International Journal of Advanced Engineering Research and Science (IJAERS)
Peer-Reviewed Journal
ISSN: 2349-6495(P) | 2456-1908(O)
Vol-8, Issue-11; Nov, 2021
Journal Home Page Available: https://ijaers.com/
Article DOI: https://dx.doi.org/10.22161/ijaers.811.38

Genetic divergence in corn with forage potential in the Municipality of Santa Maria of Barreiras-PA

Weder Ferreira dos Santos[1*], Maria Angelica Oliveira Marinho[2], Layanni Ferreira Sodré Santos[3], Joênes Mucci Peluzio[4], Marcela Cristina Agustini Carneiro da Silveira Tschoeke[1],Guilherme Benko de Siqueira[4], Fernando Barnabé Cerqueira[5],Talita Pereira de Souza Ferreira[1], Cícero Antonio Sobreira Fidelis[6], Laura Carneiro Silva[1], Magno de Oliveira[7]

[1]Federal University of Tocantins, Gurupi, Tocantins, Brazil.
Email: eng.agricola.weder@gmail.com*
[2]CEULP/ULBRA, Palmas, Tocantins, Brazil.
[3]E.M.E.I.F Ullisses Guimarães, Santa Maria of Barreiras, Pará, Brasil.
[4]Federal University of Tocantins, Palmas, Tocantins, Brazil.
[5]Faculty Guaraí, Guaraí, Tocantins, Brazil.
[6]Federal Instituteof Pará, Conceição do Araguaia, Pará,Brazil.
[7]University of Valley Taquari - Univates, Rio Grande do Sul, Brazil.
*Corresponding Author

Received: 03 Oct 2021,

Received in revised form: 14 Nov 2021,

Accepted: 23 Nov 2021,

Available online: 30 Nov 2021

Keywords -Silage, Nitrogen fertilization, Zea mays. Breeding.

***Abstract**-The objective of this work was to estimate the genetic divergences in corn with forage potential in the southern region of Pará. Two competition trials of corn cultivars were installed, one under high nitrogen (150 kg ha^{-1}from N) and another under low N (0 kg ha^{-1}from N) applied in Cobertura, a crop 2020/21 in the State of Pará (8°18’32’’S, 50°36’58’’O,150 meters of altitude). The experimental design used in each assay was randomized blocks with three replicates and 11 maize cultivars, three varieties of open pollination, one single hybrid, seven double hybrids, and one triple hybrid. The following characteristics were analyzed: plant height (AP) in cm, the height of spike (AE), stem diameter (DC), spike diameter (DE), stem and leaf pasta (MCF), spike mass (ME),and full plant mass (MTP). For the analysis of genetic divergence, dissimilarities measures were used that were determined according to the multivariate analysis model, allowing the achievement of dissimilarities, residual covariances, and means of populations. Genetic divergence was evaluated by multivariate procedures with the generalized Mahalanobis distance, the Tocher optimization clustering method, and Singh's criterion to quantify the relative contribution of the seven characteristics. By estimating Mahalanobis distances, maize genotypes AG8088PRO2 X P33-16 showed a greater distance. The Tocher method was efficient in separating the groups. The characteristics of full plant mass and mass of stem and leaf were the ones that most contributed to genetic divergence.*

I. INTRODUCTION

The figures for full corn production in Brazil in 2020/2021 crop reached 108 million tons, with a planted area of 19.5 million hectares, and average productivity of 5,543 kg ha^{1}, focusing on the second harvest, which full about 77% of grain production. Comparing these values with the 2019/2020 crop, there was an increase of 5.4% in full production [1].

The consumption of corn goes beyond domestic use, these products are used in the production of various foods, such as snacks, sweet popcorn, breakfast cereals, and children's foods, and the manufacture of loaves of bread or in the brewing and pharmaceutical industries and mining [4]. For animal consumption, corn demand in Brazil was 52.0%, 30.4% for aviculture, 13.6% for pig farming, and 8.0% for cattle [2].

Silage is a very old process used for the conservation of fodder, based on the fermentation of plant sugars and acidification (pH reduction), being one of the most used conservation methods in Brazil to ensure food supply during the dry season. Numerous forages can be used for this purpose, however, corn stands out due to highly desirable characteristics such as high productivity, low buffer power, high sugar content, and high energy content [5].

When the objective is to obtain good silage, it is indispensable to manage adequately in all stages, from planting to harvest. The use of nitrogen fertilizers is one of the indispensable stages of management and that requires a lot of care, as it is directly correlated with the high yield of the crop, especially in the case of grasses [6]. In addition, the choice of cultivar is one of the extremely important factors to be observed, because it is necessary to consider both agronomic characteristics and bromatological characteristics [7].

For the choice of cultivar, studies of genetic divergence involving corn crop have been used concerning seed quality in Santa Catarina [8], grain production in southern Brazil [9], grain production in Tocantins [10, 11, 12 and 13], oil and protein content in Tocantins [14, 15 and 16], water stress in the Tocantins [17], forage production in the semi-arid [18], and grain production in Pará [19 and 20]. However, there are few studies involving genetic divergence in corn aiming at the production of fodder in northern Brazil.

Because of the above, the objective of this study was to evaluate the genetic divergence of eleven maize genotypes with forage potential in the municipality of Santa Maria of Barreira in the southern region of the State of Pará.

II. MATERIAL AND METHODS

Two competition trials of corn cultivars were installed at Sítio Vitória (8°18'32" S, 50°36'58" O, and 150 meters of altitude), located in the municipality of Santa Maria das Barreiras–PA (Figure 1), one under low nitrogen, with 0 kg ha^{-1} of N, and another under high nitrogen, with 150 kg ha^{-1}of N, both in coverage. The doses were determined according to the lowest and highest expected productivity for the corn crop according to [21]. Sowing was carried out on November 14, 2020.

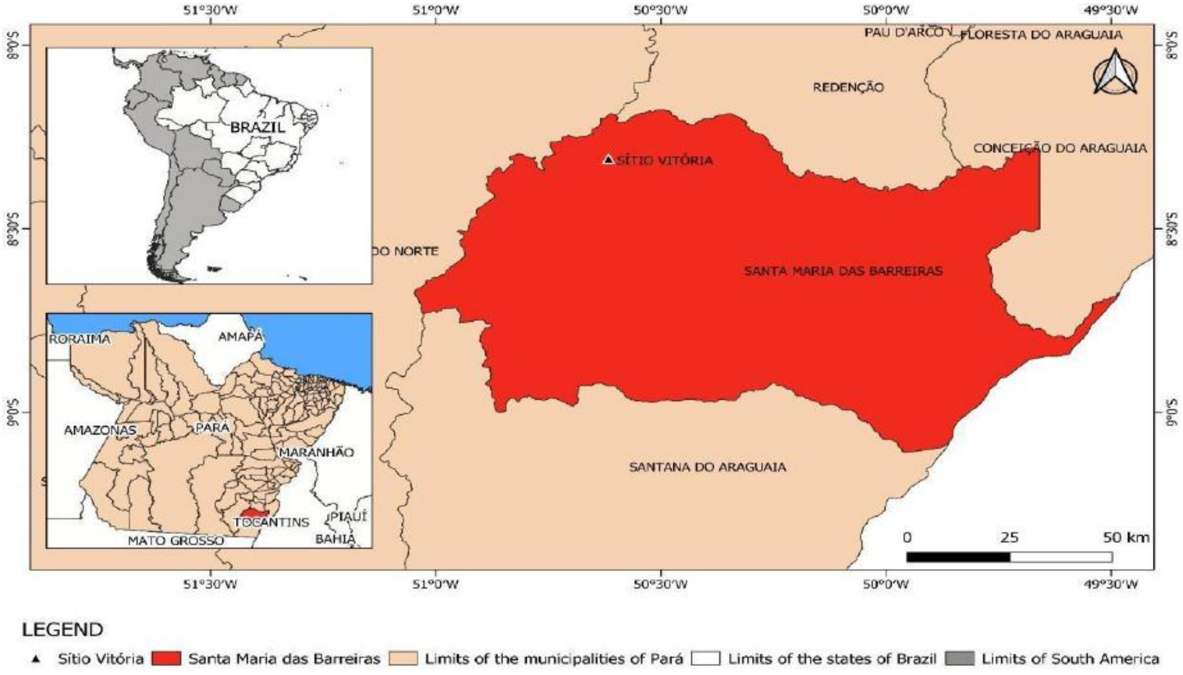

Fig.1. Location Map of Sítio Vitória, in the municipality of Santa Maria of Barreiras, State of Pará.

The region has a predominantly tropical climate according to Koppen as Aw, with rains in summer and a distinctly dry season in winter. The precipitation and temperature data obtained over the conduction period of the experiment are presented in Figure 2.

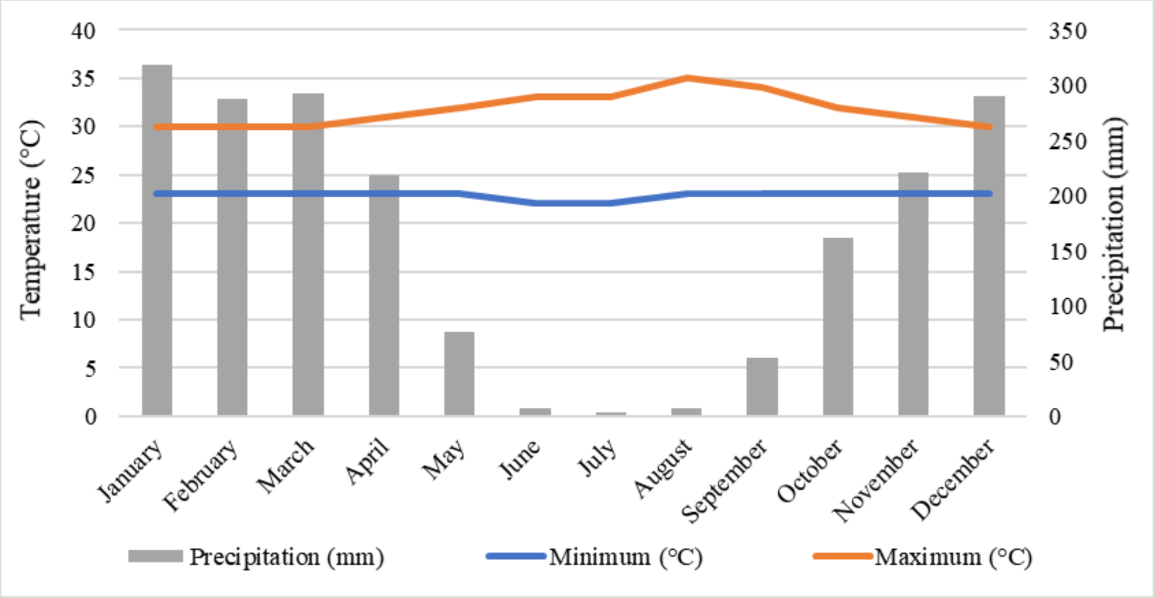

Fig.2. Precipitation climatological averages, minimum temperature, and a maximum of the municipality of Santa Maria of Barreiras, Estado of the Pará in the year of 2019.

Fonte: Climatempo [22].

The soil, representative of the study area, is of the sandy frank textural class, with very low phosphorus and calcium availability, low magnesium, and medium potassium, according to table 1 data from chemical and textural soil analysis.

Table 1. Chemical attributes and soil granulometry were used in the first epoch of the experiment. Santa Maria of Barreiras-Pará, 2018.

pH	Pmeh	K	S	Ca^{+2}	Mg^{+2}	Al^{+3}	H+Al	M.O.	C.O.
$CaCl_2$	$mg.dm^{-3}$				$cmolc.dm^{-3}$			$dag.kg^{-1}$	%
4.8	4.9	43	3.0	1.7	0.3	0.20	3.10	1.7	1.0
SB	CTCt		V%		M	Clay		Silt	Sandfull
			$mg.dm^{-3}$					%	
2.11	5.21		40		9.0	15.0		5.0	80.0

Two competition trials of corn cultivars were installed, one installed under low nitrogen, with 0 kg $ha^{-1}$of N, and the other under high nitrogen, with 150 kg $ha^{-1}$of N, both in cover. The doses were determined according to the lowest and highest expected productivity for the corn crop according to [21].

The experimental design used in each assay was randomized blocks with eleven treatments and three replications. The treatments consisted of maize cultivars, three varieties of open pollination, a single hybrid, seven double hybrids, and a triple hybrid, whose characteristics are found in Table 2.

Table 2. Agronomic characteristics of corn cultivars used in the experiment.

Nomecomercial	Base	Transgenia	Ciclo	Finalidade	Nível
AG1051	HD	C	SMP	G/MV/SPI	M/A
AG8088PRO2	HS	PRO2	P	G/SPI	A
ANHEMBI	PPA	C	P	G/SPI	B/M
BRS 3046	HT	C	SMP	MV	M/A
M274	HD	C	P	G/SPI	B/M
PR 27D28	HD	C	SP	G/SPI	B/M
P33-16*	HD				M
P33-11*	HD				M
P29-M12*	HD				M
P36-19*	HD				M
P40-8*	HD				M

HS: Simple hybrid; HD: Double hybrid; HT: Triple hybrid; PRO2: Technology VT PRO 2™; C: Conventional; P: Precocious; SMP: Semiprecocious; SP: Superprecocious; G: Grain; MV: Green corn; SPI: Silage of the whole plant; A: High; M: Medium and B: Low; * Experimental genotypes.

The experimental plot consisted of 4 rows of 5.0 m long with the spacing of 0.9 m between rows, being considered the two central rows as useful areas.

Sowing was performed in a groove with a depth of approximately 0.04 m, soon after seedling emergence, thinning was performed to obtain the spacing of 0.20 m between plants, and a final population of 55,555 plants ha^{-1}.

The cultural and phytosanitary control treatments of diseases, pests, and weeds were carried out according to the technical recommendations of the crop [23].

For soil preparation, a gradation was used followed by the leveling of the area. Pre-planting fertilization was calculated according to the levels obtained throughsoil analysis [23], 300 kg ha^{-1} of formulated 5-25-15 (N-P_2O_5-K_2O) + 0.5% Zn was applied.

The cover fertilization was performed with 150 kg ha^{-1}from N in the trial High N. The source used was urea (45% from N), totaling 333.33 kg ha^{-1}urea, it was divided into two stages, the first in stage V_4 and the second in stage V_8[21].

The harvest was carried out in the two central rows, during the period when the plant was in the R5 (hard farinaceous) stage, due to the period in which the driest matter accumulates in the plant [23].

The following characteristics were analyzed: plant height (AP) in cm, ear height (AE) in cm, stem diameter (DC) in mm, ear diameter (DE) in mm, stem mass and leaf (MCF) in g, ear mass (ME) in g, and full plant mass (MTP) in g.

For the analysis of genetic divergence, measures of dissimilarities were used that were determined according to the multivariate analysis model, allowing the obtaining of dissimilarities, residual covariances, and means of populations.

For group formation, using together with the data from high and low N, the grouping method by Optimization of Tocher [24], whose calculations were based on the Generalized Mahalanobis Distance [25], and the Singh criterion [26] were applied. to quantify the relative contribution of the seven traits evaluated in genetic divergence.

Statistical analyses were performed using the Computational Genes program [27].

III. RESULTS AND DISCUSSION

The measures of genetic dissimilarity, estimated from the Mahalanobis distance (Table 3), presented a high magnitude (31.13 to 688.29), indicating the presence of genetic variability among genotypes. [13] found magnitude (D^2= 4.8 to 79.2), [16] found a magnitude of D^2 from0.4 to 328.7 and [12] found magnitude (D^2= 4.0 to 644.6) in corn crop.

Table 3. Estimation of Mahalanobis distances ($D1^2$) maximum and a minimum of maize genotypes.

Genotype	Bigger		Minor	
	Distance D^2	Genotype	Distance D^2	Genotype
BRS 3046	271.34	(AG8088PRO2)	31.13	(P33-11)
M 274	371.82	(AG8088PRO2)	44.22	(BRS 3046)
AG8088PRO2	688.29	(P33-16)	115.49	(P36-19)
ANHEMBI	388.74	(PR 27D28)	32.68	(P29-M12)
PR 27D28	614.82	(P33-16)	181.03	(P36-19)
AG1051	530.12	(AG8088PRO2)	50.17	(M 274)
P33-16	688.29	(AG8088PRO2)	37.49	(P40-8)
P33-11	404.8	(AG8088PRO2)	31.13	(BRS 3046)
P29-M12	515.34	(PR 27D28)	32.68	(ANHEMBI)
P36-19	267.29	(P33-16)	54.73	(BRS 3046)
P40-8	487.64	(PR 27D28)	37.49	(P33-16)
Biggerdistance		688.29	(AG8088PRO2xP33-16)	
Minordistance		31.13	(BRS3046 x P33-11)	

In parentheses are represents genotype(s).

The combination of cultivars AG 8088PRO2 x P33-16 (Table 3) were considered the most divergent (D^2= 688.29), followed by PR 27D28 x P33-16 (D^2= 614.82) and AG 1051 x AG 8088PRO2 (D^2= 530.12). The shortest distances were between the combinations BRS 3046 x P33-11 (D^2 = 31.13), ANHEMBI x P29-M12 (D^2 = 32.68), P33-16 x P40-8 (D^2 = 37.49), M274 x BRS 3046 (D^2 = 44.22). Combinationsthat result in longer distances may be an indication that cultivars may come from different germplasm banks[28, 11, 12, 19, 13 and 20].

Cluster analysis by the Tocher method separates the materials into different groups so that there is intragroup homogeneity and intergroup heterogeneity [29]. By this method, the cultivars were grouped into three groups (Table 4).

Table 4. Grouping by the Tocher method, based on the dissimilarity expressed by the Generalized Mahalanobis Distance.2

Group	Access
I	BRS 3046, M 274, ANHEMBI, AG 1051, P33-16, P33-11, P29-M12, P36-19 e P40-8
II	PR 27D28
III	AG8088PRO2

The first large group separated by the Tocher method was composed of nine genotypes (BRS 3046, M 274, ANHEMBI, AG 1051, P33-16, P33-11, P29-M12, P36-19, and P40-8), the second group by a genotype (PR 27D28), and the third group formed by a genotype (AG 8088PRO2). This information confirms which genotypes are more divergent [18, 28, 11, 12, 19, 13, 20]. In this case, AG 8088PRO2 and PR 27D28, because they were the most divergent, constituted isolated groups.

The mean intergroup distances, derived from the Tocher optimization method (Table 5), indicate which groups are the most divergent. Thus, the least divergent groups were II and III (211.68) and the most divergent Groups I and III (409.11).

Table 5. Mean distances between groups formed by genetic divergence analysis in maize genotypes.3

Group	II	III
I	356.78	409.11
II		211.68

Regarding the contribution of the characteristics to the study of genetic divergence (Table 6), the one that most contributed was the full plant mass (MTP) (53.74%), followed by the mass of stem and leaf (MCF) (31.09%). The lowest contributions were: stem diameter (CD) (1.31%) and plant height (PA) (1.65%). Thus, the characteristics of the DC and AP can be discarded from future evaluations, as they contribute little to discriminate the evaluated materials, and can then reduce time, labor, and costs in the improvement programs [28, 11, 12, 19, 13 and 20].

Table 6.The relative contribution of traits in the genetic dissimilarity of genotypes.

Variable	Value in%
Plant height	1.65
Spike height	4.44
Stem diameter	1.31
Ear diameter	3.65
Stem mass and leaf	31.09
Cob mass	4.12
Full plant mass	53.74

IV. CONCLUSION

By estimating Mahalanobis distances, maize genotypes AG8088PRO2 X P33-16 showed a greater distance.

The Tocher method was efficient in separating the groups.

The characteristics of full plant mass and mass of stem and leaf were the ones that most contributed to genetic divergence.

REFERENCES

[1] CONAB - Companhia Nacional de Abastecimento. Acompanhamento Safra Brasileira de Grãos: v.6 - Safra 20/21 - n.6 - sexto levantamento. Brasília: CONAB, 2021. 106p. Disponível em: <https://www.conab.gov.br>. Acesso em: 26 out. 2021.

[2] Contini, E.,Mota, M.M.,Marra, R.,Borghi, E.,Miranda, R.A.,Silva, A.F.,Silva, D.D.,Machado, J.R. A.,Cota, L.V.,Costa, R.V.,Mendes, S.M. 2019. Milho: caracterização e desafios tecnológicos. Brasília, DF: Embrapa Milho e Sorgo. Disponível em: <https://ainfo.cnptia.embrapa.br/digital/bitstream/item/195075/1/Milho-caracterizacao.pdf>. Acesso em: 18 out. 2021.

[3] ABIMILHO – Associação Brasileira das Indústrias do Milho. Estatísticas do milho. 2021. Disponível em: <http://www.abimilho.com.br/estatisticas>. Acesso em: 27 out. 2021.

[4] Strazzi, S. 2015. Derivados do milho são usados em mais de 150 diferentes produtos industriais. Revista Visão Agrícola–USP/ESALQ. 13: 146-150.

[5] SENAR - Serviço Nacional de Aprendizagem Rural. 2011. Silagem de milho e sorgo: produção, ensilagem e utilização. Brasília: SENAR, 2011.

[6] Kappes, C.,Arf, O.,Arf, M.V.; Ferreira, J. P.,Dal Bem, E.A.; Portugal, J.R.; Vilela, R.G. 2013. Inoculação de sementes com bactéria diazotrófica e aplicação de nitrogênio em cobertura e foliar em milho. Semina: Ciências Agrárias. 34(2): 527-538.

[7] Gomes, M.S.,Von Pinho, R.G.,Ramalho, M.A.P.,Furtado, D.F. 2006. Alternativas para seleção de híbridos de milho envolvendo vários caracteres visando à produção de silage. Revista Brasileira de Milho e Sorgo. 5(3): 406-421.

[8] Prazeres, C.S., Coelho, C.M.M. 2016. Divergência genética e heterose relacionada à qualidade fisiológica em sementes de milho. Bragantia. 75(4): 411-417.

[9] Nardino, M., Baretta, D., Carvalho, I.R., Follmann, D.N., Ferrari, M., Pelegrin, A.J., Szareski, V.J., Konflanz, V.A., Souza, V.Q. 2017. Divergência genética entre genótipos de milho (Zea mays L.) em ambientes distintos. Revista de Ciências Agrárias. 40(1): 164-174.

[10] Dias, M.A.R.,Melo, A.V.,Santos, V.M.,Santos, D.P.S.,Nunes, H.V. 2018. Divergência genética entre progênies de milho na região centro-sul do estado do Tocantins. Revista Engenharia na Agricultura. 26(6): 483.

[11] Santos, W.F., Maciel, L.C., Sodré, L.F., Silva, R.M., Afférri, F.S., Freitas, J.H., Pereira, J.S. 2017. Diversidade genética em genótipos de milho para baixo nível tecnológico em Gurupi, TO. Tecnologia & Ciência Agropecuária. 11(2): 21-24.

[12] Santos, W.F., Aférri, F.S., Pelúzio, J.M., Sodré, L.F., Rotili, E.A., Cerqueira, F.B., Ferreira, T.P.S. 2018. Diversidade genética em milho sob condições de restrição ao nitrogênio. Journal of Bioenergy and Food Science, 5(2): 44-53.

[13] Silva, K.C.L.,Santos, W.F.,Afférri, F.S.,Peluzio, J.M.,Sodré, L.F. 2019. Diversidade genética em cultivares de milho de plantio tardio sob diferentes níveis de nitrogênio no Tocantins. Revista de Agricultura Neotropical. 6(3): 92-100.

[14] Santos, W.F., Pelúzio, J.M., Afférri, F.S., Sodré, L.F., Santos, D.S., Farias, T.C.M. 2014. Variabilidade genética e eficiência de uso do nitrogênio em populações de milho para teor de óleo. Revista de Ciência Agrárias. 57(3): 312-317.

[15] Santos, W.F., Afférri, F.S., Peluzio, J.M. 2015. Eficiência ao uso do nitrogênio e biodiversidade em genótipos de milho para teor de óleo. Enciclopédia Biosfera, 11(21): 2916-2925.

[16] Sodré, L.F., Santos, W.F., Ascêncio, S.D., Peluzio, J.M., Silva, R.M., Reina, E. 2017. Divergência genética em milho para baixo e alto nitrogênio visando à produção de óleo e proteína. Pesquisa Agropecuária Pernambucana, 22(1): 1-7.

[17] Melo, A.V., Santos, V.M., Lopes, T.M., Dias, M.A.R., Nunes, H.V. 2019. Divergência genética entre híbridos de milho em condições de deficiência hídrica. Revista de Agricultura Neotropical. 6(3): 66-75.

[18] Carvalho, M.N., Silveira, E.S., Menezes, B.S., Olieira, T.R.A., Oliveira, G.H.F. 2020. Caracterização e divergência genética de genótipos de milho com potencial forrageiro avaliados em região semiárida. Agri-Environmental Sciences. 6: 13-13.

[19] Santos, W.F., Milhomem, D.A., Silva, Z.D., Barbosa, A.S., Ferreira Junior, O.J., Santos, L.F.S., Santos, M.M., Ferreira, T.P.S., Maciel, L.C., Oliveira, M. 2019. Genetic divergence in corn indifferent concentrations of the powder. International Journal of Development Research, 9(11): 31099-31102.

[20] Silva, R.M., Santos, W.F., Andrade, M.R., Silva, Z.D., Santos, L.F.S., Peluzio, J.M., Bequiman, L.R.S., Luz, C.N.M., Dias, V.C., Borges, T.A.S.L., Martins, A.L.L., Oliveira, M. 2019. Agronomic Performance and Genetic Divergence in Corn (Zea mays) in the Cerrado-Amazon Ecotone. International Journal of Plant & Soil Science, 31(1): 1-7.

[21] Ribeiro, A.C., Guimarâes, P.T.G., Alvarez V.V.H. 1999. Recomendações para o uso de corretivos e fertilizantes em Minas Gerais – 5a Aproximação. Viçosa: Comissão de Fertilidade do Solo do Estado de Minas Gerais.

[22] CLIMATEMPO. 2021. Climatologia: Santa Maria das Barreiras, PA. 2021. Available at: <https://www.climatempo.com.br/climatologia/6858/santa mariadasbarreiras-pa>. Access in: 06 out. 2021.

[23] Borém, A., Galvão, J.C.C., Pimentel, M.A. 2015. Milho: do plantio à colheita. Viçosa: Editora UFV.

[24] Rao, C.R. 1952. Advanced statistical methodos in biometricresearch. New York: John Willey. 390p.

[25] Mahalanobis, P.C. 1936. On the generalized distance in statistics. Proceedings of the National Institute of Sciences of India. (2): 49-55.

[26] Singh, D. 1981. The relative importance of characters affecting genetic divergence. The Indian Journal of Genetics and Plant Breeding, 41:237-245.

[27] Cruz, C.D.,Regazzi, A.J. 2007. Modelos biométricos aplicados ao melhoramento genético. Viçosa: Imprensa Universitária, 480p.

[28] Coelho, D.R., Santos, W.F., Sodré, L.F., Pelúzio, J.M., Assunção, F.A., Pereira, J.S., Fonseca, S.L., Oliveira, M., Duarte Júnior, B.L., Silva, R.M. 2019. Genetic Divergence in Corn Genotypes in the South of the State of Pará. International Journal of Advanced Engineering Research and Science. 6(6): 471-475.

[29] Cruz, C.D., Carneiro, P.C.S., Regazzi, A.J. 2014. Modelos biométricos aplicados ao melhoramento genético. 3 ed. Viçosa: UFV. 668p.