

Abstract

Project Code : TRG5780196

Project Title : A Phylogeny of the Genus *Dimocarpus* Based on Molecular and Morphological Evidence.

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Abstract:

Dimocarpus longan, commonly known as the longan, belongs to the family *Sapindaceae*, and is one of the most economically important fruits commonly cultivated in several regions in Asia. There are various cultivars of longan throughout the Thai-Malay peninsula region, but until now no phylogenetic analysis has been undertaken to determine the genetic relatedness of these cultivars. To address this issue, 6 loci, namely ITS2, *matK*, *rbcL*, *trnH-psbA*, *trnL-I* and *trnL-trnF* were amplified and sequenced from 40 individuals consisting of 26 longan cultivars 2 types of lychee and 8 herbarium samples. The sequencing results were used to construct a phylogenetic tree using the neighbor-joining (NJ), maximum likelihood and Bayesian inference (BI) criteria. The tree showed cryptic groups of *D. longan* from the Thailand-Malaysia region (*Dimocarpus longan* spp.). This is the first report of the genetic relationship of *Dimocarpus* based on multi-locus molecular markers and morphological characteristics. Multiple sequence alignments, phylogenetic trees and species delimitation support that *Dimocarpus longan* spp. *longan* var. *obtusius* and *Dimocarpus longan* spp. *malesianus* var. *malesianus* should be placed into a higher order and are two additional species in the genus *Dimocarpus*. Therefore these two species require nomenclatural changes as *Dimocarpus malesianus* and *Dimocarpus obtusius*, respectively.

Keywords : *Dimocarpus*, longan, Phylogenetic tree, Multiple sequence alignments, species delimitation.