



Genetic variation in and spatial structure of natural populations of *Dipterocarpus alatus* (Dipterocarpaceae) determined using single sequence repeat markers

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ABSTRACT. *Dipterocarpus alatus* (Dipterocarpaceae) is widely distributed in lowland forests in central and southern Vietnam, Cambodia, Laos, Myanmar, Philippines, Thailand, and India. Due to over-exploitation and habitat destruction, the species is now threatened. The genetic variation within and among populations of *D. alatus* was investigated on the basis of 9 microsatellite (single sequence repeat, SSR) loci. In all, 268 sampled trees from 10 populations in central and southern Vietnam were analyzed in this study. The SSR data showed

a high genetic variability within populations with an average of $H_o = 0.209$ and $H_E = 0.239$. Genetic differentiation among populations was high ($F_{ST} = 0.266$), indicating limited gene flow ($N_m = 0.69$). Analysis of molecular variance showed that most genetic variation was within populations (74.96%). This study highlights the importance of conserving the genetic resources of *D. alatus* species.

Key words: *Dipterocarpus alatus*; Genetic variation; Species conservation; SSR markers