Intraspecific Diversity of Elaeocarpus Montanus Thwaites in Sri Lanka, Based on Molecular Data

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Elaeocarpus montanus Thwaites (family Elaeocarpaceae) is a medium-sized tree with nearly globular, tinged red brown colour fruits confined to the montane forests of Sri Lanka. A recent morphometric study carried out on the genus *Elaeocarpus* in Sri Lanka, based on field collected samples, revealed morphological variations among populations within the species, recognizing three phenetic groups. Given its status as an endemic species classified as vulnerable on the IUCN Red List 2020, a comprehensive taxonomic study is imperative for the conservation of *E. montanus* in Sri Lanka. Hence, the current study was aimed to reassess the phenetic groups identified through morphometric analysis and to establish a phylogenetic framework for confirming the monophyly of *E. montanus*, employing molecular sequence data. Three specimens were collected from each population, representing the three phenetic groups. The genomic DNA extractions of fresh leaf samples were carried out using the modified CTAB method with an addition step of sorbitol pre-washing. The *trn*L-*trn*F, ITS, *matK* and *trnH-psbA* regions were PCR amplified and sequenced. Phylogenetic trees were constructed based on Maximum Parsimony method, along with model-based methods, Maximum Likelihood and Bayesian Analysis. *Elaeocarpus angustifolius* was used as the out group. Although the *E. montanus* was supported as a monophyletic taxon in all analyses, the populations within the species representing the three phenetic groups, even though resolved as separate clades, were weakly supported (Posterior Probability less than 0.005) and unresolved. The sequence diversity in the selected barcoding regions was not adequate (genetic distances less than 0.002) to support the phenetic grouping. Therefore, a detailed molecular analysis of populations is necessary to reveal the levels of population diversity, isolation and the taxonomic position of *E. montanus*.

Keywords: Conservation, Molecular Data, Phylogenetics, Population Level Sub-Structuring

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