Application of DNA barcoding markers to the identification of *Hopea* species

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**ABSTRACT.** *Hopea chinensis* (synonym: *H. hongayensis*) (Dipterocarpaceae) is a threatened species found so far in only two locations: Quang Ninh (Vietnam) and Guangxi (China). The species shares many morphological characteristics with *H. mollissima* and the two species are often confused. To overcome this problem of identification and to investigate the genetic relationships of *Hopea* species with other Dipterocarp species, we sequenced three candidate DNA barcodes for the chloroplast markers rbcL, trnH-psbA, and matK. These markers were used separately and in different combinations to determine whether they could establish an accurate and effective identification system for *H. chinensis* in Quang Ninh (Vietnam). Our analyses indicated that two of the candidate DNA barcodes, matK and rbcL, performed best. We also generated a neighbor-joining phylogenetic tree and confirmed the presence of four *Hopea* species (*H. odorata*, *H. hainanensis*, *H. mollissima*, and *H. chinensis*) in nature reserves and natural parks of Vietnam. These species showed a close relationship with an average
genetic distance of 0.0045; both matK and rbcL separated all species, but their use in combination gave higher bootstrap values. The matK region was found to provide the most reliable barcode for the identification of the most closely related Dipterocarp species. Our study provides a means to identify rare Hopea species non-ambiguously and to support the protection of this decreasing natural genetic resource.

Key words: Hopea chinensis; Chloroplast DNA; Genetic relationship; Dipterocarpaceae