UNIVERSITI TEKNOLOGI MARA

ASSESSMENT OF IRAP AND REMAP MARKERS FOR EVALUATION OF GENETIC DIVERSITY OF *Eurycoma longifolia*

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ABSTRACT

Eurycoma longifolia is among the most precious medicinal herbs in Malaysia and due to the current scenario, Forest Research Institute of Malaysia (FRIM) has started to venture on the plant improvement research of the species. However, limitations on the informative genetic diversity have hindered many related further studies such as breeding programme. Thirteen Inter-retrotransposon Amplified Polymorphism (IRAP) and 12 Retrotransposon-Microsatellite Amplified Polymorphism (REMAP) markers were screened for their transferability to be used as markers for the assessment of genetic diversity of *E. longifolia* within and between three provenances; Forest Reserve of Bukit Beruang (Melaka), Forest Reserve of Kapas Island (Terengganu) and Forest Reserve of Maokil (Johor) in Peninsular Malaysia. Findings of the study showed that retrotransposon elements were presence in the DNA genome of *E. longifolia*. The screening of IRAP markers showed four single primers and two combinations of primers effectively utilized to analyse the genetic diversity of *E. longifolia*. The Percentage of Polymorphic Band (PPB) ranged from 50.0% to 100.0% and the Polymorphism Information Content (PIC) values of the markers ranged from 0.4691 to 0.8332 with the average of 0.6816. The PIC values for all primers recorded were more than 0.50 except for the combination of primers Sukkula-9900 and Copia-F, and the Heterozygosity (He) values recorded ranged from 0.5647 to 0.8517. However, screening of REMAP markers showed no interaction between retrotransposon and microsatellite markers, which implies that the markers were not effective. In term of genetic diversity assessment, the total diversity (H_T) recorded was 0.2396 and the diversity within population (H_S) was 0.2233. Coefficient of gene differentiation (G_{ST}) value recorded was 0.0680 and the value signified that there were 6.8% of the total genetic variations between the provenances and 93.2% variations among individual accessions within the provenances. In conclusion, retrotransposon elements were present in the DNA genome of *E. longifolia*, there were six IRAP markers have been effectively utilized to analyse the genetic diversity of *E. longifolia* and the genetic variations between selected provenances were lower than genetic variations within the provenances.

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