ORIGIN, DISTRIBUTION AND GENETIC DIVERSITY OF *JATROPHA CURCAS* IN INDIA

1. Principal Investigator: Dr. Rekha R. Warrier, Scientist - G

2. Duration of the Project: 2 years (2006-2008)

3. Total Budget: Rs. 4.07 lakhs

4. Objectives

- To study the diversity of *J. curcas* populations in India through isozymes and DNA based markers.

- To identify the genetic distinctiveness of the populations and arrive at unique populations.

5. Overall progress since the implementation of the project

Fifteen enzyme systems provided a total of 18 loci for the 56 accessions of *Jatropha curcas.* Twenty eight percent of the resolved isozyme loci were polymorphic on an average 26.67% were found to be polymorphic and mean observed number of alleles per locus was 1.533. Average observed heterozygosity was 0.15 and expected value was 0.14 with a gene flow value of 0.24. DNA extraction procedures were standardized to avoid latex contamination. PCR protocols were optimized by carrying out variations in $MgCl_2$ concentration, primer concentration, DNA and buffer volume. A total of 120 bands whose size ranged between 300 and 2000 bp were produced using 25 primers. Genetic identities at the RAPD level varied from 0.951 to 0.998, not significantly different from the values obtained at the isozyme level. Comparison of genetic variation showed that RAPDs consistently revealed higher levels of variability than isozymes in terms of percentage of polymorphic loci, gene flow and gene diversity. Yet, the numerical congruence between the isozyme and RAPD data suggests an indication that in *J. curcas* the isozyme data provides a fairly good picture of the genetic structure.