AGRONOMY SCIENCE AND BIOTECHNOLOGY

RESEARCH ARTICLE

Genetic variability and effect of plant arrangement on corn

Luiz Leonardo Ferreira[1], Lucas Souza Hunhoff[1], Uirá do Amaral[2], Ivan Ricardo Carvalho[3,*], Rodrigo Vieira da Silva[4], Núbia Sousa Carrijo dos Santos[1], Marilaine de Sá Fernandes[1], Francine Lautenchleger[5], Alexandre Igor de Azevedo Pereira[6], Carmen Rosa da Silva Curvêlo[6] and Murilo Vieira Loro[7]

[1]Mineiros University Center – Unifimes, Mineiros, Goiás, Brazil. [2]Federal Institute of Brasília – IFB, Planaltina, Distrito Federal, Brazil. [3]Regional University of the Northwest of the State of Rio Grande do Sul, Campus Ijuí, Brazil. [4]Instituto Federal Goiano, Campus Morrinhos, Morrinhos, Goiás, Brazil. [5]State University of the Midwest, Guarapuava, Paraná, Brazil. [6]Instituto Federal Goiano, Campus Urutaí, Urutaí, Goiás, Brazil. [7]Federal University of Santa Maria, Santa Maria, RS, Brazil. *Corresponding author, E-mail: carvalho.irc@gmail.com

ABSTRACT

One of the factors of great influence on the agronomic performance of corn plants is their population arrangement. In this respect, the objective of this work was to evaluate the effect of plant arrangement and genetic divergence in different corn genotypes. The study was conducted in the county of Mineiros-GO, Brazil. The soil is Quartzarenic Neosol (Entisol). The experimental design used was in random blocks in factorial 8x2, totaling 16 treatments corresponding to 8 corn genotypes (A8740, A8088, DKB290, DKB390, DKB177, P30F35, P30S31 and P3707) and 2 spacing between lines (0.45 m and 0.90 m), 4 repetitions. The soil preparation was done in the no-tillage system. At the end of the experiment, biometric and productivity variables were measured and analyzed using Softwares R and Genes. The analysis of variance revealed significance in the simple and main effects. Genetic divergence and the effect of plant arrangement on corn genotypes were observed, where the variables plant height, stem diameter and the thousand grain mass were the main characteristics that influenced yield. Among the analyzed genotypes, the growing of genetic material DKB390 is recommended in rows spaced at 0.45 or 0.90 m, as it has plants with ears of greater number of grains, thousand grain mass and yield, demonstrating its plasticity in adaptation to the proposed systems.

Keywords: Grain production, correlation, spacing, *Poaceae*, *Zea mays* L., canonical variables.

Citation: Ferreira, L. L., Hunhoff, L. S., Amaral, U., Carvalho, I. C., Silva, R. V., Santos, N. S. C., Fernandes, M. S., Lautenchleger, F., Pereira, A. I. A., Curvêlo, C. R. S., & Loro, M. V. (2022). Genetic variability and effect of plant arrangement on corn. *Agronomy Science and Biotechnology*, 8, 1-16 https://doi.org/10.33158/ASB.r162.v8.2022

Received: December 23, 2021.
Accepted: February 26, 2022.
Published: April 12, 2022.

English by: Luiz Leonardo Ferreira.

INTRODUCTION

The corn growing system has undergone changes over the last few years, such as the use of the direct sowing system, which has resulted in an increase in the corn growing areas under this system (Chaves Neto et al., 2018). Every crop has a critical point that is defined by intraspecific competition and maximum production point, which according to, the population corresponding to that point is the ideal one for the genotype-environment combination. The density and arrangement of plants in the canopy are of great importance in the interception and conversion efficiency of photo-synthetically active radiation for grain production (Takasu et al., 2014).

Important studies with grasses were carried out in Brazil including maize (Águila & Silva, 2021; Carvalho et al., 2022; Dubal et al., 2022; Ducatti et al., 2022; Teixeira et al., 2022; Troyjack et al., 2021). It is known that for high productive potential, regardless of the crop to be implanted, the ideal spatial arrangement for a given genotype must be found, in such a way as to express the maximum of its production potential. The corn crop is traditionally implanted in Brazil with spacing between lines of 0.80 and 0.90 m, in a conventional system (Pereira et al., 2018). However, the reduction of the spacing between the lines provides a more uniform distribution among the plants in the growing area (Ferreira et al., 2015). The use of low plant densities promotes underuse of incident radiation, decreasing crop productivity (Sangoi et al., 2019), and one of the main objectives of changing the spatial arrangement of plants is to reduce the time required for the crop to intercept as much solar radiation as possible.

In order to have a high productive potential, the ideal spatial arrangement between plants must be verified, so that plants distributed in an equidistant way compete less for nutrients, light and water. When delimiting the best plant density, material selection is also essential for a better productive response. The spacing between rows of crops, in turn, has great relations with the spatial arrangement between plants, being subject to adjustment with the main aim of reducing intraspecific competition (Foloni et al., 2014). Therefore, it is appropriate to estimate a spatial arrangement per hectare, in order to achieve greater grain production.

One of the main objectives of modifying the plant arrangement, by reducing the distance between the lines, is to shorten the time necessary for the crop to intercept the maximum of the incident solar radiation and, with this, increase the amount of energy captured per unit area and time (Takasu et al., 2014). The arrangement of plants in the field has a great influence on the agronomic performance of corn (Sangoi et al., 2019). Among the ways to manipulate this influence, the line spacing is one that has the most effect.

Recent research has shown that the reduction of line spacing in the corn crop has contributed to the increase in yield (Lima et al., 2016). For Pereira et al. (2018), changes in plant density, through spacing between lines and the distribution of plants in the growing line, provide different arrangements, and have been the focus of study by several researchers nationwide. Some recent studies have been carried out with other crops such as wheat (Silva et al., 2019, Silva et al., 2020; Bender et al., 2021), soybean (Ferreira et al., 2020), flaxseed (Muraro et al., 2018) promoting important information to enhance the agronomic performance of crops.

However, there is still an obstacle when it comes to high grain yields, which are formed by a series of processes that is defined by Silva et al. (2019), namely: water availability, soil fertility, genetic characteristics of genotypes, sowing cycle and time, row spacing, fertilization level, climatic factors, crop management and harvesting method. The plant population is one of the main factors that influence the capacity of the crop to capture resources from the environment (Silva et al., 2014). In this respect, the objective of this work was to evaluate the genetic divergence and the effect of plant arrangement on different genotypes of corn.

MATERIAL AND METHODS

The study was conducted at the Luiz Eduardo de Oliveira Sales Experimental Farm, in the county of Mineiros-GO, Brazil, located between the geographical coordinates of 17 ° 34'10 '' South latitude and 52 ° 33'04 '' West longitude, with average altitude of 760 m. The temperature is ± 22.7 °C, the average annual rainfall is 1,695 mm occurring mainly in spring and summer. The experimental area is classified as Aw type climate (hot to dry) and the soil as Quartzarenic Neosol (Entisol) (Embrapa, 2013). The analysis of the soil in the 0-20 cm layer revealed: hydrogen potential 5.7; calcium 3, magnesium 0.8, aluminum 0.2, hydrogen plus aluminum 2, cation exchange capacity 5.9, in cmolc dm^{-3}; potassium 53, phosphorus 59, sulfur 1.7, boron 0.2, copper 1.4, iron 51, manganese 23, zinc 8.3, sodium 1.5, in mg dm^{-3}; clay 223, silt 50, sand 728, organic matter 20 and organic carbon 12, in g dm^{-3}.

The experimental design used was in random blocks in factorial 8x2, totaling 16 treatments corresponding to 8 corn genotypes (A8740, A8088, DKB290, DKB390, DKB177, P30F35, P30S31 and P3707) and 2 spacing between lines (0.45 m and 0.90 m) in 4 repetitions, totaling 64 experimental units. The experimental units were composed of four rows of 4.0 m in length. The two central lines were evaluated as the useful area of each plot. The main morpho-agronomic characteristics of the corn genotypes were described in Table 1.

Table 1. Main morpho-agronomic characteristics of corn genotypes.

Hybrid		Genetics	Type[1]	Cycle[2]	Grains		
Technical	Common				TGM[3]	Color[4]	Texture[5]
AG 8740 PRO3	A8740	Agroceres	HS	E	396	YE	SMDENT
AG 8088 PRO2	A8088	Agroceres	HS	E	330	ORISH	HARD
DKB 290 PRO3	DKB290	Dekalb	HS	E	466	ORISH	SMHARD
DKB 390 PRO3	DKB390	Dekalb	HS	E	380	YE-ORISH	SMHARD
DKB 177 PRO3	DKB177	Dekalb	HS	E	402	YE-ORISH	SMHARD
30F35VYHR	P30F35	Pioneer	HS	E	310	YE-ORISH	SMDENT
30S31VYH	P30S31	Pioneer	HS	E	305	YE-ORISH	SMDENT
P3707VYH	P3707	Pioneer	HS	E	340	YE-ORISH	SMDENT

[1]HS- simple hybrid; HSm-modified simple hybrid; HD- double hybrid; HT-three way hybrid. [2]Cycle: SE-superearly; E-early; SME-semiearly. [3]TGM: Thousand grain mass (g). [4]Grain color: ORISH-Orangish; YE-yellow; OR-Orange. [4]Grain Texture: SMDENT-semidentate; SMHARD-semi-hard.

The soil was prepared in the no-tillage system. Sowing took place on 04/04/2018 reaching a population of 60 thousand plants per hectare for all combinations between genotypes and spacing. The soil correction and fertilization were carried out according to Sousa and Lobato (2004). The nitrogen source used was urea in stage V5, V9 and V11 totaling 120 kg ha^{-1} of N, phosphorus was made 120 kg ha^{-1} of P2O5 based on MAP in the sowing and potassium was used KCL with an amount of 90 120 kg ha^{-1} of K_2O in the phenological stage V5. During the execution of the experiment, the control of insects, pathogens and weeds were carried out whenever necessary, respecting the good practices of integrated pest management. For this, the following commercial products were used: Atrazine, Glyphosate, Connect, Engeo Pleno, Aproach Prima and Score Flexi. In the application of pesticides, backpack sprayer was used, with a single boom with a double fan type spray nozzle. The applications were carried out in the morning, with an average ambient temperature of 25 ºC, relative humidity above 60% and average winds of 5 km h^{-1}.

At the end of the experiment, the following characteristics were measured: plant height (PH) in centimeters; ear insertion height (EIH) in centimeters; stem diameter (SDI) in centimeters; number of rows ear (NRE) in units; number of grains per row (NGR) in units; number of grains per ear (NGE) in units; yield grain (YG) with 13% moisture in grains in sacks ha^{-1}; and the thousand grain mass (TGM) in grams. Soon after, the data obtained were submitted to the assumptions of the statistical model, verifying normality (Shapiro and Wilk, 1965) and homogeneity of variances (Steel et al., 1997).

Afterwards, the analysis of variance was carried out in order to identify the interaction between the corn genotypes - 8 x spacing between lines - 2, when verifying significant interaction these were broken down to simple effects and in the absence with main effects through the grouping of Scott-Knott means, at 5% probability. Singh's (1981) criterion was also used to quantify the relative contribution of these characteristics to genetic divergence. To group the genotypes, the Tocher method (Rao, 1952) was used. Subsequently, the variables of each spacing were subjected to Pearson's correlations in order to understand the association trend, with its significance based on a 5% probability by the t-test.

The path analysis was performed from the phenotypic correlation matrix, considering the YI as the dependent variable and PH, EIH, SDI, NRE, NGR, NGE and TGM as explanatory. Once the presence of high multicollinearity was identified among the data, the path analysis was carried out under multicollinearity, with subsequent adjustment of the k factor to the diagonal elements of the correlation matrix. After the genetic dissimilarity was carried out by the Mahalanobis algorithm, where the residual matrix was weighted, the phylogenetic tree of the distances was constructed using the UPGMA grouping, then the canonical biplot method was used, where it was possible to visualize the general variability of the experiment and multivariate trends. The character matrix data were subjected to unsupervised computer learning through Artificial Neural Networks, using the K-means and Kohonen Map algorithms (Carvalho, 2018). The analyzes were performed on the Rbio do R interface (Bhering, 2017), in addition to the Software Genes (Cruz, 2016).

RESULTS AND DISCUSSION

The analysis of variance revealed significance in the simple effect for the variables number of rows per ear and number of grains per ear ($p<0.05$). For the main effects, significance was obtained in the source of variation genotypes in plant height ($p<0.05$), ear insertion height, number of rows per ear, number of grains per row, number of grains per ear, yield and thousand grain mass ($p<0.01$), as well as, for spacing in ear insertion height ($p<0.05$), number of rows per ear, number of grains per ear ($p<0.01$) and thousand grain mass ($p<0.05$) (Table 2). This information corroborates with Silva et al. (2016), Takasu et al. (2014), Silva Júnior et al. (2017), Ferreira et al. (2019c) and Demétrio (2008). The latter states that the forms of manipulation of the plant arrangement and population density are techniques that have a great effect on corn grain yield.

The genotype x spacing interaction revealed that the DKB390 genotype in the

45 cm row spacing presented the highest averages among the others analyzed for the characteristics of ear insertion height, number of rows per ear, number of grains per ear and thousand grain mass, corroborating the work of Dourado Neto et al. (2003). Only the genotypes P30F35 and P3707 underwent changes in their means when the production system was modified for the rows 0.45 and 0.90 m (Table 3). Such information can be explained by the level of density used in planting, which causes greater intraspecific competition in the growing area, however, plant genetics can express an independent biotype in plant density.

Table 2. Summary of analysis of variances for plant height - PH, ear insertion height - EIH, stem diameter - SDI, number of rows per ear - NRE, number of grains per row - NGR, number of grains per ear - NGE, yield - YI and thousand grain mass - TGM.

		Means Square (MS)							
SV	DF	PH	EIH	SDI	NRE	NGR	NGE	YG	TGM
		(cm)	(cm)	(cm)	(unit)	(unit)	(unit)	(sacks)	(g)
GxS	7	NS	NS	NS	*	NS	*	NS	NS
Genotypes (G)	7	*	**	NS	**	**	**	**	**
Spacings (S)	1	NS	*	NS	**	NS	**	NS	*
Blocks	3	0.045	0.0025	0.008	0.09	9.46	2733.95	693.092	1828.72
Residue	45	0.019	0.005	0.06	0.53	3.86	1407.68	274.78	1525.97
CV%	-	8.75	9.06	10.95	4.57	7.68	9.15	21.12	20.27

^{NS} not significant by F test; * significant at 5% probability by F test; ** significant at 1% probability by F test

Table 3. Averages for the simple effects in ear insertion height - EIH, number of rows per ear - NRE, number of grains per ear - NGE and thousand grain mass - TGM of corn genotypes submitted to spacing of 0.45 m and 0.90 m between lines.

Genotype	------ EIH (cm) ----		----- NRE (unit)-----		------ NGE (unit) ---		------- TGM (g) -------	
	E45	E90	E45	E90	E45	E90	E45	E90
A8740	0.76 bA	0.77 bA	16.28 aA	15.80 cA	444.21 aA	425.03 bA	175.14 bA	211.26 aA
A8088	0.72 bA	0.70 bA	16.00 aA	16.25 bA	394.50 aB	460.95 aA	165.61 bA	149.60 bA
DKB290	0.84 bA	0.79 bA	16.50 aA	16.75 bA	395.50 aA	402.00 bA	182.10 bA	133.01 bA
DKB390	1.09 aA	0.98 aA	15.75 aA	16.75 bA	385.75 aA	410.75 bA	236.02 aA	243.58 aA
DKB177	0.85 bA	0.83 bA	15.50 aA	15.33 cA	380.50 aA	403.00 bA	241.08 aA	195.97 aA
P30F35	0.86 bA	0.74 bB	14.90 bA	15.50 cA	397.15 aA	398.75 bA	200.41 bA	207.19 aA
P30S31	0.82 bA	0.82 bA	14.50 bB	15.66 cA	347.50 aB	417.33 bA	187.72 bA	164.12 bA
P3707	0.84 bA	0.81 bA	16.00 aB	18.33 aA	392.50 aB	502.00 aA	238.30 aA	152.93 bB

Averages followed by the same lowercase letter in the vertical and uppercase letters in the horizontal, do not differ, by Scott Knott's test at 5% probability.

Through the splitting of the genotypes within the spacing (Table 4) it was possible to visualize that the genetic material DKB390, regardless of the distance from the planting lines, presented the plants of greater height, ears with the highest number of grains per row and yield, demonstrating its plasticity in adaptation to the proposed systems. For these characteristics, the formation of only two classes of individuals was observed, and among these the least flexible in terms of oscillation was the number of grains per row and greater amplitude in yield (Table 4). This information corroborates Dourado et al. (2003) when diagnosing a reduction in the morphological components of corn genotypes, probably due to their genetic variability. However, in research by Demétrio et al. (2008) the plant height and the ear insertion height in the plant were not influenced by the reduction of spacing between lines. For Alves et al. (2019) the production and productivity components of corn cultivars were increased with a spacing of 0.80 m between rows. Ferreira et al. (2021), showed influence on the behavior of corn hybrids when evaluated in different plant arrangements.

Table 4. Averages for the main effects on plant height - PH, number of grains per row - NGR and yield - YI of corn genotypes subjected to spacing of 0.45 cm and 0.90 m between lines.

Genotype	------PH (m) -----		------ NGR (unit) ------		--- YG (sacks ha^{-1}) ---	
	E45	E90	E45	E90	E45	E90
A8740	1.63 a	1.59 a	27.26 a	26.90 a	77.16 b	101.50 a
A8088	1.51 a	1.44 b	24.75 b	28.32 a	65.48 b	68.86 b
DKB290	1.69 a	1.67 a	24.00 a	24.00 a	72.96 b	52.61 b
DKB390	1.69 a	1.70 a	24.50 a	24.50 a	90.97 a	99.24 a
DKB177	1.74 a	1.74 a	24.50 a	26.33 a	92.15 a	78.31 b
P30F35	1.61 a	1.58 a	26.50 a	25.75 a	79.13 b	73.63 b
P30S31	1.46 a	1.38 b	24.00 a	26.66 a	65.04 b	68.53 b
P3707	1.67 a	1.62 a	24.50 a	27.33 a	93.71 b	77.44 b

Averages followed by the same letter in the lowercase vertically, do not differ, by Scott Knott's test at 5% probability.

Cluster analysis using Tocher's optimization method found that the results characterize the existence of distinct clusters under different population arrangements for both row spacing, separating the corn genotypes into 4 dissimilar groups. In the E45 spacing the concentration of 62.5%, 12.5%, 12.5% and 12.5% was observed and in the E90 spacing the concentration of 50.0%, 25.5%, 12.5% and 12.5%, for groups I, II, III and IV, respectively (Figure 1). According to Rios et al. (2010) this can probably be explained by the differential expression of genes, in the two environmental conditions. According to Melo et al. (2019), the genotypes gathered in more distant groups give an indication of being dissimilar, and can be considered as promising in artificial crosses.

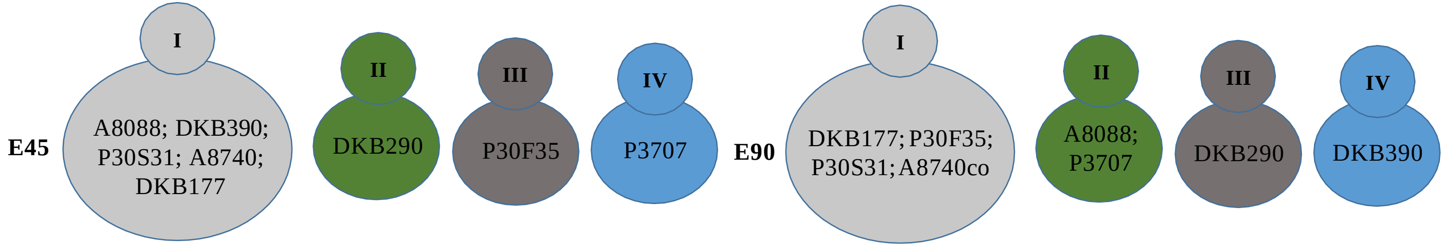

Figure 1. Grouping by the Tocher's method, based on the generalized Mahalanobis distance of the corn genotypes submitted to the spacing of 0.45 m (E45) and 0.90 m (E90) between lines.

The relative contribution of the characters to the genetic divergence of the 8 corn genotypes, in the two analyzed spacing, is shown in Figure 2. A similar contribution was observed among the characteristics with a concentration of over 99% in both spacing between TGM, NGE and YI, in descending order. These characteristics can be prioritized in the study of genetic diversity, considering the possibility of selection with lower analysis cost. Rios et al. (2010) also declared in his work low contribution of yield to genetic diversity in corn. In addition to being dissimilar, it is necessary for parents to associate high mean and variability in the characteristics to be improved (Melo et al., 2019).

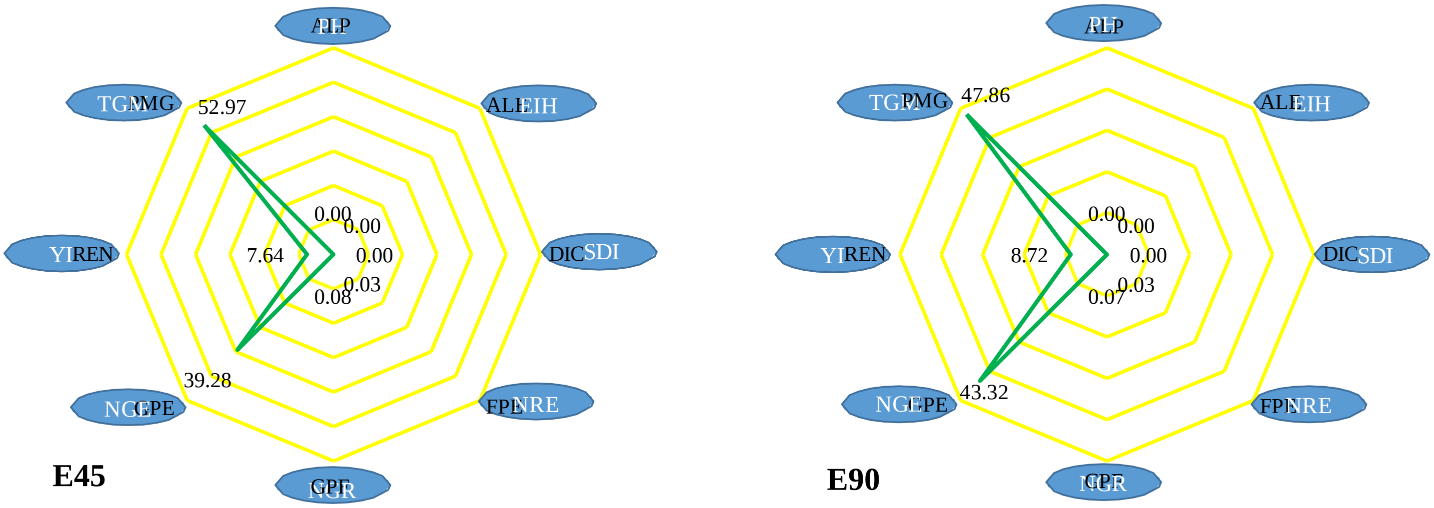

Figure 2. Relative contribution of the eight characters to the genetic divergence according to Singh (1981), of the corn genotypes submitted to the spacing of 0.45 m (E45) and 0.90 m (E90) between lines.

Although the correlation analysis is important to understand the interrelationships between the characteristics, high values do not necessarily imply a cause and effect relationship. As well as, in this work where high correlations can be observed, corroborating with Melo et al. (2019) when working with corn genotypes, as well as in Ferreira et al. (2019a) and Ferreira et al. (2019b). In the analysis of simple correlation, the formation of 2 significant pairs was observed for the spacing between lines of 0.45 m, being the YI x TGM (0.85) and NGR x NGE (0.85) (Figure 3 E45), as well as, TGM x YI (0.85), NGR x NGE (0.76) and NGE x NRE (0.66) for lines spaced at 0.90 m (Figure 3 E90). It appears that for both spacings the correlations in pairs of the components of yield of YI x TGM and NGR x NGE are marked among the analyzed genotypes (Figure 3 E45 and E90). The correlation coefficient is a measure that reflects the degree of association between the characteristics.

The estimates of direct and indirect effects in the path analysis showed very high coefficients of determination for both R2: 0.98 and R2: 0.95 spacings in lines with 0.45 and 0.90 m, respectively. Thus, the explanatory model adopted expressed the cause and effect relationship between the secondary characters and the YI of grains and the direct and indirect effects were considered significant those with loads equal to or greater than 0.1 (Ferreira et al., 2019a).

In lines spaced 0.45 m apart, the variables that had a direct effect in order of influence in the YI were TGM (0.98), NGE (0.17), NGR (0.14) and NRE (0.12), different from plants spaced at 0.90 m where all characters directly influenced the YI, following the magnitude of SDI (-0.52), PH (0.47), TGM (0.44), NGR (0.34), EIH (0.22), NRE (-

0.15) and NGE (0.12). Indirectly, the TGM was the characteristic that contributed most among the others to the YI of the corn genotypes in the two spacing analyzed (Figure 4), data which corroborates with Souza et al. (2013) where the number of grains per plant and the TGM are those that are most directly associated with YI. Santos et al. (2011) also observed estimates of the direct and indirect effects on the YI of corn genotypes.

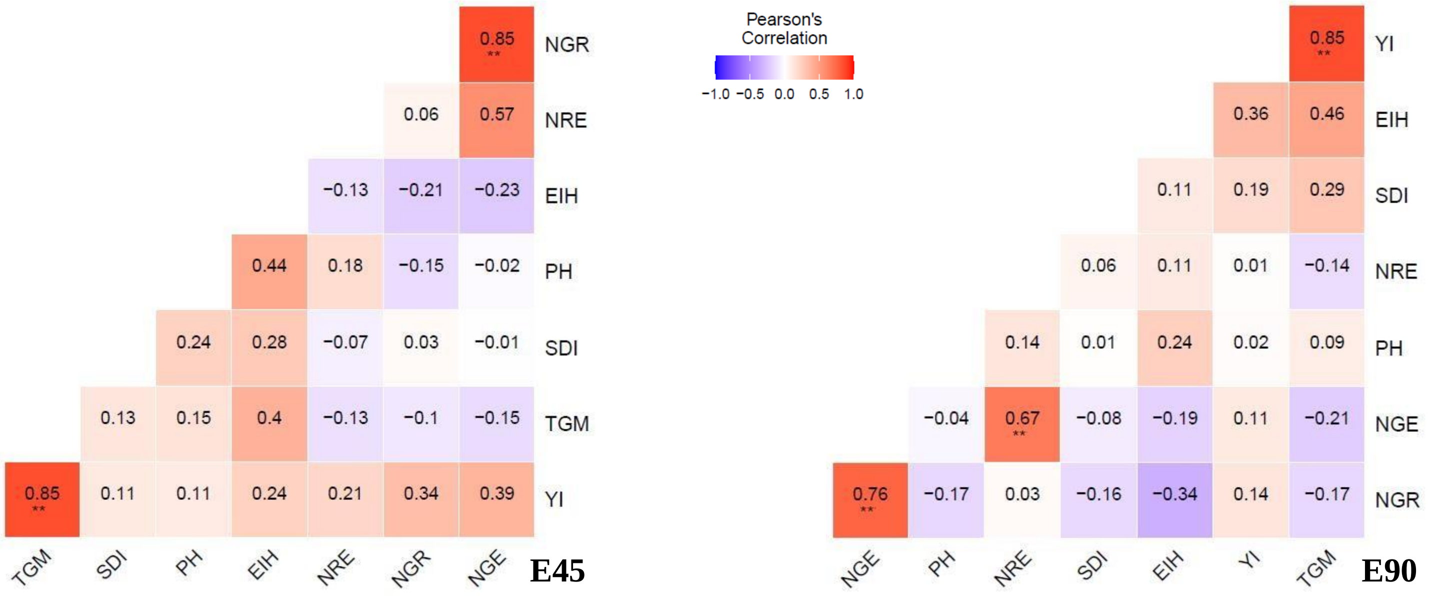

Figure 3. Phenotypic correlations network of characteristics of corn genotypes subjected to the spacing of 0.45 m (E45) and 0.90 m (E90) between lines. Significance: 0,05probability: *; 0,01 probability:**, by t test.

Biologically the plant patterns for both spacings are distinguished from each other. For high yields in the densest lines, genotypes need to present high averages in the characteristics of TGM, NGE, NGR and NRE. However, for the planting system with rows spaced at 0.90 m the plant needs to have high average values in PH, TGM, NGR and EIH, as well as a reduction in SDI, NRE and NGE (Figure 4). Works by Shi et al. (2015), demonstrated that the variability of the location of corn plants and the spacing between lines has a significant correlation with grain yield. As well as that of Sharifi and Namvar (2016) where they observed that corn biomass is altered with the plant density in addition to the line spacing.

The phylogenetic tree representative of the dissimilarity between corn genotypes subjected to spacing between lines of 0.45 and 0.90 m, obtained by the technique of the nearest neighbor, based on the average Euclidean distance, presented the formation of 2 large dissimilar groups among themselves for each spacing, with the smallest groups formed by P3707 and A8088 (Figure 5 E45), as well as, in isolation, the A8740 genotype (Figure 5 E90), respectively. These data corroborate with in which a significant effect was also detected for genotype in relation to all characters, indicating that at least one genotype differed from the others. In addition to dissimilarities, for Melo et al. (2019), it is necessary for parents to associate high mean and variability in the characteristics to be improved.

The variables in order of magnitude of greatest importance in the formation of the groups were TGM and NGE among the genotypes in the spacing between lines of 0.45 m and NGE and TGM in the spacing of 0.90 m. The greatest distances were reported between genotypes A8088 and P30F35, as well as between, A8740 and

DKB177 in plants spaced 0.45 and 0.90 m, respectively (Figure 5).

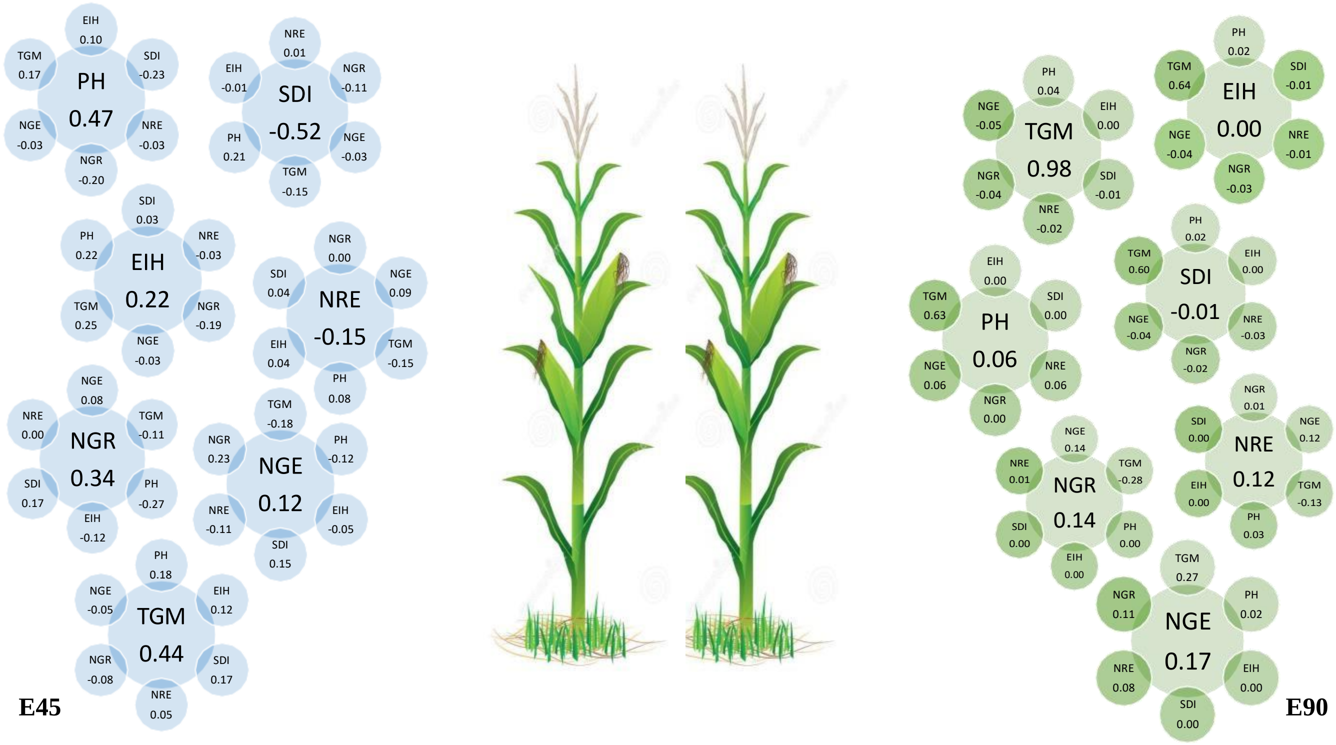

Figure 4: Causal diagram of the estimates of direct and indirect effects in the path analysis in explanatory characters plant height - PH, ear insertion height - EIH, stem diameter - SDI, number of rows per ear - NRE, number of grains per row - NGR, number of grains per ear - NGE and thousand grain mass - TGM on the yield - YI of the corn genotypes submitted to the spacing of 0.45 m (E45) and 0.90 m (E90) between lines.

E45: Coefficient of determination R2: 0.98, K value used in the analysis: 0.011, Effect of the residual variable: 0.111, Determinant of the correlation matrix between explanatory variables: 1.31E-03; E90: R2 determination coefficient: 0.95, K value used in the analysis: 0.011, Effect of the residual variable: 0.219, Determinant of the correlation matrix between explanatory variables: 1.10E-03.

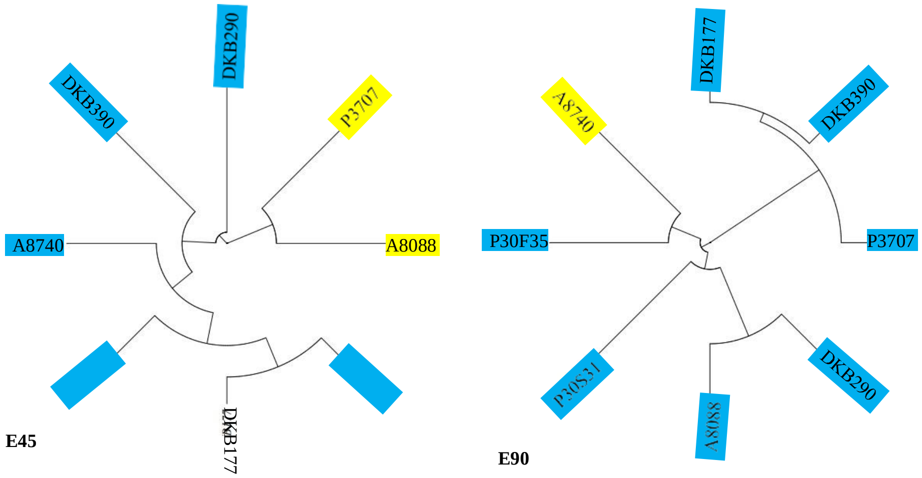

Figure 5. Phylogenetic tree built based on the Mahalanobis algorithm, with UPGMA grouping and Tocher's optimization groups of corn genotypes subjected to the spacing of 0.45 m (E45) and 0.90 m (E90) between rows, using the variables number of rows per ear - NRE; number of grains per row - NGR; number of grains per ear - NGE; yield - YI and thousand grain mass - TGM.

The analysis of canonical variables obtained through the Mahalanobis algorithm added in the two canonical axes the explanation of the variation of the data in 82.6% and 84.1% for the genotypes planted in 0.45 and 0.90 m, in this order (Figure 6). In the first growing system, affinity of the genotypes DKB390 and P3707 with NGE was observed, in addition to the genotype P30F35 with NGR (Figure 6 E45), for this purpose, in the other growing system, affinities were attributed to TGM in genotypes DKB177 and P30S31, YI for A8088 and NRE in genotype P3707 (Figure 6 E90).

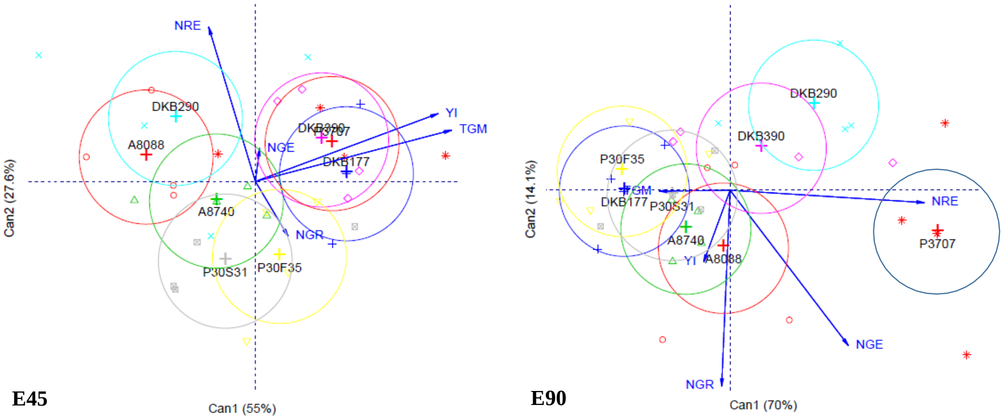

Figure 6. Analysis of canonical variables obtained through the Mahalanobis algorithm of the characters number of rows per ear - NRE; number of grains per row - NGR; number of grains per ear - NGE; yield - YI and thousand grain mass - TGM, of corn genotypes, submitted to spacing of 0.45 m (E45) and 0.90 m (E90) between lines.

The analysis of canonical variables is characterized as a multivariate technique that allows the reduction of the dimensionality of data, similar to the main components and canonical correlations. The use of this technique allows to observe characteristics that are not observed in univariate analyzes, such as, for example, the magnitude of the genotypes for each variable analyzed, as well as (Entringer et al., 2014) to compare the effects of the genotypes and estimate heritability based on the experimental averages.

The neural network was obtained by the K-means and Kohonen Map algorithms assembled through the learning rate of 0.5, with 3 rows and 2 columns, thus forming 6 centromeres, with the participation of 8 neurons from the different corn genotypes for each spacing between lines, taking the characteristics of number of rows per ear - NRE; number of grains per row - NGR; number of grains per ear - NGE; yield - YI and thousand grain mass - TGM. There was proximity to the centromeres I and IV in both spacings (Figure 7).

There was agglomeration of neurons DKB290 and P30F35 in centromere II and DKB177 and DKB390 in centromere I in plants spaced 0.45 m between lines (Figure 7 E45), clustering was also observed for neurons P30S31, P3707 and A8088 in centimeter VI in plants spaced at 0.90 m (Figure 7 E90). Azevedo et al. (2017) pointed out the high phenotypic and genotypic correlation estimated by ANN for the selection of superior genotypes. Abraham et al. (2019) proposed an ANN model to make predictions of soybean crop, concluding that the proposed model met expectations, with minimal errors, demonstrating multiple correlation between variables.

The behavior of the corn genotypes distributed in the planting systems spaced between rows at 0.45 and 0.90 m were explained by taking 8 morphological parameters. The analysis of variance performed initially demonstrated the significant differences of the variables for the simple and main effect of the sources of variation, broken down their averages in the grouping test of averages, and correlated pair-by-pair in Pearson's analysis in a varied way.

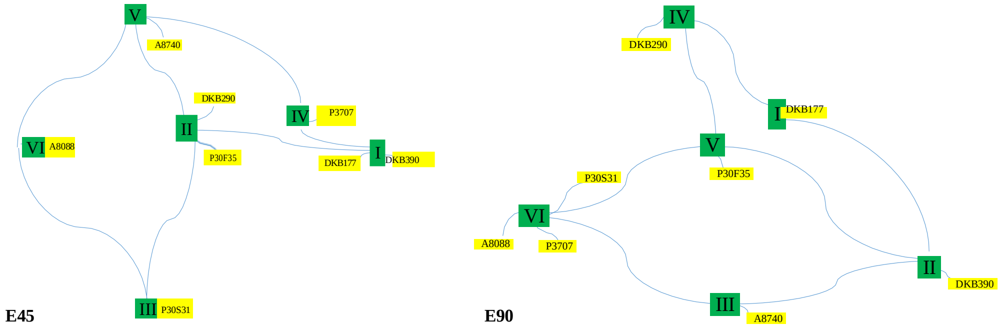

Figure 7. Artificial Neural Networks (ANNs) obtained by the K-means and Kohonen Map algorithms defining the centroides (green) and neurons (yellow) and synaptic links (blue lines), for combinations of corn genotypes, submitted to the spacing of 0.45 m (E45) and 0.90 m (E90) between lines.

Multivariate analyzes will be able to express the degree of magnitude of the contribution of the variables on the performance of the analyzed systems, and subsequently the genotypes will be worked on in the degree of similarity of patterns in the phylogenetic trees. Affinities were considered in the analysis of canonical variables, reflecting the dominance of genotypes over a given consultative variable.

CONCLUSIONS

The characteristics of plant height, stem diameter and thousand grain mass were the main characteristics that influenced the yield grain, whereas the number of grains per ear and thousand grain mass define the genetic divergence.

Among the analyzed genotypes, the growing of genetic material DKB390 is recommended in rows spaced at 0.45 or 0.90 m, as it has plants with ears of greater number of grains, thousand grain mass and yield, demonstrating its plasticity in adaptation to the proposed systems.

REFERENCES

Abraham, E. R., Reis, J. G. M., Toloi, R. C., Souza, A. E., & Colossetti, A. P. (2019) Estimativa da produção da soja brasileira utilizando redes neurais artificiais. *Agrarian*, 44(12), 261-271. DOI: 10.30612/agrarian.v12i44.9209

Águila, R. M. D., & Silva, E. F. (2021) Efficiency of crosses selection for yield in red rice through diallel analysis. *Agronomy Science and Biotechnology*, *7*(1966), 1–10. https://doi.org/10.33158/asb.r135.v7.2021

Alves, L. W. R., Montagner, A., & Pereira, J. F. (2019) Potencial produtivo de cultivares de milho no Cerrado do Amapá. Comunicado Técnico (INFOTECA-E). Macapá, AP: Embrapa Amapá.

Azevedo, A. M., Andrade Júnior, V. C., Sousa Júnior, A. S., Santos, A. A., Cruz, C. D., Pereira, S. L., & Oliveira, A. J. M. (2017) Aumento da eficiência de seleção para área foliar em couve utilizando redes neurais artificiais. *Horticultura Brasileira***,** 35(01), 14-19. https://doi.org/10.1590/S0102-053620170103

Bender, A. N., Carvalho, I. R., Martins, T., Moura, N., Silva, J. L. S., Lautenchleger, F., Ferreira, M. T., Hutra, D. J., Loro, M. V., & Souza, V. Q. (2021) Plant arrangement and its effects on yield and bromatological quality of wheat submitted to different cutting systems. *Research, Society and Development*, 10, e5301029555-10. https://doi.org/10.33448/rsd-v10i2.9555

Bhering, L. L. (2017) Rbio: A tool for biometric and statistical analysis using the R platform. *Crop Breeding and Applied Biotechnology*, 17(2), 187-190. http://doi.org/10.1590/1984- 70332017v17n2s29

Carvalho, C. R. B. (2018). Uma abordagem multivariada para redes de agrupamento Fuzzy Kohonen.

Carvalho, I. R., Ferreira, L. L. F., Conte, G. G., Amaral, G. C. L., Campos, J. N., Tomazele, A. A. S., … Loro, M. V. (2021) Effect of biostimulant on yield characters of common bean cultivars under Southwestern Goiás conditions. *Agronomy Science and Biotechnology*, *8*, 1–13. https://doi.org/10.33158/asb.r148.v8.2022

Chaves Neto, J. R., Guerra, R. C., Boscaini, R., Ledur, N. R., Travessini, M., & Costa, I. F. D. (2018) Desempenho agronômico e qualidade sanitária de grãos de milho, em função da aplicação foliar de fungicidas. *Revista Científica Rural*, 20(2), 74-90. https://doi.org/10.30945/rcr-v20i2.261

Cruz, C. D. (2016) Genes Software – extended and integrated with the R, Matlab and Selegen. *Acta Scientiarum*. 38(4), 547-552. https://doi.org/10.4025/actasciagron.v38i4.32629

Demétrio, C. S., Fornasieri, F. D., Cazetta, J. O., & Cazetta, D. A. (2008) Desempenho de híbridos de milho submetidos a diferentes espaçamentos e densidades populacionais. *Pesquisa Agropecuária Brasileira*, 43(12), 1691-1697. https://doi.org/10.1590/S0100-204X2008001200008

Dourado Neto, D., Vieira, P. A., Manfron, P. A., Palhares, M., Medeiros, S. L. P., & Romano, M. R. (2003) Efeito da população de plantas e do espaçamento sobre a produtividade de milho. *Revista Brasileira de Milho e Sorgo*, 2(3), 63-77. https://doi.org/10.18512/1980-6477/rbms.v2n03p%25p

Dubal, I. T. P., Carvalho, I. R., Pimentel, J. R., Troyjack, C., Szareski, V. J., Jaques, L. B. A., … Pedó, T. (2021) Effect of production environments on storage and physiological quality of maize seed. *Agronomy Science and Biotechnology*, *8*, 1–15. https://doi.org/10.33158/asb.r138.v8.2022

Ducatti, D. B. R., Tironi, S. P., Wordell Filho, J. A., & Mazaro, S. M. (2022) Carrageenan as an elicitor of wheat's mechanisms of defense. *Agronomy Science and Biotechnology*, *8*, 1–11. https://doi.org/10.33158/asb.r152.v8.2022

EMBRAPA - Empresa Brasileira de Pesquisa Agropecuária. (2013) *Sistema Brasileiro de Classificação de Solos*. (3ª ed.). Brasília, DF: Embrapa Solos.

Entringer, G. C., Santos, P. H. A. D., Vettorazzi, J. C. F., Cunha, K. S., Pereira, M. G. (2014) Correlação e análise de trilha para componentes de produção de milho superdoce. *Revista Ceres*, 61(3), 356-361. https://doi.org/10.1590/S0034-737X2014000300009

Ferreira, J. P., Rodrigues, R. A. F., Kaneko, F. H., Kappes, C., Arf, M. V., & Goés, R. J. (2015) Características Agronômicas do milho sob arranjos espaciais e densidades de plantas em região de cerrado. *Cultura Agronômica: Revista de Ciências Agronômicas*, 24(1), 27-44. https://doi.org/10.32929/2446-8355.2015v24n1p27-44

Ferreira, L. L., Amaral, U., Silva, C. S., Curvelo, C. R. S., & Pereira, A. I. A. (2019c) Components of Maize Crop as a Function of Doses of Polymerized Urea. *Journal of Agricultural Science*, 11(11), 185-192. DOI : 10.5539/jas.v11n11p185

Ferreira, L. L., Araujo, G. S., Carvalho, I. R., Santos, G. A., Fernandes, M. S., Carnevale, A. B., Curvelo, C. R. S., & Pereira, A. I. A. (2019b) Cause and Effect Estimates on Corn Yield as a Function of Tractor Planting Speed. *Journal of Experimental Agriculture International*, 41(5), 1-7. DOI: 10.9734/jeai/2019/v41i530417

Ferreira, L. L., Barbosa, H. Z., Carvalho, I. R., Prado, R. L. F., Curvelo, C. R. S., Pereira, A. I. A., Fernandes, M. S., Carnevale, A. B. (2019a) Effect of Biostimulants in Late Seeding of Genotypes of Zea mays L.. *Journal of Experimental Agriculture International*, 41(6), 1-9. DOI: 10.9734/jeai/2019/v41i630431

Ferreira, L. L., Mendes, S., Carvalho, I. R., Conte, G. G., Leal, F. S., Santos, N. S. C., Silva, J. G., Fernandes, M. S., Pereira, A. I. A., Curvelo, C. R. S., & Hutra, D. J. (2021) Spatial arrangement and its implications in the yield of maize cultivars. *Genetics and Molecular Research,* 20(1), 1-12. DOI: https://doi.org/10.4238/gmr18425

Ferreira, L. L., Moreira, N. V., Carvalho, I.R., Santos, N. S. C., Fernandes, M. S., Pereira, A. I. A., Curvelo, C. R. S., Silva, R. V., Amaral, U., & Silva, R. A. (2020) Spacing between rows of soybean genotypes: averages, regressions and correlations in yield levels. *Research, Society and Development*, 9, 1-17. https://doi.org/10.33448/rsd-v9i9.7793

Foloni, J. S. S., Juliano, C. C., Tiago, A. C., Norberto, A. B., Carlos, S. T., & Alexandrius, M. B. (2015) Cultivares de milho em diferentes populações de plantas com espaçamento reduzido na safrinha. *Revista Brasileira de Milho e Sorgo*, 13(3), 312-325. http://dx.doi.org/10.18512/1980-6477/rbms.v13n3p312-325

Lima, S. F., Alvarez, R. C. F., & Contardi, L. M. (2016) Influência do espaçamento entre linhas em características fito técnicas e acúmulo de massa seca de híbridos de milho**.** 2016. *Ambiência*, 12(4), 1027-1039. DOI:10.5935/ambiencia.2016. 04.nt2

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. DOI: 10.32404/rean.v6i3.2339

Muraro, D. S., Basso, C. J., Carvalho, I. R., Szareski, V. J., Cutti, L., Aguiar, A. C. M., Silva, V. A., Pinto, M. A. B., & Lautenchleger, F. (2018) Agronomic Components of Brown Linseed as a Function of Spacing. *Journal of Agricultural Science*, 10, 527. DOI:10.5539/JAS.V10N10P527

Pereira, L. B., Machado, D. S., Alves F. D. C., Brondani, I. L., Silva, V. S., Argenta, F. M., & Borchate, D. (2018). Características agronômicas da planta e produtividade da silagem de milho submetido a diferentes arranjos populacionais. *Magistra*, 29(1), 18-27.

Rao, R. C. (1952). *Advanced statistical methods in biometric research*. New York: J. Wiley.

Rios, S. D. A., Borém, A., Guimarães, P. E. D. O., & Paes, M. C. D. (2010) Divergência genética entre genótipos de milho quanto ao teor de carotenóides nos grãos. *Revista Brasileira de Milho e Sorgo*, 9(3), 277-286. http://dx.doi.org/10.18512/1980-6477/rbms.v9n3p277-28

Sangoi, L., Schmitt, A., Durli, M. M., Leolato, L. S., Coelho, A. E., Kuneski, H. F., & Vander, L.O. (2019) Estratégias de manejo do arranjo de plantas visando otimizar a produtividade de grãos do milho**.** *Revista Brasileira de Milho e Sorgo*, 18 (1), 47-60. https://doi.org/10.18512/1980-6477/rbms.v18n1p47-60

Santos, M. M., Galvão, J. C. C., Melo A. V., Adriano, R. C., Fidelis, R. R., & Corrêa, M. L. P. (2011) Efeito da fonte de nitrogênio e da época de aplicação na cultura do milho, em plantio direto, com espaçamento reduzido. *Revista Brasileira de Milho e Sorgo*, 10(1), 29-37. http://dx.doi.org/10.18512/1980-6477/rbms.v10n1p29-37

Sharifi, R. S., & Namvar, A. (2016) Plant density and intra-row spacing effects on phenology, dry matter accumulation and leaf area index of maize in second cropping. *Biologija*, 62(1). DOI: 10.6001/biologija.v62i1.3289

Shi, Y., Wang, N., Taylor, R. K., & Raun, W. R. (2015) Improvement of a ground-LiDAR-based corn plant population and spacing measurement system. *Computers and Electronics in Agriculture*, 112, 92-101. https://doi.org/10.1016/j.compag.2014.11.026

Silva Júnior, A. B., Ferreira, P. V., Cunha, J. L. X. L., Lira, R. C., & Carvalho, I. D. E. (2017) Desempenho produtivo de genótipos de milho sob diferentes espaçamentos para a produção de silagem. *Revista Ciência Agrícola*, 15(2), 1-10. https://doi.org/10.28998/rca.v15i2.3034

Silva, A. F., Schoninger, E. L., Caione, G., Kuffel, C., & Carvalho, M. A. C. (2014) Produtividade de híbridos de milho em função do espaçamento e da população de plantas em sistema de plantio convencional. *Revista Brasileira de Milho e Sorgo*, 13(2), 162-173. https://doi.org/10.18512/1980-6477/rbms.v13n2p162-173

Silva, F. A. S., & Azevedo, C. A. V. (2016) The assistat software version 7.7 ande its use in the analysis of experimental data. *African Journal of Agricultural Research*. 11(39), 3733-3740. DOI: 10.5897/AJAR2016.11522

Silva, F. L., Carvalho, I. R., Barbosa, M. H., Conte, G. G., Hutra, D. J., Moura, N., & Souza, V. Q. (2020) Sowing density and clipping management: effects on the architecture and yield of dual-purpose wheat. *Bioscience Journal*, 36(6), 2060-2067. https://doi.org/10.14393/BJ-v36n6a2020-48207

Silva, F. L., Carvalho, I. R., Szareski, V. J., Pimentel, J. R., Troyjack, C., Lautenchleger, F., Ferreira, L. L., Silva, J. A. G., Pereira, E. A., & Souza, V. Q. (2019) Forage bromatology is affected by sowing density and cutting management in dual purpose wheat. *Genetics and Molecular Research*, 18, 1-14. DOI: https://doi.org/10.4238/gmr18211

Singh, D. (1981) The relative importance of characters affecting genetic divergence. *The Indian Journal of Genetics and Plant Breeding*, 41, 237-245.

Sousa, D. M. G., & Lobato, E. (2004) Edição Cerrado: Correção do solo e adubação. Planaltina, DF: *Embrapa Cerrados*.

Souza, C. S., Andrade, A. P., Lima, J. R. S., Antonino, A. C. D., Souza, E. S., & Silva, I. F. (2013) Balanço hídrico da cultura da mamona sob condições de sequeiro. *Revista Brasileira de Engenharia Agrícola e Ambiental-Agriambi*, 17(1). https://doi.org/10.1590/S1415-43662013000100001

Takasu, A. T., Rodrigues, R. A. F., Goes, R. J., Arf, O., & Haga, K. I. (2014) Desempenho agronômico do milho sob diferentes arranjos populacionais e espaçamento entrelinhas. *Agrarian*, 23(7), 34-41.

Teixeira, E. M. M., Dias-Pereira, J., Drumond, L. C. D., God, P. I. V. G. G., & Araújo, H. H. de A. (2022) Leaf anatomy of Urochloa brizantha and Urochloa ruziziensis (Poaceae) plants subjected to different fertilization management practices. *Agronomy Science and Biotechnology*, *8*, 1–14. https://doi.org/10.33158/asb.r159.v8.2022

Troyjack, C., Carvalho, I. R., Pimentel, J. R., Junior, G. T., Szareski, V. J., Dubal, Í. T. P., … Conte, G. G. (2021) Environmental stresses and its implications on breeding of brewing barley. *Agronomy Science and Biotechnology*, *7*, 1–18. https://doi.org/10.33158/asb.r123.v7.2021