distribution in southeastern Brazil. A small genome is but one of several attributes that make *S. speciosa* an excellent candidate for genetic and genomic research. Recent improvements in DNA sequencing technology have reduced the cost of whole genome sequencing by >90%. A genome sequence for *S. speciosa*, together with an effective mutagenesis strategy, would enable the identification of genes involved in tuber formation, flower development, pigment biosynthesis, etc. The genome sequence of *S. speciosa* would serve as a basic reference for other species in the Gesneriaceae, and would be an important resource for phylogenetic studies and comparative genomics with other important taxa. Research strategies, funding, and recent progress in developing *S. speciosa* as a model for ornamental plant genomics will be discussed.

DR5 COLEMAN, CASSANDRA L. • PRITCHARD, ROSS • ROALSON, ERIC H. • CLARK, JOHN L.

Rediscovery of *Phinaea pulchella* in Cuba: implications for the independent origin of radially symmetrical flowers in the Gloxinieae

Phinaea is a genus in the flowering plant family Gesneriaceae with three widely disjunct species. The three species of *Phinaea* are known from small populations in Mexico, northern South America, and the West Indies (Cuba & Haiti). *Phinaea pulchella* is one of the few members of tribe Gloxinieae that occurs naturally in the West Indies, and is the only member of the tribe endemic to that region. It was rediscovered in Cuba during an expedition in 2008 after nearly sixty years since it was last documented. Molecular data from nuclear and chloroplast regions were generated to test the phylogenetic placement of this enigmatic taxon. Although the species is morphologically consistent with placement in *Phinaea*, molecular results strongly support that *Phinaea pulchella* does not nest with other *Phinaea* species and instead is the sister taxon to a clade with *Pearcea*, *Kohleria*, and *Diastema vexans*. If the molecular results are showing us the true phylogeny of this group, then *Phinaea* is polyphyletic and the following morphological characters of the disjunct Cuban taxon are convergent with those of *Phinaea*: erect pedicels in fruit, valves fleshy at dehiscence, opening broadly, and sticky seeds adhering to the valves after, nectary annular (or absent), corolla pure white and subrotate with a strongly reduced tube.

DR6 CLARK, JOHN L. • COLEMAN, CASSANDRA L. • MUCHHALA, NATHAN • CLAVIJO, LAURA • CLARK, JOHN R.

Diversification of *Drymonia*: multiple shifts between bee-adapted and hummingbird-adapted flowers

The neotropical plant genus *Drymonia* is exemplified by a remarkable diversity of flower shapes and colors. The classification of *Drymonia* and closely related genera is still in flux; it has been difficult historically because of the convergence of pollination syndromes associated with bird-adapted flowers. A preliminary phylogeny of *Drymonia* and closely related genera based on nuclear and chloroplast markers suggests that there have been more shifts between pollinators and associated floral traits than previously recognized, and that these shifts are the primary reason for the convergence of pouched flowers. Here, pollinator shifts that may have affected species diversity in this group are examined using ancestral states reconstruction analysis, coded as presence/absence characters. Ancestral states reconstruction patterns were inferred using both fitch parsimony implemented in Mesquite and stochastic mapping (SM) performed using SIMMAP utilizing the posterior distribution of trees resulting from the Bayesian analyses of molecular data. These results are compared and contrasted in terms of the methods used and in the results obtained. Trends in pollinator shift are explored and future directions with this research are discussed.

EDUCATION AND CONSERVATION

EC1 PENCE, VALERIE C.

In vitro methods for the conservation of *Saintpaulia* spp.

In vitro propagation and preservation methods have been tested at the Center for Conservation and Research of Endangered Wildlife with five species of *Saintpaulia* and could be utilized to supplement other tools for the conservation of these species. Plants are readily propagated from leaf cuttings and produce orthodox seeds. However, in vitro (tissue culture) methods can play a supplemental role in supporting conservation, particularly when few or no seeds are available. We have demonstrated in vitro collecting methods that can be used to initiate tissue cultures in the field, providing a method for preserving and transporting tissues while they initiate regenerative growth in vitro. Alternatively, leaves can be cultured after several days in transit. Once initiated, sterile cultures can be maintained that can avoid nematodes and infections that can compromise the utility of resulting plants for reintroduction projects. Plants can be recovered from cultures for outplantings, research, display, and education, and the cultures themselves are being used to raise funds for *Saintpaulia* conservation in situ. Finally, tissues from in vitro cultures have been successfully cryopreserved using encapsulation dehydration, providing a method for tissue banking. Taken together, these methods provide tools for researchers in the field to collect and preserve germplasm from threatened genotypes, even when they are not producing seeds at the time of collecting. Wild germplasm can thus be backed up by tissue collections, supplementing seed and living collections. These methods can play a role in an overall conservation strategy for *Saintpaulia* and could be adapted for use with other endangered Gesneriaceae.

EC2 SMITH, JEFF

Registration numbers for *Saintpaulia* species – the new system from the African Violet Society of America

For years the African Violet Society of America (AVSA) gave registration numbers to *Saintpaulia* species for AVSA show purposes. With the recent reorganization of the number of *Saintpaulia* species and a larger availability of new collections, the AVSA had a problem; how to reorganize the species registration system to reflect the taxonomic changes without losing the genetic diversity of the plants in collection. The purpose of this presentation will be to present the recently adopted AVSA species registration system that hopefully gives a working solution to this problem.

EC3 ERTELT, JONATHAN

Utilizing gesneriads as teaching tools in the classroom

Though there are exceptions, of course, many gesneriads are relatively easy to grow either on a windowsill or in a terrarium. As a family they have many attributes that make them excellent candidates for use in the classroom as teaching tools. This presentation will explore ways these plants could be easily used to demonstrate many basics of botany and plant studies across the age levels from elementary school through college and graduate programs.

EC4 CLARK, JOHN R. • KATZENSTEIN, JEANNE

The Gesneriad Conservation Alliance

The Gesneriad Conservation Alliance, a partnership between The Gesneriad Society, Inc. and the Gesneriad Research Center at Selby Gardens, is tasked with developing and implementing ex situ conservation strategies to preserve endangered, poorly known, or otherwise rare gesneriads. The Gesneriad Research Center is responsible for devising scientifically based strategies for managing these collections and to inform conservation growers of the tasks and responsibilities of maintaining species for conservation. The Gesneriad Society and certified conservation growers in the Society are responsible for growing and maintaining the specimens of concern. In this way, the two institutions are partnering to manage what we are calling the *metacollection of rare and endangered gesneriads* – a dispersed collection of plants that are maintained and managed by individuals around the world as part of a single collection.

EC5 SOLTIS, PAMELA S.

iPlant Collaborative and My-Plant.org

My-Plant.org is a freely available, phylogenetically structured social networking website for plant scientists, educators, and other interested parties. Users can easily share information, collaborate, and stay on top of the latest news in their field. Members can view and contribute to information, including image galleries, forum discussions, and access to external sources of data, for specific clades of interest. Most importantly, because the network is based on the phylogeny of green plants, My-Plant.org members are able to associate quickly with others who share common scientific interests. This enables members of the plant sciences community to interact in a way not previously possible. Plans for new features will be presented, and ideas for new functionalities will be sought from the participants in the conference.

POSTERS

P1 ONOFRE DE ARAUJO, ANDRÉA • PERRET, MATHIEU

Systematic revision of the Brazilian endemic genera *Mandirola* and *Goyazia*

In the framework of a revision of the Brazilian Gloxinieae, the genera *Mandirola* (3 spp., i.e., *M. ichthyostoma*, *M. multiflora* and *M. rupestris*) and *Goyazia* (3 spp. i.e., *G. petraea*, *G. rupicola* and *G. villosa*) were analyzed using morphological and phylogenetic data. The goal of this study was to clarify species delimitation and relationships among these taxa endemic from Central Brazil. Results indicate a lack of clear morphological boundaries between the three species of *Mandirola*. We suggest that these three species geographically distributed between the Brazilian States Minas Gerais and Pará (plus one recently discovered occurrence in NE of São Paulo State) should be synonymized into a single broadly defined species *M. hirsuta* (based on the earliest available epithet for this group). Phylogenetic relationships among *Mandirola* and *Goyazia* species and their position in the tribe Gloxinieae were inferred using seven molecular markers (ITS, ncpGS, trnLF, arpB-rbcL, rps16, rpl16, and matK) and samples representative of the main Gloxineae linages including all Brazilian taxa (excepted *G. villosa* and *M. multiflora*). We found that *Mandirola* and *Goyazia* form a well supported clade and that *Goyazia* is not monophyletic but embedded within *Mandirola*. Based on this result, we propose to combine the three *Goyazia* species into *Mandirola*. However, the paraphyly of *Mandirola* s.s. pointed out by molecular data conflict with morphological data indicating that further investigation in this species complex *Mandirola/Goyazia* is still needed.

P2 PUGLISI, CARMEN • MÖLLER, MICHAEL

Phylogenetic studies on *Paraboea*

Paraboea comprises about 100 species distributed throughout Southeast Asia, from China to Sulawesi. The genus is highly diverse in fruit and inflorescence morphology, including straight- and twisted-fruited species and species with terminal, subterminal and axillary inflorescences. *Paraboea* has a characteristic matted indumentum on the lower leaf surface which distinguishes it from *Boea*. Although preliminary molecular studies have indicated a potential paraphyly of *Paraboea* with *Trisepalum*, the latter is morphologically distinguishable by the calyx and the stigma. It also has narrower distribution, being found mainly in Thailand and Burma. Here we present an extended molecular investigation on the clade containing *Paraboea*, *Trisepalum* and closely allied genera, the *Boea* group. The DNA regions examined are the chloroplast trnL-F intron-spacer and the nuclear ITS. The data have been analysed using maximum parsimony and Bayesian inference. The study will shed light on the species and genus relationships within the *Boea* group.

P3 HSIN, KUAN-TING • WANG, CHUN-NENG

Genetic structure and conservation of a rare actinomorphic Gesneriaceae species in Taiwan, *Conandron ramondioides*

Conandron ramondioides, a monotypic Gesneriaceae species with actinomorphic flowers, has a widely disjunct distribution, in Southeast China, Taiwan and southern Japan. Due to its specific habitat requirement, it can only survive on wet limestone slopes under primary forest canopies. To investigate the genetic structure of this rare plant, we use genome-wide AFLP markers to survey the variation among and within five populations in Taiwan. A low genetic diversity was found within populations, but a high genetic differentiation was observed between populations. These results imply that the populations of *C. ramondioides* in Taiwan are highly fragmented remnants of a previously continuous distributed species. Despite the fact that natural populations of *C. ramondioides* are widely isolated from each other, the pollinators were not found during the field work, and yet seed sets are still observed in the field. Flower section examination suggests that the flowers may be autogamous; the anthers dehisce introrsely and come in contact with the stigma when the corolla abscises. This species is estimated as a near threat species according to IUCN. Habitat restoration of all field populations is necessary to prevent *C. ramondioides* from becoming extinct.

P4 HSU, HAO-CHUN • WANG, CHUN-NENG

A tale of Darwin's Gloxinia – the genetics of floral symmetry transition in *Sinningia speciosa*

Sinningia speciosa provides us with an intriguing opportunity to elucidate the genetic mechanisms of floral symmetry changes. Darwin himself described the peloric *Sinningia speciosa* cultivar as an actinomorphic mutant that arose from its zygomorphic wild ancestor; the cultivar is now commonly known as Darwin's Gloxinia. In our study, we crossed zygomorphic wild-type with actinomorphic peloric plants, and the F1 hybrid was selfed to establish an F2 population. Flowers produced by F1 hybrids were all zygomorphic, suggesting that the wild-type character is dominant. In the F2, floral symmetry segregated into a 3:1 ratio, zygomorphic to actinomorphic respectively, indicating that one gene is involved. We investigated the role of CYCLOIDEA (CYC) in this process, as it is known to control dorsiventral identity in snapdragon flowers. We found a single copy of SsCYC (Sinningia CYC) in *Sinningia*, as predicted from our genetic studies. We also found a deletion in the SsCYC coding region, causing a frame-shift and premature stop codon in the peloric *Sinningia*. Genotyping all individuals in the F2 population showed a complete association with the segregation of the trait of floral symmetry and the presence of the defunct SsCYC. Gene expression studies showed that SsCYC is only present in developing floral buds of wild-type *Sinningia*, but not at any developmental stage of peloric flowers. This is the first demonstration that Darwin's Gloxinia is loss of function mutation, in SsCYC. We currently attempt to transform wild-type SsCYC into peloric plants to directly confirm the role of SsCYC in determining floral asymmetry.

P5 SUMMERS, CARLY F. • MARGENTHALER, ELAINA • CLARK, JOHN R.

On the origin and diversification of the monophyletic Pacific clade in the genus *Cyrtandra*: recent insights from sampling along the southeast Asia-Pacific interface

With approximately 600 species, *Cyrtandra* is the largest genus of gesneriad and occupies the greatest range for any genus in the family, extending throughout southeast Asia and into the Pacific. *Cyrtandra* is also the only genus in the family to colonize the remote Pacific Islands. The monophyletic Pacific clade represents approximately half of all known species in this genus, but its origins and relationship to more mainland lineages of *Cyrtandra* remain largely unclear. Recent research points to a greater Fiji-Samoa region as a potential center of origin for the Pacific clade, but several gaps in species sampling remain, particularly along the southeast Asia-Pacific interface, a region centered on Fiji and extending north to the Philippines and southeast to Samoa. This study builds on previous work on *Cyrtandra* and includes increased sampling from a recent expedition to the Solomon Islands in addition to other samples acquired through international collaborations. We use maximum likelihood and Bayesian phylogenetic methods to analyze plastid and nuclear ribosomal sequence data for these samples. Results from this study are evaluated in the context of Pacific-wide lineage radiations and parallels with other Pacific plant lineage radiations are discussed. (part of a contributed paper, PT11)

P6 MARGENTHALER, ELAINA • SUMMERS, CARLY F. • BENZING, DAVID • HOLST, BRUCE K. • CLARK, JOHN L. • CLARK, JOHN R.

Comparative phylogenetic analysis of the origin and frequency of epiphytism among three disparate plant families: Bromeliaceae, Gesneriaceae, and Orchidaceae

Epiphytism has evolved numerous times across disparate plant lineages including mosses, ferns and seed plants. Although thousands of species exhibit epiphytism and many of these have a high tolerance for the often xeric environment of forest canopies, no single character is unique to epiphytic plants. Adaptations that counter aridity are numerous (e.g., CAM metabolism, drought-deciduousness) and are shared by epiphytes and terrestrials alike. However, by retracing and studying the evolutionary history of epiphytes, we may identify unique combinations of characters or heretofore unknown factors affecting the success of these plants. In this study, we utilize phylogenetic comparative methods to explore the independent origin and evolution of epiphytism among three disparate seed plant families, each containing a relatively high percentage of epiphytic genera: Bromeliaceae (Poales), Gesneriaceae (Lamiales), and Orchidaceae (Asparagales). By providing a phylogenetic framework to study epiphytism, we may better understand how these groups are both similar and radically different from one another. Using extensive sampling across bromeliads, gesneriads, and orchids from Marie Selby Botanical Gardens living collection, and sequence data from GenBank, we analyze plastid and nuclear ribosomal genic regions using maximum likelihood and Bayesian phylogenetic methods to construct phylogenetic trees. Parsimony, likelihood and Bayesian methods are then used to reconstruct the origin and evolution of various structures and physiologies along these evolutionary topographies. We interpret the evolution of epiphytism in terms of shared, derived characters and the frequency and distribution of these characters among the three families. We also compare various methods for reconstructing life history traits and the relative strengths and weaknesses of these methods are explored.

P7 LOVOY, ZACHARY WEIL • CLARK, JOHN L.

The Gesneriaceae image library – A tool for field biologists

Recognizing plant diversity is a major obstacle for field biologists. The most pronounced example is when working in areas of high diversity such as tropical rainforests where even common plants are difficult to identify. We developed an image library of Gesneriaceae that is easily downloaded to an iPod with the goal of creating a rapid identification tool for biologists. This project made use of digital images of field collections of Gesneriaceae from the New World tropics. We used pre-existing file storage applications that can hold the entirety of our image library on an iPod.

P8 YI-GANG, WEI • FANG, WEN • MÖLLER, MICHAEL

Gesneriaceae of South China

We published a monograph introducing Gesneriaceae species from South China, the center of diversity of Old World taxa. Here, more than 350 species of Gesneriaceae are known. Among the authors, we conducted hundreds of field trips over 16 years, and obtained extensive first-hand data on their situation in the field. We introduced some species into cultivation after carefully studying their ecological requirements. This book sums up this work that started in 1993, and covers more than 85% of the species in this family in southern China and 65% of the species in this family in China. Of these, some are new species and one a new genus, *Litostigma* Y.G.Wei, F.Wen & M.Möller, that forms an important link between basal and advanced lineages of subfamily Didymocarpoideae. This demonstrates that the botanically significant karst region in Southern China still holds surprises and will undoubtedly yield more systematic jewels in the future. Regarding the contents of the book, each species is illustrated with color pictures, described in detail, including additional information (e.g., chromosome numbers where available), comparison to similar species, information on their current status in the field and threats, a proposed IUCN status, and information on horticultural aspects. This work combines classical taxonomy with input from modern molecular phylogenetic work where appropriate. The Guangxi Institute of Botany, Chinese Academy of Sciences, is one of the most important academic research centers for Gesneriaceae in China, and desires to introduce Chinese representatives of this plant family to a wider audience through this book. (also an oral presentation, F4)

P9 KEENE, JEREMY • BALLARD, HARVEY E.

A systematic revision of *Diastema* and *Monopyle* (Gloxinieae)

Diastema and *Monopyle* are two closely related genera within the tribe Gloxinieae (Gesneriaceae). They are both terrestrial understory herbs distributed from Central America southward through northern South America. *Monopyle* may include other taxa that have not been properly circumscribed, while *Diastema* is still undergoing active alpha-taxonomic investigation at the species level. Molecular data for the genera is also lacking – with only a small sample of the taxa being added to the overall tribal classification. A collection trip to South America for fresh specimens will allow for examination of the ecological factors impacting the species and the overall habit of the plants. The purpose of this research is to use herbarium and field collected specimens to do an in depth morphological and molecular study of the group. The products of this research will include a molecular phylogeny for the genera showing distribution patterns, determine the placement of the *Diastema/Monopyle* clade within Gloxinieae, publish new species, and write a monographic treatment for the genera.

P10 KARTONEGORO, ABDULROKHMAN

The Genus *Rhynchoglossum* in Malesia

A revision of the genus Rhynchoglossum (Gesneriaceae) in Malesia is presented. Seven species are recognized in this treatment including *R. borneense* Merr., *R. klugioides* C.B. Clarke, *R. medusothrix* B.L. Burtt, *R. merrilliae* Kraenzl., *R. obliquum* Blume, *R. spumosum* Elmer and *R. spec. nov.*. *Rhynchoglossum obliquum* is known as a widespread species found throughout the region. *Rhynchoglossum merrilliae* and *R. spumosum* are endemic to the Philippine Islands while *R. borneense* and *R. medusothrix* are endemic to Borneo. *Rhynchoglossum* sp. nov., a new species from Sulawesi, is newly described and illustrated. Morphological descriptions, distribution maps, ecological habitats, collector's notes, and notes are provided. An identification key and a list of collections seen are included.

P11 SPADA, ALBERTO • MÖLLER, MICHAEL • NISHII, KANAE • WANG, CHUN-NENG

Pattern formation during *Streptocarpus rexii* development

In the genus *Streptocarpus* (Gesneriaceae), the shoot unit was termed 'phyllomorph' and seedlings do not establish a SAM during embryogenesis and exhibit 'anisocotyly'. Recent molecular advances on model plants uncovered crucial roles for gene–hormone interactions in meristem fate and cell specification, which may be the key to understanding the genetic/physiological background of the unorthodox morphogenesis in *Streptocarpus*. In the species *Streprocarpus rexii*, exogenous application of plant hormones, such as GA and CK, affects anisocotyly, and cause a relocation of the meristematic cells from the lamina/petiolode junction to a central position of a conventional SAM. The expression patterns of SrWUS and SrSTM, (WUS and STM orthologs, two of the major players in meristem formation and maintenance in model plants) follow these relocated meristematic areas. Auxin has little effect on the morphogenesis of *S. rexii* seedlings, however, if TIBA or NPA (both auxin transport antagonist) are applied, the seedlings remain isocotyly and shoot development is initiated. These experiments show us that hormone imbalance between the cotyledons at the isocotylous stage is the first step of the establishment of anisocotyly and affect gene expression. Hormone genes crosstalks in *Streptocarpus* development is an emerging key research area, and *S. rexii*, with its multiple vegetative forms, provides an ideal study system to shed light on the diversity of molecular pathway/s involved in plant diversification.

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