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Improvement of taxonomical classification of the Lauraceae family using DNA barcoding and RAD-seq approaches

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Abstract

The economically and ecologically significant Lauraceae family is a predominantly woody plant family comprising roughly 50 genera and up to 3,500 species. However, the systematic classification of Lauraceae has been controversial due to the poorly resolved taxonomy of this family, which makes it difficult to accurately identify species for their conservation management, proper uses and understanding of their ecological function. In order to address the establishment of a reliable barcoding reference database and phylogenetic relationships within the family, leaf samples had been previously collected from four different land use types: (1) logged-over primary rain forest (old growth forest), (2) jungle rubber agroforestry, (3) rubber plantations, and (4) oil palm plantations in Jambi Province, Sumatra, Indonesia. In addition, their nucleotide sequences were also generated using the *rbcL* and *matK* genes. The phylogenetic tree constructed from the *rbcL, matK*, and their concatenated sequences show the distinct phylogenetic placements among the examined Lauraceae species, as well as authenticate the morphologically identified Lauraceae species. The *trnH-psbA, rpb2* and ITS genes will also be used to generate sequencing data for initial species identification. However, closely related species are not well resolved at these markers. Therefore, RAD-seq (restriction site-associated DNA sequencing) will be applied to provide a more in-depth view of the phylogenetic relationships among the species within the family, to develop SNPs without relying on the reference genomes and to identify species-diagnostic markers. The results will be instrumental for a better understanding of the evolutionary history of the Lauraceae and the assessment of species diversity for the conservation of the tropical forest ecosystem.

Keywords: DNA barcoding, Lauraceae, phylogeny, RAD-seq, SNP markers, species identification

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