GENETIC DIVERSITY OF KELAMPAYAN USING DOMINANT DNA MARKERS BASED ON INTER-SIMPLE SEQUENCE REPEATS IN SARAWAK

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Abstract

Neolamarckia cadamba (Roxb.) Bosser, or locally known as kelampayan, is a fast-growing timber species which produces one of the best sources of raw material for the plywood industry and also for the pulp and paper industry. It has been selected as one of the promising plantation tree species for large-scale planted forest development in Sarawak. Therefore, the molecular characterization of this indigenous tropical tree species is needed to maintain its high quality. Inter-simple sequence repeats (ISSR) markers were used in this study to determine the genetic diversity of kelampayan in three progeny trial blocks at the Landeh Nature Reserve, Semengok, Sarawak. The seeds were collected from the selected mother trees located at the Pasai Bon, Niah and Lawas seed production areas (SPAs) in Sarawak. Three ISSR primers, namely $(GTG)_6$, $(AG)_{10}$ and $(AC)_{10}$, that yielded reproducible, informative and scorable fragments were chosen for ISSR analysis. A total of 64 loci were generated of which 45.3–74.6% of the loci were identified as polymorphic bands with the size ranging from 500 bp to 2 kb among 247 kelampayan progenies selected in the present study. Molecular diversity based on Shannon's diversity indices (I) among 247 trees ranged from 0.268 to 0.350. In general, the kelampayan trees in the three progeny trial blocks exhibited a high level of molecular diversity and DNA polymorphism compared with its natural populations. This preliminary information will form the base for kelampayan tree improvement and conservation programmes.