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Genetic diversity and importance of agronomic traits in cowpea genotypes in conditions of low technological level in Piaui[1]

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ABSTRACT

The aim of the study was to evaluate the genetic diversity, agronomic traits and promising combinations of cowpea genotypes under conditions of low technological level in the region south of Piaui. The experiment was conducted in rainfed condition in the experimental area of the Federal Institute of Piauí, Uruçuí - PI, in DBC with four replications. We used 10 genotypes of commercial cultivars. The following variables were evaluated: Cycle; Number of pods /plants; Number of grains/pods; Weight of 100 grains and yield. The genetic divergence was obtained by Mahalanobis distance and clustering by UPGMA method. The genotypes BRS Tumucumaque, BRS Pajeú and BRS Guariba are promising for cultivation in the first crop under conditions of low technological level in the Cerrado region of Piauí. The combinations of genotypes BRS Tumucumaque and BRS Imponente, BRS Tumucumaque and BRS Aracê, BRS Guariba and BRS Imponente, BRS Guariba and BRS Aracê and BRS Pajeú and BRS Imponente have great potential for use in breeding programs to obtain promising segregating populations for grain yield and other attributes. The traits weight of 100 grains, cycle and number of grains per pod have the greatest contribution to the genetic diversity in the studied population.

Keywords: *Vigna unguiculata*; genetic variability; characterization of cultivars.

INTRODUCTION

The Cowpea (*Vigna unguiculata* (L.) Walp) is a leguminous plant of great importance and prominence in human food in different regions of the world, because of its versatility and appreciable nutritional composition, combined with low requirement in soil fertility and tolerance to high temperatures and drought, allowing it to be grown in tropical regions, under rainfed regime (Freire Filho *et al.*, 2011; Ramos *et al.*, 2015; Silva *et al.*, 2018; Araújo *et al.*, 2019).

He Brazilian production occurs especially in the first and second seasons in the North, Northeast and Midwest regions due to their traits of earliness and tolerance to water deficit, in addition to low cost and the obtaining of the good yields (Freire Filho *et al.,* 2011; Araújo *et al.*, 2018; Barros *et al.*, 2021). In the agricultural year 2022/2023, the estimated total Brazilian production of cowpea was 643,100 tons of grain, grown in an area of 1,297,900 hectares, with average grain yield around 496 kg ha-1. In the north and northeast regions, the estimated area with the cultivation of cowpea for the same agricultural year was 1,186,300 hectares, with production of 536,600 tons of grain, corresponding to more than 80% of all national production (Conab, 2023).

In Piauí, the cowpea is configured as an indispensable crop in local subsistence, especially in families with limited conditions, to be an important income generator, since first the destination of production is geared to meet the family itself, getting the surplus facing marketing (Bertini

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et al., 2010; Freire Filho *et al.*, 2011; Silva & Neves, 2011; Andrade *et al.*, 2013).

Despite the importance, cowpea has its genetic potential underexplored in the state, given that genotypes that are either traditional or from breeding programs conducted in other regions, with different soil and climatic conditions, are used in most plantations, and its cultivation is carried out mostly by small farmers with little technical knowledge and little knowledge of the environment, as well as limited economic power (Silva *et al.*, 2014; Sousa *et al.*, 2017; Silva *et al.*, 2018).

With the study of genetic diversity, it is possible to know the best the materials genetic combinations, making it possible to obtain superior genotypes for segregating generations, thus identifying divergent individuals and assisting in the choice of combinations more promising and favorable to crosses, allowing the formation of new genetic combinations (Cruz & Regazzi, 2001; Santana *et al.*, 2019).

Some studies have been conducted on the genetic divergence of cowpea (Santos *et al.*, 2012; Santos *et al.*, 2014). However, cowpea needs to be further explored, because the species has a wide genetic variability in different environments for virtually all traits of agronomic interest, such as the number of pods and number of grains, weight of one hundred grains and yield grains.

Therefore, the aim of the study was to evaluate the genetic diversity, agronomic traits and promising combinations of cowpea genotypes under conditions of low technological level in the region south of Piaui.

MATERIAL AND METHODS

The experiment was conducted in the experimental area of the Federal Institute of Piaui - IFPI, in the municipality of Urucui, located south of the state of Piauí (7º 13' 46" S, 44º 33' 22" W and altitude of 167 m asl). The climate of the region is Aw, according to Köppen's classification, with average annual rainfall of 1.069 mm and average annual temperature of 27.2 ºC. The mean temperature (ºC) and precipitation (mm) during the experiment conduction period were daily collected (Figure 1).

The experiment was conducted in the agricultural year 2018/2019, with sowing on December 11 and harvest between February 18 and 23. The previous cultivation of the area was conducted with corn. The soil of the experimental area is classified as oxisol, whose main chemical characteristics in the 0-20 cm depth layer are: ph (cacl2): 5.7; Mo: 15.8 g kg-1; P (mehlich-1): 4.0 mg dm-3; K: 0.06 cmolc dm-3, ca: 2.82 cmolc dm-3; Mg: 1.57 cmolc dm-3; Al: 0.0 cmolc dm-3; H + al: 0.62 cmolc dm-3; Sb (sum of bases) = 4.45 cmolc dm-3; V (base saturation) = 87.8%. These determinations were performed before the installation of the experiment, through soil collections in the 0-20 cm layer. Then, the conventional tillage was carried out with a plow and a sowing. The treatments consisted of 10 cowpea genotypes, all commercial cultivars selected by the cowpea breeding program of Embrapa Meio Norte (Table 1).

The experimental design was a randomized blocks (RBD) with four replicates. Each experimental plot consisted of four 5-m-long rows, spaced apart by 0.5 m, considering the two central rows as the evaluation area (useful), disregarding 0.5 m of each end, totaling 4 m2, totaling 80 plants per useful area. Before sowing, the area was furrowed and fertilized

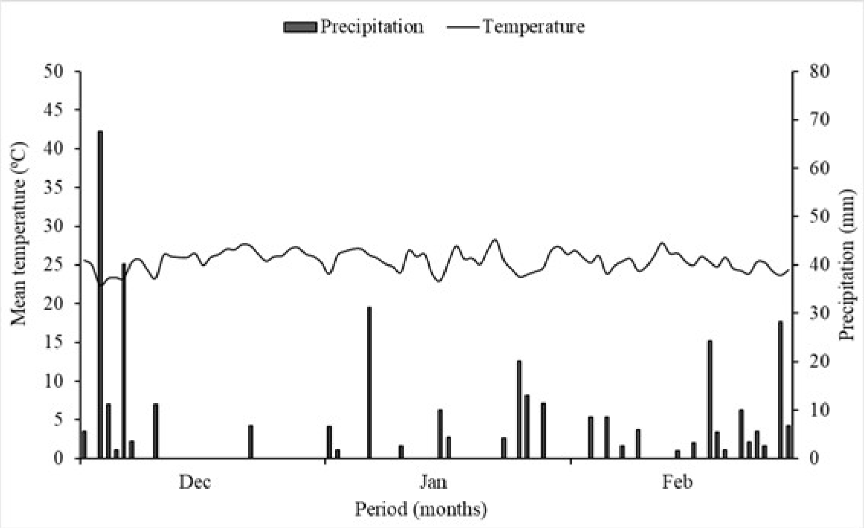

Figure 1: Daily climatic data of mean temperature (ºC) and precipitation (mm), during the experiment conduction period, from December 2018 to February 2019, in Uruçuí, Piauí, Brazil. Source: INMET, 2019.

Table 1: Agronomic traits of cowpea genotypes (commercial cultivars) used in the experiment

Cultivars	Subclass	Plant Size	Cycle*	Growth habit
BRS Guariba	Plain-white	Semi-erect	Early	Indeterminate
BRS Tumucumaque	Plain-white	Semi-erect	Semi-early	Determinate
BRS Cauamé	Plain-white	Semi-erect	Early	Indeterminate
BRS Xiquexique	Plain-white	Semi-prostrate	Early	Indeterminate
BRS Novaera	Rough-white	Semi-erect	Semi-early	Indeterminate
BRS Imponente	Rough-white	Semi-erect	Early	Indeterminate
BRS Itaim	Black-eyed	Erect	Early	Determinate
BRS Marataoã	Cream color	Semi-prostrate	Semi-early	Indeterminate
BRS Pajeú	Cream color	Semi-prostrate	Semi-early	Indeterminate
BRS Aracê	Green	Semi-prostrate	Semi-early	Indeterminate

*: Early = between 60 and 70 days; Semi-early = between 71 and 80 days.

using a mechanized seeder. Sowing was performed manually, distributing 16 seeds per linear meter. After seedling emergence, thinning was done keeping the average stand of ten plants per meter, which corresponds to a population of 200.000 plants per hectare (Cardoso *et al.*, 2005).

Fertilization was applied according to the results of the soil analysis of the experimental area and based on the recommendations for the cowpea crop (Melo *et al.*, 2005). Fertilization at sowing was performed with 250 kg ha-1 of NPK formulated fertilizer (5-30-15). At 25 days after sowing, nitrogen fertilization was applied as top-dressing at a dose of 20 kg ha-1, in a continuous strip at 0.10 m from the plant row, with ammonium sulfate as source.

Weed control was performed with manual weeding at 15 and 30 days after seedling emergence. With regard to the management of the culture, monitoring of the culture was carried out and alternative applications of insecticides based on Thiamethoxam and Acetamiprid, in dosages of 200g/ha and 250g/ha, respectively, in order to control the whitefest (*Bemisia tabaci*). The applications were performed via knapsack sprayer in the early stages of pest infestation during the crop cycle.

The cultivars were evaluated until they reached the ideal growth stages for their evaluations. We evaluated the following agronomic traits: Cycle to maturity - period of days between sowing and almost all dry pods; Number of pods/plant (nº) - relationship between total number of pods and total number of plants collected; Number of grains/pod (nº) - relationship between total number of grains and total number of pods; Weight of 100 grains (g) - determined by collecting and counting 4 samples of 100 grains per experimental unit followed by weighing with standardization in the moisture content of the grains to 13%; Grain yield (kg ha-1) - obtained by weighing the grains produced by the plants of the useful area of the plot, corrected to 13% moisture, converted into kg ha-1, after manual harvesting and mechanized threshing. To determine the number of pods/plants, number of grains/pod and weight of 100 grains, 10 plants were collected in the useful area of each plot, after physiological maturity of each cultivar (R9).

The data were submitted to analysis of variance by the F test and the means were compared by the Scott-Knott test at 5% probability level. Clustering of genotypes was performed by Unweighted Pair Group Method with Arithmetic Mean (UPGMA), using the Generalized Mahalanobis Distance a from a cutoff at approximately 20% of the maximum distance. The contribution of the characters was assessed through the methodology of Singh (1981). For the processing of statistical analysis, we used the computer software Genes (Cruz, 2013).

RESULTS AND DISCUSSION

There was a significant difference ($p < 0.05$) by the F test between genotypes for all traits, showing the occurrence of genetic diversity among the genotypes studied (Table 2). The cowpea genotypes composed three groups regarding the cycle: cultivars BRS Itaim, BRS Imponente and BRS Xiquexique were the earliest compared to the other genotypes, with an average of 65 days of cycle. BRS Aracê, BRS Marataoã and BRS Pajeú were the latest ones

Table 2: Average values of the traits cycle, yield components and grain yield of ten cowpea genotypes under rainfed condition in the Cerrado biome. Uruçuí, Piauí, Brazil 2018/2019

Genotypes	Cycle (day)	Pods per plant (n)	Grains per pod (n)	Weight of 100 grains (g)	Grain yield (kg ha^{-1})
BRS Guariba	70 b	15 b	12.2 c	21.5 c	1,354 a
BRS Marataoã	74 a	11 c	14.6 a	18.4 d	794 b
BRS Novaera	71 b	19 a	10.4 d	23.5 b	640 b
BRS Itaim	65 c	22 a	12.9 b	23.0 b	572 b
BRS Pajeú	74 a	8 c	13.6 b	21.0 c	1,388 a
BRS Tumucumaque	71 b	14 b	12.1 c	22.0 b	1,379 a
BRS Aracê	74 a	14 b	12.9 b	15.6 e	938 b
BRS Cauamé	70 b	11 c	11.2 d	19.8 c	866 b
BRS Imponente	65 c	15 b	10.1 d	32.6 a	851 b
BRS Xiquexique	65 c	10 c	14.7 a	17.6 d	765 b
Overall average	71	13.9	12.5	21.5	955.1
CV (%)	1.7	19.1	8.6	5.0	26.1
MS	51.3**	70.7**	10.2**	85.2**	379186.7**

** Significant at 1% by the F test; Means followed by the same letter in the column do not differ from each other by the Scott-Knott test at 5% significance. MS = Mean Square; CV = Coefficient of Variation.

(average of 74 days), followed by BRS Cauamé, BRS Guariba, BRS Novaera and BRS Tumucumaque (between 70 and 71 days) (Table 2). Earliness is relevant in plant breeding, because early genotypes are likely to enable the reduction of risks due to the action of climatic factors, as very high temperatures in the flowering stage and the lack of humidity in the grain filling period in months of little rain (Teixeira *et al.*, 2010; Vale *et al.*, 2015).

For the number of pods per plant, the genotypes BRS Itaim and BRS Novaera stood out with the highest averages observed, with 22 and 19 pods, respectively, not differing statistically. BRS Pajeú, BRS Marataoã, BRS Cauamé and BRS Xiquexique showed the lowest number of pods, making up the group with the lowest average for this trait. The other genotypes had averages between 14 and 15 pods per plant (Table 2). In relation to the number of grains per pod, four groups of distinct means and therefore significant were formed, where the superior genotypes were BRS Xiquexique (14.7) and BRS Marataoã (14.6). BRS Aracê, BRS Pajeú and BRS Itaim did not differ, as well as the genotypes BRS Imponente, BRS Novaera and BRS Cauamé, which had the lowest values for the number of grains per pod (Table 2).

The values found here were higher than the averages reported by Sousa *et al.* (2017), who obtained values from 5.93 to 14 for pods per plant and 12.51 to 14.56 for grains per pod, in a study with genotypes and lines of cowpea. Also, in relation to the aforementioned authors, there was the formation of only one group for the character number of pods per plant, with an overall average of 9.70 and, for the number of grains per pod, two groups were formed with an overall average of 12.30. Teixeira *et al.* (2010) verified that BRS Marataoã also stood out for the character number of grains per pod. Barros *et al.* (2021) concluded in their work that the increase in temperatures promotes a high rate of aborted flowers reflecting the amount of pods and consequently the crop yield. Santos *et al.* (2012) state in their work that a greater number of pods per plant is one of the components that strongly contribute to greater grain production in cowpea. However, this statement was not evident in this study since the genotypes BRS Itaim and BRS Novaera had lower yield (Table 2).

Regarding the traits weight of 100 grains, the genotypes were distributed into five groups, and there was comprehensive genetic variability among the cowpea genotypes evaluated, with averages ranging from 15.6 g to 32.6 g (Table 2). The commercial cultivar BRS Imponente had the highest weight of 100 grains, although it obtained the lowest values for the trait number of grains per pod, thus demonstrating that its grains are compensated by weight. Values greater than these results are in accordance with those found by

Santos *et al.* (2012). The BRS Tumucumaque, BRS Itaim and BRS Novaera showed no significant differences among their means, as well as BRS Cauamé, BRS Pajeú and BRS Guariba. The lowest value observed for weight of 100 grains was obtained by BRS Aracê (Table 2).

Sousa *et al.* (2017), evaluating this same trait, found only a single group, with masses ranging from 13.86 to 17.54 g, and BRS Tumucumaque had the highest average observed. According to some authors, there is a greater acceptance of cowpea beans with weight above 18 g (Freire Filho *et al.*, 2011; Silva & Neves, 2011). Probably, one of the factors that may have contributed to this result is linked to the particularity that each genotype responds differently to soil and climatic conditions and management imposed by different treatments, influencing, in this case, the plant metabolism via distribution of photoassimilates to different amounts of grain, which caused variations in grain weight between genotypes.

As for grain yield, two groups of genotypes were formed, the most productive being composed of BRS Pajeú (1,388 kg ha-1), BRS Tumucumaque (1,379 kg ha-1) and BRS Guariba (1,354 kg ha-1), with no significant difference between these genotypes. Despite having obtained the highest values for the number of pods per plant, the BRS Itaim and BRS Novaera genotypes showed the lower values for the grain yield, with means of 572 kg ha-l and 640 kg ha-1, respectively, not differing statistically between the other genotypes, that have values of less than a thousand kilograms (Table 2).

There was no direct relationship between the number of pods and grain yield, since the genotype BRS Pajeú had the lowest number of pods (8) and, nonetheless, showed the highest yield (Table 2), as well as the genotypes BRS Itaim and BRS Novaera, which were the least productive, since they obtained the highest number of pods per plant, which partially disagrees with the results of Santos *et al.* (2012).

These results were higher compared to those found by Sousa *et al.* (2017), who obtained average yield of around 588 kg ha-1 when working under rainfed conditions. Silva *et al.* (2018) achieved higher grain yield results among the commercial cultivars BRS Marataoã (2,399.97 kg ha-1) and BRS Pajeú (2,011.86 kg ha-1). Teixeira *et al.* (2010) obtained yield values around 2,221 kg ha-1 with the commercial cultivar BRS Guariba, and overall average of 1,307 kg ha-1 in their work.

The cowpea genotypes showed a satisfactory average grain yield, higher than the national average, considering the agricultural years 2019/2020 to 2021/2022 (Conab, 2023). It is known that several factors can affect the plant behavior in different production environments (Araújo *et al.*, 2019; Ramos *et al.*, 2015; Santana *et al.*, 2019; Sousa *et al.*, 2017), whose distinctions, especially of climate and soil, interfere in the responses of each genotype according to the specificities of the place of production.

The correct recommendation of commercial cultivars to be adapted in certain regions is important to have better yield gain, taking into account the evaluation of genotypes, including the knowledge of the main morphoagronomic components of the plant under the conditions of plant growth, soil and climate of the place of cultivation, management, production system and technological level, which ultimately contribute to the appropriate choice of genotype by the producer (Teixeira *et al.*, 2010; Santos, 2013; Júnior *et al.*, 2017).

The UPGMA clustering, based on the Mahalanobis distance, allocated the cowpea genotypes into four groups from a cutoff at approximately 20% of the maximum distance (Figure 2). According to the dendrogram, group I and group II had the largest number of genotypes, both with the same amount grouped (4): BRS Marataoã, BRS Xiquexique, BRS Aracê and BRS Pajeú composed group I, and BRS Guariba, BRS Tumucumaque, BRS Cauamé and BRS Novaera composed group II. Group III was defined by BRS Itaim and group IV by BRS Imponente.

There was absolute similarity between genotypes of group II regarding the maturation cycle (Table 2), however, the BRS Guariba and BRS Tumucumaque genotypes showed statistically similar mean values for most traits evaluated. The other genotypes of the group obtained between the weight of 100 grains and number of grains per pod the average values with the most similar behavior among the items evaluated. Similarly, in group I, the genotypes BRS Xiquexique and BRS Marataoã obtained statistically equal means for most traits evaluated (Table 2). For this group, the results for cycle to maturity, number of pods per plant and yield were the most similar. These results provide subsidies for the possibility of proximity between the genotypes of the respective groups in the conditions evaluated, corroborated by the degree of genetic similarity found in figure 2.

Gonçalves *et al.* (2014), with UPGMA grouping, also obtained the same number of groups among accessions of traditional bean, in which these materials, when verified in the same group, showed similar genetic traits, while between groups there was heterogeneity between their an-

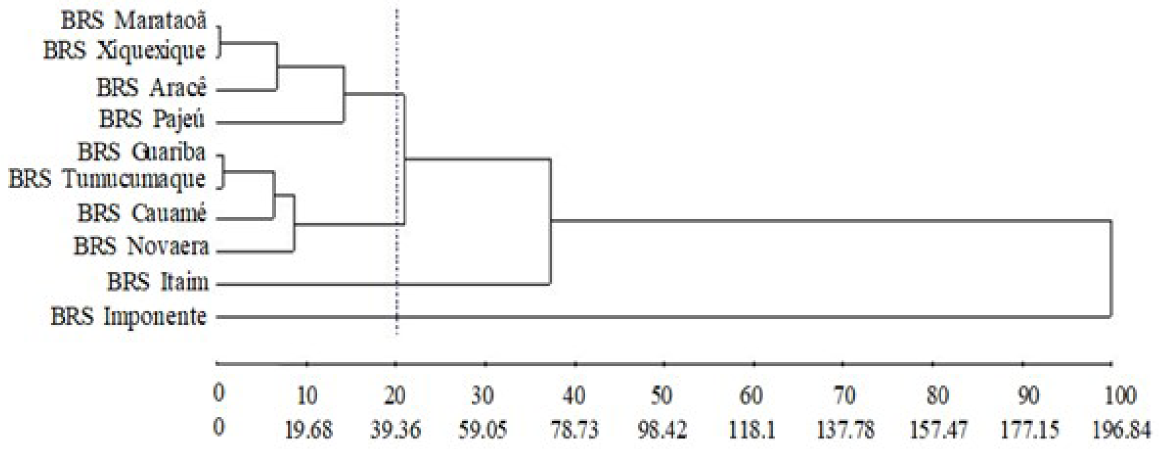

Figure 2: Dendrogram representative of genetic dissimilarity among 10 cowpea genotypes, obtained by the UPGMA clustering method, using the generalized Mahalanobis distance as a measure of dissimilarity. Dotted line: cutoff in the dendrogram at approximately 20% of the maximum distance, forming 4 groups of genotypes.

alyzed traits. Among the most used statistical procedures to estimate the genetic distance through morphological characters, we highlight the generalized Mahalanobis distance (D2), as it considers the existence of correlations between the analyzed characters (Cruz & Regazzi, 2001).

Sousa *et al.* (2017) claim that combinations between genotypes from different groups can enable the generation of promising populations. However, it is important to note that the Mahalanobis distance can be estimated only when the experimental design employs the use of replicates, so that we can measure the environmental effects on the genetic composition (Cargnelutti Filho *et al.*, 2010).

Table 3 shows the measures of genetic dissimilarity of cowpea genotypes evaluated, estimated from the Mahalanobis distance. The distance between the values found was quite high for most crosses between genotypes. The highest value of dissimilarity was D2 = 325.75 between the genotypes BRS Aracê and BRS Imponente, revealing the great genetic variability between them and identifying them as parents that are highly capable of forming segregating populations. The lowest dissimilarity value found was between the genotypes BRS Marataoã and BRS Xiquexique, equal to D2 = 0.72, pointing them as the most similar genotypes among the others (Table 3), since they are part of the same group of genetic dissimilarity (Figure 2), thus suggesting that these genotypes may have lower traits of interest in genetic crossing, because there is a high probability of the genetic potential of the descendants being less than that of the parents.

According to Barros (2019), it is essential to know the genetic distance, in view of the possibility of choosing parents that will give rise to segregating populations. In his work conducted with cowpea, the same author observed a maximum value of genetic divergence equal to D2 = 86.76 and a minimum of D2 = 0.36, values lower than those observed in this study.

It is also verified in table 3 that all genotypes when crossed with BRS Imponente showed high values of dissimilarity, indicating this genotype as the most divergent among all evaluated. Among these values, the combinations BRS Imponente and BRS Xiquexique (D2 = 298.95), BRS Imponente and BRS Marataoã (D2 = 272.99), BRS Imponente and BRS Pajeú (D2 = 202.96) stood out due to the strong divergence. The commercial genotype BRS Itaim also deserves attention in the selection for having high value of genetic divergence with other genotypes, such as BRS Pajeú (D2 = 108.44), BRS Aracê (D2 = 100.90), BRS Xiquexique (D2 = 112.21) and BRS Imponente (D2 = 118.23). These results were higher than those reported by Sousa *et al.* (2017), who found greater dissimilarity among cowpea genotypes Branquinho and UFTfc-19, with a value of D2 = 41.36.

The genotypes that composed the similar traits (Figure 2), showed, notably, values of lower genetic di-

Table 3: Genetic dissimilarity among ten cowpea genotypes in relation to five characters, based on the generalized Mahalanobis distance (D^2)

Genotypes	2	3	4	5	6	7	8	9	10
1	34.0	14.68	41.31	20.76	1.34	41.75	10.60	143.39	42.30
2		50.31	98.87	18.07	32.77	13.96	41.78	272.99	0.72
3			31.46	44.35	15.19	63.69	21.51	114.09	61.01
4				108.44	53.27	100.90	40.41	118.23	112.21
5					13.97	43.67	37.09	202.96	22.47
6						46.25	14.65	140.03	41.12
7							40.61	325.75	12.26
8								155.13	47.78
9									298.95

(1) BRS Guariba, (2) BRS Marataoã, (3) BRS Novaera, (4) BRS Itaim, (5) BRS Pajeú, (6) BRS Tumucumaque, (7) BRS Aracê, (8) BRS Cauamé, (9) BRS Imponente and (10) BRS Xiquexique.

vergence, recorded when there was an interaction between the two groups the members (Table 3). The combinations between the genotype BRS Pajeú and BRS Imponente (D2 = 202.96), as well as between the genotypes BRS Tumucumaque and BRS Imponente (D2 = 140.03) and between BRS Guariba and BRS Imponente (D2 = 143.39) are considered good options for crossing and obtaining promising populations, considering the agronomic traits yield and grain weight, which meet the requirements of farmers and consumers, respectively, as they were the most significant genotypes regarding these aspects (Table 3).

Other combinations were also promising for yield, namely BRS Tumucumaque and When the distances are high, the indications of greater variability between genotypes are more promising and, thus, the interactions of these combinations can be indicated as parents to compose a base population of a breeding program (Sousa *et al.*, 2017). According to Santana *et al.* (2019), the cross between very divergent genotypes may enable better genetic combinations, becoming more relevant when both have good agronomic yields.

The relative contribution of the characters to the genetic dissimilarity of the ten genotypes evaluated, according to the method proposed by Singh (1981), can be observed in table 4. The weight of 100 grains showed the highest relative contribution to dissimilarity among genotypes evaluated with contribution of 48.89% (Table 4). In addition to this trait, the cycle until physiological maturity and the number of grains per pod were the traits that most contributed to dissimilarity among the genotypes evaluated, with 31.11% and 11.92%, respectively (Table 4).

Cabral *et al.* (2011) concluded in their experiment that the characters number of pods per plant, weight of one hundred grains and number of grains per pod were the ones that had greater potential for identification of superior genotypes for grain yield. Santos *et al.* (2014) found that the traits pod length and weight of one hundred grains showed greater contribution to divergence in cowpea genotypes. Thus, in this work, the use of these characters for the selection of parents in a breeding program would have good efficiency, diverging partially from the results obtained by Sousa *et al.* (2017).

Moreover, knowing the parameters between the characters of interest for the selection allows the breeder to know the level of interaction between the characters of economic importance, since the selection on a given character can change the behavior of the other (Correa *et al.*, 2015).

According to Silva *et al.* (2014), knowledge about the association between the main morphoagronomic components of the plant is necessary because it indicates how the selection for a character influences the expression of other characters of interest. There has been disagreement in studies of genetic divergence with cowpea about the components that definitely contribute to its divergence. For Santos *et al.* (2014), pods and weight of 100 grains were more sensitive to provide divergence between the genetic groups among genotypes; Sousa *et al.* (2017) found as contributions for the divergence of yield, the number of days for the ripening of fruits, the number of days for maturation the pods and the number of grains per pod; Santana *et al.* (2019) obtained the

Table 4: Relative contribution of the characters to the genetic dissimilarity of 10 cowpea genotypes according to the method proposed by Singh (1981)

Characters	Value (%)
Cycle	31.11
Pods per plant	3.39
Grains per pod	11.92
Weight of 100 grains	48.89
Grain yield	4.67

characters for divergence, the weight of pods, beginning of flowering and pod length the most contributed to the genetic diversity of the genotypes evaluated. Mendonça *et al.* (2018) attribute this alternation of values for the contribution to the choice of traits and the group of genotypes studied.

CONCLUSIONS

The genotypes BRS Tumucumaque, BRS Pajeú and BRS Guariba are promising for crops in the first season under conditions of low technological level in the Cerrado region of Piauí.

The combinations between the genotypes BRS Tumucumaque and BRS Imponente, BRS Tumucumaque and BRS Aracê, BRS Guariba and BRS Imponente, BRS Guariba and BRS Aracê and between BRS Pajeú and BRS Imponente present great potential for use in breeding programs aimed at obtaining of promising segregating populations in terms of grain yield and other attributes.

The characters weight of 100 grains, maturation cycle and number of grains per pod present the greatest contribution to the genetic divergence in the studied population.

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