GENETIC DIVERSITY ANALYSIS OF *JATROPHA CURCAS* L. USING SNP-BASED HAPLOTYPES FOR GENES CONTROLLING FATTY ACID BIOSYNTHESIS AND LIPID BREAKDOWN IN SEEDS


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*Jatropha curcas* L. (2n=2x=22) is becoming a popular non-food oleaginous crop in several developed countries for its proposed value in the biopharmaceutical industry. Despite the potentials of its oil-rich seeds as a renewable source of biodiesel and an interest in large-scale cultivation, relatively little is known with respect to population genetics and plant genomics. We recently performed genomic DNA markers and FCSS analyses to gain insights on ploidy variation and heterozygosity levels of multiple accessions, and genomic relationships among commercial varieties and locally dominant ecotypes grown in different geographical areas (Ambrosi et al., 2010 Diversity 2(5): 810-836). Seeds commercialized worldwide seem to include a few closely related genotypes showing high degrees of homozygosity for single varieties and very low genetic diversity between varieties. For a better understanding of oil production and accumulation in *J. curcas* seeds, it would be useful to clone and characterize genes controlling key steps of FA biosynthesis and lipid breakdown pathways. Gene bank searches and bioinformatic analyses allowed us to select a number of genes encoding for enzymes involved in lipid metabolism. Some of these genes were previously isolated in *J. curcas* (i.e., acetyl-CoA carboxylase I-II, 3-ketoacyl-ACP I- II and III, acyl-ACP desaturase, and acyl-ACP thioesterase I-II), and their nucleotide and amino acid sequences were retrieved directly from the NCBI databases. Other genes were cloned and bioinformatically characterized in the present study (i.e., ATP-citrate lyase, 3-ketoacyl-ACP reductase, 3-hydroxyacyl-ACP dehydrase, enoyl-ACP reductase and acyl-CoA dehydrogenase). Genomic DNA samples deriving from an available core collection were used for multiple sequence alignments and discovery of functional SNPs. Replicated cDNA samples produced by retrotranscription of mRNAs from mature seeds were also obtained and used for comparative gene expression studies by means of quantitative Real-time PCT assays. This information was then exploited for haplotyping single accessions belonging to a worldwide collection of *J. curcas* commercial and local varieties to find out the most representative and discriminant SNP markers related to FA biosynthesis and lipid metabolism genes.