

JacEST - Sequencing of Expressed Sequence Tags in *Jatropha curcas*

Bomfim, V.C, Pitta, L., Mehana-Neto, A., Paulillo, L.C. M.S., Ferrão-Gonzales, A.D.,
Moreau, V.H.

Núcleo de Biotecnologia (NuBiotec), Faculdade de Tecnologia e Ciências (FTC),
Salvador, BA, Brazil.

Jatropha curcas is a plant from *Euphorbiaceae* family used as oil source and medicinal ends in India, China and Africa. *J. curcas* is expected to be a promise oil source for the biodiesel production due to its oil characteristics, yields of oil production and adaptivity, mainly to the Brazilian North-East region. Few genetic sequences are available from *J. curcas* in the Genebank and lack of genetic information shell became one of the obstacles to the genetic enhancement of the plant. Few details about gene sequences and expression are known or published. Acknowledgment about genes expression in response to environmental conditions and plant management would be important for genetic selection and enhancement of this plant for industrial farming. In this work, we build a whole-plant cDNA library from *J. curcas* in standard growing conditions. cDNA library was ligated to plasmid vectors and prepared for DNA sequencing and further genes identification. For this end, methods for aseptic germination and cultivation of the plant were developed in order to reduce microbial DNA contamination from seeds and soil used. Tissue-specific libraries are being built as well and will help us to characterize gene expression in different tissue and development steps of the plant. Sequences of the genes expressed in *J. curcas* will possibly direct the research in specific metabolic pathways of the plant and allow one to select and manipulate genetic characteristics desired for industrial cultivation and oil production. Supported by FAPESB.