

**Myrteae phylogeny, calibration, biogeography and diversification patterns:  
Increased understanding in the most species rich tribe of Myrtaceae**

**ABSTRACT**

Myrteae (c. 2500 species; 51 genera) is the largest tribe of Myrtaceae and an ecologically important group of angiosperms in the Neotropics. Systematic relationships in Myrteae are complex, hindering conservation initiatives and jeopardizing evolutionary modelling. A well-supported and robust phylogenetic hypothesis was here targeted towards a comprehensive understanding of the relationships within the tribe. The resultant topology was used as a base for key evolutionary analyses such as age estimation, historical biogeography and diversification rate patterns. One nuclear (ITS) and seven chloroplast (*psbA-trnH*, *matK*, *ndhF*, *trnI-trnF*, *trnQ-rps16*, *rpl16* and *rpl32-trnL*) DNA regions for 115 taxa representing 46 out of the 51 genera in the tribe were accessed and analysed using maximum likelihood and Bayesian inference tools for phylogenetic reconstruction. Dates of diversification events were estimated and contrasted using two distinct fossil sets (macro and pollen) in BEAST. The subsequent dated phylogenies were compared and analysed for biogeographical patterns using BioGeoBEARS and diversification rates using BAMM. Myrteae phylogeny presents strong statistical support for three major clades within the tribe: Australasian group, Myrtus group and Main Neotropical Lineage. Dating results from calibration using macrofossil are an average of 20 million years older and show an early Paleocene origin of Myrteae, against a mid-Eocene one from the pollen fossil calibration. Biogeographic analysis shows the origin of Myrteae in Zealandia in both calibration approaches, followed by a widespread distribution throughout the still-linked Gondwana continents and diversification of Neotropical endemic lineages by later vicariance. Best configuration shift indicates three points of acceleration in diversification rates, all of them occurring in the Main Neotropical Lineage. Based on the reconstructed topology, several new taxonomic placements were recovered, including: the relative position of *Myrtus communis*, the placement of the *Blepharocalyx* group, the absence of generic endemism in the Caribbean, and the paraphyly of the former *Pimenta* group. Distinct calibration approaches affect biogeography interpretation, increasing the number of necessary long distance dispersal events in the topology with older nodes. It is hypothesised that biological intrinsic factors such as modifications of embryo type and polyploidy might have played a role in

accelerating shifts of diversification rates in Neotropical lineages. Future perspectives include formal subtribal classification, standardization of fossil calibration approaches and better links between diversification shifts and trait evolution.