

A Transcriptomic and Proteomic Analysis of Developing and Germinating *Jatropha curcas* L. Seeds

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Although the potential of *J. curcas* seeds as a biodiesel source is widely recognised, very little is known about the patterns of oil and protein deposition during seed development and the mobilisation of these reserves during germination. The availability of this knowledge would be of importance for the creation of new genotypes tailored to meet the demands of the biodiesel industry. As a first step in this direction, two cDNA libraries from developing seeds and from germinating seeds were prepared and used to generate an EST database containing 12978 sequences, representing 6724 unique transcripts (4392 developing seeds, 2332 germinating seeds). In this database are represented most of the genes involved in fatty acid biosynthesis and degradation and proteinases involved in protein mobilisation. Also represented are transcript related to several allergenic proteins and to the metabolism of phorbol esters, the main toxic components of the seeds. The EST database is now being used as a primary databank for protein identification by mass spectrometry. Proteome reference maps corresponding to solubility based proteins fractions (albumins, globulins, glutelins and gliadins) of developing and germinating seeds were prepared. These reference maps allowed us to identify the protein spots corresponding to different developmental stages.

Kew words: *Jatropha curcas*, oil seeds, transcriptomics, proteomics

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