

A target capture approach for phylogenomic analyses at multiple evolutionary timescales in rosewoods (*Dalbergia* spp.) and the legume family (Fabaceae)

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December 17, 2021

Abstract

Understanding the genetic changes associated with the evolution of biological diversity is of fundamental interest to molecular ecologists. The assessment of genetic variation at hundreds or thousands of unlinked genetic loci forms a sound basis to address questions ranging from micro- to macro-evolutionary timescales, and is now possible thanks to advances in sequencing technology. Major difficulties are associated with i) the lack of genomic resources for many taxa, especially from tropical biodiversity hotspots, ii) scaling the numbers of individuals analyzed and loci sequenced, and iii) building tools for reproducible bioinformatic analyses of such datasets. To address these challenges, we developed a set of target capture probes for phylogenomic studies of the highly diverse, pantropically distributed and economically significant rosewoods (*Dalbergia* spp.), explored the performance of an overlapping probe set for target capture across the legume family (Fabaceae), and built a general-purpose bioinformatics pipeline. Phylogenomic analyses of *Dalbergia* species from Madagascar yielded highly resolved and well supported hypotheses of evolutionary relationships. Population genomic analyses identified differences between closely related species and revealed the existence of a potentially new species, suggesting that the diversity of Malagasy *Dalbergia* species has been underestimated. Analyses at the family level corroborated previous findings by the recovery of monophyletic subfamilies and many well-known clades, as well as high levels of gene tree discordance, especially near the root of the family. The new genomic and bioinformatics resources will hopefully advance systematics and ecological genetics research in legumes, and promote conservation of the highly diverse and endangered *Dalbergia* rosewoods.

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