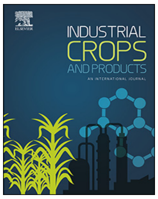
Industrial Crops & Products 119 (2018) 290–293

Contents lists available at ScienceDirect

Industrial Crops & Products

journal homepage: www.elsevier.com/locate/indcrop



Selection of *Jatropha curcas* families based on temporal stability and adaptability of genetic values

Rodrigo Silva Alves[a], Leonardo de Azevedo Peixoto[a], Paulo Eduardo Teodoro[a], Lidiane Aparecida Silva[a], Erina Vitório Rodrigues[b], Marcos Deon Vilela de Resende[a], Bruno Galveas Laviola[b], Leonardo Lopes Bhering[a,*]

[a] *Universidade Federal de Viçosa, Avenida Peter Henry Rolfs, s/n, Campus Universitário, Viçosa, MG, 36570-000, Brazil*
[b] *Embrapa Agroenergia, Parque Estação Biológica (PqEB), Asa Norte, Brasília, DF, 70770-901, Brazil*

ARTICLE INFO

Keywords:
Jatropha curcas L.
Mixed model methodology
Repeated measure
HMRPGV method
Genetic selection

ABSTRACT

Despite its numerous important traits for biodiesel production, little research exists on the *Jatropha curcas* crop, mainly with respect to repeated measures over time (crop years). The present study was thus developed to evaluate repeated measures over time in *Jatropha curcas* and examine the applicability and efficiency of the harmonic mean of the relative performance of genetic values (HMRPGV) method in the selection of families for yield, stability, and adaptability, simultaneously. The work involved data from the evaluation of 730 individuals of 73 half-sib families, in a complete randomized block design, during six crop years, for the trait grain yield. Restricted maximum likelihood/best linear unbiased prediction (REML/BLUP) procedure was performed to estimate the variance components and predict the genetic values. Ten crop years must be evaluated to obtain 80% of the maximum coefficient of determination and 90% accuracy in terms of genetic gain from selection. The efficiency of performing 10 measurements compared with the situation in which only one measurement is used was 67%. The HMRPGV method has great potential in the selection of *Jatropha curcas* families for yield, stability, and adaptability, simultaneously.

1. Introduction

Jatropha curcas (*Jatropha curcas* L.) stands out among the biofuel-producing plants by virtue of its various agronomic traits such as high oil content in the seeds (Berchmans and Hirata, 2008), high oil-to-biofuel conversion efficiency compared with other species (Pu et al., 2011), drought tolerance (Becker and Makkar, 2008), fast growth and easy propagation (Openshaw, 2000), the possibility of cultivation at high altitudes, and production life of more than 50 years (Nithiyanantham et al., 2012). Moreover, *Jatropha curcas* seeds are composed of 35% oil, which after extracted consists of 47% crude fat and 25% crude protein (Akintayo, 2004). *Jatropha curcas* oil has important characteristics compared with other vegetable oils, e.g. better oxidation stability, and lower viscosity (Bailis and McCarthy, 2011). Nevertheless, despite its numerous important traits for biodiesel production, little research exists on the *Jatropha curcas* crop, mainly with respect to repeated measures over time (crop years).

Experimental analysis with repeated measures over time on the same individual has some peculiarities, since the many crop years are correlated with each other and there may be heterogeneity of variance and covariance among crop years. Repeated-measures analysis allows for the prediction of genetic values for each crop year individually and for all crop years simultaneously, in addition to identifying the variance structure over crop years. Therefore, it is possible to understand the behavior of a trait over time and consequently more accurately perform genetic selection. In this regard, the full repeatability model, also called repeatability model plus genotype × measurement (G × M) interaction, has come to be a useful strategy to analyze repeated measures over time in plant breeding (Resende, 2007).

In an investigation aimed at genetic selection based on temporal stability and adaptability of genetic values, Resende (2004) proposed the harmonic mean of the relative performance of genetic values (HMRPGV) method within the mixed model methodology. This method allows for a simultaneous selection for yield, stability, and adaptability. The following are some of the many advantages of HMRPGV method: genotype effects are assigned as random effects, meaning this method estimates the genotypic and non-phenotypic stability and adaptability; it can be used for unbalanced experiments; it can be fitted for experiments with heterogeneity variance and correlated errors within block or crop years; it does not depend on estimation or interpretation of

---

[*] Corresponding author.
E-mail address: leonardo.bhering@ufv.br (L.L. Bhering).

https://doi.org/10.1016/j.indcrop.2018.04.029
Received 17 April 2017; Received in revised form 28 February 2018; Accepted 14 April 2018

other parameters such as regression coefficient; it allows for the elimination of the G × M interaction residue, as it considers heritability for this effect; it generates results in the same magnitude as the phenotypic values; and it estimates genetic gain for the three attributes simultaneously (Resende, 2007).

Experiments in the literature have tested strategies for genetic selection in *Jatropha curcas* (Bhering et al., 2013; Junqueira et al., 2016; Peixoto et al., 2016), but none of them considered the temporal stability and adaptability of genetic values in the selection of families. The present study was thus proposed to evaluate repeated measures over time in *Jatropha curcas* and examine the applicability and efficiency of the HMRPGV method in the selection of families for yield, stability and adaptability, simultaneously.

2. Material and methods

2.1. Experimental data

The experiment was implemented in November 2008 in the experimental field of Embrapa Cerrados, Planaltina – DF, Brazil (15°35′30” S and 47°42′30” W; 1007 m asl), as a completely randomized block design with two replicates and five plants per plot. Plants were arranged at 2 m from each other in rows spaced 4 m apart. All management practices were based on Carels et al. (2013). The experiment consisted of a performance evaluation of 730 individuals of 73 half-sib families. Plants were evaluated for grain yield (kg plant^{-1}) during six crop years, from 2010 to 2015.

2.2. Statistical analysis

Restricted maximum likelihood/best linear unbiased prediction (REML/BLUP) procedure was performed to estimate the variance components and to predict the genetic values, according to Resende (2016). The statistical model, associated with the evaluation of repeated measures at the individual level, in completely randomized block design, was determined by the following equation:

$$y = Xm + Za + Wp + Qi + Ts + e,$$

in which y is the vector of phenotypic values; m is the vector of the measure-replicate combinations effects plus the overall mean (fixed effect); a is the vector of individual additive genetic value effects (assumed random); p is the vector of plot effects (assumed random); i is the vector of G × M interaction effects (random effect); s is the vector of permanent environmental effects (assumed random); e is the vector of residuals (random effect); and X, Z, W, Q, and T are the incidence matrices for m, a, p, i, and s effects, respectively. The m vector is associated with all measures in all replicates, and it fits simultaneously for the replicate, measure, and replicate × measure (R × M) interaction effects (Resende, 2016).

For the random effects of the model, significance for the likelihood ratio test (LRT) was tested using chi-square statistics with one degree of freedom. Coefficients of determination were obtained as follows:

$$c_i^2 = \sigma_i^2/\sigma_{Phen}^2,$$

in which σ_i^2 is the variance of effect i and σ_{Phen}^2 is the phenotypic variance. The individual repeatability is obtained as follows:

$$\rho = (\sigma_{Genotype}^2 + \sigma_{Plot}^2 + \sigma_{\text{Permanent environment}}^2)/\sigma_{Phen}^2.$$

The efficiency of use of m measurements in each plant compared with the use of only one measurement, in terms of genetic gain from selection, is obtained by:

$$E = \{m/[1 + (m - 1) \times \rho]\}^{0.5}.$$

This expression is valid for asexual and sexual strategies (Resende, 2015).

Determination is obtained as shown below:

$$D = (m \times \rho)/(m \times \rho + 1 - \rho).$$

The accuracy of the use of m measurements in each plant compared with the use of only one measurement, in terms of genetic gain from selection, is obtained by:

$$Acc = \sqrt{D}.$$

As proposed by Resende (2004), a method to rank genotypes considering the yield and stability simultaneously is the harmonic mean of genetic values (HMGV). When considering the yield and adaptability simultaneously, the recommended approach is the relative performance of genetic values (RPGV) over crop years.

Harmonic mean of the genetic values (HMGV) of each family were obtained as follows:

$$\text{HMGV}_i = \frac{n}{\sum_{j=1}^{n} \frac{1}{\text{GV}_{ij}}}.$$

in which n is the number of crop years (n = 6) where genotype i was evaluated; GV ij is the genetic value of family i in crop year j, expressed by the ratio of the mean in this crop year.

Relative performance of the genetic values (RPGV) of each family was obtained by:

$$\text{RPGV}_i = \frac{1}{n}\frac{\sum_{j=1}^{n} \text{GV}_{ij}}{\text{M}_j},$$

in which M_j is the mean grain yield in crop year j.

The simultaneous selection for yield, stability, and adaptability is given by the harmonic mean of the relative performance of the genetic values (HMRPGV), obtained as shown below:

$$\text{HMRPGV}_i = \frac{n}{\sum_{j=1}^{n} \frac{1}{\text{RPGV}_{ij}}}.$$

HMRPGV*OM corresponds to HMRPGV multiplied by the overall mean of all crop years, providing the mean genotypic value penalized by the instability and capitalized by the adaptability. Selective accuracy and selection gain were obtained following Resende (2016).

Statistical analyses were performed using Selegen REML/BLUP (Resende, 2016) and R (R Development Core Team, 2017) software.

3. Results

Significant genotype, plot, G × M interaction, and permanent environment effects ($P < 0.01$) were detected by the LRT (Table 1). Thus, according to the LRT, the full model was the most suitable to estimate the genetic parameters and predict the genetic values. The variance

Table 1

Deviance, likelihood ratio test (LRT), variance components, and coefficient of determination for the trait grain yield (kg plant^{-1}), evaluated in 730 individuals of 73 *Jatropha curcas* half-sib families, during six crop years.

Effect	Deviance	LRT	Variance component	Coefficient of determination
Genotype	−1986.28	9.53**	0.0416	0.1073 ± 0.0141
Plot	−1836.71	159.10**	0.0489	0.1263
G × M interaction	−840.45	1155.36**	0.1163	0.3002
Permanent environment	−1912.07	83.74**	0.0199	0.0514
Residue	–	–	0.1607	0.4148
Full model	−1995.81	–	–	1.0000

** Significant at the 0.01 probability level according to the chi-square test. The null hypothesis was that the full and reduced models did not differ.