

High level of molecular and phenotypic biodiversity in *Jatropha curcas* accessions from Central America compared to those from Africa, Asia and South America

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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 [1]. *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, *Jatropha curcas* is still a wild species and no varieties with desirable traits for specific growing conditions are available, which makes growing *Jatropha* a risky business [2]. The low phenotypic and genetic variability found in materials from Africa, Asia and South America [3, 4, 5 & 6] display the need for new sources of genetic variation in *Jatropha curcas* that can be used in breeding programs. Such genetic variation was identified in Central America.

This study analysed phenotypic and genetic variation in a new collection 182 accession from Central American, Asia, Africa and South-America.

Methodology

In the Global *Jatropha* Evaluation Programme (JEP; www.jatropha.wur.nl), a collection of 182 *J. curcas* accessions was established from Central America, South America, Africa and Asia. Genetic evaluation by different DNA marker (Target region amplification (TRAP), Simple sequence repeat (SSR) and Amplified Fragment Length Polymorphism (AFLP)) were used to establish the relationship and diversity amount the collection.

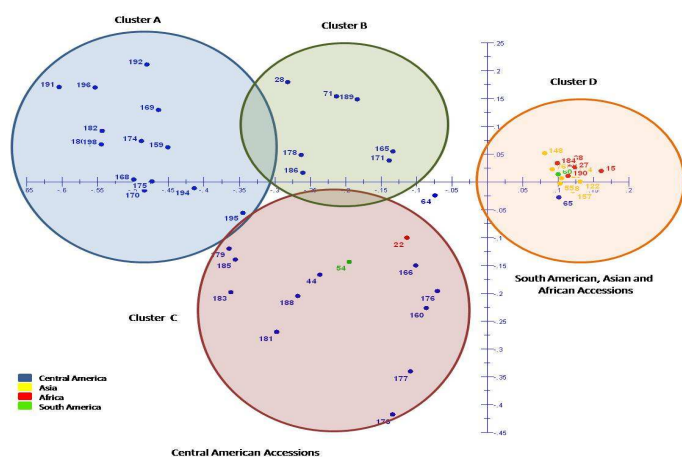


Figure 1. Principal component analysis plot for *Jatropha curcas* accessions of the JEP germplasm collection

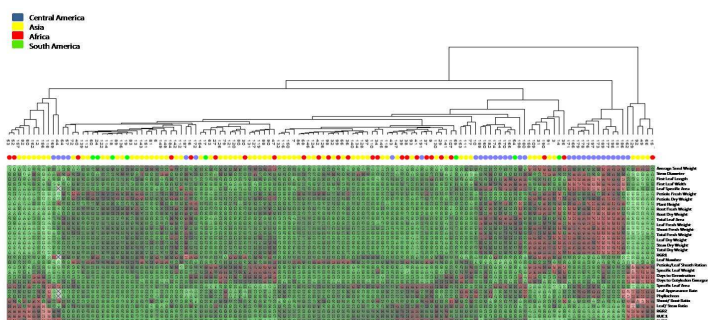


Figure 2. Morphology-based UPGMA dendrogram of *Jatropha curcas* accessions in the JEP collection.

Phenotypic evaluation were done on the collection by measuring different traits as seed oil content, fatty acid composition, relative growth rate (RGR), Network assimilation rate (NAR) and specific leaf area (SLA) in the seedling stage on the basis of a greenhouse experiment in Wageningen, The Netherlands.

Results.

Genetic variation was assessed with DNA-markers and by measuring early growth traits, seed oil content and fatty acid composition of the oil. Accession from Asia, Africa and South America cluster together in the cluster D (Fig.1). Central America accessions showed the higher genetic variability and are present in all cluster (Fig. 1). The Central American accessions of *Jatropha curcas* showed the highest level of DNA-marker variation.

The set of Central American accessions also showed the highest level of phenotypic variation for early growth traits, seed oil content and fatty acid composition (Fig 2). Central American accessions contained a higher level of linoleic acid (43.09%) and a lower level of oleic acid (34.51%) in seed oil than accessions from other continents. The heritability values for almost all the early growth traits was high (50%-88%) indicating a strong gene influence for the variation on almost all the traits evaluated. Except for petiole length and weight. A high level of genetic variation was found for RGR and its components SLA, LWR and NAR in our collection. In order to interpret the impact of an increase in RGR by plant breeding better, it will help to realise that an increase of only 10 % in RGR can result in a difference of 20 % in absolute dry matter accumulation in 60 days. Such improvements in early growth would be large enough to justify selection for early growth in breeding programs of *Jatropha*.

Conclusion

A wide range of genetic variation was found in a global set of *Jatropha curcas* accessions in which the Central America accessions showed the highest level of genetic variation. From this new set of accessions, varieties can be selected directly for establishing *Jatropha curcas* production fields now and parents can be chosen as starting point of new breeding programs.

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