



Abstract

Phylogenetic Discordance between Species Tree and Functional Gene Trees of Fagaceous Genera [†]

Min-Xin Luo , Chien-Ti Chao, Jui-Tse Chang and Pei-Chun Liao * 

Department of Life Science, National Taiwan Normal University, Taipei 116059, Taiwan

* Correspondence: pcliao@ntnu.edu.tw

[†] Presented at the 3rd International Electronic Conference on Forests—Exploring New Discoveries and New Directions in Forests, 15–31 October 2022; Available online: <https://iecf2022.sciforum.net/>.

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 reconstructed 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 understand 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 will 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



Citation: Luo, M.-X.; Chao, C.-T.; Chang, J.-T.; Liao, P.-C. Phylogenetic Discordance between Species Tree and Functional Gene Trees of Fagaceous Genera. *Environ. Sci. Proc.* **2022**, *22*, 27. <https://doi.org/10.3390/IECF2022-13045>

Academic Editor:
Filippos Aravanopoulos

Published: 15 October 2022

Publisher's Note: MDPI stays neutral with regard to jurisdictional claims in published maps and institutional affiliations.



Copyright: © 2022 by the authors. Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<https://creativecommons.org/licenses/by/4.0/>).

Supplementary Materials: The presentation material of this work is available online at <https://www.mdpi.com/article/10.3390/IECF2022-13045/s1>.

Author Contributions: Conceptualization, P.-C.L.; methodology, M.-X.L. and P.-C.L.; formal analysis, M.-X.L.; collecting samples, M.-X.L. and C.-T.C.; writing—original draft preparation, M.-X.L. and P.-C.L.; writing—review and editing, C.-T.C. and J.-T.C.; project administration, P.-C.L.; funding acquisition, P.-C.L. All authors have read and agreed to the published version of the manuscript.

Funding: This research was financially supported by the National Science and Technology Council (NSTC) of Taiwan (109-2621-B-003-003-MY3 and 110-2628-B-003-001) to P.-C.L. This article was also subsidized by the National Taiwan Normal University (NTNU).

Institutional Review Board Statement: Not applicable.

Informed Consent Statement: Not applicable.

Data Availability Statement: Not applicable.

Conflicts of Interest: The authors declare no conflict of interest.