Patterns of genetic structure and variation of merkus pine (*Pinus merkusii*) in Indonesia

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Abstract

The genetic structure and variation of *Pinus merkusii* from two natural populations in Sumatra and one artificial population (seed orchard) in Java were evaluated using isoenzymes as genetic markers. Moderate levels of genetic variation were found in a conservation stand in Aceh (Sumatra) and a seedling seed orchard in Java included in the present study, while no variation was observed in a population from a national park in Kerinci (Sumatra). Genetic variation measures of the seed trees, progenies (embryos) and effective pollen in these populations were determined using eight isoenzyme loci (GOT-B, GOT-C, GOT-D, PGM-A, PGM-B, SKDH-A, NDH-A and FDH-A). In both of the variable populations 80% of the loci were polymorphic. Analysis of the seed trees showed that effective number of alleles per locus (A/L), allelic diversity (v), gametic diversity (v_{gam}) and total population differentiation ($\delta_T = H_e$) in the population from Aceh (Sumatra) were 2.0, 1.544, 40.953 and 0.361 respectively, while in the population of Java they were 2.4, 1.630, 62.516 and 0.395 respectively. At the progeny level (embryo level), the above measures for the population from Aceh were 2.0, 1.565, 46.023 and 0.362 respectively, while in the population from Java they were 2.4, 1.636, 63.448 and 0.389 respectively.

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