

Evolution and biogeography of *Memecylon*

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Abstract

Premise

The woody plant group *Memecylon* (Melastomataceae) is a large clade occupying diverse forest habitats in the Old World tropics and exhibiting high regional endemism. Its phylogenetic relationships have been previously studied using ribosomal DNA with extensive sampling from Africa and Madagascar. However, divergence times, biogeography, and character evolution of *Memecylon* remain uninvestigated. We present a phylogenomic analysis of *Memecylon* to provide a broad evolutionary perspective of this clade.

Methods

One hundred supercontigs of 67 *Memecylon* taxa were harvested from target enrichment. The data were subjected to coalescent and concatenated phylogenetic analyses. A timeline was provided for *Memecylon* evolution using fossils and secondary calibration. The calibrated *Memecylon* phylogeny was used to elucidate its biogeography and ancestral character states.

Results

Relationships recovered by the phylogenomic analyses are strongly supported in both maximum likelihood and coalescent-based species trees. *Memecylon* is inferred to have originated in Africa in the Eocene and subsequently dispersed predominantly eastward via long-distance dispersal (LDD), although a reverse dispersal from South Asia westward to the Seychelles was postulated. Morphological data exhibited high levels of homoplasy, but also showed that several vegetative and reproductive characters were phylogenetically informative.

Conclusions

The current distribution of *Memecylon* appears to be the result of multiple ancestral LDD events. Our results demonstrate the importance of the combined effect of geographic and paleoclimatic factors in shaping the distribution of this group in the Old World tropics. *Memecylon* includes a number of evolutionarily derived morphological features that contribute to diversity within the clade.