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CHALLENGES IN TROPICAL ECOLOGY AND CONSERVATION - GLOBAL PERSPECTIVES

SPECIES DELIMITATION, HYBRIDIZATION AND SPECIES HABITAT ASSOCIATIONS IN THE GENUS SYMPHONIA (CLUSIACEAE) ON MADAGASCAR

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Tropical rainforest tree genera often comprise multiple closely-related species occurring in sympatry but the genetic mechanisms that explain such sympatric coexistence are poorly understood. Inter-specific hybridization has been proposed as a key mechanism in the maintenance of highly diverse communities, potentially retarding the (local) extinction of rare species and also allowing the sharing of beneficial genetic variants across species borders. The genus *Symphonia* (Clusiaceae) diversified on Madagascar, where ca. 20 endemic species have largely overlapping ranges. *Symphonia* species are difficult to distinguish morphologically because of trait variation within species, poorly defined species boundaries and scarcity of discriminant characters for species delimitation.

We set out to test the role of hybridization in shaping patterns of genetic variation and species delimitation of the genus *Symphonia* in Madagascar. We sampled over 400 trees from three regions in eastern Madagascar, where hybridization among multiple species of the genus is expected to take place, genotyped them at 20 nuclear SSRs (nuSSRs), as well as sequenced the internal transcribed spacer (ITS) region in a representative subsample. A phylogeny was built from ITS sequences and we used genetic clustering approaches on "blind samples" (i.e., without using morphology) for taxon delimitation using nuSSRs. We then examined the spatial distribution of genetic clusters and assessed the hybridization history of the genus in Madagascar.

We discovered three major gene pools in *Symphonia*, which were sub-structured into 13 minor gene pools that could be assigned to 13 potential species. Gene pools occurred frequently in sympatry, suggesting a role of hybridization in maintaining high genetic diversity in the genus. Flow cytometry and nuSSR scoring identified three tetraploid and ten diploid species. Clustering analysis was congruent with morphological characters in *S. clusioides*, *S. eugenioides*, *S. microphylla*, and *S. nectarifera,* but did not support other described taxa such as *S. fasciculata*, *S. sessiliflora* and *S. louvelii*. Overall, we found evidence for hybridization and introgression between multiple species and a habitat-specific distribution of sympatric clusters in several locations.

GLOBAL PATTERNS IN PALM ABUNDANCE

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Palms (Arecaceae) are an iconic and diverse group that provide myriad ecosystem services in tropical forests. For example, palms account for 7 of the top 20 'hyperdominant' tree species of the Amazon. While previous work has examined global patterns of palm diversity, we currently lack a quantitative global analysis of palm abundance patterns. Given the many morphological and physiological differences between palms and dicotyledonous trees, the responses of these groups to environmental change drivers are likely to differ. As a result, a better understanding of palm dominance will help identify knowledge gaps and ultimately improve the predictive ability of global vegetation models.

Using a dataset of > 1,000 globally-tropical forest plots distributed, we quantified (1) relative abundance of arborescent palms versus dicot trees across regional, continental, and global scales, and (2) how relative abundance of arborescent palms is related to abiotic variables. We show that arborescent palm abundance is extremely lower in the African and Asian tropics compared to Neotropical sites. We then examined spatial variation in palm abundance considering evolutionary, biogeographical, and ecological hypotheses, and use statistical models to examine relationships between palm abundance and plot-level environmental covariates. We introduce some novel hypotheses regarding the dominance of the arborescent palm life form in the New World.

Merian Award Applicant