



## **Variability, Association and Selection of Promising Characters for Breeding Creole Maize**

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### **Authors' contributions**

*This work was carried out in collaboration among all authors. Author LON designed the study and performed the statistical analysis. Authors VBS and JGVM managed the analyses of the study. Authors YRF and ACA managed the literature searches. Authors MMN and ABF supported at the experimental design and traits evaluations. Authors AFBL and CFC reviewed the manuscript and suggested some alterations. All authors read and approved the final manuscript.*

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### **ABSTRACT**

Genetic variability is the main characteristic when seeking to select promising genotypes for plant breeding. Thus, the objective of this work was to investigate the genetic variability in agronomic and morphological characteristics of traditional varieties of maize, in addition to determining the degree of association and the selection of variety and promising characters to be explored in programs of genetic breeding of Creole maize. The experiment was conducted at the Federal University of Acre (UFAC), Rio Branco - Acre, in the 2017/2018 harvest period. A randomized block design was used, with five replications. The treatments were four varieties of Creole maize (V1, V2, V3 and V4) from

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the Vale do Juruá region and another hybrid cultivar LG 3040 (HI). The morpho-agronomic characteristics were evaluated in the useful area of the plots: days to silking (DS), days to anthesis (DA), plant height (PH) and height ear insertion (HEI), stem diameter (SD), mass of ear (ME), length ear (LE), diameter ear (DE), total grain mass (TGM), mass of 100 grain (M100G), grain moisture (GM) and grain productivity (GP). The data were subjected to analysis of variance and comparison of means. The values of genotypic and phenotypic variance were also estimated, heritability in the broad sense, selection accuracy, phenotypic, genotypic and environmental correlation, in addition to the principal component analysis (PCA). Variations in characteristics were found between the varieties of Creole maize and their interrelations, showing greater influence of ME, PH, TGM, M100G, DE and GP in the expression of the phenotype. Therefore, it is concluded that there is genetic variability in the characteristics evaluated, with emphasis to V4 that showed superior performance allowing direct selection of the characteristics SD, ME, TGM and M100G to be incorporated into an breeding program.

*Keywords: Zea mays; biometric; genetic parameter; heritability.*

## 1. INTRODUCTION

Maize (*Zea mays* L.) is among the most cultivated and produced cereals on the planet due to its high genetic diversity, its nutritional value, the breadth of use, in addition to the generation of income [1]. Brazil is the third largest producer of the grain in the world with an estimated production of 108,068.7 thousand tons and average productivity of 5,543 kg ha<sup>-1</sup> in the 2019/2020 harvest [2]. Due to its ability to adapt to different environmental conditions, it has a wide distribution throughout Brazilian territory, although with differences in productivity between the regions [2].

Corn is grown from small rural properties on family farming, to large tracts of land that involve high use of technology and skilled labor [3]. In economically developed regions, the crops are designated for the cultivation of hybrid and transgenic maize, while in regions where there is a predominance of family farming, the cultivated type is usually traditional varieties. The crops at family farming operations are obtained through several generations of cultivation under low technological level, allowing producers certain independence in acquiring seeds from the market, rescuing themselves annually from crops [1].

Traditional varieties have lower productivity than improved cultivars due to their broad genetic base. Although they do not guarantee high yield in the short term, they can perform similarly to conventional varieties when using low technology [4]. Thus, the genetic variability present in the traditional maize population represents a source of favorable alleles for the genetic response to biotic and abiotic adverse factors, providing greater long-term yield stability [5].

The use of local varieties is still a common practice since it is produced under low cost and offer alternatives for the sustainability of small producers. In addition, the genetic plant breeding of these varieties can be done on the farmers property in cooperation with the farmers, who are well-aware of these Creole materials [6]. However, there is a demand from plant breeders for information about these varieties in the phenotypic and genotypic characterization, to get more comprehensive knowledge for selection of promising parental genotypes for a maize breeding program [7].

Studies on the variability in maize characteristics, especially those associated with yield, using parameters such as estimated means, genotypic-phenotypic variances, heritability and correlation coefficients, are important sources for selecting promising parental genotypes for the improvement of Creole maize through breeding, in addition to knowing the genetic variability of the material [8].

Thus, the objective of this study is to verify the genetic variability in agronomic and morphological characteristics of traditional varieties of Creole corns, and to determine the degree of association in selecting promising characters of Creole maize to be utilized through plant breeding programs.

## 2. MATERIAL AND METHODS

The experiment was conducted at the Federal University of Acre, located in the municipality of Rio Branco, in the State of Acre (07 ° 07 'S and 66 ° 30' W in datum WGS84), in the 2017/2018 crop period. According to the international classification of Köppen, the climate of the region

is an Am type, characterized as being hot and humid, with maximum temperatures ranging from 29.7 °C to 32.8 °C, and minimum from 16.1 °C to 21.8 °C, average rainfall of 1,994 mm per year and relative humidity between 80.5% and 87.9% throughout the year [9].

Before the experiment establishment, soil chemical analysis in the experimental area was carried out. The results are showing that at the depth from 0 - 20 cm, pH = 5.09; P = 9.86 mg dm<sup>-3</sup>; K = 35.19 mg dm<sup>-3</sup>; MO = 12.05 g dm<sup>-3</sup>; Al = 0.63 cmolc dm<sup>-3</sup>; Ca = 1.31 cmolc dm<sup>-3</sup> and Mg = 0.69 cmolc dm<sup>-3</sup>.

The soil was prepared thirty days before sowing by plowing, harrowing and application of agricultural lime at a dose of 2.0 t ha<sup>-1</sup>, based on the soil chemical analysis. Fertilization was carried out according to the chemical characteristics of the soil, using 60 kg P ha<sup>-1</sup>, 80 kg K ha<sup>-1</sup> and 120 kg N ha<sup>-1</sup>, adjusting the distribution of fertilizers per linear meter.

The experiment was set up in randomized block design with five replications. As treatment, four traditional maize varieties (V1, V2, V3 and V4) obtained from the Vale do Juruá region and one hybrid cultivar LG 3040 (HI) were used. The plots consisted of four planting lines of 5 m long, with a spacing of 1 meter between rows and 0.50 m between plants, using the two central rows as useful area for evaluation of all variables.

Sowing was carried out manually in November 15, 2017, with four seeds per hole. Twenty one days after planting, thinning was done leaving only two plants per hole. During the experiment, two manual weeding and nitrogen fertilization (N) were carried out at stages V4 and V7, when the corn plant has 4 and 7 fully expanded leaves, respectively. Pest control was done with neem oil (*Azadirachta indica*) applications.

In the plants of each useful area, days to silking (DS) and days to anthesis (DA) were evaluated, observing the number of days when 50% of the plants in the plot had fully exposed tassel and the exposure of the stigma style on the ear, respectively.

At the time plants were in stage R3 (92 DPA), all the plants in each plot were evaluated for the following variables: plant height (PH) and ear insertion (HEI), measuring from the soil surface to the base of the soil flag-leaf and highest ear, respectively. In the same plants, the stem

diameter (SD) was measured with the aid of a digital caliper (mm).

At the harvest that occurred 120 days after sowing, the mass of ears (ME) was determined by obtaining the weight with a digital scale of all ears harvested, without the presence of straw. Still, all the ears were taken to measure the length ear (LE), measuring from the basal end to the apical end, the diameter of the ear (DE) using the caliper (mm), was measured in the middle third.

For the total grain mass (TGM), the grains of the ears were weighed (g), using the analog scale. Therefore, it was possible to verify the mass of 100 grains (M100G). Through a small sample of grains from each portion, the grain moisture (GM) (%) at the time of harvest was verified, with a moisture analyzer model G650. The verification of grain productivity (GP) was achieved by the total weight of grains obtained in each plot, corrected to a standard humidity of 13% and transformed to kg ha<sup>-1</sup>.

In the statistical analysis, to assess the existence of genetic variability between traditional corn varieties (treatments), analyzes of variances were performed according to the statistical model:  $Y_{ij} = \mu + G_i + B_j + \epsilon_{ij}$ , in which 'μ' represents the average general, 'G<sub>i</sub>' was the effect of the genotype; 'B<sub>j</sub>' the block effect, and 'ε<sub>ij</sub>' was the experimental error effect.

The data were submitted to the verification of the normalities of the residuals by the Shapiro and Wilk test [10], and homogeneity of variances by the Bartlett test with the aid of the statistical software [11]. Subsequently, the analysis of variance of the data was performed by the F test, followed by the comparison of the averages by the Tukey test [12], both at the level of 5% probability.

Based on the mean squares of the analysis of variance, the genotypic ( $\sigma_g^2$ ) and phenotypic ( $\sigma_f^2$ ) components were obtained by the equations,  $\sigma_{f(x)}^2 = \text{MSP}_{(x)}/r$  and  $\sigma_{g(x)}^2 = \text{MSP}_{(x)} - \text{MSR}_{(x)}/r$ , respectively, in which:  $\sigma_{f(x)}^2$  = phenotypic variance of x;  $\sigma_{g(x)}^2$  = genetic variance of the character x; MSP = mean square of the progeny; MSR = mean square of the residue and r = number of repetitions. In addition, heritability was obtained in the broad sense  $h_a^2 = \frac{\sigma_g}{\sigma_f}$ , the ratio between the genetic variance ( $\sigma_g$ ) and the phenotypic variance ( $\sigma_f$ ) [13].

The selection accuracy was obtained using the formula:  $rgg = \sqrt{1 - VEG/\sigma^2g}$  where: VEG = variance of the error of the genotypic values and  $\sigma_g$  = genotypic variance [14].

For correlation analysis, the following expressions were used [15]: phenotypic correlation:  $rP = \frac{AP_{xy}}{\sqrt{AST_x * AST_y}}$ ; genotypic correlations:  $rG = \frac{\sigma_{gxy}}{\sqrt{\sigma_{gx} * \sigma_{gy}}}$ ; and environmental:

$rE = \frac{APE_{xy}}{\sqrt{ASR_x * ASR_y}}$ , in which:  $\sigma_{g_{xy}} = AP_{xy} - APE_{xy}/r$ ;  $\sigma_{gx} = AST_x - ASR_x/r$ ;  $\sigma_{gy} = AST_y - ASR_y/r$ , where:  $AP_{xy}$ : average product associated with the characters X and Y;  $APE$  = average product associated with the error;  $AST$  = average square of the treatment;  $ASR$  = average square of the residue;  $\sigma_{gxy}$  = genotypic covariance estimator between the characters X and Y;  $\sigma_{gx}$  and  $\sigma_{gy}$  = are the estimators of the genotypic variances of the characters X and Y, respectively.

The significance of the correlation coefficients for each variable was assessed by the t test and the Bootstrap method with 5,000 simulations, at the levels of 1% and 5% of probability.

The analysis of variance, comparison of means, genetic parameters, phenotypic, genotypic and environmental correlation coefficients, and the gain by selection for all evaluated characters, were obtained with the aid of the statistical program Genes [16].

The principal component analysis (PCA) was carried out in order to detect grouping and

relationship between characteristics and genotypes using the prcomp command of the statistical software R [11].

### 3. RESULTS AND DISCUSSION

In view of the results, it is noteworthy that the pattern of the ears harvested showed typical characteristics of each variety evaluated (Fig. 1). The results found are essential in the choice of superior genotypes, since variability is essential to obtain progress in maize breeding programs [13].

For the characters plant height and ear insertion, V4 showed higher averages among the tested varieties, and the stem diameter (SD) was statistically equal between the varieties (Table 1). It is noteworthy that for the total mass of ears (ME), V4 presented values higher than those of the other Creole varieties, being clear its low ear yield only when compared with the hybrid.

The varieties studied showed plant height and ear insertion patterns similar to the hybrid, except for V4. According to Silveira et al [17], the Creole varieties of corn are characterized by having high plant vigor and height ear insertion, in addition to a diversity of qualitative characteristics that are favorable for adaptation in different environments. However, it is recommended that the height of the plant and the height of the ear be smaller, with a larger stem diameter, so that the plants do not suffer breakage and achieve greater production [18].

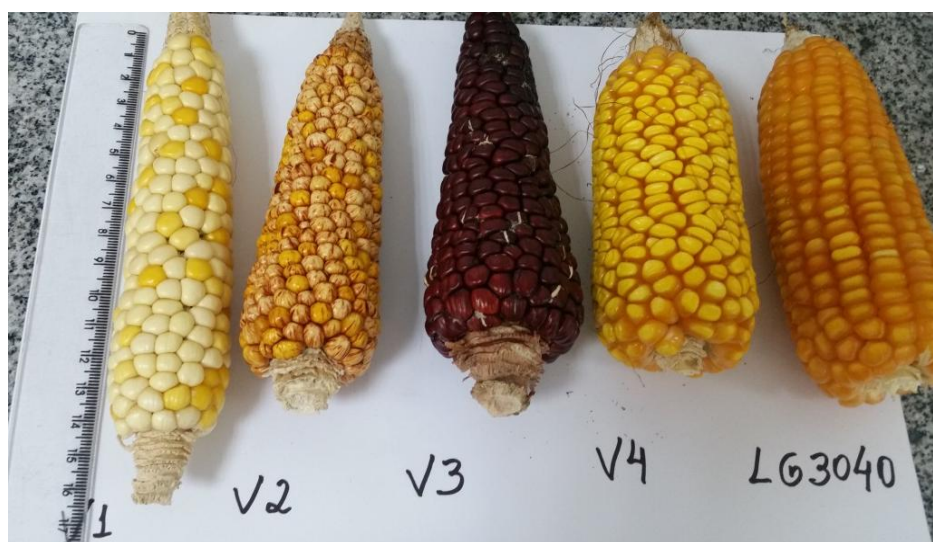


Fig. 1. Ears of Creole and hybrid varieties, observed after harvest

**Table 1. Evaluation of plant height (PH), height of ear insertion (HEI), stem diameter (SD) and mass of ear (ME) by the Tukey test**

Varieties	Average Comparison			
	HP (m)	HEI (m)	SD (mm)	ME (kg)
V1	1.49 b	0.81 b	12.63 a	1.00 bc
V2	1.43 b	0.78 b	12.52 a	0.83 c
V3	1.45 b	0.80 b	13.73 a	0.93 c
V4	2.01 a	1.17 a	14.39 a	1.92 b
HI	1.28 b	0.66 b	13.11 a	3.73 a

\* Means with different letters in the column differ statistically ( $P < 0.05$ ) from each other by the Tukey test

The variables HP and HEI are characterized as the best factors for selection of strains within the genetic breeding, since when the lowest height of the plant and the lowest insertion of the ear, the lodging index of the plants is minimal [19]. In this way, the smaller stem diameter can increase the percentage of bedridden and broken plants, being harmful for harvesting, both mechanized and manual, and can even make it unfeasible with losses of production in the corn crop [20].

The results for ear mass demonstrate the superiority of the V4 variety among the local breeds. However, it should be noted that the ear weight is considered to be one of the essential components of yield, as heavier ears have a higher potential for high productivity [21]. This reinforces the positive intrinsic relationship that the mass of ears has with the productivity attributes, [22].

Comparisons revealed statistically significant differences ( $p < 0.05$ ) between varieties for days to silking (DS), diameter (DE) and length (LE) of ear, but with only male flowering (FM) showing statistically similar means between varieties (Table 2).

The hybrid presented ears with larger diameters (47.03 mm), but with a shorter length. On the other hand, the V4 had a larger diameter (40.17 mm) among the traditional varieties, followed by the greater length (10.53 cm) of the ear (Table 2). According Olivoto et al [23], the length and diameter of the ear is influenced by the expression of the genotype and suffers little

influence from the environment and reflects high yield. Thus, the featured variety has intrinsic characteristics of ears suitable for plant breeding aiming at high yields.

In regard to flowering season, tassel emission occurred simultaneously between varieties V1, V2, V3, V4 and HI, with values between 60 and 75 days. For days to silking, the stigma style was first emitted in the hybrid cultivar at 61 days, and in the Creole varieties after 83 days. However, it is observed that the emission of male flowering, in all evaluated genotypes occurred before days to silking, mainly due to the fact that corn has a protandic characteristic [24].

The interval between days to anthesis and days to silking is a feature of great importance in maize cultivation because synchrony establishes late and uneven fertilization, which leads to a reduction in grain production due to pollen and ovule abortion [25]. There was a lack of synchronization between the flowering among the evaluated genotypes; it was shorter for the hybrid, and from 13 to 33 days between the traditional varieties.

For the parameter total grain mass (kg), it was observed that the hybrid was superior ( $p < 0.05$ ) to Creole varieties. However, the variety V4 and the HI differ significantly from the others for mass of 100 grains. Regarding grain yield, varieties V3 and V4 showed similar productivity ( $p > 0.05$ ) to that of the hybrid cultivar (Table 3), but were not different of V1 and V2 in this aspect.

**Table 2. Evaluation of diameter ear (DE), length ear (LE), days to anthesis (DA) and days to silking (DS) using the Tukey test**

Varieties	Average Comparison			
	DE (mm)	LE (cm)	DA (days)	DS (days)
V1	31.36 c	12.20 a	75 a	88 a
V2	32.56 c	10.39 ab	66 a	99 a
V3	31.95 c	10.78 ab	65 a	83 ab
V4	40.17 b	10.53 ab	74 a	90 a
HI	47.03 a	9.70 b	60 a	61 b

\* Means with different letters in the column differ statistically ( $P < 0.05$ ) from each other by the Tukey test

**Table 3. Evaluation of total grain mass (TGM), mass of 100 grains (M100G), grain moisture (GM) and productivity (PD) by the Tukey test**

Varieties	Average Comparison			
	TGM (g)	M100G (g)	GM (%)	PD (kg ha <sup>-1</sup> )
V1	752.20 b	17.43 b	19.20 bc	1141.08 b
V2	637.20 b	14.51 b	15.80 c	1098.15 b
V3	740.00 b	16.49 b	16.80 c	1531.93 ab
V4	1424.00 b	28.94 a	29.40 a	2687.55 ab
HI	2984.00 a	32.62 a	28.00 ab	3009.21 a

\* Means with different letters in the column differ statistically ( $P < 0.05$ ) from each other by the Tukey test

The Creole varieties had a lower total mass of grains than the hybrid, but V4 had a mass of 100 grains higher than the other Creole varieties. According to Li et al. [26], the mass of maize grains is dependent of the genotypes used, since some varieties have grains with smaller and lighter kernels, which consequently reduces the productive potential per plant. Thus, selection of genotypes with greater grain mass is essential to obtain gains in a maize breeding program.

Grain productivity ranged from 1098.15 to 2687.55 kg ha<sup>-1</sup> for the Creole varieties, but not being significantly different among them. The hybrid variety was the most efficient, showing the highest productivity, with 3009.21 kg ha<sup>-1</sup>. However, according to Bianchetto et al. [27], traditional varieties present yield values equal to or higher than improved cultivars when they are inserted in crops with low use of technologies. Such fact can be verified in this work, since the V4 and V3 presented productivity averages statistically similar to the hybrid.

In general, maize varieties when grown in a traditional system tend to stand out, compared to commercial hybrid cultivars. This is due to the fact that Creole corn has genotypes with a broad genetic base, capable of better responding to abiotic and biotic stresses [28]. Thus, the use of the V4 variety proves to be an alternative for sustainable production, as it can reduce production costs with inputs, in addition to minimizing the use of technological packages.

The estimation of the genetic parameters of a population provides information about the nature of the genes that are involved in the inheritance of the characters, in addition to assessing whether a phenotypic characteristic can evolve through natural and artificial selection [29]. In this experiment, genetic parameters were estimated for all characters measured based on analysis of variances, excluding the hybrid variety (Table 4). Significant differences detected in the analysis of variance demonstrate the existence of genetic

variability between varieties in relation to the evaluated characters. This is a very favorable situation for breeding, marking being possible the selection of varieties, whose phenotypic values of the characters were more influenced by the genetics of the individuals. The phenotypic variance is the result of the combined action of genetic and environmental effects, with genetic variance being the most important component for breeding [30].

The characteristics that showed the greatest genetic expression in the phenotype were HEI, SD, ME, DE, LE, TGM, M100G, GM and PD, while days to silking responded with greater environmental variance. According to Allier et al. [31], one of the main factors that determines the response to selection in a breeding programs is the genetic variance of the evaluated characteristics. Thus, our results reveal promising attributes for selection, as it is the genetic factor that most determines expression in most characteristics of traditional varieties of corn.

Maize is a crop with a very varied cycle, with flowering conditioned to the eminent characteristics of the genotypes and in most of the environmental conditions imposed by the cultivation sites [32]. Thus, the low genetic variation for days to silking found in this study can be explained by the fact that the reproductive phases can be influenced by the environment regarding the temporal variation of precipitation, humidity, temperature and photoperiod [33].

The morpho-agronomic characters that showed high heritability ( $h^2$ ) were PH (97.26%), HEI (94.24%), SD (70.55%), ME (82.82%), DE (93.10%), TGM (76.80%), M100G (90.11%), GM (92.08%) and PD (83.79%), showing that the phenotypic variation in the evaluated population is due to genetic effects. On the other hand, LE (60.29%), DS (18.57%) and FM (38.82%) had a low estimate of heritability, indicating that the

environment had a greater influence on their results.

The heritability of a trait corresponds to the fraction of the selection differential that can cause genetic alteration in the generation of offspring. Thus, it acts as a filter that determines the efficiency with which a population can respond to phenotypic selection [29]. Values of  $h^2$  above 70% are considered high. However, they vary according to the character studied and thus help in the effective selection of characteristics based on phenotypic expression, assisting in the adoption of a simple selection method focused on genetic improvement [34].

The genotypic coefficient variation (CVg%) is commonly used to describe the specific characteristics in addition to comparing the genetic variability expressed for each attribute, where CVg values greater than 5% are considered high for the evaluated trait [35].

The highest genetic coefficients were HEI (20.35%), SD (5.67%), ME (39.04%), DE (11.73%), LE (5.89%), TGM (35, 59%), M100G (31.98%), GM (29.46%) and PD (42.03%), while the smallest went PH (2.09%), DA (0.96%) and DS (3.11%). The results reveal genetic variability in the population for the characters with the highest CVg value, enabling the selection of these characteristics when aiming at future genetic gains.

In the ratio between the coefficient of genetic variation (CVg) and the environmental variation (CVe), the characters PH (2.66), HEI (1.81), DE (1.64), M100G (1.34), GM (1.52) and PD (1.01) presented high values, revealing that the greatest contributions of the characteristics were of genetic origin. On the other hand, the variables SD (0.69), ME (0.98), LE (0.55), TGM (0.81), DA (0.35) and DS (0.21) presented values too lower, which reflects a marked environmental interference in the expression of these characteristics. In such a way, Clovis et al. [36] observed by the CVg / CVe ratio that a large part of the variation in the characteristics evaluated in corn was due to genetic variance, with few variables being influenced by environmental causes.

Selective accuracy (rgg) is a parameter that refers to the correlation between the true genotypic value and the values estimated or predicted from the data obtained in the experiment, being classified as very high ( $rgg \geq 0.90$ ), high ( $0.70 \leq rgg < 0.90$ ), moderate ( $0.50 \leq$

$rgg < 0.70$ ) and low ( $rgg < 0.50$ ) [14]. Thus, the results showed that there was high precision in the values predicted for PH (0.98), HEI (0.97), ME (0.91), DE (0.97), M100G (0.95), GM (0.96), PD (0.91), SD (0.84) and LE (0.78), except DA (0.62) and DS (0.43), indicating a high correlation between the genotypic value true of the characteristics and the predicted with the experimental information [37].

The analysis of phenotypic, genetic and environmental correlation carried out in this study for the morpho-agronomic characters in the populations of Creole maize, revealed a total of 84 pairs of significant correlations. In addition, it was observed that the genotypic correlations showed magnitudes higher than the environmental ones (Table 5), which is desirable for breeders, as it makes it possible to achieve faster progress than by simply selecting the desired character.

Correlation analysis is a statistical technique that measures the degree and the association between two characteristics, where the positive relationship components show that the increases are proportional, while the negative coefficients indicate inversely proportional associations [21]. However, knowledge of the phenotypic, genetic and environmental correlation between the characters becomes essential in the simultaneous selection of correlated characteristics, even if the attribute of interest reveals low heritability or when it is difficult to measure [38].

Correlation coefficient estimates are useful in identifying the characteristics of the components that can be used to improve maize productivity [39]. Among the evaluated characters, it can be highlighted for being positively correlated genetically with the grain yield (PD), the characteristics SD ( $rG = 1.26$ ), ME ( $rG = 1.09$ ), TGM ( $rG = 1.13$ ), M100G ( $rG = 1.09$ ), DE ( $rG = 1.01$ ) and GM ( $rG = 1.08$ ). Thus, traditional varieties of corn that have a larger stem diameter, mass of ear, grain mass and the high diameter of ears may favor the increase in grain productivity.

From the obtained correlations, greater relevance is directed towards associations with grain yield, as it is the main characteristic desired in breeding programs [8,31,40]. The results indicate that the direct selection of the SD, ME, TGM and M100G characteristics for breeding purposes can induce indirect genetic gains in corn productivity.

**Table 4. Summary of genetic parameters of the characteristics: plant height (PH), height of ear insertion (HEI), stem diameter (SD), mass of ear (ME), diameter ear (DE), length ear (LE), total grain mass (TGM), mass of 100 grain (M100G), grain moisture (GM), days to anthesis (DA), days to silking (DS) and productivity (PD)**

Variables	$\sigma_F$	$\sigma_A$	$\sigma_G$	$h^2$	CVg (%)	CVg/CVe	rgg
PH	0,00	0,00	0,00	97,26	2,09	2,66	0,98
HEI	0,35	0,02	0,33	94,24	20,35	1,81	0,97
SD	0,80	0,23	0,57	70,55	5,67	0,69	0,84
ME	0,25	0,04	0,21	82,82	39,04	0,98	0,91
DE	17,10	1,18	15,92	93,10	11,73	1,64	0,97
LE	0,69	0,27	0,42	60,29	5,89	0,55	0,78
TGM	130180,59	30196,81	99983,78	76,80	35,59	0,81	0,87
M100G	42,46	4,20	38,26	90,11	31,98	1,34	0,95
GM	38,84	3,07	35,77	92,08	29,46	1,52	0,96
DA	0,00	0,00	0,00	38,82	0,96	0,35	0,62
DS	42,32	34,46	7,86	18,57	3,11	0,21	0,43
PD	549667,17	89082,15	460585,02	83,79	42,03	1,01	0,91

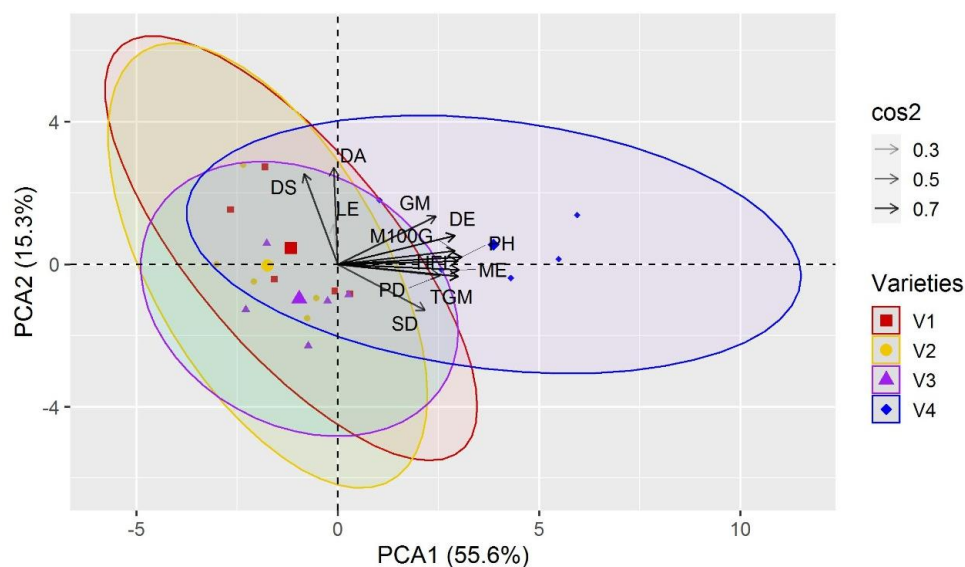
*Nota:  $\sigma_F$ : phenotypic variance;  $\sigma_g$ : genetic variance,  $\sigma_A$ : environmental variance,  $h^2$ : heritability in the broad sense, CVg (%): genotypic coefficient variation, CVg/CVe: ratio between the coefficient of genetic variation (CVg) and the environmental (CVe), rgg: accuracy*



**Table 5. Estimates of the phenotypic (rF), genetic (rG) and environmental (rE) correlation coefficients of the characteristics of the creole varieties of maize**

Variáveis		HEI	SD	ME	LE	TGM	M100G	DE	GM	DA	DS	PD
PH	rP	0,99**	0,76 <sup>ns</sup>	0,99**	-0,25 <sup>ns</sup>	0,99**	0,99**	0,98*	0,99**	0,70 <sup>ns</sup>	-0,07 <sup>ns</sup>	0,95 <sup>ns</sup>
	rG	1,00**	0,85 <sup>ns</sup>	1,06**	-0,33 <sup>ns</sup>	1,08**	0,99**	1,00**	0,99**	0,99**	-0,44 <sup>ns</sup>	0,99**
	rE	0,93**	0,63**	0,59**	-0,36 <sup>ns</sup>	0,72**	0,14 <sup>ns</sup>	0,55 <sup>+</sup>	0,16 <sup>ns</sup>	-0,27 <sup>ns</sup>	-0,48 <sup>+</sup>	0,55 <sup>+</sup>
HEI	rP		0,81 <sup>ns</sup>	0,99**	-0,32 <sup>ns</sup>	0,99**	0,99**	0,98*	0,98*	0,64 <sup>ns</sup>	-0,09 <sup>ns</sup>	0,97*
	rG		0,98 <sup>ns</sup>	0,99**	-0,66 <sup>ns</sup>	0,99**	1,07**	0,99**	1,03**	1,14**	-0,09 <sup>ns</sup>	1,04**
	rE		0,52 <sup>+</sup>	0,54 <sup>+</sup>	-0,07 <sup>ns</sup>	0,67**	0,13 <sup>ns</sup>	0,54 <sup>+</sup>	0,23 <sup>ns</sup>	-0,23 <sup>ns</sup>	-0,25 <sup>ns</sup>	0,49 <sup>+</sup>
SD	rP			0,80 <sup>ns</sup>	-0,41 <sup>ns</sup>	0,83 <sup>ns</sup>	0,81 <sup>ns</sup>	0,78 <sup>ns</sup>	0,75 <sup>ns</sup>	0,27 <sup>ns</sup>	-0,49 <sup>ns</sup>	0,93 <sup>ns</sup>
	rG			0,88 <sup>ns</sup>	-0,58 <sup>ns</sup>	0,89 <sup>ns</sup>	0,94 <sup>ns</sup>	0,91 <sup>ns</sup>	0,87 <sup>ns</sup>	0,94 <sup>+</sup>	-0,76 <sup>ns</sup>	1,26**
	rE			0,59 <sup>+</sup>	-0,09 <sup>ns</sup>	0,66 <sup>+</sup>	0,39 <sup>ns</sup>	0,26 <sup>ns</sup>	0,29 <sup>ns</sup>	-0,51 <sup>+</sup>	-0,45 <sup>+</sup>	-0,20 <sup>ns</sup>
ME	rP				-0,24 <sup>ns</sup>	0,99**	0,99**	0,97*	0,99**	0,70 <sup>ns</sup>	-0,15 <sup>ns</sup>	0,96*
	rG				-0,48 <sup>ns</sup>	1,01**	1,06**	1,06**	1,06**	1,42**	0,31 <sup>ns</sup>	1,09**
	rE				0,39 <sup>ns</sup>	0,98**	0,65 <sup>+</sup>	0,35 <sup>ns</sup>	0,30 <sup>ns</sup>	-0,32 <sup>ns</sup>	-0,43 <sup>+</sup>	0,30 <sup>ns</sup>
LE	rP					-0,25 <sup>ns</sup>	-0,19 <sup>ns</sup>	-0,46 <sup>ns</sup>	-0,13 <sup>ns</sup>	0,48 <sup>ns</sup>	-0,40 <sup>ns</sup>	-0,39 <sup>ns</sup>
	rG					-0,53 <sup>ns</sup>	-0,37 <sup>ns</sup>	-0,64 <sup>ns</sup>	-0,29 <sup>ns</sup>	0,84 <sup>ns</sup>	-1,40**	-0,59 <sup>ns</sup>
	rE					0,34 <sup>ns</sup>	0,37 <sup>ns</sup>	0,13 <sup>ns</sup>	0,47 <sup>ns</sup>	0,16 <sup>ns</sup>	0,12 <sup>ns</sup>	0,07 <sup>ns</sup>
TGM	rP						0,99**	0,97*	0,98**	0,68 <sup>ns</sup>	-0,17 <sup>ns</sup>	0,97 <sup>ns</sup>
	rG						1,08**	1,07**	1,12**	1,49**	0,01 <sup>ns</sup>	1,13**
	rE						0,64 <sup>+</sup>	0,48 <sup>ns</sup>	0,32 <sup>ns</sup>	-0,36 <sup>ns</sup>	-0,41 <sup>+</sup>	0,36 <sup>ns</sup>
M100G	rP							0,95*	0,99**	0,72 <sup>ns</sup>	-0,19 <sup>ns</sup>	0,96*
	rG							1,00**	1,08**	1,32**	-0,56 <sup>ns</sup>	1,09**
	rE							0,36 <sup>ns</sup>	0,07 <sup>ns</sup>	-0,26 <sup>ns</sup>	0,11 <sup>ns</sup>	0,11 <sup>ns</sup>
DE	rP								0,94 <sup>ns</sup>	0,54 <sup>ns</sup>	0,43 <sup>ns</sup>	0,95*
	rG								0,99 <sup>ns</sup>	0,96 <sup>+</sup>	0,06 <sup>ns</sup>	1,01**
	rE								0,31 <sup>ns</sup>	-0,17 <sup>ns</sup>	0,08 <sup>ns</sup>	0,63 <sup>+</sup>
GM	rP									0,78 <sup>ns</sup>	-0,16 <sup>ns</sup>	0,93 <sup>ns</sup>
	rG									1,31**	-0,33 <sup>ns</sup>	1,08**
	rE									-0,04 <sup>ns</sup>	-0,09 <sup>ns</sup>	-0,17 <sup>ns</sup>
DA	rP										-0,19 <sup>ns</sup>	0,51 <sup>ns</sup>
	rG										-2,19**	0,84 <sup>ns</sup>
	rE										0,56 <sup>+</sup>	0,09 <sup>ns</sup>
DS	rP											-0,24 <sup>ns</sup>
	rG											-0,574 <sup>ns</sup>
	rE											-0,044 <sup>ns</sup>

\*\* e \*: Significant at 1 and 5% probability by T test; ++ and +: Significant at 1 and 5% - respectively - by the Bootstrap method with 5,000 simulations



**Fig. 2. Analysis of main components of the characteristics and varieties of Creole maize**

On the other hand, it is observed that the magnitude of the significant environmental correlation coefficients, mainly in the character pairs PH x PD, HEI x PD and DE x PD, indicate that the environment positively influences the phenotypic expression of these characters. Such associations need attention to avoid errors at the time of selection, since the associations arising from the correlations of the environment result from a non-inheritable and unpredictable fraction in the mutual expression of characters [38].

In the analysis of main components (Fig. 2), the first two axes explained 70.9% of the variability of the individuals, showing a strong relationship between the morpho-agronomic characteristics of the Creole varieties. Thus, the analysis of main components contributes significantly to a good indirect selection of characteristics that are capable of increasing grain yield, in addition to identifying lower and upper genotypes, reducing agricultural losses [19].

The general interpretation of the PCA analysis is centered on the percentage variation of the data that are explained by the cartesian plans [41]. Thus, there was variation in the characteristics between the traditional maize varieties and their interrelations, evidencing the greater influence of the variables ME, PH, TGM, M100G, DE and PD in the expression of the phenotype. Still, it is possible to observe that the evaluated characteristics are grouped with the V4 genotype, making it clear that the variety has high variability in characteristics.

The relationship between genotype and environment is what determines the phenotypic phenomenon of the plant, and it is accepted that thousands of genes are involved in its life cycle to adjust each physical characteristic and its interrelationships [42]. However, the interest in evaluating the relative contribution between the characteristics resides in the possibility of selecting characters that most contribute to the expression of the genotype in breeding programs, reducing work, time and money spent on experimentation [40].

#### 4. CONCLUSION

Given the above, it is concluded that there is genetic variability among the traditional varieties of the Creole corn studied, with V4 showing superior performance among creoles and productive potential similar to the hybrid.

The characteristics of stem diameter, mass of ear, total grain mass, mass 100 grain and diameter ear are highly correlated with traditional corn productivity, these being the main characters capable of providing direct gains in grain productivity in the breeding programs.

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## COMPETING INTERESTS

Authors have declared that no competing interests exist.

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