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THE GENETICS STRUCTURE OF THREE THREATENED *HOPEA* SPECIES (DIPTEROCARPACEAE) IN THE PROTECTED AREAS OF VIETNAM

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ABSTRACT

A total of 237 samples from ten populations of three threatened species (Hopea chinensis (Merr.) Hand.-Mazz. (native to coastal islands in a Quang Ninh province), H. odorata Roxb. (in lowland forests) and H. hainanensis Merr. et Chun. (in only two provinces (Ninh Binh and Thanh Hoa)) was studied the genetics structure based on ten SSR primers. The results showed that inbreeding was only significant in an island population of H. chinensis, a bottleneck event could be detected in H. odorata and H. hainanensis populations. Allele frequency and genetic diversities were lowest for H. hainanensis. Population inbreeding was only significant in an island population of H. chinensis whereas indications of a bottleneck event could be detected in populations of H. odorata and H. hainanensis. Bayesian analysis and F_{ST} values suggested high genetic divergence between populations in H. hainanensis (F_{ST} = 0.230) and H. odorata (F_{ST} = 0.251) even at about one hundred km distance. This study highlights the importance of conserving the genetic resources of Hopea species in different protected areas and at short geographic distance. It is proposed to search in more detail for potential inbreeding effects of the endangered H. chinensis and for bottleneck events in natural and planted stands of the other species.

KEYWORDS: *Dipterocarp, Hopea, Tropical Tree, Inbreeding, Bottleneck, Microsatellites, Vietnam*

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