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Understanding phylogenetics and natural hybridization in Sri Lankan temperate woody bamboos: *Arundinaria* (Poaceae: Bambusoideae) based on low copy nuclear markers

The award money was used to support DNA sequencing (PCR, cloning, and high-throughput sequencing) mainly for two low copy nuclear markers: RNA polymerase II (RPB2) and G protein alpha subunit (gpa1) for twelve species. Good quality sequences were obtained for RPB2, though the cloning was not satisfactory for some taxa of gpa1. Thus, I decided to focus only on RPB2 along with the other two low copy nuclear markers (supported by a Lois H. Tiffany Award, Iowa State University) poly-A binding protein gene (pabp1) and cellulase protein gene (pvcel1). This is an ongoing study and currently I’m sequencing an additional 24 taxa for RPB2 to better understand the phylogenetic relationships within the Sri Lankan *Arundinaria* (*Kuruna*) clade and among the other temperate woody bamboo clades and also to understand the potential role of hybridization in the evolution of native Sri Lankan *Kuruna* species.
Phylogeny, inflorescence evolution, and historical biogeography in *Buddleja* L.

I used the ASPT graduate student research grant I received to help fund a field trip in October 2013 to Eastern Cape province in South Africa, where I collected 22 specimens representing six species of *Buddleja* for my research on the systematics of the genus. I am currently analyzing data and preparing a manuscript on the phylogenetic relationships within the trip Buddlejeae, with a focus on the genus *Buddleja*. The field trip supported by the ASPT grant allowed me to include molecular data from the African specimens in my study, which proved to be crucial for analyses of evolutionary patterns, as the African taxa are the earliest diverging members in the genus. In addition to inferring relationships among species, I am also testing hypotheses about historical biogeography and the evolution of inflorescence form and floral morphology.
Investigating the impact of hybridization on diversification: A case study in the plant genus *Heuchera*

The project funded by the ASPT uses phylogenomic data to infer ancient hybridization in the genus *Heuchera* (coral bells; Saxifragaceae) by (1) producing an improved species tree estimate analyzed by a pluralistic approach using concatenation and coalescence and (2) providing numerous gene trees in order to search for the genomic historical-mosaicism expected of taxa with a history of hybridization (likely to be underestimated with few loci), using such tools as concordance factors and networks. The original proposal intended to use an amplicon sequencing protocol; however several sources of funding materialized since that date that have allowed us to obtain reference whole-genome shotgun sequences from our taxa of interest and upgrade to a sequence capture protocol aimed at intron-containing genes (probes based on a low-coverage reference genomic assembly of *Heuchera parviflora* performed by us and transcriptome data from the 1KP project). All lab work has taken place as a visitor to the Mandel lab at the University of Memphis; the project is ongoing with library preparation just recently completed and sequence capture slated to be completed shortly.
Population genetics and species limits of *Artocarpus odoratissimus* Blanco (Moraceae)

This project uses microsatellite markers to investigate the origins, diversity, and species limits of *Artocarpus odoratissimus* Blanco (Moraceae), an underutilized tropical tree crop native to Borneo. The funds from ASPT were used to fund microsatellite analysis of ca. 100 samples collected in the summer of 2013 in Sabah, Malaysia, for 14 loci (nuclear and chloroplast), which formed the core of our data collection. The analysis supported our hypothesis that a wild type characterized by a longer indumentum is genetically distinct. The project is ongoing as we await the arrival of additional samples being collected by a collaborator in the Philippines (where the species was likely introduced from Borneo). We hope to write up the results for publication in early 2015.
Molecular phylogeny and monograph of *Epistephium*, a key towards the understanding of the evolution of leaf venation and habitat in Vanilloideae (Orchidaceae).

I used the funds to travel to Bogota (Colombia) and Caracas (Venezuela) where I reviewed *Epistephium* specimens housed in COL, HPUJ, COAH and VEN. Based on this material and the ones I have on loan from AMES, F, K, MO, NY, and US, I have been able to solve some questions regarding *Epistephium* species and distribution. Although the absence of a short pseudo-petiole was not always obvious, the convergence of the main veins in the apical portion of the blade in *E. scleroophyllum* was found to be a new useful character to distinguish it from *E. subrepens* (matching the determination based on the dissection of the flowers). My new data reduced the range of *E. scleroophyllum* to Brazil and Bolivia as I correctly identified the material cited in Flora de la Guayana and a recent article on the Colombian Epistephiums as *E. subrepens*. To fully resolve the complex group of Epistephiums with sessile leaves, I plan to perform a morphometric analysis of the vegetative and floral organs. I’m still obtaining data of the specimens photographed in this and other trips to South America (501 specimens) and reviewed in the USA (597 specimens) in order to have a complete dataset.
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Shirley and Alan Graham Graduate Student Research Award  

Gene Chimerism, Horizontal Gene Transfer, and the Origin of Modern Fern Diversity  

This award allowed me to conduct fieldwork in Florida and western North Carolina to collect critical hornwort samples, and to do additional genome walking experiments to confirm the presence of neochrome gene in hornworts. The results from this study were published this year in PNAS, and received quite substantial media attention, including The New York Times, The Economist, National Geographic, Scientific American, Current Biology and Nature Reviews Genetics. I am really grateful for this graduate student research grant.  

Enigmatic Non-Twining Vines: Evolution and Systematics of *Matelea* subgenus *Chthamalia* (Gonolobinae, Apocynaceae)

Funding from ASPT allowed me to conduct fieldwork in Chihuahua, Mexico for two weeks last August (2014). While there, I collaborated with Dra. Socorro Gonzalez Elizondo of the herbarium at CIIDIR, Durango to collect multiple populations of six species of *Matelea* subgenus *Chthamalia* (Gonolobinae, Apocynaceae). Three of the species are quite rare and known only from a handful of specimens; one had not been collected for more than eighty years! While there, approximately 100 voucher specimens (including associated species) and silica material were collected that will be used to support morphological study, species descriptions, and collection of molecular data. I am in the process of obtaining molecular data including hundreds of nuclear genes, nrDNA, complete cpDNA, and partial mtDNA. These will be used to estimate phylogenetic relationships which, in turn, will allow me to study patterns of character evolution for interesting morphological aspects of these plants including their growth habit and floral morphology.
Elucidating the polyploidy complexes within *Callisia* Loef. Section *Cuthbertia* (Commelinaceae)

The funds awarded to me by ASPT were used in two aspects of my research. Half of the funds were used to help finance several plant collecting trips in the southeastern U.S. during summer 2013. During these trips, plant material of *Callisia graminea*, *C. rosea*, and *C. ornata* was collected. Most of necessary fieldwork throughout Georgia, South Carolina, North Carolina and Virginia has been completed. The remaining half of the funds was used to pay part of my expenses involved in amplifying and sequencing the *trnL*-F and ITS regions of the collected samples. The results of these analyses were presented at the Botany 2014 meeting in Boise, Idaho. This project is ongoing, and the ASPT research grant has contributed significantly towards my dissertation research.
Phylogeny and systematics of the genus *Lachemilla* (Rosaceae) in the Andes.

I used the ASPT Graduate Student Research grant to cover a portion of expenses associated with fieldwork in the páramos of Colombia during September 1 to October 16, 2013. *Lachemilla* is distributed along the mountains of Mexico, Central America and especially South America, with Colombia being the center of diversity of this group. On this trip, I collected 165 specimens, representing 22 species and 4 potential new species. As part of my ongoing dissertation research, these specimens are being used to study the phylogeny and evolution of this group, with a particular focus on the role of polyploidy and hybridization in the diversification of *Lachemilla*. Preliminary results were presented at the Botany 2014 meeting in Boise, Idaho, where I showed using high-throughput sequence data that polyploidy in *Lachemilla* can be attributed to both autopolyplody and allopolyploidy, and that hybridization likely played a key role in the initial diversification of the clade.
Systematics and evolution of *Guzmania* (Bromeliaceae): exploring a Neotropical radiation with phylogenomics

ASPT funding was used to help defray costs associated with the next-generation sequencing of whole plastome datasets for nearly a quarter of the total species represented in my dataset. Data generation for my project is nearly complete and genomic analyses are ongoing. Results are being written up for use in my Master thesis and then for subsequent publication in a major botanical journal. Thank you ASPT for your support.
Phylogeography and species limits in Spiranthes (Orchidaceae): Implications and applications for conservation.

The ASPT Graduate Student Research Grant allowed me to increase population and loci sampling for several rare species of Spiranthes, including dozens of populations from the taxonomically challenging Spiranthes cernua species complex, and a new cryptic species in this complex that I am describing from northern Arkansas (research ongoing). Additionally, this grant supported ESEM research, microsatellite development via NextGen Sequencing, and travel to collect a rare cryptic species of Spiranthes endemic to Florida that has been lost under taxonomic confusion for 109 years. The support of ASPT allowed me to gain a more complete understanding of this long lost and cryptic species, while simultaneously developing dozens of microsatellites that will illuminate its conservation genetics. Lastly, support from ASPT has helped inform our understanding of hybridization within Spiranthes, revealing that it occurs far less frequent than it is commonly thought.
Biome conservatism in the Neotropics? A case study in Bignoniaceae

I used the funds provided by the ASPT grant to cover travel expenses for field work in Brazil. To unravel patterns of biome conservatism and biome shifts in the Neotropics, I am collecting members of the large Neotropical plant family Bignoniaceae with a focus on Jacarandaeae, the earliest diverging lineage of the family. Brazil is the center of diversity for this group, containing up to 40 of the ca. 50 species in the tribe. In only six days in the field, I have made collections of five species of *Jacaranda*, the larger of the two genera in the group (the other genus is *Digomphia*, containing only three species). Ultimately, using novel high-throughput sequencing techniques and statistical phylogenetic analyses, I aim to (A) detect early diversification events in Bignoniaceae and (B) estimate diversification rates and correlate biome conservatism and biome shift events with these diversification rates across the family.
Geneious! Simplified Genome Skimming Methods for Phylogenetic Systematic Studies: A Case Study in Oreocarya (Boraginaceae)

Funds from the ASPT research grant allowed me to sequence several additional samples for my study examining the feasibility of using NGS genome skimming to study recalcitrant lineages like Oreocarya (Boraginaceae). The genus Oreocarya is a good example of a group lacking both species-level resolution and genomic resources. My work details methods that can be implemented in the user-friendly program Geneious that make NGS genome skimming accessible to even the least tech-savvy systematists. The nuclear ribosomal cistron, the plastome, and 12 mitochondrial genes were recovered by processing 100 bp single-end Illumina HiSeq 2000 reads in Geneious using a combination of de novo and reference-guided assemblies. I conclude that genome skimming represents a much-improved primary data collection over PCR+Sanger when cpDNA, nrDNA, and mtDNA are the target sequences. I have completed my research and M.S. degree. My publication will be in the December issue of Applications in Plant Sciences.
Systematics and evolution of the tribe Leucopaxilleae (Fungi: Agaricales)

Funds provided by the ASPT were used to buy reagents and cover sequencing costs to build a phylogeny of the family Tricholomataceae. These funds greatly contributed to my research by allowing me to increase the taxon and gene sampling. I was able to expand my project to perform a systematic revision of the family Tricholomataceae rather than only studying the tribe Leucopaxilleae. As a result I generated a multi-gene phylogeny on which to base a modern systematic revision of the Tricholomataceae s.str., and proposed four new genera. This project is completed and currently in press in the journal *Taxon*. 
Species of a new generation: the integration of next gen sequencing, distributional, and morphological data for species delimitation.

Funding from the ASPT has allowed me to travel throughout the southeastern United States and collect flowers and leaf material at the population level for integrative morphometric and molecular investigations of species boundaries and phylogenetic relationships in *Asarum* section Hexastylis. These collections have been used in three papers that are currently in review, one of which is a description of a new species. Furthermore, the material collected forms the core of a NSF DDIG that I have been awarded, with DNA sequencing scheduled to begin this month.
Evolution and systematics of *Claytonia lanceolata* sensu lato: Untangling polyploid origins in a challenging species complex.

I received an ASPT award that allowed me to make a long road trip to the Klamath and Siskiyou regions of northern California and southern Oregon to find localities and collect samples of a new species of tuberous perennial *Claytonia* that I am describing. Among other things, the funds offset a car rental over three weeks of travel -- ultimately, adding additional DNA sequences from previously unsampled populations around the southwestern edge of the distributional range of *C. lanceolata* sensu lato. Most importantly, I used these funds to visit a site near Mt. Shasta where two taxa from the *C. lanceolata* species complex are apparently hybridizing. Adding samples from this area to my phylogenetic dataset will greatly improve our understanding of species boundaries in the group. Look for my phylogenetics of *Claytonia* section *Claytonia* paper to be submitted to Systematic Botany soon!
Speciation and hybridization in *Caltha leptosepala* s.l. (Ranunculaceae): Disentangling the subalpine marsh-marigold species complex.

Our studies of *Caltha leptosepala* s.l. are focused on understanding refugial dynamics of the species complex at the last glacial maximum, as well as deeper divergences (e.g. allopatric speciation driven by orogeny). We are also investigating ploidy-level and genome-size differences between populations and lineages through karyological studies and flow cytometry analyses. Funding from ASPT was used for travel and supported me in reaching northern populations (Kenai Peninsula of Alaska, pictured here) and sympatric/hybrid zones (Oregon and Washington) where I collected leaf material for DNA studies, whole plant specimens for studying morphology, and seeds to allow propagation of material for cytology. Studies are currently in progress, with preliminary (chloroplast and nuclear ribosomal DNA) data showing divergence between a Rocky Mountain and a coastal (Cascade and Sierra Nevada) clade, with hybrids between these lineages forming around the Columbia River Basin of Washington and Oregon. I am grateful for the support and encouragement from ASPT, and am deeply enjoying the work with this beautiful and complex group of marsh-marigolds.