

# Phylogenetic Discordance Between Species Tree and Functional Gene Trees of Fagaceous genera <sup>†</sup>

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**Abstract:** Fagaceae species predominate a diverse range of habitats in the northern hemisphere and are critical to the ecosystem and economy. The high morphological and genetic diversity of these species serves as the foundation for adaptation to environmental stress. To comprehend the diversity, an evolutionary viewpoint is required. However, we found extensive conflicts among gene trees at the genus level, resulting in inconclusive phylogenetic inferences based on various genetic markers. Unresolved phylogeny would affect taxonomy, biogeographic inference, and ancestral state. In this study, we aimed to look deeply into the source of phylogenetic discordance in Fagaceae. We sampled 65 species from six genera (*Fagus*, *Lithocarpus*, *Quercus*, *Castanea*, *Castanopsis*, and *Notholithocarpus*) and obtained 603,809 SNPs from transcriptome sequences. In addition to concatenated and coalescence-based approaches for phylogenetic inference, we also reconstruct 256 gene topologies to investigate conflict among nuclear genes. Our results show that the conflicts arise mainly from the relationship between *Lithocarpus* and *Quercus*, with approximately 34% of genes supporting the two genera as a sister group. We also try to know why the genes of minority topologies are different from those of majority topologies. To answer the question, we performed a functional enrichment analysis to determine the function of the minority topological genes. According to the GO terms, their functions are primarily related to cellular structure or organelle. In the following step, we would investigate whether the main sources of discordance are introgression, incomplete lineage sorting, or selection.

**Keywords:** Fagaceae; transcriptomes; phylogenomics; topological test; gene trees; species trees; GO terms

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