

Isozyme polymorphism to detect genetic diversity of *Jatropha curcas* (L.) in India

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ABSTRACT

The Indian Government identified *Jatropha curcas* L. as the most suitable tree-borne oilseed for the production of bio-diesel. The species has spread to many parts of India due to its ability to withstand adverse conditions. Breeding of inter and intra specific *Jatrophas* for the exploitation of hybrid vigour is one of the most economical means of tree improvement. To study the genetic base of the species distributed in India, 55 accessions of *J. curcas* from Jammu to Kanyakumari and Jodhpur to Kolkata were assessed using isozyme markers. Fifteen enzyme systems were evaluated for their efficacy in distinguishing the accessions. While three (formate dehydrogenase, malate dehydrogenase and peroxidase) were found useful, twelve did not exhibit any variation and had fixed monomorphic alleles. Each polymorphic enzyme system produced one well resolved polymorphic region except peroxidase which had three. On an average 4 loci (26.67%) were found to be polymorphic (P) and mean observed number of alleles per locus (A) was 1.533. Average observed heterozygosity (H_o) was 0.1082 and expected value (H_e) was 0.0993 with and gene flow $Nm = 0.2177$ showing low level of genetic variation among different accessions suggesting poor segregation of genes over generations. The isozyme variation was measured by standard gene diversity measures using POPGENE v. 1.32. Dendrograms revealed very low heterozygosity leaving little scope for exploitation of hybrid vigour and suggesting that initiating breeding programmes with Indian land races may not lead to substantial genetic gain, vigorous seed set and higher volumes of oil yield.

Key words: *Jatropha curcas*, isozymes, genetic variability, dendrogram, heterozygosity

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