



Genetic characterization of red-colored heartwood genotypes of Chinese fir using simple sequence repeat (SSR) markers

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ABSTRACT. The present study investigated the genetic characterization of red-colored heartwood Chinese fir [*Cunninghamia lanceolata* (Lamb.) Hook.] in Guangxi using 21 simple sequence repeat (SSR) markers and analyzes of the genetic variation (N = 149) in samples obtained from five sites in Guangxi Province, China. The number of different alleles and the Shannon's information index per locus ranged from 3 to 12 and from 0.398 to 2.258 with average values of 6 and 1.211, respectively, indicating moderate levels of genetic diversity within this germplasm collection. The observed and expected heterozygosity ranged from 0.199 to 0.827 and from 0.198 to 0.878 with an average of 0.562 and 0.584, respectively. Although, the mean fixation index was 0.044, indicative of a low level of genetic differentiation among germplasms, analysis of molecular variance revealed considerable differentiation (99%) within the

samples. The neighbor-joining dendrogram revealed that the majority of red-colored Chinese fir genotypes were apparently not associated with their geographic origins. Further analysis by STRUCTURE showed that this Guangxi germplasm collection could be divided into three genetic groups comprising 76, 37, and 36 members, respectively; these were classified into mixed groups with no obvious population structure. These results were consistent with those of the cluster analysis. On the whole, our data provide a starting point for the management and conservation of the current Guangxi germplasm collection as well as for their efficient use in Chinese fir-breeding programs.

Key words: Red-colored heartwood; Chinese fir; Genetic diversity; Genetic differentiation; Molecular marker