WAGENINGEN UR
For quality of life

Global Evaluation of genetic variability in *Jatropha curcas*

L.R. Montes[1,2,3], C. Azurdia[3], R.E.E. Jongschaap[1], E.N. van Loo[1], E. Barillas[4], R. Visser[2] & L. Mejia[3]

Introduction

Jatropha curcas is a multi-purpose tree, originally growing in countries of the equatorial Americas, from where it has been spread to other tropical countries (Heller, 1996). Jatropha seeds are rich in oil and when extracted, pure plant oil can be used directly to produce light, warmth and electricity, or it can be used as a feedstock for bio-diesel. For this reason Jatropha is an attractive crop and it is rapidly introduced in commercial plantations and various rural development programs, as it may contribute with income generation and efficiency increase of rural and agricultural processes.

However, *J. curcas* is a wild species and no varieties with desirable traits for specific growing conditions are available, which makes growing Jatropha a risky business (Jongschaap *et al.*, 2007). The low phenotypic and genetic variability found in materials from Africa and Asia (e.g. Basha and Sajutha, 2007) display the need for new sources of genetic variation in *J. curcas* that can be used in breeding programs. Such genetic variation was identified in Latin America, especially in Guatemala.

Methodology

Around 225 accessions of *J. curcas* have been collected from over 30 countries in Latin America, Africa and Asia. Samples were analyzed (AFLP) at San Carlos University in Guatemala and by NBS-profiling in the Netherlands at Wageningen University and Research centre - Plant Research International (Van der Linden *et al.*, 2004).

Results

High phenotypic variation was found in all material from Latin America, such as in plant architecture (Figure 1).

Wild accession of J. curcas from Guatemala (left) and accession 'Cabo verde' from Nicaragua (right).

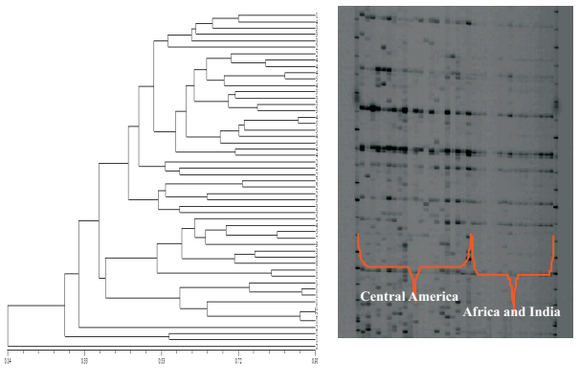

Figure 2. Dendrogram with Guatemalan accessions (left) and NBS-profiling with Central American, African and Indian accessions (right).

Genetic variability was low in African and Indian *J. curcas* accessions, but high genetic variability was found in Latin American accessions (Figure 2). This genetic variation will be used in breeding programs.

Conclusions

- Low genetic variation found in African and Indian accessions of *J. curcas*.
- High genetic variation found in Guatemalan and other Latin American accessions of *J. curcas*.
- New molecular marker technology (patent free): conserved sequence based on NBS-gene family.
- Intercrossing 'elite' *J. curcas* (e.g. 'Cabo verde') with low toxic and toxic Guatemalan accessions as starting point for breeding.
- Genetic analysis of segregating population now possible.

Literature

- Basha, S. D. and M. Sujatha, 2007. Inter and intra population variability of *Jatropha curcas* (L.) characterized by RAPD and ISSR markers and development of population-specific SCAR markers. Euphytica 156:375–386.
- Heller, J., 1996. Physic nut. *Jatropha curcas* L. Promoting the conservation and use of underutilized and neglected crops. 1. Institute of Plant Genetics and Crop Plant Research, Gatersleben/ International Plant Genetic Resources Institute, Rome.
- Jongschaap, R. E. E., W. J. Corré, P. S. Bindraban, and W. A. Brandenburg, 2007. Claims and Facts on *Jatropha curcas* L. Plant Research International B.V., Wageningen, the Netherlands, Report 158, 42 pp + annexes.
- Van der Linden, C. G., D. C. A. E. Wouters, V. Mihalka, E.Z. Kochieva, M. J. M. Smulders and B. Vosman, 2004. Efficient targeting of plant disease resistance loci using NBS profiling. Theor. Appl. Genet . 109: 384-393.

Wageningen UR Plant Breeding
P.O. Box 16
6700 AA Wageningen, The Netherlands
Tel: 0317 48 60 81 – Fax: 0317 48 34 57
E-mail: luisrodolfo.montesosorio@wur.nl

[1] **Plant Research International B.V**
[2] **Wageningen University, the Netherlands.**
[3] **San Carlos University, Faculty of Agriculture (FAUSAC), Guatemala.**
[4] **Biocombustibles de Guatemala S.A., Guatemala.**