Oil content increase and toxicity reduction in jatropha seeds through family selection

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A B S T R A C T

The objectives of this study were to verify the existence of genetic variability among half-sib families and select the best families in order to increase oil content and reduce toxicity in jatropha seeds. The experiment was carried out in complete randomized block design with two replications and five plants per plot, during five crop years (2010–2014). Plots were evaluated for grain yield (g/plant) and for weight of 100 seeds (g), and in the year of 2014, seed oil content and phorbol ester concentration (mg/g) were also evaluated. Analysis of variance was carried out considering genotypes as random, and from this analysis, genetic parameters were estimated for the characteristics of interest. Diversity analysis was carried out using the Mahalanobis distance matrix. Tocher and UPGMA clustering methods were also used. Gain with selection was estimated using the method of direct selection on the main variable and indirect selection on the other variables, based on the selection of the former. Different selection indexes wegain) in order to estimate the gain and select the top 20 families. The mulre also used (classic, base index, sum of ranks, multiplicative index and index based on the desired tiplicative index was the best index for jatropha because using this index we obtained gain for all traits together. It was concluded that there is genetic variability among half-sib families, and that selected families by multiplicative index made it possible to increase oil content and decrease toxicity in jatropha seeds.

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1. Introduction

Currently, the worldwide concern regarding the emission of toxic gases, which enhances the greenhouse effect and contribute to climate change, has been a commonplace subject of various international meetings (Naylor et al., 2007). Thus, many countries have invested lots of money on research of promising species for biofuel production (Bailis and Baka, 2011). Among these species, jatropha (Jatropha curcas L.) has stood out by the high oil content found in its seeds, and for the ability of transforming this oil into biofuel (Berchmans and Hirata, 2008; Pu et al., 2011).

Jatropha has numerous characteristics that makes it an economically viable crop, such as drought tolerance, since it can be grown in areas with less than 200 mm rainfall (Becker and Makkar, 2008); fast-growth; and easy propagation (Openshaw, 2000). Also, it can be grown in almost all altitudes, and plants can be productive for up to 50 years (Nithiyanantham et al., 2012). Moreover, jatropha has an average of 35% seed oil content, and the oil extracted from the seeds has 24.6% crude protein and 47.2% crude fat (Akintayo, 2004). This oil has good oxidation stability, when compared to soybean oil; low viscosity, when compared to castor oil; and low pour point, when compared to palm oil (Bailis and Mccarthy, 2011).

Although seeds are rich in oil and crude protein, they are highly toxic to animals and humans (Liberalino et al., 1988). Seeds toxicity makes the cultivation of this crop unfeasible, since it is necessary to make profit not only from the oil sale, but also from jatropha cake, which is a by-product extracted from the seeds used in animal feed (Nithiyanantham et al., 2012). Phorbol ester is the main substance

responsible for the toxicity of jatropha seeds (Adolf et al., 1984) and its concentration has varied from 2 to 6 mg/g of dry matter in toxic genotypes, and from 0 to 1.8 mg/g in nontoxic genotypes (Nithiyanantham et al., 2012). Thus, there is a need to achieve highly productive genotypes, with high seed oil content and with the lowest level of toxicity as possible. Once it is almost impossible to find this genotype in nature, it is necessary to use all the tools of a breeding program in order to find genotypes with characteristics similar to the ideal ones.

The success of a breeding program requires that appropriate selection methods are used so that each selection cycle keeps the genetic variability of the population and the high means of the characteristics of interest (Bhering et al., 2013). Thus, the estimate of genetic parameters, such as genetic variance and heritability, becomes crucial for proper selection of genotypes that will be used in the next selection cycle (Laviola et al., 2010). Many studies have been carried out in order to estimate genetic parameters and establish a jatropha base population (Bhering et al., 2013; Laviola et al., 2012, 2010; Spinelli et al., 2015). However, most of these studies aim at genetic gain in one or a few characteristics of economic interest.

Selection of superior genotypes should be simultaneously carried out for several characteristics of interest. However, this may hinder the selection of genotypes, especially when there are characteristics with negative genetic correlation. One way to minimize this problem is the use of selection indexes, which select individuals and simultaneously increase the mean of all characteristics. Therefore, the objectives of this study were to verify the existence of genetic variability among half-sib families collected throughout Brazil, and to select families with higher grain yield (grams/plant), higher seed oil content (Percentage) and lower toxicity.

2. Material and methods

The experiment was implemented in February 2009, in a complete randomized block design with 2 replications, and 5 plants per plot, arranged in rows, spaced 4 m between rows and 2 m between plants. All management practices were based on Carels et al. (2013) and Bahadur et al. (2012). The experiment consisted of the performance evaluation of 179 jatropha half-sib families.

During 5 crop years, from 2010 to 2014, plots were evaluated for grain yield (g/plant) and weight of 100 seeds (g). Seed oil content (percentage) and phorbol ester concentration in seeds (mg/g) were evaluated only in the year of 2014.

Analysis of variance and BLUP was carried out for each characteristic by the Genes software (Cruz, 2013), using data of the means of plots, in order to test the hypothesis of significant genetic variance among the means of half-sib families.

The following statistical model was used for oil content and phorbol ester concentration measured in one year only:

ANOVA

$$Y_{ijk} = \mu + B_j + F_i + \epsilon_{ijk},$$

with $i = 1, 2, \ldots 179$ families; e $j = 1, 2$ blocks.

where: Y_{ijk} is the observation in the k-th plant, in the i-th family, of the j-th block; μ is the population general mean; F_i is the effect of the i-th family, in which $F_i \sim \text{NID}(0, \sigma_g^2)$; b_j is the effect of the j-th block, in which $b_j \sim \text{NID}(0, \sigma_d^2)$; ϵ_{ij} is the effect of environmental variation among families, in which $\epsilon_{ij} \sim \text{NID}(0, \sigma^2)$.

BLUP

$$y = X_m + Z_g + W_p + e$$

where: Y is the observation in the k-th plant, in the i-th family, of the j-th block; μ is the population general mean (fixed); g is genotypic
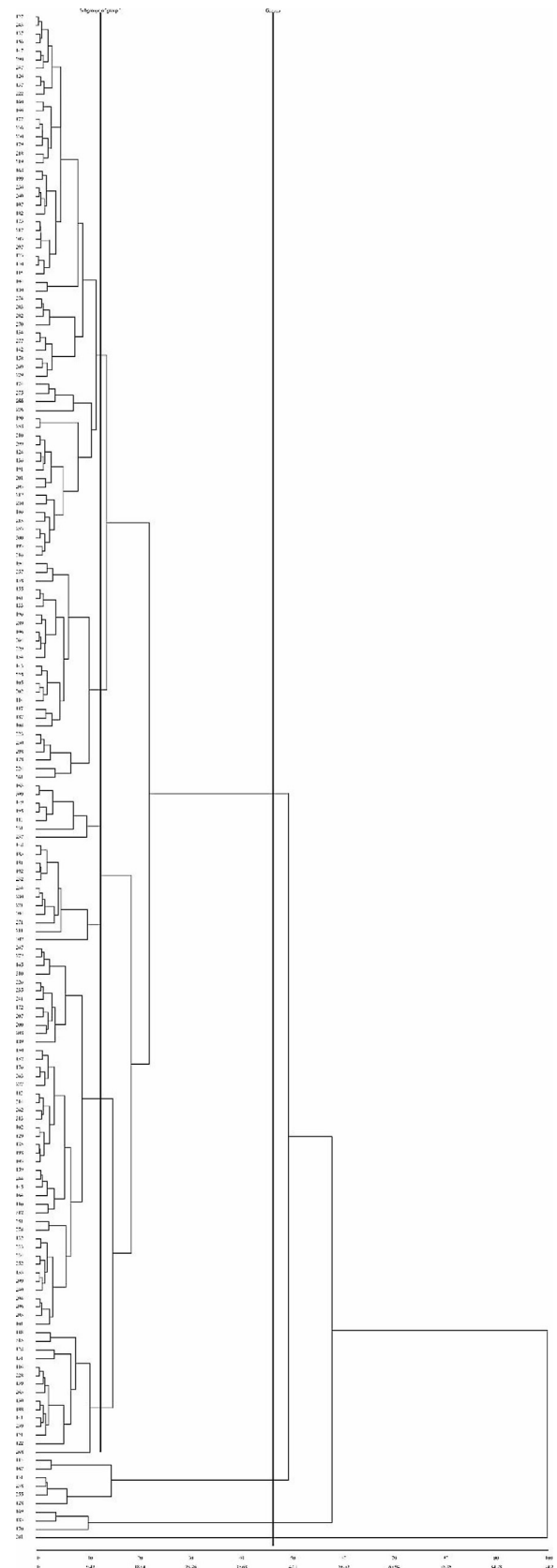

Fig. 1. Clustering of 179 jatropha half-sib families using UPGMA method performed using Mahalanobis distance. The traits used to estimated Mahalanobis distance were yield, weight of 100 seeds, oil content and phorbol ester.