



Diversity and genetic parameter estimates for yield and its components in *Jatropha curcas* L.

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ABSTRACT. *Jatropha curcas* L. is one of the most promising oilseeds for biodiesel and biokerosene production, but few basic studies or breeding programs have been conducted for the species. We estimated genetic parameters and diversity based on 10 yield traits in 77 half-sib progenies of *J. curcas* after 52 months in the field, and evaluated correlations between them and the oil content of the seeds. The mean grain yield per plant was 377.9 g (ranging from 169.8 to 772.1 g) and the mean oil content was 36.2% (ranging from 30 to 39.6%). Moderate estimates of heritability at the mean progeny level were obtained for the length of the fruit (84.7%), length (69.1%) and width (68.2%) of the seed, and grain yield per plant (62.2%). Oil content was only positively and significantly correlated with 100-seed weight. Our study revealed a range of possible crosses to be investigated in *J. curcas*. Progeny production should be evaluated over several crop seasons for the accurate selection of the best progenies.

Key words: Correlation between traits; Grain yield; Heritability; Oil content; Physic nut breeding program; Pooled analysis

INTRODUCTION

Due to the demand for clean and renewable energy, liquid fuels of plant origin, such as biodiesel and ethanol, have gained recognition on the world economic stage. The search for alternatives to fossil fuels requires the evaluation of renewable sources with low environmental impact (Matos et al., 2012). Therefore, the development of appropriate techniques and raw materials for energy generation is essential.

Scientists and large corporations in the energy sector have promoted *Jatropha curcas* L. as one of the most promising oilseed species for biodiesel and biokerosene production. *J. curcas* seeds are rich in oleic acid (above 50%) and have high oil content (above 36%). Governments and their financing agencies have made resources available for research, and incentives for large-scale planting (Dias et al., 2012). This rising interest in *J. curcas* has created demand for the development of improved cultivars of the species. However, caution on the part of researchers and producers is necessary for the success of the crop for biodiesel production. There are few *J. curcas* breeding programs compared to other oilseed crops, such as soybean, cotton, peanut, and sunflower (Freitas et al., 2011). According to Rocha et al. (2012), technical limitations have impeded the full insertion of the species in the Brazilian energy matrix. Uneven maturation of the fruit and low grain yield are two hurdles that have limited the economic viability of this crop (Dias et al., 2007).

For a breeding program to be successful, it is necessary to investigate estimates of the genetic parameters of the main traits, the genetic associations between them, and the genetic variability available. Through such studies, the most adequate selection method and the traits that may be obtained through selection are defined. However, studies on the genetic parameters of the main traits of *J. curcas* are few in number (Kaushik et al., 2007; Rao et al., 2008; Das et al., 2010; Freitas et al., 2011; Laviola et al., 2012; Bhering et al., 2013; Shabanimofrad et al., 2013), and are not easily compared because they involve plants at different stages. In addition, most of them studied young plants and have not dealt with grain yield and oil content in the seeds of adult plants. Rocha et al. (2012) also observed that there have been few studies that have estimated genetic components and gain through selection, taking into consideration repeated measures and the evaluation of plants at a productive age.

Knowledge of the associations between traits is of extreme importance, particularly if selection for one of them presents difficulties caused by low heritability and/or measurement and identification (Cruz et al., 2012). Associations between yield traits of *J. curcas* must be studied by breeders, particularly regarding the oil content of the seeds, which is the target characteristic in breeding for biodiesel. However, few studies on this species have investigated this characteristic (Ginwal et al., 2004; Kaushik et al., 2007; Freitas et al., 2011; Biabani et al., 2012; Wani et al., 2012; Shabanimofrad et al., 2013).

Information regarding the degree of genetic diversity between and within natural populations, at and outside the center of origin, is necessary for the search for genotypes and populations that are potentially valuable for breeding (Achten et al., 2010). According to Dias et al. (2012), Mexico is the center of domestication and also diversity of *J. curcas*. In Brazil, the northern region of the State of Minas Gerais has genotypes with a high oil content, which led Dias et al. (2012) to propose that region to be considered a secondary center of diversity for the species. Studies that have evaluated the genetic and phenotypic diversity of *J. curcas* progenies have been conducted in India (Kaushik et al., 2007; Rao et al., 2008; Das et al., 2010; Wani et al., 2012), China (Sun et al., 2008), Brazil (Laviola et al., 2010; Freitas et al., 2011), Mexico (Ovando-Medina et al., 2011; Fresnedo-Ramírez and Orozco-Ramírez, 2013), and Malaysia (Biabani et al., 2012; Shabanimofrad et al., 2013).

The aim of this study was to evaluate the genetic parameters and diversity of progenies of *J. curcas* for yield and its components, as well as to investigate correlations between these traits and the oil content of the seeds.

MATERIAL AND METHODS

A total of 77 half-sib progenies of *J. curcas* originating from different regions of Brazil and Cambodia were evaluated, with 75 of them considered to be regular and 2 as control progenies (Table 1). The regular progenies were equally distributed across four trials, all in randomized blocks with four replications and four-plant plots spaced at 2 x 2 m, with two common progenies as controls. The trials were conducted at the Araponga Experimental Field (20°39'S, 42°32'W; 823 m above mean sea level), Minas Gerais, Brazil, in November 2008 by direct sowing. Trials 1, 2, 3, and 4 included the progenies UFVJC 1 to 20, UFVJC 21 to 38, UFVJC 39 to 58, and UFVJC 59 to 75, respectively. The two control progenies were UFVJC 76 and 77. This design resulted in precise and easily conducted trials. In addition, the use of common control progenies, which are the most grown in Brazil, facilitated an accurate joint analysis. Crop treatments, such as liming, fertilization, and pest and disease control, were conducted according to Dias et al. (2007).

Table 1. Collection locations of the 77 *Jatropha curcas* L. progenies studied.

Code	No. of progenies	State of origin	Country
UFVJC 1-34, 36, 40, 46-57, 59, 66, 69-73, 76-77	57	Minas Gerais	Brazil
UFVJC 38, 41, 44-45, 74	5	São Paulo	Brazil
UFVJC 42-43	2	Mato Grosso	Brazil
UFVJC 37	1	Tocantins	Brazil
UFVJC 75	1	Pernambuco	Brazil
UFVJC 35	1	Ceará	Brazil
UFVJC 64	1	Maranhão	Brazil
UFVJC 60	1	Pará	Brazil
UFVJC 65	1	Rondônia	Brazil
UFVJC 58	1	Rio Grande do Sul	Brazil
UFVJC 39	1	Mato Grosso do Sul	Brazil
UFVJC 67-68	2	Unknown	Cambodia
UFVJC 61-63	3	Unknown	Brazil

The 10 traits evaluated after 52 months (4.4 years) in the field were fruit production (FrPd), grain yield per plant (GYP), oil content of the seeds (OC), 50-fruit weight (50FrW), percentage of shell in the fruit (SFr), length (LFr) and width (WFr) of the fruit, 100-seed weight (100SW), and length (LS) and width (WS) of the seed. For the evaluation of FrPd (g), fruits were collected from each plant and the ground and weighed; the GYP (g) was based upon the SFr of each progeny; the OC (%) was determined using nuclear magnetic resonance (Oxford Instruments, model MQC -23-27 ISO 10565, 300 baker avenue, suite 150, Concord, MA 01742, USA) on seeds from all of the plants; the 50FrW (g) was determined by randomly selecting 50 fruits from each progeny per block and weighing them; and the SFr (%) was calculated by dividing the shell weight of the 50 fruits by their total weight and multiplying the result by 100. Of the 50 fruits evaluated for 50FrW, a random sample of fruits and seeds was removed from each progeny per block for evaluation of LFr, WFr, LS, WS (mm), and 100SW (g). For LFr, WFr, LS, and WS (mm), a random sample of 10 fruits and seeds was evaluated with a digital caliper rule; the 100SW (g) was determined by weighing 100 randomly selected seeds.

Data related to FrPd, GYP, and OC at the level of individual plants and per trial were

obtained by the block method, with information within plots. For 50FrW, SFr, LFr, WFr, 100SW, LS, and WS, the analyses were based on a sample of the fruits and seeds of the plants that constituted the plots, respecting the block design. The mean plot values for FrPd, GYP, and OC were added to the data for the other traits, and a pooled analysis of variance (ANOVA) of the four trials was conducted. Initially, a single ANOVA for each trial was conducted using the following model:

$$Y_{ij(k)} = \mu + T_i + B_j + \varepsilon_{ij} \quad (\text{Equation 1})$$

where $Y_{ij(k)}$ is the value observed in the i^{th} progeny in the j^{th} block for trial k , μ is the overall mean value for trial k , T_i is the effect of the i^{th} progeny for trial k , B_j is the effect of the j^{th} block for trial k , and ε_{ij} is the random error for trial k . Subsequently, a pooled ANOVA of the trials was conducted, with the sum of squares adjusted for treatments (regular and control progenies) (Table 2) according to the following model:

$$Z_{ijk} = \mu + T_i + B_{j(k)} + E_k + TcE_{ik} + \varepsilon_{ijk} \quad (\text{Equation 2})$$

where Z_{ijk} is the value evaluated in the i^{th} treatment (regular progeny and control progeny) in the j^{th} block for trial k , μ is the overall mean value of the trial, T_i is the adjusted effect of the i^{th} treatment, $B_{j(k)}$ is the effect of the j^{th} block within the k^{th} trial, E_k is the effect of the k^{th} trial, TcE_{ik} is the effect of the interaction between the control progeny and the trial, and ε_{ijk} is the random error.

For comparisons between progenies in the different trials, a correction of the values obtained for each one was performed by removing the environmental effects estimated based on the value of the controls. Therefore, those progenies evaluated in unfavorable environments were compensated, and values obtained from those evaluated in favorable environments were reduced.

To study associations between the traits evaluated and the oil content of *J. curcas* seeds, Pearson and partial phenotypic correlation coefficients were obtained. Estimates of the mean genotypic variance, heritability at the mean progeny level, intraclass correlation at the plot level, genetic coefficient of variation (CV_g), and relative coefficient of variation ($CV_r = CV_g / CV_e$) for all 10 traits were obtained.

Genetic variability was quantified in two steps. Firstly, dissimilarity between the progenies in the 10 traits evaluated was estimated using the Mahalanobis generalized distance (Rao, 1952), which considers the residual correlation between the traits and is one of the most used measures in divergence studies. Secondly, using the distance matrix generated, the optimization method proposed by Tocher (Rao, 1952) was used to form diversity clusters. After cluster formation, for greater discrimination the Tocher method was used on the cluster with the greatest number of progenies. The ANOVAs, estimations of the genetic parameters, correlations, and cluster analyses were conducted using the GENES software (Cruz et al., 2012).

RESULTS

Statistical analysis

Based on the results of the pooled ANOVA (Table 2), significant differences were found between the trials for all of the traits evaluated, except OC. For the control progenies x trial interaction,

FrPd and GYP were significant at the 5 and 1% levels of probability, respectively. There were significant differences between the adjusted treatments (75 regular progenies and two control progenies) in all of the traits, except SFr. Regarding precision, the experimental coefficients of variation were 21.7 and 21.2% for FrPd and GYP, respectively, and ranged from 1.7 to 6.6% for the other traits (Table 2).

The mean values of the regular progenies were greater than or similar to the mean values of the control progenies, with FrPd and GYP standing out.

Genetic parameter estimates

The highest estimates of heritability at the mean progeny level were for LFr (84.7%), LS (69.1%), WS (68.2%), and GYP (62.2%) (Table 3). Regarding the variability between progenies, FrPd and GYP exhibited considerable genotypic variability (Table 3), with genotypic coefficients of variation of 12.9 and 13.4%, respectively. WFr, LS, and WS had lower genotypic coefficients of variation (1.0, 1.2, and 1.3%, respectively). The genetic parameter estimates obtained in the present study were of the same order of magnitude as those reported in the literature (Table 4).

Table 2. Summary of pooled analysis of variance results for 10 traits in 77 progenies of *Jatropha curcas* L.

Sources of Variation	df	Mean squares ^a									
		FrPd	GYP	OC	50FrW	SFr	LFr	WFr	100SW	LS	WS
locks/Trial	12	16,626.36	85,30.78	5.93	186.10	6.42	2.32	0.70	44.47	0.09	0.11
Trial	3	888,281.78	463,824.97	1.74	2,794.76	25.54	19.03	3.66	596.54	2.98	2.03
Control x Trial	3	47,115.86	26,820.58	0.27	35.09	6.50	0.34	0.25	1.15	0.08	0.04
Adjusted Progenies	76	30,079.56	16,928.37	2.76	92.16	4.39	5.45	0.39	24.75	0.31	0.13
Error	237	12,250.36	6,398.25	1.34	51.53	3.46	0.83	0.19	11.34	0.09	0.04
Total	331										
Mean		510.05	377.95	36.21	130.83	28.05	28.39	20.73	69.71	17.81	10.60
Mean (regular progenies)		514.01	380.81	36.27	130.94	28.08	28.42	20.74	69.79	17.81	10.60
Mean (control progenies)		472.96	351.21	35.63	129.75	27.80	28.12	20.65	68.93	17.80	10.63
CV (%)		21.70	21.16	3.20	5.49	6.63	3.22	2.10	4.83	1.72	1.90

^aValues in bold and underlined are significant at the 1 and 5% levels of probability, respectively, by the F test. CV, coefficient of variation; FrPd, fruit production; GYP, grain yield per plant; OC, oil content; 50FrW, 50-fruit weight; SFr, percentage of shell in the fruit; LFr, fruit length; WFr, fruit width; 100SW, 100-seed weight; LS, seed length; WS, seed width.

Table 3. Genetic parameter estimates for 10 traits in 77 half-sib progenies of *Jatropha curcas* L.

Estimates	FrPd (g)	GYP (g)	OC (%)	50FrW (g)	SFr (%)
V_g	4457.301	2632.53	0.355	10.158	0.23
h^2	59.27	62.20	51.41	44.09	21.36
RI (%)	26.68	29.15	20.92	16.47	6.36
CV_g (%)	12.99	13.47	1.64	2.43	1.73
CV_r	0.59	0.64	0.51	0.44	0.26
Mean	510.05	377.95	36.21	130.83	28.05
Minimum	223.19	169.86	30.00	97.40	21.96
Maximum	1057.47	772.17	39.61	158.50	41.63
Estimates	LFr (mm)	WFr (mm)	100SW (g)	LS (mm)	WS (mm)
V_g	1.153	0.051	3.351	0.053	0.022
h^2 (%)	84.70	51.89	54.16	69.15	68.22
RI (%)	58.04	21.24	22.80	35.91	34.92
CV_g (%)	3.78	1.09	2.62	1.29	1.39
CV_r	1.17	0.51	0.54	0.74	0.73
Mean	28.39	20.73	69.71	17.81	10.60
Minimum	24.06	19.44	51.10	16.83	9.67
Maximum	37.30	22.04	81.30	19.36	11.18

V_g , mean genotypic variance; h^2 , mean heritability at the progeny level; RI, intraclass correlation at the plot level; CV_g , genetic coefficient of variation; CV_r , relative coefficient of variation (CV_g/CV_e ratio); FrPd, fruit production; GYP, grain yield per plant; OC, oil content; 50FrW, 50-fruit weight; SFr, percentage of shell in the fruit; LFr, fruit length; WFr, fruit width; 100SW, 100-seed weight; LS, seed length; WS, seed width.

A relative coefficient of variation value greater than 1 was only obtained for LFr (1.17); for the other traits, it ranged from 0.2 to 0.7. GYP and OC were the most important traits from a crop improvement perspective, and had mean values of 377.9 g (ranging from 169.8 to 772.1 g) and 36.2% (ranging from 30.0 to 39.6%), respectively (Table 3).

Table 4. Genetic parameter estimates of *Jatropha curcas* L. traits in previous studies.

Traits	Age (months)	\hat{h}_a^2 (%) ^a	\hat{h}_r^2 (%) ^b	CV _g (%) ^c	References
LS	-	77.00		2.45	Kaushik et al. (2007)
LS	60	82.14		5.44	Rao et al. (2008)
LS	24	85.40		3.38	Shabanimofrad et al. (2013)
WS	-	57.00		2.00	Kaushik et al. (2007)
WS	60	77.77		11.34	Rao et al. (2008)
WS	24	81.80		1.94	Shabanimofrad et al. (2013)
100SW	-	96.00		8.83	Kaushik et al. (2007)
100SW	60	93.16		7.34	Rao et al. (2008)
100SW	24	80.50		7.04	Shabanimofrad et al. (2013)
100SW	36	95.80		18.10	Das et al. (2010)
100SW	20		65.29	4.81	Bhering et al. (2013)
GYP	36	77.10		66.20	Das et al. (2010)
GYP	24		65.00	77.37	Laviola et al. (2012)
GYP	20		62.92	29.01	Bhering et al. (2013)
GYP	24	71.70		48.95	Shabanimofrad et al. (2013)
OC	-	99.00		8.83	Kaushik et al. (2007)
OC	60	99.61		11.67	Rao et al. (2008)
OC	36	79.50		5.73	Rocha et al. (2012)
OC	48	78.50		6.36	Rocha et al. (2012)
OC	24	67.60		6.98	Shabanimofrad et al. (2013)

^aBroad-sense heritability. ^bNarrow-sense heritability. ^cGenotypic coefficient of variation. GYP, grain yield per plant; OC, oil content; 100SW, 100-seed weight; LS, seed length; WS, seed width.

Associations between traits

Pearson and partial phenotypic correlation coefficients were obtained to investigate associations between the traits and their causes and effects (Table 5). The traits that had the most significant partial correlations were FrPd and GYP (0.99), GYP and SFr (-0.82), FrPd and SFr (0.81), and LFr and LS (0.62). Regarding the OC, Pearson correlations revealed highly significant associations with GYP (0.41), SFr (-0.48), FrPd (0.39), and 50FrW (0.34). The partial correlations only found a significant association with 100SW (0.41).

Diversity analysis

Initially, we detected five distinct clusters of progenies (Table 6). Cluster 1 contained most of the progenies (70), followed by cluster 2 (2), cluster 3 (3), and clusters 4 and 5 (1 each). The greatest intercluster distance was between clusters 3 and 5, followed by 4 and 5, 2 and 3, and 1 and 5 (Table 6). Later, we only found one cluster, which was composed of 70 progenies. This was divided into 16 distinct subclusters, with subcluster 1.1 containing most of the progenies (20), followed by 1.2 (13), 1.3 (10), 1.4 (8), 1.5 (3), subclusters 1.6 to 1.10 (2 each), and the rest contained one progeny each (Table 6).

Table 5. Pearson (above the diagonal) and partial (below the diagonal) correlations between *Jatropha curcas* L. traits.

Trait ^a	FrPd	GYP	OC	50FrW	SFr	LFr	WFr	100SW	LS	WS
FrPd	1	0.99	0.39	-0.11	-0.46	-0.21	-0.17	<u>-0.28</u>	-0.44	<u>-0.29</u>
GYP	0.99	1	0.41	-0.12	-0.51	<u>-0.22</u>	-0.20	<u>-0.29</u>	-0.46	<u>-0.29</u>
OC	-0.14	0.15	1	0.34	-0.48	0.00	-0.13	0.22	-0.14	-0.21
50FrW	0.13	-0.14	0.08	1	0.15	0.44	0.60	0.76	0.36	<u>0.22</u>
SFr	0.81	-0.82	0.03	-0.07	1	<u>0.23</u>	0.44	0.20	0.38	0.18
LFr	0.13	-0.14	-0.11	0.15	-0.16	1	0.18	<u>0.27</u>	0.64	-0.32
WFr	-0.17	0.18	-0.16	0.45	<u>0.28</u>	0.15	1	0.62	<u>0.28</u>	0.50
100SW	0.15	-0.16	0.41	0.39	-0.17	-0.05	<u>0.24</u>	1	0.43	0.49
LS	-0.22	0.21	-0.07	0.18	<u>0.26</u>	0.62	-0.32	<u>0.25</u>	1	0.11
WS	0.05	-0.06	-0.23	-0.10	-0.14	-0.59	0.36	<u>0.29</u>	<u>0.29</u>	1

^aValues in bold and underlined are significant at the 1 and 5% levels of probability, respectively. FrPd, fruit production; GYP, grain yield per plant; OC, oil content; 50FrW, 50-fruit weight; SFr, percentage of shell in the fruit; LFr, fruit length; WFr, fruit width; 100SW, 100-seed weight; LS, seed length; WS, seed width.

Table 6. Clusters and relative intercluster distances (RID) of 77 progenies of *Jatropha curcas* L. based on 10 traits.

Cluster	Progenies																			
1																				
1.1	6	12	14	20	22	26	29	30	32	35	38	43	45	46	47	49	50	52	53	56
1.2	1	2	3	9	15	18	19	28	36	51	54	58	76							
1.3	4	7	34	37	40	62	63	65	74	77										
1.4	5	23	59	64	66	70	71	73												
1.5	42	44	57																	
1.6	39	48																		
1.7	69	72																		
1.8	60	68																		
1.9	27	67																		
1.10	33	61																		
1.11	8																			
1.12	25																			
1.13	21																			
1.14	17																			
1.15	11																			
1.16	13																			
2	24	75																		
3	10	41	55																	
4	16																			
5	31																			
Clusters (RID)	1				2				3				4				5			
1	(35.04)				(126.12)				(150.15)				(148.03)				(418.03)			
2					(7.51)				(471.76)				(287.17)				(100.50)			
3									(17.75)				(211.34)				(977.39)			
4													-				(608.38)			
5																	-			

DISCUSSION

To obtain the correct mean values of the progenies, the control progenies x trial interaction should not be significant, so that the behavior of the control progenies only reflects the quality of the environment evaluated. The only traits that exhibited this significant interaction were FrPd and GYP (Table 2), where the progenies that were evaluated in an environment that was favorable to their performance had their mean values reduced for purposes of comparison; the mean values of the others increased because of the environmental effect. Therefore, for each progeny, it was necessary to adjust the values obtained in relation to these traits for the purpose of a joint evaluation of the trials, and a more efficient evaluation regarding the behavior of the progenies.

Genetic variability existed between the 77 progenies, particularly for yield components, which exhibited the highest CV_g values. This variability could be used in breeding programs by selecting progenies that obtain higher GYP values than our mean value of 377.9 g, because there was great variation (169.8 to 772.1 g) that could be exploited in future generations. In addition, this trait exhibited a heritability of 62.2%, demonstrating that selecting the best progenies can result in genetic gain.

Regarding the OC of *J. curcas* seeds, the mean value in the present study was 36.2%, and ranged from 30.0 to 39.6%. When the genetic parameters for OC in the 77 progenies were evaluated, a fairly high coefficient of heritability (51.4%) and low CV_r value (0.5) were obtained. According to Vencovsky (1987), if the relative value of the CV_r is near or above 1 for maize progenies, there is a high probability of genetic gain from selection, which suggests that the trait may be easily worked with in genetic breeding programs. Therefore, there is a possibility of gain from selecting the best progenies, e.g., by selecting plants with an OC above the mean value found in this study (36.2%). However, despite being one of the main traits for *J. curcas* breeding, gain from selection would not easily be obtained because of the low CV_r value obtained in the present study.

Importantly, we found a higher mean OC (36.2%) and greater variation (30.0 to 39.6%) in *J. curcas* seeds than that reported in the literature (Table 7). *J. curcas* GYP is related to genetic potential, crop field management, and the age of the plant, as it is a perennial species. Studies on *J. curcas* from different regions and at different ages have obtained a wide range of values for GYP (Table 7). *J. curcas* reaches its productive potential after four to five years in the field (48 to 60 months). The present study used plants after 52 months in the field, and the mean GYP was 377.9 g and ranged from 169.8 to 772.1 g. Although there have been few studies conducted on plants older than 48 months, the GYP observed in this study proved to be expressive, which increases the expectation for production in the next years. Plants that maintain an expressive grain yield and above-average OC should receive special attention in our breeding program.

We found significant associations between OC and four other traits using Pearson correlations, whereas an association with only one trait was found using partial correlations. This indicates that the partial correlation coefficient is a more informative measure of relationships between traits, because cause and effect cannot be inferred from simple correlations (Table 5). In addition, partial correlations are more informative regarding the relationships between traits because they take into account the effects of other traits on the association studied. To better evaluate associations between traits, they should be measured in consecutive crop years to obtain long-term data.

When evaluating 25 *J. curcas* accessions from India, Ginwal et al. (2004) found a significant correlation between OC and 100SW (0.79). A significant phenotypic correlation, although negative, was observed by Kaushik et al. (2007) between OC and LS (-0.47). The results of the present study support those of Ginwal et al. (2004) regarding the association between OC and 100SW, as well as the Kaushik et al. (2007), who reported a positive, significant correlation between them (0.23).

Freitas et al. (2011) and Wani et al. (2012) did not find an association between OC and the traits that they studied, and Biabani et al. (2012) did not find a correlation between OC and 100SW. However, they found a significant negative correlation between OC and GYP (-0.59). Shabanimofrad et al. (2013) found significant, positive correlations between OC and LS (0.38) and OC and 100SW (0.44). Some workers have found an association between OC and 100SW as we did in the present study, but evaluations should be performed over several crop seasons to investigate whether this association is maintained over time.

Table 7. Means and ranges of grain yield per plant and seed oil content of *Jatropha curcas* L. obtained by previous studies.

Country	Age (months)	Oil content (%)	Grain yield per plant (g)	Reference
India	-	33.0 (28.0-38.8)		Kaushik et al. (2007)
India	60	33.70 (29.85-37.05)	147.8 (36.6-263.9)	Rao et al. (2008)
India	36		84.7 (34.8-196.4)	Das et al. (2010)
Brazil	36	36.10 (23.30-39.0)		Rocha et al. (2012)
Brazil	48	33.70 (27.10-40.20)		Rocha et al. (2012)
India	30	32.37 (22.43-35.46)	432.4 (222-635)	Wani et al. (2012)
Brazil	24		175.8 (52.8-782.0)	Laviola et al. (2012)
Malaysia	24	32.35 (24.40-35.53)	282.8 (107.2-745.7)	Shabanimofrad et al. (2013)
Brazil	20		175.9 (57.1-537.1)	Bhering et al. (2013)

In addition to genetic parameter estimates of the main traits and associations between them, the success of a breeding program depends on knowledge of the genetic diversity available. Studies on *J. curcas* diversity have been conducted in different regions of the world (Table 8). In the present study, the formation of five clusters was observed, revealing the existence of genetic diversity in the progenies. The two progenies from Cambodia (UFVJC 67 and UFVJC 68) that were evaluated were clustered with those from Brazil, which demonstrates that, in accordance with the results of Freitas et al. (2011) and Biabani et al. (2012), geographical diversity does not necessarily reflect genetic diversity. A similar result was obtained by Ricci et al. (2012), who, working with *J. curcas* plants collected from different geographical regions (Brazil, Cape Verde, Cuba, Mozambique, and Senegal), reported the formation of two clusters, with one cluster composed of plants from Brazil, Mozambique, and Senegal and the other of plants from Cuba and Cape Verde.

Table 8. Genetic diversity of *Jatropha curcas* L. evaluated by cluster analysis obtained by previous studies.

No. of progenies or accessions	Location	No. of Clusters	Reference
24	India	6	Kaushik et al. (2007)
32	India	4	Rao et al. (2008)
110	Brazil	5	Laviola et al. (2010)
6	Indonesia, Malaysia, Philippines, and India	3	Biabani et al. (2012)
48	Malaysia	6	Shabanimofrad et al. (2013)
64	Brazil, Cape Verde, Cuba, Mozambique, and Senegal	2	Ricci et al. (2012)

Our study revealed a range of possible crosses to be investigated in *J. curcas*. Broad genetic variability is important in a breeding program, because divergent genotypes with a high OC and grain yield should be selected for the production of hybrids, and their fixation by cloning.

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REFERENCES

- Achten WMJ, Nielsen LR, Aerts R, Lengkeek AG, et al. (2010). Towards domestication of *Jatropha curcas*. *Biofuels* 1: 91-107. <http://dx.doi.org/10.4155/bfs.09.4>
- Bhering LL, Barrera CF, Ortega D, Laviola BG, et al. (2013). Differential response of *Jatropha* genotypes to different selection methods indicates that combined selection is more suited than other methods for rapid improvement of the species. *Ind. Crops Prod.* 41: 260-265. <http://dx.doi.org/10.1016/j.indcrop.2012.04.026>
- Biabani A, Rafii MY, Saleh GB, Shabanimofrad M, et al. (2012). Phenotypic and genetic variation of *Jatropha curcas* L. populations from different countries. *Maydica* 57: 164-174.
- Cruz CD, Carneiro PCS and Rezazzi AJ (2012). Modelos biométricos aplicados ao melhoramento genético, Vol 1, 4th Edn. Editora UFV, Viçosa.
- Das S, Misra RC, Mahapatra AK, Gantayat BP, et al. (2010). Genetic variability, character association and path analysis in *Jatropha curcas*. *World Appl. Sci. J.* 8: 1304-1308.
- Dias LAS, Leme LP, Laviola BG, Pallini Filho A, et al. (2007). Cultivo de pinhão-mansão (*Jatropha curcas* L.) para produção de óleo combustível. Suprema, Viçosa.
- Dias LAS, Missio RF and Dias DCFS (2012). Antiquity, botany, origin and domestication of *Jatropha curcas* (Euphorbiaceae), a plant species with potential for biodiesel production. *Genet. Mol. Res.* 11: 2719-2728. <http://dx.doi.org/10.4238/2012.June.25.6>
- Freitas RG, Missio RF, Matos FS, Resende MDV, et al. (2011). Genetic evaluation of *Jatropha curcas*: an important oilseed for biodiesel production. *Genet. Mol. Res.* 10: 1490-1498. <http://dx.doi.org/10.4238/vol10-3gmr1146>
- Fresnedo-Ramírez J and Orozco-Ramírez Q (2013). Diversity and distribution of genus *Jatropha* in Mexico. *Genet. Resour. Crop Evol.* 60: 1087-1104. <http://dx.doi.org/10.1007/s10722-012-9906-7>
- Ginwal HS, Rawat PS and Srivastava RL (2004). Seed Source variation in growth performance and oil yield of *Jatropha curcas* Linn. in Central India. *Silvae Genet.* 53: 186-192.
- Kaushik N, Kumar K, Kumar S, Kaushik N, et al. (2007). Genetic variability and divergence studies in seed traits and oil content of *Jatropha* (*Jatropha curcas* L.) accessions. *Biomass Bioenergy* 31: 497-502. <http://dx.doi.org/10.1016/j.biombioe.2007.01.021>
- Laviola BG, Rosado TB, Bhering LL, Kobayashi AK, et al. (2010). Genetic parameters and variability in physic nut accessions during early developmental stages. *Pesq. Agrop. Bras.* 45: 1117-1123. <http://dx.doi.org/10.1590/S0100-204X2010001000010>
- Laviola BG, Alves AA, Gurgel FL, Rosado TB, et al. (2012). Estimates of genetic parameters for physic nut traits based in the germplasm two years evaluation. *Cienc. Rural* 42: 429-435. <http://dx.doi.org/10.1590/S0103-84782012000300008>
- Matos FS, Oliveria LR, Freitas RG, Evaristo AB, et al. (2012). Physiological characterization of leaf senescence of *Jatropha curcas* L. populations. *Biomass Bioenergy* 45: 57-64. <http://dx.doi.org/10.1016/j.biombioe.2012.05.012>
- Ovando-Medina I, Sánchez-Gutiérrez A, Adriano-Anaya L, Espinosa-García F, et al. (2011). Genetic diversity in *Jatropha curcas* populations in the state of Chiapas, Mexico. *Diversity (Basel)* 3: 641-659. <http://dx.doi.org/10.3390/d3040641>
- Rao CR (1952). Advanced statistical methods in biometric research. John Wiley, New York.
- Rao GR, Korwar GR, Shanker A and Ramakrishna YS (2008). Genetic associations, variability and diversity in seed characters, growth, reproductive phenology and yield in *Jatropha curcas* (L.) accessions. *Trees (Berl.)* 22: 697-709. <http://dx.doi.org/10.1007/s00468-008-0229-4>
- Ricci A, Chekhovskiy K, Azhaguvel P, Albertini E, et al. (2012). Molecular characterization of *Jatropha curcas* resources and identification of population-specific markers. *BioEnergy Res.* 5: 215-224. <http://dx.doi.org/10.1007/s12155-011-9150-6>
- Rocha RB, Ramalho AR, Teixeira AL, Laviola BG, et al. (2012). Eficiência da seleção para incremento do teor de óleo do pinhão-mansão. *Pesq. Agrop. Bras.* 47: 44-50. <http://dx.doi.org/10.1590/S0100-204X2012000100007>
- Shabanimofrad M, Rafii MY, Megat Wahab PE, Biabani AR, et al. (2013). Phenotypic, genotypic and genetic divergence found in 48 newly collected Malaysian accessions of *Jatropha curcas* L. *Ind. Crops Prod.* 42: 543-551. <http://dx.doi.org/10.1016/j.indcrop.2012.06.023>
- Sun Q-B, Li L-F, Li Y, Wu G-J, et al. (2008). SSR and AFLP markers reveal low genetic diversity in the biofuel plant *Jatropha curcas* in China. *Crop Sci.* 48: 1865-1871. <http://dx.doi.org/10.2135/cropsci2008.02.0074>
- Vencovsky R (1987). Herança quantitativa. In: Melhoramento e produção do milho. 2nd edn. (Paterniani E and Viégas GP, eds). Fundação Cargill, Campinas, 137-214.
- Wani TA, Kitchlu S and Ram G (2012). Genetic variability studies for morphological and qualitative attributes among *Jatropha curcas* L. accessions grown under subtropical conditions of North India. *S. Afr. J. Bot.* 79: 102-105. <http://dx.doi.org/10.1016/j.sajb.2011.10.009>