Analysis of Genetic Diversity using RAPD Markers for Intraspecific Breeding in *Jatropha curcas*

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Abstract—Jatropha curcas L., an important biofuel feedstock was introduced in the country as one of the tree borne oilseed crop in India. The major limitation is its non-stable yield. Jatropha being perineal can be accommodated in problematic soils with dual purpose of improving the soil condition and also as a feedstock resource. Improving the yield potential of Jatropha is still a viable challenge. For the intra-specific breeding program to be successful, accessing the genetic diversity of the parents with molecular markers will be highly beneficial.

A total of 30 diverse germplasm consisting of 15 high yielding (1.5 -2.0 kg/plant) and 15 low yielding (> 0.75 kg/plant) Jatropha accessions were subjected to random amplified polymorphic DNA (RAPD) analysis to see if they are distinct at molecular level using 26 RAPD primers. The genetic association among genotypes was evaluated by calculating the Jaccard's similarity coefficient based on shared bands produced by primersusing NTSYS-PC20software. The dendogram was formed based on UPGMA, Principle component analysis (PCA) was performed to generate a two and three dimensional representation of genetic relationshipamong 30 genotypes of J.curcas

The result showed the selected primers showed high polymorphism (PIC values 0.439 – 0.867) among the 30 accessions. The dendrogram based on the similarity co-efficient divided the 30 accessions into two major clusters and the accessions from high yielding range formed one cluster and the low yielding accessions in another cluster. PCA also led to the segregation of theaccessions into the distinct groups, which reflected their clear grouping based on the seed yield trait. Thus the grouping of the parental accessions based on the yield for intra-specific breeding was reconfirmed at the molecular level. Hybridization involving these diverse accessions can be followed by molecular marker based selection for yield improvement.