Universidade Federal Rural do Semi-Árido
Pró-Reitoria de Pesquisa e Pós-Graduação
https://periodicos.ufersa.edu.br/index.php/caatinga

ISSN 0100-316X (impresso)
ISSN 1983-2125 (online)
http://dx.doi.org/10.1590/1983-21252022v35n106rc

VARIABILITY OF F_2 PROGENIES OF CASTOR BEAN BY MEANS OF MORPHOAGRONOMIC DESCRIPTORS[1]

GEAN CARLO SOARES CAPINAN[2]*, SIMONE ALVES SILVA[3], DEOCLIDES RICARDO DE SOUZA[3], LAURENICE ARAUJO DOS SANTOS[3], ILNEIDE BRAZ SANTOS DE JESUS[3]

ABSTRACT - Morphoagronomic characterization is a basic requirement to identify a phenotypic profile of a population. The quantification of variability allows efficient selection of superior and divergent genotypes. Thus, this study aimed to estimate the variability among 490 genotypes and seven strains, from an F_2 population of *Ricinus communis* L., in 35 morphoagronomic traits and 12 agronomic traits. For qualitative descriptors, the entropy technique was used in the percentage frequencies of each category, computing its level using the coefficient of Rényi (1961). Quantitative descriptors were subjected to analysis of variance by the F test, and Tukey test was performed at 1% probability level. Of the morphoagronomic traits used, 13 were related to plants, nine were related to inflorescence, six were related to fruits and seven were linked to seeds, in addition to 12 agronomic traits. The material was arranged in the field with families (strains of five families) interspersed with their respective parents (controls). Stem color, shape and number of racemes collected, main color, type of secondary color and hundred-seed weight have high variability in the population, with formation of 68 groups as a function of genetic similarity. The possibility of selection as to the number of racemes harvested is clear, so it is possible to identify genotypes with higher number, aiming to enhance crop yield.

Keywords: *Ricinus communis* L.. Genetic improvement. Entropy.

VARIABILIDADE DE PROGÊNIES F_2 DE MAMONEIRA POR MEIO DE DESCRITORES MORFOAGRONÔMICOS

RESUMO - A caracterização morfoagronômica é requisito básico para identificar um perfil fenotípico de uma população. A quantificação da variabilidade permite seleção eficiente de genótipos superiores e divergentes. Deste modo, esse trabalho teve como objetivo, estimar a variabilidade entre 490 genótipos e sete linhagens, oriundos de população F_2 de *Ricinus communi* L., em 35 caracteres morfoagronômicos e 12 agronômicos. O nível de frequência e entropia dos descritores qualitativos foi estimado com o procedimento de Renyi. Os quantitativos foram submetidos à análise de variância pelo teste F, sendo realizado o teste de Tukey a 1%, e agrupados pelo método de otimização de Tocher por meio da similaridade genética. Dos descritores morfoagronômicos utilizados, 13 foram referentes às plantas, nove relacionados à inflorescência, seis direcionados aos frutos, sete ligados às sementes e 12 agronômicos. O material foi disposto em campo com famílias (linhagens de cinco famílias) intercaladas com seus respectivos parentais (testemunhas). A coloração do caule, forma e número de racemos colhidos, coloração principal, tipo de coloração secundária e peso de cem sementes possuem elevada variabilidade na população com formação de 68 grupos em função da similaridade genética. Evidencia-se a possibilidade de seleção, quanto ao número de racemos colhidos, podendo identificar os genótipos com maior número, visando potencializar o rendimento da cultura.

Palavras-chave: *Ricinus communis* L.. Melhoramento genético. Entropia.

*Corresponding author
[1]Received for publication in 08/12/2020; accepted in 08/30/2021.
Article extracted from the doctoral thesis of the first author.
[2]Instituto Federal de Educação, Ciência e Tecnologia Baiano, Itapetinga, BA, Brazil; gean.capinan@ifbaiano.edu.br – ORCID: 0000-0001-6189-7040.
[3]Center for Agrarian, Environmental and Biological Sciences, Universidade Federal do Recôncavo da Bahia, Cruz das Almas, BA, Brazil; sas@ufrb.edu.br - ORCID: 0000-0002-3017-6133, drsouza@ufrb.edu.br – ORCID: 0000-0002-4599-952X, lasagro@hotmail.com - ORCID: 0000-0003-1367-279X, ilneidebraz@hotmail.com - ORCID: 0000-0002-3940-3005.

INTRODUCTION

Castor bean (*Ricinus communis* L.) has great economic relevance, for being a crop that requires a large volume of labor, generating several jobs, and the oil extracted from its seeds is used in several industrial segments (COSTA et al., 2015).

The species has a mixed reproductive system, in which both self-fertilization and cross fertilization occur, with cross rates varying according to size and/ or type of branching (SAVY FILHO, 1999), contributing to result in great genetic variability and hence diversification in morphological descriptors, such as color of fruits and stems, types of seeds, presence of waxiness among others (AZEVEDO et al., 2001). Thus, knowledge on a population is fundamental to access its variability (ELLEGREN; GALTIER, 2016), enabling the selection of parents which can direct genetic improvement programs of the species (SALIHU et al., 2019).

The use of morphoagronomic characterization contributes to making the selection process less costly and easy to perform, based on the phenotype that results in numerous pieces of information. Several studies such as those conducted by de Silva et al. (2019) and Bezerra Neto et al. (2010) use this methodology in the characterization of species, revealing variability among genotypes for the morphoagronomic traits evaluated, concomitantly allowing a performance evaluation.

The evaluation of genetic diversity can be performed by observing the level of entropy using the Rényi's (1961) coefficient, which makes it possible to indicate phenotypic classes for the qualitative characteristics observed, indicating the balance existing in the proportion between the frequency of genotypes in the various phenotypic classes. The recognition of the most closely related genotypes aims to gather parents into groups, using a measure of dissimilarity or similarity, explaining homogeneity within the group and heterogeneity between groups.

The objective of this study was to evaluate the genetic divergence in 490 strains and seven castor bean progenitors in order to identify the performance of the population in relation to the morphoagronomic descriptors proposed by the Ministry of Agriculture, Livestock and Food Supply - MAPA and by the Center for Genetic Improvement and Biotechnology of the Federal University of Recôncavo da Bahia.

MATERIAL AND METHODS

The study was carried out from 2016 to 2018, in the experimental area of the Center for Agrarian, Environmental and Biological Sciences of the Federal University of Recôncavo da Bahia, on the campus of Cruz das Almas – Bahia, Brazil. The municipality (12° 40'39" S, 39° 40'23" W) is located at 220 m altitude and has average temperature of 24.5 °C, relative humidity of 82% and annual precipitation of 1,197 mm. According to the Köppen's classification system, the climate in the region is a zone of transition between Am (monsoon climate) and Aw (tropical climate with dry season in winter) (C1 type), and is dry and sub-humid. The soil in the experimental field is classified as a *Latossolo Amarelo distrófico* (Ultisol) - A horizon with moderate to sandy clay texture (EMBRAPA, 2006).

To conduct the experiment, hybridizations were performed using eight divergent parents in 2016, forming 24 families, of which 17 were selected based on the superiority of the traits of interest for the NBIO/UFRB Program for Genetic Improvement of the Species. Each family was grown during the year 2017, being evaluated and self-fertilized to generate seeds to be used in 2018, after confirming the superiority of the best constitutions. With the results and selection, the parents $UFRB_{318}$, $UFRB_{317}$, $UFRB_{321}$, $UFRB_{322}$, $UFRB_{323}$, $UFRB_{319}$ and $UFRB_{320}$, as well as the seeds of hybrid families F01, F02, F03, F04 and F05, began to make up in 2018 the F_2 population of the present study.

The arrangement of the experimental material in the field was five families interspersed with two controls, a derivation of the augmented block design (FEDERER, 1956), with controls equivalent to common treatments (parents) and families equivalent to regular treatments (strains - F_2), totaling 880 genotypes, of which only 497 were used, due to losses by death during the experiment. The area was prepared conventionally and then received basal fertilization at the dose of 20 $kg.ha^{-1}$ of N, 80 $kg.ha^{-1}$ of P and 40 $kg.ha^{-1}$ of K. Planting was carried out by direct seeding using three seeds per genotype.

Each genotype was characterized in the F_2 population, by a single observer always at the same observation time, following the phenotypic classes for 35 morphometric descriptors of the Ministry of Agriculture, Livestock and Food Supply (BRASIL, 2008), namely: 13 referring to plants: anthocyanin pigmentation of the hypocotyl - APH, insertion of the primary raceme - IPR, stem diameter - STD, average length of stem internodes - ALSI, number of stem internodes - NSI, stem waxiness - STWX, stem color - STC, upper side of the lamina - USL, pigmentation of the midrib - PMR, waxiness on the upper side of the lamina - WXUSL, color of the upper side of the lamina - CUSL, plant stature - PST and plant architecture - PARC; nine related to inflorescence: flowering - FLO, male flowers in racemes - MFR, location of male flowers in raceme - LMFR, stigma color - STGC, raceme density - RD, number of racemes harvested - NRH, length of primary raceme - LPR, effective length of primary raceme - ELPR, raceme shape - RSH; six related to the fruits: fruit waxiness - FWX, fruit color - FC, presence of spines on the fruits - PSF, density of fruit

spines - DFS, color of fruit spines - CFS, dehiscence of fruits - DEF; eight related to the seeds: main color of the seed - MCS, presence of secondary color - PSC, secondary color of the seed - SCS, type of secondary color - TSC, seed shape - SSH, caruncle protuberance - CARP, 100-seed weight - 100SW and yield of seeds per fruit - YSF; and 13 agronomic traits: raceme length - RL, effective raceme length - ERL, number of seeds per plant - NSP, weight of fruits per raceme - WFR, number of fruits per raceme - NFR, weight of racemes per plant - WRP, weight of seeds per raceme - WSR, number of seeds on the primary raceme - NSPR, weight of seeds per plant - WSP, number of fruits per plant - NFP, oil content in the seeds - OCS and yield - YLD. These descriptors were measured in accordance with the Form of Instructions for Conducting Testes of Distinguishability, Homogeneity and Stability of Castor Bean (*Ricinus communis* L.) Crops based on the images of Document 192 (MILANI, 2008) and the 13 quantitative descriptors established by the Center for Genetic Improvement and Biotechnology of the Federal University of Recôncavo da Bahia - NBIO/UFRB, as relevant to the program (Table 1).

Table 1. Keywords proposed by the Ministry of Agriculture, Livestock and Food Supply - MAPA (BRASIL, 2008) and proposed by the Center for Genetic Improvement and Biotechnology of the Federal University of Recôncavo da Bahia. Cruz das Almas, BA, Brazil.

Until 10 days after emergence		
Descriptors	Evaluation	Phenotypic class
1. Anthocyanin Pigmentation of the Hypocotyl (APH)	Observe visually if there is presence or absence.	1. Absent or 2. Present
Full flowering of primary raceme.		
2. Insertion of the Primary Raceme (IPR).	Measure with a tape measure from the soil to the point of insertion of the primary raceme.	1. Low (< 50cm); 2. Medium (51 to 100cm); 3. High (> 100cm).
3. Stem Diameter (STD).	Measure in the middle third of the stem, with digital caliper.	1. Thin (< 3cm); 2. Medium (3 to 6cm); 3. Thick (> 5cm).
4. Average Length of Stem Internode (ALSI).	Obtained by the NSI/IPR ratio.	1. Short (< 2cm); 2. Medium (3 to 5cm) or 3. Long (>5 cm).
5. Number of Stem Internodes (NSI).	Quantity of scars present on the stem.	1. Low (up to 15); 2. Medium (16 to 18) or 3. High (> 19).
6. Stem Waxiness (STWX).	Record if there is presence or absence of wax on the stem.	1. Absent or 2. Present.
7. Stem Color (STC).	Phenotypic classes of MAPA (BRASIL, 2008).	1. Light green; 2. Medium green; 3. Dark green; 4. Pinkish green; 5. Pinkish; 6. Red; 7. Reddish brown or 8. Purple.
8. Upper Side of the lamina (USL).	According to the angle formed by the lamina.	1.Flat. 2. Slightly tapered. 3. Tapered.
9. Pigmentation of the Midrib (PMR).	Color of veins on the lower side of mature leaves.	1. Greenish and 2. Reddish.
10. Waxiness on the Upper Side of the Lamina (WXUSL).	Observe on the upper lamina of mature leaves.	1. Absent and 2. Present.
11. Color of the Upper Side of the Lamina (CUSL).	Color observed on the side.	1. Light green; 2. Medium green; 3. Dark green; 4. Pink; 5. Reddish green. 6. Red
12. Male Flowers in Racemes (MFR).	Check for the presence of male flowers.	1. Absent and 2. Present.
13. Location of Male Flowers in Racemes (LMFR).	Observe whether the male flowers are mostly at the bottom of the primary raceme.	1. Predominant at the bottom of the raceme and 2. Interspersed with female flowers.
14. Stigma Color (STGC).	Observe in the first raceme the color of the stigma before pollination.	1. Yellowish; 2. Greenish; 3. Orangish; 4. Reddish and 5. Pinkish.
From emergence to the beginning of female flowering of the first raceme.		
15. Flowering (FLO).	Subtraction of germination data from flowering date.	1. Early (up to 30 days); 2. Medium (31 to 60 days) and 3. Late (above 60 days).

Table 1. Continuation.

Until 10 days after emergence		
Descriptors	Evaluation	Phenotypic class
Full flowering of the last commercial raceme.		
16. Plant Stature (PST).	Measure with a tape measure from the soil to the apex of the highest branch.	1. Very short (< 100 cm); 2. Short (101 to 150 cm); 3. Medium (151 to 200 cm); 4. Tall (201 to 250 cm) and 5. Very tall (> 250 cm)
17. Plant Architecture (PARC).	Photograph plants for analysis.	1. Erect; 2. Semi-erect and 3. Open.
18. Number of Racemes Harvested (NRH).	Count how many racemes were produced.	1. Low (up to 3); 2. Medium (4 to 7) or 3. High (> 7).
19. Length of Primary Raceme (LPR).	Measure with a ruler from the apex of the first raceme to the scar of the first node.	1. Short (< 31 cm); 2. Medium (31 to 50 cm) or 3. Long (> 51 cm).
Immature fruits of the first raceme		
20. Raceme Density (RD).	Phenotypic classes of MAPA (BRASIL, 2008).	1. Sparse; 2. Intermediate and 3. Compact.
21. Raceme Shape (RSH).	Phenotypic classes of MAPA (BRASIL, 2008).	1. Globose; 2. Cylindrical and 3. Conical.
22. Fruit Waxiness (FWX).	Evaluations performed visually.	1. Absent. 2. Present.
23. Fruit Color (FC).	Phenotypic classes of MAPA (BRASIL, 2008).	1. Yellowish; 2. Light green; 3. Medium green; 4. Dark green; 5. Pinkish green. 6. Pink; 7. Red or 8. Purple.
24. Presence of Spines on the Fruits (PSF).	Evaluations performed visually	1. Absent or 2. Present.
25. Density of Fruit Spines (DFS).		1. Low; 2. Medium or 3. High;
26. Color of Fruit Spines (CFS).	Phenotypic classes of MAPA (BRASIL, 2008).	1. Yellowish; 2. Light green; 3. Medium green; 4. Dark green; 5. Pinkish green. 6. Pink; 7. Red or 8. Purple.
Mature fruits or racemes		
27. Dehiscence of Fruits (DEF).	According to the quantity of open fruits.	1. Dehiscent; 2. Semi-dehiscent or 3. Indehiscent.
Seeds harvested from mature fruits.		
28. Presence of Secondary Color (PSC).	Evaluations performed visually	1. Absent. 2. Present.
29. Main Color of the Seed (MCS).	Corresponding to the predominant color.	1. White; 2. Yellowish; 3. Reddish; 4. Light brown; 5. Medium brown; 6. Dark brown; 7. M-Reddish brown. 8. Grayish or 9. Black.
30. Secondary Color of the Seed (SCS).	Phenotypic classes of MAPA (BRASIL, 2008).	1. White; 2. Yellowish; 3. Reddish; 4. Light brown; 5. Medium brown; 6. Dark brown; 7. M-Reddish brown. 8. Grayish or 9. Black.
31. Type of Secondary Color (TSC).	Phenotypic classes of MAPA (BRASIL, 2008).	1. Mottled; 2. Streaked or 3. Spotted.
32. Seed Shape (SSH).	According to its shape.	1. Round or 2. Ellipsoid.
33. Caruncle Protuberance (CARP).	Evaluated visually.	1. Light or 2. Accentuated.
34. 100-seed weight at 9% moisture (100SW).	Phenotypic classes of MAPA (BRASIL, 2008).	1. Low (< 40 g); 2. Medium (41 to 55 g) or 3. High (> 55 g).
35. Yield of Seeds per Fruit (YSF).	Percentage of seed weight by fruit weight.	1. Low (< 60%); 2. Medium (61 a 80%) or 3. High (> 80%).
36. Number of fruits per raceme (NFR).	Average count of the number of fruits from the first four racemes.	Descriptors suggested by NBIO (2014).

Table 1. Continuation.

Until 10 days after emergence		
Descriptors	Evaluation	Phenotypic class
37. Number of Seeds on the Primary Raceme (NSPR).	Count of the number of seeds in the first raceme.	Descriptors suggested by NBIO (2014).
38. Number of Seeds per Raceme (NSR).	Average count of the number of seeds in the first four racemes.	Descriptors suggested by NBIO (2014).
39. Weight of Seeds per Raceme (WSR).	Average weight of seeds in the first four racemes.	Descriptors suggested by NBIO (2014).
40. Weight of Seeds per Plant (WSP).	Sum of the weight of seeds from the first four racemes.	Descriptors suggested by NBIO (2014).
41. Number of Fruits per Plant (NFP).	Count of the number of fruits from the first four racemes.	Descriptors suggested by NBIO (2014).
42. Number of Seeds per Plant (NSP).	Count of the number of seeds from the first four racemes.	Descriptors suggested by NBIO (2014).
43. Weight of Racemes per Plant (WRP).	Weight of the first four racemes, using an analytical balance.	Descriptors suggested by NBIO (2014).
44. Weight of Fruits per Raceme (WFR).	Average weight of fruits from the first four racemes, using an analytical balance.	Descriptors suggested by NBIO (2014).
45. Yield (YLD).	Estimated for each plant in kg ha^{-1}.	Descriptors suggested by NBIO (2014).
46. Raceme Length (RL).	Average length of the first four racemes.	Descriptors suggested by NBIO (2014).
47. Effective Raceme Length (ERL).	Measurement from the apex of the raceme to the last peduncle.	Descriptors suggested by NBIO (2014).
48. Weight of Fruits per Plant (WFP)	Sum of the weight of fruits from the first four racemes.	Descriptors suggested by NBIO (2014).

Regarding the descriptors, the percentage frequencies of each category and the entropy level of these traits (H) were calculated using the Rényi's (1961) coefficient, with entropy being used as a measure of the frequency of the distribution of (n) strains $P = (p_1, p_2 \ldots p_s)$, in which: $p_1 = f_i/n$ and $(p_1 + p_2 + \ldots + p_s = 1)$ provided that $n = (f_1 + f_2 + \ldots + f_s)$, where $f_1, f_2, \ldots f_n$ are the counts of each of the classes (s) in the observed descriptor.

To estimate the genetic similarity (GS=dii'), among all pairs of genotypes, the simple coincidence index was used to generate the genetic dissimilarity matrix, which was used to measure the distances between genotypes and subsequent clustering by the Tocher's optimization method (CRUZ; CARNEIRO, 2003). For the quantitative descriptors, the data were subjected to analysis of variance (ANOVA) by the F test, and the Tukey test was performed at 1% probability level. The analyses were performed using R software (R Development Core Team, 2017) and GENES software (CRUZ, 2014).

RESULTS AND DISCUSSION

The results showed the existence of genetic variability. Among the 35 morphometric traits evaluated, 62% had values higher than 0.60, with formation of classes, which allows speed in direct access to the genotype of interest. Nevertheless, 38% showed values below 0.6 and in some cases 0.0, with one or a few unbalanced classes (Table 2). The descriptors presented with few classes and low homogeneity in frequencies can be classified as of low entropy and, therefore, are little informative in terms of variability, but usable.

Entropy ranged from zero (0.0) for APH, WXUSL, MFR, LMFR, PSF and SSH to 1.22 for MCS. Equivalent results were found by Silva et al. (2019), who evaluated the castor bean germplasm bank of the Federal University of Recôncavo da Bahia and found 100% of APH. The level of entropy is related to the number of phenotypic classes and their proportion in the study population, so a great variation is possible (VIEIRA et al., 2008).

The descriptors that had the highest number of classes and frequency distributed proportionally in the classes bring with them greater variability within the studied population. In this context, MCS showed entropy of 1.22, revealing six classes, 44.1% of black color, a result equivalent to that found by Silva et al. (2019), demonstrating equitable and homogeneous distribution.

Table 2. Descriptors, phenotypic classes, frequencies of genotypes in classes and entropy level (H) evaluated in 497 genotypes. Cruz das Almas-BA, Brazil.

Descriptor	Classes	Frequency (%)	Entropy (H)
APH - Anthocyanin Pigmentation of the Hypocotyl	1. Absent	100.0	0.00
	2. Present	0.0	
FLO - Flowering	1. Early	97.8	0.11
	2. Medium	0.2	
	3. Late	2.0	
IPR - Insertion of the Primary Raceme	1. Low	87.7	0.46
	2. Medium	6.2	
	3. High	6.0	
STD - Stem Diameter	1. Thin	96.4	0.14
	2. Medium	3.6	
	3. Thick	0.0	
ALSI - Average Length of Stem Internode	1. Short	0.4	0.72
	2. Medium	49.9	
	3. Long	49.7	
NSI - Number of Stem Internodes	1. Low	57.1	0.72
	2. Medium	42.3	
	3. High	0.6	
STWX - Stem Waxiness	1. Absent	80.3	0.49
	2. Present	19.7	
STC - Stem Color	1. Light green	0.2	0.86
	2. Medium green	5.2	
	3. Dark green	0.0	
	4. Pinkish green	6.8	
	5. Pinkish	0.8	
	6. Red	10.7	
	7. Reddish brown	76.3	
	8. Purple	0.0	
USL - Upper Side of the Lamina	1. Flat	71.6	0.62
	2. Slightly tapered	28.4	
	3. Tapered	0.0	
PMR - Pigmentation of the Midrib	1. Greenish	13.1	0.39
	2. Reddish	86.9	
WXUSL - Waxiness on the Upper Side of the Lamina	1. Absent	100.0	0.00
	2. Present	0.0	
CUSL - Color of the Upper Side of the Lamina	1. Light green	78.9	0.61
	2. Medium green	0.0	
	3. Dark green	20.3	
	4. Pinkish	0.0	
	5. Reddish green	0.2	
	6. Red	0.6	
	7. Purple	0.0	
MFR - Male Flowers in Racemes	1. Absent	100.0	0.00
	2. Present	0.0	

Table 2. Continuation.

Descriptor	Classes	Frequency (%)	Entropy (H)
LMFR - Location of Male Flowers in Racemes	1. Predominant at the bottom of the raceme	100.0	0.00
	2. Interspersed with female flowers	0.0	
STGC - Stigma Color	1. Yellowish	0.0	0.62
	2. Greenish	26.4	
	3. Orangish	0.0	
	4. Reddish	73.6	
	5. Pinkish	0.0	
RD - Raceme Density	1. Sparse	17.9	0.66
	2. Intermediate	77.1	
	3. Compact	5.0	
RSH - Raceme Shape	1. Globose	30.6	1.02
	2. Cylindrical	50.9	
	3. Conical	18.5	
FWX - Fruit Waxiness	1. Absent	22.5	0.63
	2. Present	77.5	
FC - Fruit Color	1. Yellowish	0.4	0.62
	2. Light green	4.6	
	3. Medium green	86.5	
	4. Dark green	8.0	
	5. Pinkish green	0.2	
	6. Pink	0.0	
	7. Red	0.2	
	8. Purple		
PSF - Presence of Spines on the Fruits	1. Absent	100.0	0.00
	2. Present	0.0	
DFS - Density of Fruit Spines	1. Low	2.8	0.70
	2. Medium	70.4	
	3. High	26.8	
CFS - Color of Fruit Spines	1. Yellowish	0.2	0.82
	2. Light green	3.0	
	3. Medium green	1.8	
	4. Dark green	0.0	
	5. Pinkish green	23.3	
	6. Pink	1.4	
	7. Red	9.9	
	8. Purple	60.4	
PST - Plant Stature	1. Very short	32.6	0.92
	2. Short	58.4	
	3. Medium	8.7	
	4. Tall	0.4	
	5. Very tall	0.0	
PARC - Plant Architecture	1. Erect	35.0	1.09
	2. Semi-erect	38.2	
	3. Open	26.8	

Table 2. Continuation.

Descriptor	Classes	Frequency (%)	Entropy (H)
NRH- Number of Racemes Harvested	1. Low	59.0	0.80
	2. Medium	37.2	
	3. High	3.8	
LPR - Length of Primary Raceme	1. Short	86.1	0.43
	2. Medium	13.5	
	3. Long	0.4	
DEF - Dehiscence of Fruits	1. Dehiscent	67.0	0.69
	2. Semi-dehiscent	32.0	
	3. Indehiscent	1.0	
PSC - Presence of Secondary Color	1. Absent	98.4	0.09
	2. Present	1.6	
MCS - Main Color of the Seed	1. White	0.2	1.22
	2. Yellowish	0.0	
	3. Reddish	0.0	
	4. Light brown	0.2	
	5. Medium brown	4.2	
	6. Dark brown	28.0	
	7. Reddish brown	23.3	
	8. Grayish	44.1	
	9. Black	0.0	
SCS - Secondary Color of the Seed	1. White	1.8	0.15
	2. Yellowish	0.0	
	3. Reddish	0.0	
	4. Light brown	97.8	
	5. Medium brown	0.0	
	6. Dark brown	0.4	
	7. Reddish brown	0.0	
	8. Grayish	0.0	
	9. Black		
TSC - Type of Secondary Color	1. Mottled	17.7	0.93
	2. Streaked	20.7	
	3. Spotted	61.6	
SSH- Seed Shape	1. Round	0.0	0.00
	2. Ellipsoid	100.0	
CARP - Caruncle Protuberance	1. Light	40.2	0.68
	2. Accentuated	59.8	
YSF - Yield of Seeds per Fruit	1. Low	64.4	0.71
	2. Medium	34.2	
	3. High	1.4	
100SW - 100-seed weight at 9% moisture	1. Low	51.5	1.06
	2. Medium	27.2	
	3. High	21.3	

On the other hand, PST showed entropy of 0.92, distributed in four classes, being 32.6% very low, 58.4% low, 8.7% medium, and 0.4% high. The result shows that 162 genotypes are very short and, therefore, are of interest for the breeding program of the species conducted by NBIO, since shorter genotypes may result in higher yields (SOUZA-SCHLICK et al., 2018; PIVETTA; ZANOTTO; TOMAZ, 2017) and can be explored to increase the frequency of these genes in the next generations.

For the NRH, the entropy level was 0.92, distributed in three classes, 59.0% with low, 37.2% with medium and 3.8% with a high number of racemes harvested. Among the genotypes evaluated, 18 stood out for the increase in yield, as they had higher production of harvested racemes. Although the increase in the number of racemes tends towards a higher production of seeds, there are other components of equal importance, such as number and weight of seeds (AZEVEDO; BELTRÃO; 2007).

100-seed weight (100SW) is a trait directly related to crop yield (DEVIDE; CASTRO; CARVALHO; 2019). In the present study, 51.5% of the genotypes had high 100SW, 27.7% had medium and 21.3% had low, being possible to identify that 256 genotypes were superior for this trait, standing out as the most productive.

The traits linked to production stood out, including YSF, expressing frequencies of 64.4%, 34.2% and 1.4%, respectively for low (up to 60%), medium (between 61 and 80%) and high YSF (above 80%), with entropy of 0.71. Devide, Castro and Carvalho (2019) found lower values when studying the cultivars IAC Guarani, AL Guarany 2002 and IAC 2028, with yield of seeds per fruit ranging from 48.5% to 53.8%. These values outside the range found in the study may be related to the fact that the authors are evaluating cultivars with a high degree of homozygosis and, therefore, with lower possibilities of segregation. The DEF has 0.69 entropy and three classes, 67% semi-dehiscent, 32% indehiscent and 1.0% of dehiscent genotypes. Fruit dehiscence results in losses of 2% to 45%, forcing premature harvests, leading to a decrease in oil content due to loss of yield (LAVANYA et al., 2018). Semi-dehiscent fruits promote a lower production cost, and there were 332 genotypes meeting this demand in the breeding, demonstrating that there is high potential in the selection to meet the demand of the breeding program.

Plants with open architecture have overlapping of leaves, which reduces photosynthetic efficiency, resulting in low yield, besides hindering cultural practices and mechanized harvesting, due to the branches (WANG et al., 2021), behavior contrary to those shown by plants considered erect and semi-erect (GONDIM; BELTRÃO; PEREIRA, 2014). Thus, in the present study, 173 genotypes show an erect PARC, most adequate conformation to facilitate management. In this case, entropy was 1.09, distributed as follows: 35% erect, 38.2% semierect and 26.8% open.

The spines give the fruits a natural barrier against the attack of harmful insects in the crop (MORAES et al., 2011), contributing to the healthy and consequent increase in production. In the evaluation performed, it was found that all genotypes have these structures, revealing entropy of 0.0. However, the DFS manifested in different quantities, showing entropy of 0.70, separating the group of genotypes into three distinct classes, 2.8% of them with low, 70.4% with medium and 26.8% with high number of spines.

The entropy for raceme density (RD) was 0.66, a value considered of median magnitude, classifying 17.9% of the genotypes as of intermediate density, 77.1% with sparse and 5.0% as compact density. With the results obtained, 25 genotypes show potential of exploration for the breeding program of the species conducted by NBIO/UFRB, since more compact racemes tend to have a higher number of fruits and, consequently, a higher yield (RUKHSAR; PATEL, 2018).

Castor bean undergoes intense variation in stem color (STC), which was confirmed in the present study by the entropy of 0.86 and the classification of genotypes of this population in 0.2% with light green color, 0.8% pinkish, 5.2% medium green, 6.8% pinkish green, 10.7% red and 76.3% reddish-brown. Silva et al. (2019) found a variation of 30.77% for light green color and only 0.96% for red.

ALSI made it possible to distribute the population in three classes, 49.9% with medium, 49.7% with long and 0.45% with short length, and entropy of 0.72. For having a direct relationship with ALSI, NSI showed a similar behavior when distributing the genotypes in its three classes, being 57.1%, 42.3% and 0.6% as low, medium and high NSI, respectively, revealing entropy of 0.72. These two descriptors maintain a strong relationship, because in the search for plants with shorter stature, the ideal is that they have higher NSI with the ALSI between the medium to short classes, ensuring better robustness for the plant, hence minimizing lodging (PINTO et al., 2011). Thus, the population has 250 genotypes with medium and short ALSI and 213 genotypes with medium and high NSI, which may result in greater advances.

When evaluating the frequency, it was possible to identify its manifestation and identify those traits that, even at low frequency, are sources of interest for possible selection and fixation of these genes. Thus, it was possible to verify the presence of anthocyanin color in 100% of the genotypes (Table

2), which is important for plants, as anthocyanins act as antioxidants, defense mechanism and perform biological function for plants (LOPES et al., 2017).

For FLO, entropy was 0.1, with 97.8% of genotypes considered late (above 60 days), 0.2% early with flowering up to 30 days and 2.0% with medium earliness (between 31 and 60 days). As there intervals between harvests, the seeds can lose quality due to their permanence in the field; thus, maintaining an early flowering is expected, seeking not only to standardize the early harvests, but also to reduce the effect of the environment on the trait. Late flowering implies late harvest, which can cause losses in yield. Plants with early flowering (up to 30 days) or of medium earliness (31 to 60 days) reduce the time of permanence as well as the effects of the environment on trait and consequently on production. Although most genotypes behaved as late, it was possible to select 10 genotypes with the characteristics of interest for breeding.

IPR had an entropy of 0.46, classifying the genotypes as 6% with high, 87.7% with medium and 6.2% with low insertion. Plants with low insertion heights, possibly for having better carbon partition, may produce more racemes and can be distributed in arrangements with smaller spacing, for greater yield (PINTO et al., 2011). Thus, 29 genotypes with standard that meet the interest of the breeding program were identified.

For LPR, the population had 86.1% with short, 13.5% with medium and only 0.4% with long length of raceme, inducing an entropy value of 0.43. LPR has a positive correlation with seed size, number of fruits, fruit weight, seed weight and number of seeds, as reported by Thatikunta and Prasad (2001). For the exploration of the LPR in the study population, only the genotypes $UFRB_{410}$ and $UFRB_{412}$ stand out from the others.

STD showed entropy of 0.14, with 96.4% classified as thin and 3.6% classified as medium diameter. This is an important trait for providing support to the plant, and medium values facilitate mechanized harvesting and avoid tipping over, increasing yield. There were 17 genotypes with this phenotypic class.

In many cases, descriptors serve to elucidate or verify the definition of taxonomic categories and, for this reason, are used, even without direct influence on yield, in the differentiation between its constitutions (SILVA; SANTOS, 2019), serving as a standard, such as: upper side of the lamina (0.60), color of the upper side of the lamina (0.56), waxiness on the upper side of the lamina (0.0), fruit color (0.62), fruit waxiness (0.53), color of fruit spines (0.82), presence of male flowers in the raceme (0.0), location of male flowers in the raceme (0.0), secondary color of seeds (0.15), type of secondary color (0.93), seed shape (0.0) presence of secondary color (0.09), caruncle protuberance (0.68). Waxiness, when present, gives the plant defense against water deficit, making it more efficient (ZHENGBIN et al., 2011).

Thus, in the present study it was possible to identify great potential in the genotypes, since some express a set of descriptors correlated with yield, namely: $UFRB_{325}$, $UFRB_{330}$, $UFRB_{344}$, $UFRB_{336}$, $UFRB_{337}$, $UFRB_{421}$, $UFRB_{424}$, $UFRB_{429}$, $UFRB_{433}$, $UFRB_{443}$, $UFRB_{445}$, $UFRB_{452}$, $UFRB_{504}$, $UFRB_{523}$, $UFRB_{527}$, $UFRB_{528}$, $UFRB_{529}$, $UFRB_{537}$, $UFRB_{588}$, $UFRB_{627}$, $UFRB_{632}$, $UFRB_{652}$, $UFRB_{705}$, $UFRB_{709}$, $UFRB_{710}$, $UFRB_{737}$, $UFRB_{780}$, $UFRB_{789}$, $UFRB_{455}$, $UFRB_{488}$, $UFRB_{519}$, $UFRB_{520}$, $UFRB_{532}$, $UFRB_{540}$, $UFRB_{544}$, $UFRB_{549}$, $UFRB_{556}$, $UFRB_{559}$, $UFRB_{563}$, $UFRB_{569}$, $UFRB_{570}$, $UFRB_{571}$, $UFRB_{574}$, $UFRB_{573}$, $UFRB_{590}$, $UFRB_{595}$, $UFRB_{606}$, $UFRB_{614}$, $UFRB_{622}$, $UFRB_{640}$, $UFRB_{641}$, $UFRB_{648}$, $UFRB_{651}$, $UFRB_{652}$, $UFRB_{653}$, $UFRB_{658}$, $UFRB_{700}$ and $UFRB_{701}$.

However, for considering the first segregating population, these genotypes represent the presence of promising variability, and advanced generations by self-fertilization are necessary to conduct this population through method of improvement, in order to fix the traits of interest with selection of elite strains that will be evaluated in performance tests or use of selection strategies assisted by molecular markers in the F2 generation, identifying, without the effect of the environment, individuals with traits of interest (SILVA; SANTOS, 2019).

The analysis of variance for quantitative descriptors (Table 3) showed significant differences at 1% probability level, by the F test, for all 14 quantitative traits, analyzed in the 490 genotypes evaluated.

The CV ranged from 6.27% for OCS to 59.23% for WSP. For Silva et al. (2012), the CV obtained in this experiment express the polygenic nature of the traits, which are influenced by the environment, revealing differences between genotypes or treatments. The amplitude between the values of the coefficient of variation makes it possible to infer that this behavior is directly linked to the presence of genetic variability among the families, allowing the inclusion of these traits in genetic distance studies (ELLEGREN; GALTIER, 2016).

Among the agronomic traits, the obtained variation ranged from 7 to 56 cm for RL and from 1 to 65 units for NFR; consequently, NSR ranged from 3 to 197 units, with weight between 1.66 and 116.36 g, and these characteristics were highly correlated. These values were close to those found by Silva et al. (2019), when conducting the study for characterizing and evaluating the performance of castor bean strains and parents in the germplasm bank of UFRB. YLD reached a maximum value of 4,098.77 $kg.ha^{-1}$, with an average value of 1006.85

kg.ha^{-1}. These results were higher than that mentioned by CONAB for the 2017/2018 season, with an average yield for the Bahia state on the order of 631 kg.ha^{-1} (CONAB, 2018). This data reflects positive exploration potential for the program, positively affecting the selection.

The evaluated genotypes have variability, with possible selection of superior constitutions in the conduction of this population, to obtain high genetic gains for several descriptors, most of which with desirable traits from the agronomic point of view.

Table 4 shows a significant difference between genotypes for most of the evaluated traits, except for NSR and WSP.

Table 3. Summary of the analysis of variance for 14 quantitative descriptors, evaluated in 490 genotypes and seven parents of castor bean. Cruz das Almas-BA, Brazil.

Descriptors	Mean Square	F	Mean	Minimum	Maximum	CV (%)
RL (cm)	94.93	19.26**	23.88	7.00	56.00	30.48
ERL (cm)	27.82	28.13**	17.51	4.00	46.00	37.93
WRP (g)	8.000	7.27**	185.60	18.00	578.00	51.28
NFR (unt)	81.83	3.78**	16.95	1.00	65.00	54.01
NFP (unt)	1,309.00	3.83**	67.99	4.00	258.00	54.21
WFR (g)	449.34	7.36**	43.90	4.00	137.00	51.28
WSR (g)	180.38	6.41**	26.13	1.66	116.36	56.68
WSP (g)	2,630.00	3.24**	97.12	6.63	465.43	59.23
NSPR (unt)	2,209.00	6.54**	130.65	15.00	354.00	40.85
NSR (unt)	485.33	3.31**	44.06	2.99	196.93	55.84
NSP (unt)	7,689.00	3.35**	169.59	11.95	787.73	57.54
YLD (kg.ha^{-1})	23,819.00	6.99**	1008.41	91.89	4,098.77	53.85
WFP (g)	7,116.45	7.47**	176.98	15.98	712.83	52.29
OCS (%)	143.74	14.5**	44.19	23.4	51.83	6.27

**,* Significant at 1% and 5% probability levels by F-test.
RL - Raceme length; ERL - Effective raceme length; WRP - Weight of racemes per plant; NFR - Number of fruits per raceme; NFP - Number of fruits per plant; WFR - Weight of fruits per raceme; WSR - Weight of seeds per raceme; WSP - Weight of seeds per plant; NSPR - Number of seeds on the primary raceme; NSR - Number of seeds per raceme; NSP - Number of seeds per plant and YLD - Yield; WFP - Weight of Fruits per Plant; OCS - Oil Content in the Seeds.

For RL and ERL, the parent $UFRB_{323}$ stood out, a condition achieved in the family F01 ($UFRB_{322}$ X $UFRB_{319}$), for NSP, in which the genotypes are slightly superior, despite not differing from the other ones. As for WFR, the parent $UFRB_{319}$ outperforms the others, although it shows results equivalent to those of the parents $UFRB_{318}$, $UFRB_{317}$ and the families F05 ($UFRB_{321}$ x $UFRB_{322}$) and F03 ($UFRB_{322}$ X $UFRB_{323}$), with average values above the others. $UFRB_{321}$, together with F01, reached higher values for the number of fruits per raceme, standing out from the others. The highest value of WRP was obtained in $UFRB_{319}$, which was slightly superior to the parents $UFRB_{318}$ and $UFRB_{317}$ and the families F02 ($UFRB_{320}$ X $UFRB_{317}$), F03 and F05, hence being superior to all others (Table 4).

For the OCS, the parents have slightly higher levels than the families evaluated, especially the parents $UFRB_{323}$ (47.40), $UFRB_{321}$ (46.48%), $UFRB_{317}$ (45.60) and the family 05 (Table 4). Due to the possible influence of polygenic actions on the oil content, the additive effects of genes that interfere in its determination possibly cause different thresholds of expression in subsequent populations.

The NSR has superiority in the parents $UFRB_{317}$ and $UFRB_{323}$ and in the family F01. For WSR and WFR per plant, the parent $UFRB_{319}$ was superiority to the others, standing out with weights of 33.97g and 236.49g, respectively. Although $UFRB_{321}$ and the family F01 were superior to the others, they were equivalent in terms of NFP. For YLD, the parent $UFRB_{319}$, despite having higher values, does not differ statistically from $UFRB_{317}$ and from the hybrid family F02, with values on the order of 1,356.37 kg.ha^{-1}, 1,246.63 kg.ha^{-1} and 1,257.09 kg.ha^{-1}. The results demonstrate superiority for some hybrid families, as well as for some parents, which can be explored for the indication of those constitutions that add a greater number of traits of interest to the breeding program of castor bean conducted by NBIO/UFRB.

Table 4. Comparison of means by Tukey test (P<0.01) in genotypes and parents of castor bean, in the F_2 population. Cruz das Almas-BA, Brazil.

	TRAITS						
GEN	RL	ERL	NSP	NSR	WFR	NFR	WRP
$UFRB_{317}$	29.36b	22.29bc	191.65ab	50.41 a	54.22ab	19.79ab	227.51ab
$UFRB_{318}$	18.55e	13.05g	140.13ab	37.62 a	43.35abc	14.22ab	184.35abc
F04	25.82c	19.79cd	154.31ab	39.53 a	33.25c	14.58ab	141.95c
F02	19.94e	14.45fg	182.63ab	46.95 a	54.72ab	17.33ab	229.92ab
$UFRB_{321}$	23.47d	17.84e	204.22ab	52.50 a	36.78bc	20.92 a	154.41bc
$UFRB_{323}$	31.54a	24.70a	177.68ab	46.28 a	35.18c	17.00ab	146.34c
F05	29.53b	23.34b	171.88ab	46.64 a	51.03abc	16.79ab	219.00abc
$UFRB_{319}$	22.17de	18.81d	203.00ab	50.75 a	58.97 a	19.74ab	249.24 a
$UFRB_{320}$	21.16de	15.75ef	133.36ab	33.34 a	35.31c	15.73ab	146.15c
F01	23.86d	17.68e	212.74a	53.19 a	34.04c	21.04 a	143.96c
F03	16.92d	11.12g	134.50ab	35.99 a	46.25abc	14.24ab	198.40abc
$UFRB_{322}$	23.72d	13.04g	113.04b	31.87 a	38.06bc	11.52b	164.33bc
GEN	NSPR	WSR	WSP	NFP	WFP	YLD	OCS
$UFRB_{317}$	160.07 a	30.80abc	117.88 a	79.99ab	218.52ab	1246.63ab	45.60abc
$UFRB_{318}$	95.13cd	26.78abc	94.97 a	56.86ab	175.93abc	989.75abc	44.80cd
F04	132.45abcd	19.70c	75.93 a	58.31ab	134.08c	763.21c	44.96cd
F02	123.95abcd	33.09ab	114.72 a	69.70ab	219.44ab	1257.09ab	43.50e
$UFRB_{321}$	153.77ab	22.47bc	88.66 a	83.69 a	147.13bc	846.00bc	46.48a
$UFRB_{323}$	161.48 a	20.25c	77.35 a	67.99ab	141.94c	809.00c	47.40a
F05	143.29abc	29.33abc	111.31 a	67.16ab	204.13abc	1173.74abc	46.06ab
$UFRB_{319}$	128.59abcd	33.97 a	120.71 a	78.97ab	236.49 a	1356.37a	44.52d
$UFRB_{320}$	124.98abcd	20.61c	75.20 a	62.94ab	141.25c	812.20c	43.43e
F01	162.54 a	21.25c	85.14 a	84.15 a	136.17c	782.98c	45.31bcd
F03	96.47bcd	27.94abc	106.62 a	56.95ab	184.98abc	1063.65abc	43.17e
$UFRB_{322}$	82.29d	23.53abc	87.59 a	46.09b	152.25bc	875.41bc	41.05f

Note. Means followed by equal uppercase letters in the column do not differ statistically from each other by Tukey test, 1% probability level. RL - Raceme length; ERL - Effective raceme length; WRP - Weight of racemes per plant; NFR - Number of fruits per raceme; NFP - Number of fruits per plant; WFR - Weight of fruits per raceme; WSR - Weight of seeds per raceme; WSP - Weight of seeds per plant; NSPR - Number of seeds on the primary raceme; NSR - Number of seeds per raceme; NSP - Number of seeds per plant; YLD - Yield and OCS - Oil content in the seeds.

Cluster analysis revealed 68 distinct clusters (Table 5). It was possible to observe the formation of a large cluster consisting of 155 genotypes, five median clusters consisting of 14 to 54 genotypes and the other small clusters, formed by less than 13 genotypes. In the group of small clusters, it is observed that 20 of them had only one genotype, indicating that such genotypes are the most divergent compared to the others; however, other 17 groups were formed by only two genotypes each, highlighting their importance regarding dissimilarity compared to the others, and these genotypes were possible targets of selection, because they are distinct.

Table 5. Clusters of 490 genotypes and seven parents, established by the Tocher's method, based on genetic dissimilarity, number of genotypes established in each cluster and mean genetic dissimilarity within each cluster. Cruz das Almas, BA, Brazil.

Clusters	Genotypes	N° of genotypes	Dissimilarity
01	$UFRB_{368; 369; 356; 357; 371; 625; 622; 623; 337; 531; 519; 330; 650; 332; 586; 544; 521; 535; 526; 525; 520; 649; 431; 523; 529; 433 424; 434; 739; 653; 528 533; 658; 327; 641; 448; 449; 635; 636; 432; 648; 632; 427; 450; 484; 383; 382; 642; 654; 446; 429; 425; 483; 480; 633; 643; 634; 656; 444; 749; 437; 447; 638; 482; 322; 481; 426; 665; 436; 441; 631; 487; 485; 416; 721; 660; 661; 443; 663; 637; 667; 442; 748; 445; 318; 326; 336; 730; 640; 479; 724; 719; 706; 486; 718; 720; 715; 716; 727; 713; 731; 723; 677; 683; 712; 389; 722; 711; 323; 670; 495; 732 681; 682; 674; 686; 675; 676; 717; 490; 672; 678; 728; 668; 452; 462; 465; 466; 467; 469; 729; 376; 662; 664; 725; 726; 478; 679; 669; 494; 685; 644; 474; 645; 688; 707; 703; 477; 708; 705; 464; 489; 709; 471; 461 and 468.}$	155	0.21
02	$UFRB_{439; 440; 438; 639; 451; 800; 390; 496; 700; 704; 502; 492; 505; 497; 499; 498; 510; 501; 508; 500; 503; 493; 509; 504; 507; 696; 470; 454; 459; 473; 476; 460; 456; 673; 512; 453; 455; 680; 684; 463; 472; 475; 458; 457; 516; 514; 517; 515 and 699.}$	54	0.19
03	$UFRB_{805; 806; 810; 812; 807; 808; 813; 809; 782; 793; 792; 803; 811; 747; 783; 796; 786; 784; 797; 321; 745; 794; 760; 761; 742; 755; 744; 756; 757; 754; 746; 758 and 759.}$	33	0.20
04	$UFRB_{580; 596; 599; 600; 577; 576; 543; 579; 578; 581; 588; 590; 584; 592; 587; 589; 595; 802; 352; 591; 691; 409; 666; 403; 695; 693 and 701.}$	26	0.19
05	$UFRB_{624; 629; 628; 627; 617; 388; 618 and 626.}$	8	0.19
06	$UFRB_{687; 692;694; 690; 689;781;659; 394; 406; 398; 395; 401; 400 and 714.}$	14	0.13
07	$UFRB_{768; 769; 770; 772; 778; 766; 776; 777; 763; 762; 767; 775; 764; 765; 771 and 773.}$	16	0.18
08	$UFRB_{787; 788; 518; 790; 789; 791; 608 and 795.}$	8	0.17
09	$UFRB_{358; 362; 359; 372; 366; 363; 365; 593; 361; 354; 370; 355; 360 and 328.}$	14	0.19
10	$UFRB_{380; 671;375; 374; 397; 381; 391; 411; 399; 373; 402; 422 and 419.}$	13	0.18
11	$UFRB_{537; 547; 324; 541; 737; 655; 329; 345; 545; 342 and 339.}$	11	0.16
12	$UFRB_{554; 555; 556; 552; 553; 56 and 551.}$	7	0.18
13	$UFRB_{377; 378; 619; 412; 414 and 404·}$	6	0.15
14	$UFRB_{549; 550 and 548·}$	3	0.16
15	$UFRB_{558; 561; 565; 560; 571 and 564·}$	6	0.16
16	$UFRB_{559; 562; 569; 570 and 568·}$	5	0.19
17	$UFRB_{613; 620; 605; 607; 610; 698; 702 and 621.}$	8	0.19
18	$UFRB_{734; 736; 527; 750; 522; 524 and 540}$	7	0.20
19	$UFRB_{325; 335; 331; 334; 343 and 344.}$	6	0.17
20	$UFRB_{353; 367; 542 and 386.}$	4	0.18
21	$UFRB_{384; 387; 413 and 410.}$	4	0.11
22	$UFRB_{606; 611; 604 and 710.}$	4	0.19
23	$UFRB_{743; 753; 735; 733 and 738}$	5	0.18
24	$UFRB_{779; 780 and 614.}$	3	0.19
25	$UFRB_{320; 539; 601; 630 and 597.}$	5	0.19
26	$UFRB_{379; 612; 774 and 697.}$	4	0.15
27	$UFRB_{651; 751 and 557.}$	3	0.14
28 and 29*	$(UFRB_{647; 652 and 657})$ and $(UFRB_{418, 615 and 546})$	3	0.17
30 and 31*	$(UFRB_{319; 348 and 349})$ and $(UFRB_{428; 430 and 646})$.	3	0.20
32	$(UFRB_{435 and} U_{741})$.	2	0.11
33	$(UFRB_{573 and 574})$.	2	0.19
34 to 36*	$(UFRB_{393 and 396})$; $(UFRB_{491 and 511})$ and $(UFRB_{567 and} UFRB_{572})$.	2	0.17
37 to 41*	$(UFRB_{364 and 575})$; $(UFRB_{385 and 392})$; $(UFRB_{566 and 582})$; $(UFRB_{333 and 602})$ and $(UFRB_{423 and 603})$.	2	0.20
42 to 48*	$(UFRB_{408 and 417})$; $(UFRB_{415 and 740})$; $(UFRB_{420 and 421})$; $(UFRB_{506 and 804})$; $(UFRB_{532 and 534})$; $(UFRB_{583 and 801})$; and $(UFRB_{338 and 341})$.	2	0.22
49 to 68*	$UFRB_{585; 798; 538; 350; 799; 317; 405; 488; 598; 752; 351; 513; 530; 346; 594; 785; 407; 616; 536 and 609·}$	1	

*Within parentheses, genotypes belonging to the same group, with equivalent number and dissimilarity. Note. Hybrid family F01: $UFRB_{630}$ to $UFRB_{732}$; F06: $UFRB_{519}$ to $UFRB_{629}$; F12:$UFRB_{424}$ to $UFRB_{518}$; F16: $UFRB_{324}$ to $UFRB_{423}$; and F17:$UFRB_{733}$ to $UFRB_{813}$. Parent: $UFRB_{318}$; $UFRB_{317}$; $UFRB_{321}$; $UFRB_{322}$; $UFRB_{323}$; $UFRB_{319}$ and $UFRB_{320}$.

The genotypes within each group showed mean genetic distance below 0.21, that is, the mean similarity within the groups was higher than 0.79, making it possible to assume that the clusters formed are homogeneous (Table 5). The establishment of groups with homogeneity within the clusters of genotypes and with heterogeneity between the groups can be the starting point for a thorough

evaluation in the selection and indication of the genotypes to be used in breeding programs.

The results point to the possibility of accessing genotypes belonging to divergent groups, which can be evaluated for traits of interest, and with possibilities of selection to form a select group of genotypes to be used in the breeding program of castor bean conducted by NBIO/UFRB.

CONCLUSIONS

The F_2 population has genotypes with high seed yields, with the possibility of fixing the most promising ones at the time of direct or indirect selection, to guide the breeding program of the species.

REFERENCES

AZEVEDO, D. M. P. et al. In: AZEVEDO, D. M. P.; LIMA, E. F. (Eds.). **O Agronegócio da mamona no Brasil**. Campina Grande, PB: Embrapa Algodão, 2001. v. 1, p. 121-160.

AZEVEDO, D. M. P.; BELTRÃO, N. E. M. **O Agronegócio da Mamana no Brasil**. 2. ed. Campina Grande, PB: Embrapa Algodão; Embrapa Informação Tecnológica, 2007. 504 p.

BEZERRA NETO, V. F. et al. Descritores quantitativos na estimativa da divergência genética entre os genótipos de mamoneira, utilizando análises multivariadas. **Revista Ciência Agronômica**, 41: 294-299. 2010.

BRASIL. **Instruções para execução dos ensaios de distinguibilidade, homogeneidade e estabilidade de cultivares de mamona (Ricinus communis L.)**. 2008. DOU nº 147, de 01/08/2008, seção 1, 2008. p. 147: 14–15. Disponível em: <http:// www.agricultura.gov.br/arq_editor/file/vegetal/RegistroAutorizacoes/Formularios%20Prote%C3%A7%C3%A3o%20Cultivares/MAMONA%20FORMULARIO%2001%2008%202008%20P.doc>. Acesso em: 05. fev. 2021.

CONAB - Companhia Nacional de Abastecimento, 2018. **Observatório Agrícola: Acompanhamento da safra brasileira. Grãos.** Disponível em: <24 ttps://data.gessulli.com.br/file/2018/12/11/H103633-F00000-D108.pdf/>. Acesso em: 15 mai. 2019.

COSTA, L. V. et al. BIODIESEL: mamona e dendê como culturas energéticas. **Revista Eletrônica de Energia**, 5: 90-99, 2015.

CRUZ, C. D.; CARNEIRO, P. C. S. **Modelos biométricos aplicados ao melhoramento genético**. v. 2. Viçosa, MG: UFV, 2003. 585 p.

CRUZ, C. D. et al. **Modelos biométricos aplicados ao melhoramento genético.** 3. ed. Viçosa, MG: UFV, 2014. 668 p.

DEVIDE, A. C. P.; CASTRO, C. M.; CARVALHO, C. L. Manejo semiperene de mamona em duas densidades de plantio na safrinha. **Revista Brasileira de Energia Renováveis**, 8: 29-40, 2019.

ELLEGREN, H.; GALTIER, N. Determinantes da diversidade genética. **Nature***,* 17: 422-433, 2016.

EMBRAPA – Empresa Brasileira de Pesquisa Agropecuária. Centro Nacional de Pesquisas de Solos. **Sistema Brasileiro de Classificação de Solos**. 2. ed. Rio de Janeiro, RJ: Embrapa Solos, 2006. 306 p.

FEDERER, W. T. Augmented (hoonuiaku) designs. **Hawaian Planters' Record**, 55: 191-208, 1956.

GONDIM, T. M. S.; BELTRÃO, N. E. M.; PEREIRA, W. E. Plasticidade fenotípica da mamoneira precoce sob diferentes arranjos espaciais em consórcio com feijão caupi. **Revista Ciência Agronômica**, 45: 128-137, 2014.

LAVANYA C. et al. Genetics Classical, Cytogenetics, and Traditional Breeding in Castor Bean. In: KOLE, C.; RABINOWICZ, P. (Eds.) The Castor Bean Genome. **Compendium of Plant. Genomes**. Springer, Cham. 2018.

LOPES, T. J. et al. Antocianinas: uma breve revisão das características estruturais e da estabilidade. **Revista Brasileira de Agrociência**, 13: 291-297, 2007.

MILANI, M. **Descritores de mamona utilizados pela Embrapa Algodão**. Campina Grande, PB: Embrapa Algodão, 2008. 39 p.

MORAES, W. et al. Epidemiologia e manejo do mofo cinzento da mamona. **Nucleus,** *8: 1-12, 2011*.

PINTO, C. M. et al. Mamona consorciada com girassol em plantios defasados: análise de trilha da produtividade e seus componentes. **Revista Verde de Agroecologia e Desenvolvimento Sustentável**, 6: 219-229, 2011.

PIVETTA, L. G.; ZANOTTO, M. D.; TOMAZ, C. A. Crescimento de híbridos de mamona sob densidades populacionais adensadas. **Revista Ceres**, 64: 399-412. 2017.

R CORE TEAM. R. **A language and environment**

for statistical computing. Áustria: R Foundation for Statistical Computing, 2017.

RÉNYI, A. **On measures of entropy and information**. Fourth Berkeley Sympo- sium, Berkley, 1960. p. 547-561, 1961.

RUKHSAR, M. P.; PATEL, D. J. Variabilidade genética, associação de caráter e estudos de divergência genética em mamona (*Ricinus communis* L.), **Annals of Agrarian Science**, 16: 143-148, 2018.

SALIHU, B. Z. et al. Avaliação da diversidade genética de genótipos promissores de mamona (*Ricinus communis* L.) na Nigéria. **Notulae Scientia Biologicae**. 11: 467-474, 2019.

SAVY FILHO, A. Melhoramento da Mamona. In: BORÉM, A. (Org.). **Melhoramento de Espécies Cultivadas**. Viçosa, MG: UFV, 1999. p. 385-407.

SILVA, A. R. et al. Characterization and performance of castor bean lineages and parents at the UFRB germplasm bank. **PLoS One**, 14: e0209335, 2019.

SILVA, D. F. P. et al. Diversidade entre mangueiras, baseada em caracteres dos frutos. **Revista Ceres**, 59: 225-232. 2012.

SILVA, S. A.; SANTOS, L. A. Melhoramento Genético de Oleaginosas. In: CHAVES, L. H. G.; FRANCISCO, P. R. M.; VASCONCELOS, A. C. F. (Eds.). **Oleaginosas e Hortaliças sob diferentes Manejo de Cultivo: Coletânea de Estudos**. Campina Grande, PB: EPGRAF, 2019. v. 1, p. 78-85.

SOUZA-SCHLICK, G. D. et al. Mepiquat Chloride Effects on Castor Growth and Yield: Spraying Time, Rate, and Management. **Crop Science**, 58: 880-891, 2018.

THATIKUNTA, R.; PRASAD, D. Analysis *Ricinus communis* L.. Research Notes. **Agricultural Journal**, 88: 705-707, 2001.

VIEIRA, E. A. et al. Variabilidade genética do banco de germoplasma de mandioca da Embrapa Cerrados acessada por meio de descritores morfológicos. **Científica**, 36: 56-67, 2008.

ZHENGBIN, Z. et al. Advances a water use efficiency, **Critical Reviews in Biotechnology**, 31: 1–13, 2011.

WANG, Z.et al. Bulked segregant analysis reveals candidate genes responsible for dwarf formation in woody oilseed crop castor bean. **Scientific Reports**, 11: 1-15, 2021.