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W. Hardy Eshbaugh Graduate Student Research Grant

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Systematic affinities of Early Cretaceous mosses of western North America – an inquiry into the deep history of bryophytes

I traveled to California and worked in Dr. Mihai Tomescu’s lab at Humboldt State University for a period of four months. To study the bryophyte fossils I learned to section the rocks serially using the cellulose acetate peel technique. We described and assigned taxonomically a new fossil moss, Tricarinella crassiphylla gen. et sp. nov., which marks the oldest record for family Grimmiaceae and sub-class Dicranidae. We wrote the manuscript during my stay in California and this study was recently published in Annals of Botany (doi: 10.1093/aob/mcy015; also attached). I also contributed as a co-author to a comprehensive review of the bryophyte fossil record (currently in press in an Elsevier special volumen; page proofs attached) and I initiated the description of three other fossil mosses with polytrichaceous affinities. While at Humboldt State University, I also took Marie Antoine’s bryophyte diversity course. Finally, I presented my work as first author at the national meeting of the Botanical Society of America in Fort Worth (Texas). My research work on fossil mosses and collaboration with Dr. Tomescu’s lab is ongoing.
The generous funds from the ASPT were used for sequencing double digest RAD (ddRAD) libraries of all taxa in *Chloropyron* (Orobanchaceae). These specimens were collected from herbarium sheets to show the utility of herbarium specimens for producing genomic scale data using reduced representation sequencing techniques, as well as to resolve relationships in a rare and unique clade of western North American annuals. The empirical portion of this research has concluded and the resulting manuscript has been accepted at Systematic Botany. This work has spurred computation work to better understand the effects of missing data in reduced representation sequencing through simulations. These two studies comprised the two chapters of my MS thesis, which was completed in June 2017, and I have since become a PhD student at Yale University in the Department of Ecology and Evolutionary Biology.
Dylan Cohen
Department of Botany, Rancho Santa Ana Botanic Garden

Elucidating species relationships, biogeography, and floral evolution within the Andean *Loasa* s.l. using Next-Gen approaches

The money I received from the ASPT was extremely helpful in facilitating my first field work season to Chile in January 2017. I was able to collect over 25 specimens from central and southern Chile. My project is currently ongoing as I just completed a second season of field work from Argentina. I am planning to sequence DNA from both Chile and Argentina this summer. If all goes according to plan I intend to complete my PhD dissertation by May of 2020.
Jenna Dorey
Department of Biology, New York Botanical Garden

Reconstructing the evolutionary history of an Asian-North American disjunction in sedges Carex (Cyperaceae)

The ASPT Graduate Student Research Grant was used to fund field work and collecting specimens for my dissertation research on Carex section Laxiflorae. I used the funding for myself and my collaborator to travel from Okayama to Toyama, Japan, where we spent multiple days collecting Carex with local scientists. During this trip we collected Carex vaniotii, a Japanese endemic found at high elevation, which had not been recorded in Japan for several decades. Thanks to the ASPT Graduate Student Research Grant I was able to sample all of my target taxa in Japan, and reconstructed the phylogeny for over 60 taxa using six different gene regions. However, many low level branches remained unresolved, so I am now expanding my analysis to include ddRAD seq data for 216 individuals.
For my dissertation research, I am exploring the diversity of the fern family Thelypteridaceae. As currently circumscribed, five of the 30 genera are non-monophyletic, and several others have never been tested. My goal is to revisit generic circumscriptions based on molecular phylogeny, and identify morphological characteristics that can be used to diagnose monophyletic genera. In collaboration with Emily Sessa at the University of Florida and Alan Smith at UC Berkeley, among others, I have sampled ~600 of the 1000 species in the family, which are currently being sequenced for 500 low-copy nuclear loci. Of particular interest are Antillean Goniopteris, North American Parathelypteris, and Christella sect. Pelazoneuron, which will be the focus of more detailed taxonomic study. The support received from ASPT allowed me to visit herbaria and study collections at HUH, US, NY, MICH and UC. Visits to those institutions contributed to the publication of a new species, Chingia fijiensis Game, S.E. Fawc. & A.R. Sm., and facilitated the preparation of two other manuscripts: “Evolution of Perine Morphology in Thelypteridaceae” and “Phegopteris excelsior sp. nov. (Thelypteridaceae), the North American tetraploid beech fern.”
Thanks to the funds I received from ASPT, I was able to collect and sequence 20 new samples of *Besleria* (Gesneriaceae) from Colombia, increasing the number of accessions to ca. 150 specimens (representing 80 species out of the 165 in total). These samples were collected during a field trip in Colombia’s Andes organized from January to February 2016 in the department of Valle del Cauca and Choco. The phylogenetic analysis of these samples has contributed to elucidate the interspecific relationships within *Besleria*, especially between the Andean and the Brazilian species. This phylogenetic result allowed us to further investigate the biogeographic history of the group that shaped its current distribution. The work is in the writing phase and will be submitted to Molecular Phylogenetic Evolution and will form one chapter of my PhD thesis which I will defend in July 2018.
Luiz Henrique Martins Fonseca
Department of Botany, Universidade de São Paulo
Systematics, Phylogeny and Diversification of *Adenocalymma* (Bignonieae, Bignoniaceae)

The grant received from ASPT was used to cover the expenses to visit the four major herbaria in USA. More specifically, I used the amount to cover my daily expenses in Chicago to visit the Field Museum herbarium, Saint Louis to visit the Missouri Botanical Garden herbarium, Washington DC. to visit the Smithsonian herbarium and New York to visit the New York Botanical Garden herbarium. The data I collected during the visits were used for the analyzes presented in my Ph.D. thesis, completed last year. I am also using these data on my ongoing postdoctoral research.
A population genetics approach to phylogeny clarification

After challenges with my proposed project proved insurmountable, I completed a study of the genetic diversity and connectivity to other bays of eelgrass (*Zostera marina*) in Morro Bay, California. I found that, despite a loss of over 95% of the cover of eelgrass in Morro Bay, genetic diversity remained relatively high. Additionally, I found that Morro Bay is genetically differentiated from Northern populations. Despite this clear genetic differentiation, I also found clear evidence of gene flow into the bay. This research is under final revision for publication in *Estuaries and Coast*. 

Julia Harenčár,
Department of Biology, California Polytechnic State University
Closing the Rift: Investigating the Evolutionary History of the Ledebouriinae (Scilloideae, Asparagaceae)

Thanks to the ASPT award I was able to travel to Tanzania to make collections of Ledebouria from Eastern Africa. In total, I made 21 collections throughout the central part of the country. This project is currently ongoing since specimens are only just awakening from their year-long dormancy. This summer I will characterize their morphology, extract DNA and begin sequencing for phylogenetic analyses.
Nuclear phylogeny of the drought-adapted and desiccation-tolerant notholaenid fern clade (Pteridaceae)

The funding is preliminarily being used on DNA extraction, amplification, and sequencing. Thanks for the funding from ASPT, so that I could reconstruct robust species phylogeny among notholaenids ferns using by incorporating nuclear DNA sequences. I present my preliminary results in Botany 2017 using the title “Low-copy nuclear data for notholaenid ferns (Pteridaceae) corroborate plastid phylogeny over traditional morphological groupings“, and I am currently preparing a manuscript for submitting to peer-reviewed journal. The researches funded by this grant facilitates my current plans to use notholaenids as a model system for examining the function and evolutionary significance of farina in desert-adapted ferns.
The ASPT Graduate Student Research Grant helped fund a short specimen collecting expedition on the islands of Oahu; allowing me to visit the following trails on the Koolau (Poamoho, Schofield-Waikane, Kipapa) and Waianae (Mount Kaala) mountain ranges on the island of Oahu in the summer of 2017. In total, 25 specimens comprising 7 – 8 species were collected, and were instrumental in ensuring the taxonomic coverage of Hawaiian taxa was more or less complete for my phylogenetic study. While a target-enrichment high-throughput sequencing approach for samples collected was originally proposed in the initial proposal, subsequent primer validation and optimization results, and the possibility of allotetraploidy in the group, rendered the approach risky. As such, I opted for a genome skimming approach instead to sequence the plastomes of the taxa in my study. Sequencing of 136 samples (most of those collecting on this afore-mentioned Oahu trip included) was completed in mid April, and I am now currently analyzing the results. Preliminary bioinformatic analyses suggest that the multiplexed sequencing strategy worked, and I obtained an average plastome sequencing depth of around 50 X.
I am conducting a phylogenomic analysis of *Liatris* to elucidate modes of speciation and patterns of niche diversification within this young clade. I used funding from the ASPT for my first field season, during which I collected specimens of 15 *Liatris* species. I have conducted field work in Florida and Alabama (two of the most *Liatris* rich states) and in some of the Southeast’s most unique ecosystems (such as Alabama’s ketona-dolomite glades and the scrubs of the Lake Wales Ridge in Florida), generated sequence data for 22 of 37 species, and conducted preliminary analyses with these data.
The ASPT graduate student research grant has helped fund collection of my taxa of interest (Dicerandra) across the SE United States. Because of this grant, I will be able to include two subspecies/varieties that are very poorly understood into my broader phylogenetic analysis of the group. I am currently in the process of extracting DNA from my wild-collected specimens and developing RNA probes to utilize a target capture approach to build my phylogeny. It is because of the opportunity afforded to me by the ASPT grant that I plan to be completed with data collection and analyses within the coming year.
I used the funds to purchase research materials mainly plant DNA extraction kits and lysing matrices that were used for DNA extractions from nearly 100 silica-dried leaf tissue samples. DNA extractions were then amplified and sequenced for selected nuclear and chloroplast gene regions to analyze the phylogenetic relationships among the focal taxa. Currently, the research project is at the data analysis stage. The awarded funds contributed me to accelerate the data generation process for downstream analyses.
Discovering change using herbarium specimens: plant phenology, distributions, and biological outliers

I examined phenological shifts in 87 species in 12 genera of Asteraceae by assessing over 13,000 herbarium specimens and monitoring 12 species (1 from each genus) in the field over the course of a flowering season. Because of award funds, I was able to develop a novel approach to approximating peak flowering of specimens from percentages of reproductive structures on the specimens. I found that spring-flowering and fall-flowering species have diverging responses to warming, which may lead to a “dead zone”—or period of scarce floral resources—during the hot summer months. My phenological research informed my contributions to two publications: Willis et al. 2017, *Trends in Ecology and Evolution*, and Yost et al. 2018, *Applications in Plant Sciences*. I plan to submit the core findings of my research in summer 2018 for publication.
Dawson Martin White
Department of Biological Sciences, University of Illinois at Chicago

Unlocking herbarium genetic resources with target-capture NGS sequencing

These funds were used for purchasing DNA library preparation supplies (KAPA HyperPrep Kit) to sequence 530 nuclear genes from 163 *Erythroxylum* species. I am currently in the early stages of analyzing these data. These funds were helpful in reaching the necessary budget for this project ($5,500) and I was lucky to receive other grants that really made the research possible. I would like to comment that, given their high cost, it is risky to award grants for NGS DNA sequencing projects and not provide the full amount requested on the proposal. If I had not received several other grants, this money from ASPT might not have been used as described.