

## Undergraduate Research Symposium May 19, 2017 Mary Gates Hall

### Online Proceedings

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#### POSTER SESSION 2

Commons East, Easel 44

1:00 PM to 2:30 PM

##### **A Phylogeny of Tecomeae: Bringing New Insights to New World Plant Diversity**

Paige Pauline (Paige) Fabre, Senior, Biology (Plant)

Mary Gates Scholar

Mentor: Richard Olmstead, Biology, Burke Museum

The Neotropics contain about 100,000 seed plant species, amounting to ca. 37% of the world's species. The Olmstead lab is currently investigating Bignoniaceae, a plant family comprised of 82 genera and ca. 827 species distributed primarily in the Neotropics. There are 8 recognized clades in Bignoniaceae. One clade, Tecomeae, include 12 genera and approximately 55 species, with species distributed in North and South America, Southeast and Central Asia, and Australia. To create a phylogeny for Tecomeae, I gathered all available sequence data and DNA for species in the tribe from both the Olmstead lab and GenBank. Then, DNA from samples of additional species were extracted using the DNeasy Plant Mini Kits. Three different regions of DNA were sequenced, including two chloroplast regions (*ndhF* and *rpl32-trnL*) and one nuclear region (*ITS*). I amplified these regions via Polymerase Chain Reaction and sequenced the DNA using an ABI genetic analyzer in the UW Biology Department Center for Comparative Genomics. Sequences for all species were edited and aligned using Geneious. Phylogenetic analyses were performed in both Maximum Likelihood and Bayesian frameworks using RAxML and MrBayes. Creating a phylogeny for the Tecomeae is a crucial step toward deciphering the evolutionary history of Bignoniaceae. The overarching goal of our research is to not only create a phylogeny for Tecomeae, but for all 827 species within the Bignoniaceae family. Having a phylogenetic tree for Tecomeae allows us to identify when important divergences occurred, giving us an improved picture of how Bignoniaceae diversified and, ultimately, a better understanding of Neotropical diversification as a whole.

#### SESSION 2N

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##### **FOREST ECOLOGY AND EVOLUTION**

Session Moderator: Gregory Ettl, Forest Resources

MGH 288

3:30 PM to 5:15 PM

\* Note: Titles in order of presentation.

##### **A Molecular Phylogeny and Classification of Neospartoneae : The Evolutionary Relationships among *Diostea*, *Neosparton*, and *Lampaya***

Meng Lu, Junior, Exchange - Arts & Sciences

Mentor: Richard Olmstead, Biology, Burke Museum

Mentor: Laura Frost

The Verbenaceae, commonly known as the verbena family, consists of mainly tropical trees, shrubs, lianas, and herbs. Verbenaceae's diversity is highest in Latin America (where this family is primarily distributed) and Africa. Early classifications of this family relied on morphological traits. A molecular phylogenetic study was recently undertaken to assess and revise those classifications. Verbenaceae now include 35 genera and about 1000 species. In the current classification of Verbenaceae, there is one new tribe called Neospartoneae which consists of three small genera of Argentine species (*Diostea*, *Neosparton*, and *Lampaya*). According to the morphological traits, *Diostea* and *Neosparton* exhibit similar male reproductive characters and an ephedroid habit (many-branched shrubs with cylindrical, striate stems) while *Diostea* and *Lampaya* share fruit characteristics. Previous studies turned into the molecular data and tried to figure out the relationships between genera of this tribe by chloroplast DNA sequences (loci: *ndhF*, *trnLF*, *ccsA*, *matK*, *rbcL*, *rpoC2*, *rps3*). However, the evolutionary relationships remain unresolved. In my study, I used nuclear DNA sequences (loci: *ITS*, *ETS*, *PPR123*, *PPR42*, *PPR11*, *PPR70*, *PPR91*) to provide a more robust molecular data and try to figure out the phylogenetic relationships in Neospartoneae. I extracted DNA from samples collected in Latin America. After doing PCR and purifying the PCR products, I conducted the sequencing reaction. After editing sequencing data manually, I aligned the nuclear DNA sequences to analyze data and produce the phylogenetic trees with maximum likelihood and Bayesian methods. The updated phylogeny improves our knowledge of evolutionary relationships among *Diostea*,

*Neosparton, and Lampaya.*