



## Evolutionary history of tropical tree species complexes: species delimitation and adaptive genetic variation in the Brazil nut clade (Lecythidaceae)

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**CHALLENGES IN  
TROPICAL ECOLOGY AND CONSERVATION -  
GLOBAL PERSPECTIVES**

## PARALLEL RADIATIONS IN NEOTROPICAL ANNONACEAE TRACK NEOGENE UPHEAVAL OF THE SOUTH AMERICAN CONTINENT

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Much of the immense present day biological diversity of Neotropical rainforests originated from the Miocene onwards, a period of geological and ecological upheaval in South America. We assess the impact of the Andean orogeny, drainage of lake Pebas, and closure of the Panama Isthmus on two clades of tropical trees (*Crematosperma*, c. 31 spp.; and *Mosannona*, c. 14 spp.; both Annonaceae).

Phylogenetic inference revealed similar patterns of geographically restricted clades and molecular dating showed diversifications in the different areas occurred in parallel, with timing consistent with Andean vicariance and Central American geodispersal. Ecological niche modelling approaches show phylogenetically conserved niche differentiation, particularly within *Crematosperma*. Niche similarity and recent common ancestry of Amazon and Guianan *Mosannona* species contrasts with dissimilar niches and more distant ancestry of Amazon, Venezuelan and Guianan species of *Crematosperma* suggesting that this element of the similar patterns of disjunct distributions in the two genera is instead a biogeographic parallelism, with differing origins. The results provide further independent evidence for the importance of the Andean orogeny, the drainage of Lake Pebas, and the formation of links between South and Central America in the evolutionary history of Neotropical lowland rainforest trees.

## EVOLUTIONARY HISTORY OF TROPICAL TREE SPECIES COMPLEXES: SPECIES DELIMITATION AND ADAPTIVE GENETIC VARIATION IN THE BERTHOLLETIA CLADE (LECYTHIDACEAE)

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Tropical tree species complexes harbour closely related species that display shared alleles and that are difficult to delimit using phylogenetic approaches. Such species complexes arise when lineage sorting is slow due to large effective population sizes typical in trees, when diversification is accompanied by interspecific gene flow, or due to a combination of both processes. The concerned species are often difficult to distinguish morphologically due to high phenotypic trait variation. The large intraspecific variation typical of tree species complexes promotes adaptive processes, suggesting that species complexes are important in the diversification of tropical tree biodiversity. The evolutionary histories of these systems remain however poorly understood.

We here investigated the evolutionary history of tropical tree species complexes by examining the phylogeny and population genetic processes in sympatric taxa of the Bertholletia clade (Brazil nut clade, Lecythidaceae) in French Guiana. We sampled 192 individuals belonging to 26 tree species of the Bertholletia clade and sequenced them at nine plastid, eight mitochondrial and 134 putative nuclear loci derived from double-digest restriction site associated DNA sequencing (ddRAD-Seq). Phylogenetic methods recovered the expected large sub-clades within the Bertholletia clade, but genetic clustering methods were needed to delimit species within these clades. Some common species such as *Eschweilera coriacea*, harboured several sympatric gene pools, indicative of hitherto undescribed cryptic species. Outlier detection methods revealed that few single nucleotide polymorphisms (SNPs) were strongly diverged among gene pools, whereas a significant portion of SNPs was more shared than expected *a priori* in sympatric populations. The local pattern of allele sharing pointed to hybridization, rather than incomplete lineage sorting. Taken together, our results suggest that hybridization is important for adaptive evolution in tropical tree species complexes.

