PhD Dissertation Defense

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Title: Systematics and Evolution of *Commiphora* Jacq. (Burseraceae) in Madagascar

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ABSTRACT

The myrrh genus, *Commiphora*, comprises a clade of nearly 200 species of shrubs and trees that grow in warm tropical regions in Africa, Madagascar, the Arabian Peninsula, the Indian sub-continent, and South America. *Commiphora* is the most species-rich genus in the frankincense and myrrh family, Burseraceae, and species belonging to it are ecologically important throughout their range in eastern, sub-Saharan Africa and western Madagascar. Aromatic oleoresins extracted from several species have been used extensively as an olfactory aesthetic and medicine with demonstrated pharmacological benefits throughout both antiquity and contemporary time. Despite its diversity and ecological and economical significance, evolutionary relationships in the genus are poorly understood and few studies have sought to reconstruct the phylogenetic history of *Commiphora*. As a result, relationships of this widespread group of plants are not well characterized. Species of *Commiphora* are morphologically diverse and the genus provides an opportunity to study the evolutionary significance of traits such as the presence of thorns, production of oleoresins, and diverse types of indumentum. This dissertation research seeks to reconstruct the evolutionary history of *Commiphora*, with an emphasis on species in Madagascar, all of which are endemic. Toward this objective, we have applied molecular phylogenetic methods to resolve infrageneric relationships in the genus using molecular markers developed from three approaches. The first approach samples molecular markers that have been designed from previously published and widely sampled genetic loci for phylogenetic reconstruction in angiosperm genera, including two nuclear ribosomal markers (ETS and ITS) and three chloroplast spacers (*ndhF-rpl32*, *psbA-trnH*, and *trnD-trnT*). Our second approach uses molecular markers designed from a bioinformatics pipeline specifically targeting conserved genetic loci predicted to be within close proximity to more informative, intronic regions of the genome. The third approach was transcriptome-enabled and utilizes microfluidic PCR techniques and Illumina MiSeq to sample a set of putative shared, single-copy nuclear genomic loci. We screened 192 primer pairs for their phylogenomic utility in *Commiphora*. 91 of these primer pairs amplified a single product and 49 sequenced loci were used for comparative phylogenetic analyses to reconstruct evolutionary relationships among species of Malagasy *Commiphora*. Our results suggest that previous attempts to circumscribe the diversity of *Commiphora* produce unnatural groups, *Commiphora* has experienced complex biogeographic radiations, diversity in the genus is characterized by strong geographic structure, and expanded taxonomic and genomic sampling improves our ability to discern infrageneric groups. We have also begun a partial and ongoing revision of the genus in Madagascar, including a revision of six species, five of which are new. We outline priorities for future studies in this group, including expanded taxonomic revision and molecular systematics research to improve species delimitation and better understand evolutionary trajectories. A key priority is to sample species from tropical east Africa.