



## **Rethinking the systematics, evolution and biogeographic history of the mahogany family (Meliaceae).**

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Meliaceae is an economically valuable family of c. 740 species, with a high diversity of lifeforms and habitats throughout its predominantly pantropical distribution. Despite the economic and biological importance of the family, infra-familial relationships remain unclear. Further, recent fossil evidence brings the assumed African origin of the family into question. In an effort to resolve the phylogeny of Meliaceae and reconstruct its biogeographic history, we generated the first, genus-complete tree of the family using the Angiosperm353 loci. This tree improves the resolution of phylogenetic relationships for much of the tree, and indicates that many tribes and genera are not monophyletic and are in need of taxonomic revision. We also find evidence for a history of genome duplication and historic hybridisation within some clades of the family. We conducted a sequential divergence dating and ancestral area analysis on a species-level Meliaceae tree generated through the combination of our NGS data and Sanger data from GenBank, which sheds light on recent biogeographic history, but results in ambiguous ancestral areas for deeper nodes. We are now using a combined-evidence phylogenetic model under a Fossilized-Birth-Death process where tree topology, divergence ages and ancestral areas are simultaneously estimated, and informed by fossil age and locality.

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