

Molecular characterization of *Jatropha curcas* germplasm using inter simple sequence repeat (ISSR) markers in Peninsular Malaysia

ABSTRACT

Molecular characterization and evaluation of germplasm was carried out using 10 Inter simple sequences repeat (ISSR) on 48 accessions of *Jatropha curcas* (L) collected from three states (Kelantan, Selangor and Terengganu) in Peninsular Malaysia. The stem cuttings of these *J. curcas* accessions were collected, raised in the nursery and then transferred to the experimental site at University Agricultural Park. The 48 *J. curcas* accessions were grouped into three different populations based on the state from where they were collected. Percentage polymorphism in these three populations ranged from 90.75% (Terengganu) to 100% (Kelantan). Analysis of molecular variance (AMOVA) showed that 94 % of the total variation was observed within the populations while variation among the populations accounted for the remaining 6%. A dendrogram produced by Unweighted Pair Group Method with Arithmetic Mean (UPGMA) based on Nei's genetic distance grouped the whole germplasm into 11 distinct clusters. Based on the information from this dendrogram, accessions that are far from each other by virtue of genetic origin and diversity index are strongly recommended to be used as parent for crossing. This will bring about greater genetic diversity, thus resulting into increase in selection gain. This will also lead to high productive index in terms of increase in fruit yield per hectare, oil yield, seed weight and other yield components. Therefore, accessions, B-01-03, T-01-09, B-04-01 and T-01-01 could be crossed with accessions D-04-02, B-05-05, B-01-04, and D-01-06 for the improvement of *J. curcas* in future breeding program.

Keyword: AMOVA; Genetic diversity; ISSR; *Jatropha curcas* L; Molecular breeding; Selection gain