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GENETIC DIVERGENCE IN CORN INDIFFERENT CONCENTRATIONS OF THE POWDER

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ABSTRACT

The main purpose of the study was to determine the genetic divergence among the ten corn genotypes cultivated in the 2017/2018 crop in the municipality of Santa Maria das Barreiras-PA. The work consisted basically of making an experiment with corn genotypes at different concentrations of potassium (high, low and general (low + high)). Both experiments were conducted in randomized blocks, with line spacing 0.9 meters, a total of three repetitions for each potassium concentration. The characteristics evaluated in each assay were plant height, spike height, spike diameter, spike length, number of grains in the spike row, number of rows on the cob and productivity. Genetic divergence was determined from the generalized Mahalanobis Distance method and the grouping of genotypes with genetic similarity was estimated by the Tocher optimization method, both in order to select the best maize genotypes for the genetic breeding program. Potassium doses influenced the grouping of genotypes. The characteristic PROD, can be used in breeding programs aimed at low and high use of inputs. It presents the need for improvement conduction in different tests.

INTRODUCTION

The corn crop (*Zea mays* L.) is one of the main, if not the most important among all cereals cultivated worldwide. This is given its applicability, in the feeding of humans and animals (Rigon, 2013). In animal feeding, corn is the main energy ingredient in the food chain. Of which we can highlight, not ruminants such as poultry and pigs. Thus, about 70 to 80% of this cereal is processed directly in diets for the production of animal protein such as milk, eggs, and meats (Borém, 2015). In Brazil, the amount of total corn produced in 2018/2019 can reach 95.2 million tons, about 18% more than the last harvest, which was compromised by climatic problems in the second

crop. The total planted area was stimulated in 4996.7 hectares, presenting a fall of 2.3% in the first crop. In the second harvest, an increase of 6.4% of total production is expected (De ACCN, 2019). Potassium (K) is listed as the second most important nutrient in a plantation, getting just behind the nitrogen (N). Its enzymatic activity is related to the movement of carbohydrates, oxidative phosphorylation and the osmotic potential of the cells, performing control of the stomatal opening and closing, and giving the plant more tolerant to drought. The lack of this nutrient in the plant causes a significant reduction in photosynthesis, increased respiration and a considerable increase in soluble nitrogen compounds, Low growth of Planta, tissue fragility and greater sensitivity to dry periods, moreover, its deficiency can be noticed in the

older leaves, from which we perceive the yellowing of tips, what we call Chlorosis. One of the interesting mechanisms of fertilization by K, and its interaction in response to the phosphorus (P), promotes even greater water conservation in the leaves, the development of the cell wall and the protection against some pests and diseases (Carvalho, 2013; Santos, 2013 and Alves, 2015). Due to the great edaphoclimatic variations in Brazil, the corn plantations are subject to constant variables, thus the K concentration used via fertilization is calculated from the physicochemical analysis of the soil, where sway a recommendation table, that disregards some important criteria, such as interaction between the various soil components, as the concentration of the same varies with the type of soil used, the concentration of Ca and Mg, at the initial level of the soil, and the genetic components of corn (Andreotti, 2001). The analysis of genetic divergence among several species of corn is common and quite popular among specialists in culture. Trey aims to select more promising methods and genotypes, which allows a consider- able reduction of costs and the time it takes, crossing genotypes, which are not of interest to the producer (Nardino, 2017). Thus, the priority objective is to locate and select genotypes that have more productive characteristics, for the breeding program. From the study of these different genotypes, we analyze them, identifying the best parents and consequently, obtaining hybrids with greater heterotic effects, which allows us to have greater segregation in gene recombinations when we cross relatives of these selected hybrids (Cruz, 2014). The development of genetic diversity through technical of multivariate analyses is essential in the ge- netic improvement programs, since the proportion of existing genotypes is enormous, which makes it diffi- cult to select these genetically divergent genes, that will be crossed to obtain the desired genotype (Cruz, 2011). There are different techniques and models for analyzing genetic dissimilarity in corn, of which are more prominent, the analysis techniques of the principal components and the mean dissimilarity of the genotypes studied, of these techniques the most used and the generalized distance of Mahalanobis that works with experiments with repetitions, in addition to taking into account the relationship of all evaluated characters and the Tocher optimization method (Cruz, 2014). With the advent of new technologies and studies, these techniques became more common among corn- growing specialists and breeders (Nardino, 2017; Dotto, 2007 and Prazeres, 2016). Based on this model, the main objective of the work was, to estimate the genetic divergence, based on morphological traits and components of the production of ten corn genotypes on different concentrations of K in the 17/18 crop in Santa Maria das Barreiras, State of the Pará.

MATERIALS AND METHODS

Two corn genotypes competition trials were conducted at Sítio Vitoria, located in the municipality of Santa Maria das Barreiras, State of the Pará. The genotypes were cultivated under high K condition (90 kg ha^{-1}) and low K (0 kg ha^{-1}) applied in coverage. Sowing was performed on December 20, 2017.

The experimental design used in each assay was randomized blocks with ten treatments and three replications. The treatments consisted of ten genotypes obtained in the municipality, namely: ANHEMBI, BR 206, BRS 3046, ORION, CATIVERDE, PR27D28, AG 1051, AL BANDEIRANTE, AG 8088 and 2B655PW.

The experimental portion used was composed of four five-meter-long lines, spaced with 0.9 m between lines. At harvest, the two central lines of each row were used, Discarding 0.50 meters from the ends of the rows. The conventional soil tillage system was used, with a harrowing followed by the leveling of the area. Pre-planting fertilization was performed using 450 kg ha^{-1} of NPK of 5-25-15 + 0,5 Zn, for the two trials.

The sowing was carried out in order to obtain 55555.55 plants ha^{-1}. The cover fertilization was performed only with K, in the Stadium V4 and V6 (completely open sheets), potassium chloride as s source of K. The dosage was 0 and 90 kg ha^{-1} of K. Fertilization in the low and high K environment according to recommendation of Galvão and Miranda (Galvão, 2014). Cultural tracts, such as phytosanitary control against diseases, pests, and weeds were performed ac- cording to the technical recommendations of the culture (Prazeres, 2016). And the evaluated characters were: plant height, spike height, spike diameter, spike length, number of grains per row, number of rows per spike and total productivity. The descriptors of the characteristics were used according to the Brazilian Agrolivestock Research Company -EMBRAPA (EMBRAPA, 2010).

A study of the genetic divergence for each K dose was performed, and the generalized Mahalanobis distance was used, as a measure of dissimilarity, taking into account the degree of dependence between the variables studied. For the establishment of similar groups, the hierarchical agglomerative method of optimization pro- posed by Tocher was applied (EMBRAPA, 2010), whose calculations were also based on the generalized Mahalanobis distance. The Singh criterion (1981) was also used to quantify the relative contribution of the characteristics evaluated in the genetic divergence (Rao, 1952). Statistical analyses were performed using the Genes program (Singh, 1981).

RESULTS AND DISCUSSION

The measures of dissimilarity measures evaluated from the Mahalanobis generalized distance technique in the experiment performed in Santa Maria are evaluated in Table 1. They present a high magnitude (3.49 to 545.11), indicating the presence of genetic variability among genotypes. Santos *et al*. (2018) found magnitude (4.0 to 644.6). Already Sodré *et al*. (2017) found a magnitude of 0.4 to 328.7. These magnitudes are close to that of Table 1.

In the Low K assay, the genotypes presented lower distances were AL BANDEIRANTE and PR27D28 (D^2= 3.49), BRS 3046 and PR27D28 (D^2= 11.85), AG 1051 and PR27D28 (D^2= 14.42), AG 8088 and 2B655PW (D^2= 16.95). The longest distances were CATIVERDE and AG 8088 (D^2= 255.99), ANHEMBI and CATIVERDE (D^2= 192.14), 2B655PW and CATIVERDE (D^2= 181.49), BR 206 and AG 8088 (D^2=164.63). The knowledge of genetic distances among genotypes may help in the choice of parents for future crossings, enabling time savings, labor and financial resources in future studies [14]. For the High K dose, the smallest distances were BR 206 and BRS 3046 (D^2= 22.57), BRS 3046 and BR 206 (D^2= 22.57), CATIVERDE and BRS 3046 (D^2= 26.80), ORION and BR 206 (D^2= 27.52), PR27D28 and CATIVERDE (D^2= 29.11). The longest distances were AL BANDEIRANTE and ANHEMBI (D^2= 545.11), AG 8088 and

Erro! Indicador não definido.. Dissimilarity mean of the ten genotypes evaluated in different potassium concentrations

Genotypes	Low K				High K				General			
					Distance D² between genotypes							
	Larger		Minor		Larger		Minor		Larger		Minor	
AG 1051	99.86	AG 8088	14.42	PR27D28	301.36	ANHEMBI	31.73	2B655PW	64.92	AG 8088	21.38	ORION
CATIVERDE	255.99	AG 8088	46.00	PR27D28	176.18	ANHEMBI	26.80	BRS 3046	142.45	AG 8088	12.43	PR27D28
BR 206	164.63	AG 8088	21.74	AG 1051	364.34	AG 8088	22.57	BRS 3046	188.75	AG 8088	14.02	BRS 3046
AL BAND.	120.08	AG 8088	3.49	PR27D28	545.11	ANHEMBI	94.48	PR27D28	167.92	AG 8088	22.46	BRS 3046
AG 8088	255.99	CATIVERDE	16.95	2B655PW	366.32	AL BAND.	34.62	2B655PW	188.75	BR 206	13.37	2B655PW
2B655PW	181.49	CATIVERDE	16.95	AG 8088	316.41	ANHEMBI	31.73	AG 1051	124.09	BR 206	13.37	AG 8088
PR27D28	127.07	AG 8088	3.49	AL BAND.	263.98	ANHEMBI	29.11	CATIVERDE	133.07	AG 8088	7.28	BRS 3046
BRS 3046	120.53	AG 8088	11.85	PR27D28	291.68	AG 8088	22.57	BR 206	157.98	AG 8088	7.28	PR27D28
ANHEMBI	192.14	CATIVERDE	38.99	AG 8088	545.11	AL BAND.	133.45	ORION	143.43	AL BAND.	62.87	AG 1051
ORION	138.01	ANHEMBI	46.99	AG 1051	239.70	AG 8088	27.52	BR 206	120.11	AG 8088	21.38	AG 1051
Greater general distance	255.99		(CATIVERDE and AG 8088)		545.11		(AL BAND. and ANHEMBI)		188.75		(BR 206 and AG 8088)	
Shorter overall distance	3.49		(AL BAND. and PR27D28)		22.57		(BR 206 and BRS 3046)		7.28		(PR27D28 and BRS 3046)	

Source: Elaboration of the authors.

Table 2. Grouping of genotypes by the Tocher optimization method, based on the dissimilarities in the different assays

Group	High	Low	General
	Access		
I	BR 206, BRS 3046, ORION, CATIVERDE, PR27D28 and AG 1051	AL BAND., PR27D28, BRS 3046, AG 1051 and BR 206	PR27D28, BRS 3046, CATIVERDE, BR 206, AL BAND., ORION and AG 1051
II	AG 8088 and 2B655PW	AG 8088, 2B655PW and ANHEMBI	AG 8088 and 2B655PW
III	AL BAND.	ORION	ANHEMBI
IV	ANHEMBI	CATIVERDE	

AL BANDEIRANTE (D^2= 366.32), BR 206 and AG 8088 (D^2= 364.34), 2B655PW and ANHEMBI (D^2= 316.41). In the General trial, the smallest distances were PR27D28 and BRS 3046 (D^2= 7.28), CATIVERDE and PR27D28 (D^2= 12.43), AG 8088 and 2B655PW (D^2= 13.37). The longest distances were BR 206 and AG 8088 (D^2= 188.75), AL BANDEIRANTES and AG 8088 (D^2= 167.92), BRS 3046 and AG 8088 (D^2= 157.98). Simon *et al*. (2012), Recommends avoiding hybridization between genotypes with shorter distances, which would decrease the success of higher hybrids. Based on the distances obtained, the largest was in the general assay, among the genotypes AL BAN- DEIRANTE and ANHEMBI (D^2= 545.11), on the other hand, the shortest distance was in the Low K test among the genotypes AG 8088 and PR27D28 (D^2= 3.49). This allows us to deduce that the K concentration influences the development of the genotype, that is, plants that had no problem with the absence of K developed normally, as for those who had problems with the absence of the same, developed lithe their characters, so they obtained the lowest values of dissimilarity measures. In the grouping analysis by the Tocher optimization method (Table 2), four distinct groups were formed in the High K and Low K assay and three groups for general testing. The genotypes BR 206, BRS 3046, PR27D28 and AG 1051 are present in group I in all assays, which allows us to affirm that both genotypes have some genetic similarity among themselves. In group II, the genotypes AG 8088 and 2B655PW are found

in the three trials. In groups with only one genotype, they are in group III in all assays and in group IV only in the Low K and High K assays.

Table 3. Intra-group and intergroup distances by the Tocher optimization method

Groups	High	Low	General
	Distance		
I x II	182.93	94.52	112.52
I x III	144.86	61.07	90.64
I x IV	203.49	65.88	
II x III	298.72	116.55	76.20
II X IV	330.16	209.87	
III x IV	545.11	122.06	

Source: Elaboration of the authors.

According to Cruz *et al*. (2014) groups formed by one genotype indicate in the direction that the same is more divergent in relation to the other. The Intergroup dissimilarity (Table 3) performed through the Tocher optimization method allows for more accurate detailing, which groups have greater genetic divergence among themselves (CRUZ *et al*., 2014). The largest distance between the groups studied was between group III and IV (545.11), followed by group II and IV (330.16) in the High assay K.

The shortest distance of genetic dissimilarity was between group I and III (61.07) and between-group I and IV (65.88) in the Low K assay. What was observed in the experiment is that the most distinctive groups in the case of group III and IV presented a higher degree of genetic dissimilarity among themselves, which favors the formation of two contrasting groups. This result suggests that there is then the possibility of the genotypes obtained to present genetic divergence among themselves and consequently heterosis in combination of genotypes. The largest intergroup distances involving the groups reinforce the fact that the genotypes in distinct groups are divergent (Table 1). Thus, the groups that have a greater distance between them should contain more divergent genotypes (Santos, 2018). To analyze the characteristics that most contributed to genetic divergence among the genotypes, pre- sented in Table 4. The great interest in assessing the relative importance of the characteristics (Table 4) lies in the possibility of using only characteristics that most contributed to discriminate the genotypes, reducing this way, labor, time and cost spent on experimentation (ROTILI *et al.*, 2012).

Table 4. Characteristics that will contribute more to the genetic divergence of the 10 genotypes studied

Variable	High	Low	General
		Value in %	
Spike Height (SH)	32.67	9.57	12.46
Plant height (PH)	13.20	0.30	8.90
Spike diameter (SD)	16.87	11.17	18.42
Spike length (SL)	8.86	9.05	9.08
Number of grains in the cob row (NGR)	1.48	14.79	10.45
Number of rows on the cob (NR)	4.62	20.90	7.11
Productivity (PROD)	22.30	34.21	33.58

Source: Elaboration of the authors.

The characteristics SH, PROD and SD (High K), PROD, NR and NGR (Low K), PROD, SD and SH (General), are the most contributed to genetic divergence (Table 4).

Conclusion

Potassium levels influenced the genotype grouping. The PROD feature can be used in breeding programs aimed at low and high use of inputs. There is a need to conduct breeding in different assays.

Acknowledgements

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