Original Article

CORRELATIONS AND GENETIC PARAMETERS IN MAIZE HYBRIDS

CORRELAÇÕES E PARÂMETROS GENÉTICOS EM HÍBRIDOS DE MILHO

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ABSTRACT: The study of the genetic control of agronomic traits and heritage through estimates of genetic parameters of a population allows inferences about its genetic variability and which can be expected of gain with selection. Know the correlations among traits of interest for selection allows to the breeder know the degree of association among traits of economic importance, given that the selection of certain trait changes the behavior of the other. With the aim to estimate genetic parameters and identify agronomic traits correlated with the grain yield of maize hybrids, an experiment was conducted at the State University of Mato Grosso do Sul - University Unit of Aquidauana (UEMS/UUA). The experimental design was a randomized block with four replications. Treatments consisted of 20 maize hybrids. The traits evaluated were: plant height, first ear height, stem diameter, ear diameter, ear length, number of rows per ear, number of kernels per row, hundred grain weight and grain yield. The hybrids XB9010, P30F53, 20A78HX, XB6012, P3340, AG9010 and XB7253, obtained the highest grain yield and mass of one hundred grains. The population has a genetic variability and potential for selection of all traits. Based on the evaluated genetic parameters, mass of hundred grains can be used at the direct selection of genotypes with high grain yield.

KEYWORDS: Morphoagronomic traits. Productive components. *Zea mays* L.

INTRODUCTION

One of the main cereals grown in the world is the maize (*Zea mays* L.), main raw material of international pig and poultry farming (PATERNIANI; FIELDS, 2005; TEODORO et al., 2014a). Brazil is one of the largest maize producers in the world, with 14 million hectares and a production higher than 80 million tons, with an average yield 5,115 kg ha^{-1} (CONAB, 2013). However, this yield is considered low when compared with the productive potential of genotypes available in the market. One of the main aims of maize breeding is obtaining genotypes with high capacity grain (LEMES et al., 1992; TEODORO et al., 2015). However, grain yield is a trait in which genetic inheritance is complex because results from the involvement of several small effect genes on the phenotype (CRUZ et al., 2014).

The study of the genetic control of agronomic traits and heritage through estimates of genetic parameters of a population allows inferences about its genetic variability and which can be expected of gain with selection. Know the correlations among traits of interest for selection allows to the breeder know the degree of association among traits of economic importance, given that the selection of certain trait changes the behavior of the other. The breeder to define appropriate strategies for achieving superior genotypes based on the most important traits (FERREIRA et al., 2009) uses the estimates obtained.

The use of correlated traits also constitutes one of the main ways to increase the selection efficiency of a trait. Cruz et al. (2014) emphasized the importance of correlations, affirming that these estimates quantify the possibility of direct gains by selection on correlated traits. Thus, in breeding programs of maize crop, is very important the knowledge of the traits that contribute to greater grain yield, as this facilitates the selection of genotypes and can direct the selection methodology (LEMES et al., 1992; TEODORO et al., 2014b).

In order to generate information that can contribute to the genetic improvement of maize crop, the study aimed to evaluate the agronomic performance of 20 maize hybrids grown in the Brazilian Savanna and identify, based on different genetic parameters and correlations, which characters can be used in the selection genotypes with high grain yield.

MATERIAL AND METHODS

The experiment was conducted in the Universidade Estadual de Mato Grosso do Sul, municipality of Aquidauana, region situated in Savanna-Pantanal ecotone (20º27'S and 55º40'W), with average altitude of 170 m. The soil of the area is classified as Ultisol Dystrophic of sandy texture,

according to the criteria established by Embrapa (2013). The chemical properties of the layer 0 - 0.20 m are: pH (H_2O) = 6.2; Al exchangeable ($cmol_c$ dm^{-3}) = 0.0; Ca+Mg ($cmol_c$ dm^{-3}) = 4.31; P (mg dm^{-3}) = 41.3; K ($cmol_c$ dm^{-3}) = 0.2; Organic matter (g dm^{-3}) = 19.74; V (%) = 45; m (%) = 0.0; Sum of bases ($cmol_c$ dm^{-3}) = 2.3; CEC ($cmol_c$ dm^{-3}) = 5.1. The regional climate, according to the classification of Köppen, is "Aw" (Savanna Tropical). The experiment was conducted among February to May of 2012 and accumulated rainfall over was 450 mm, with maximum and minimum average temperatures of 33.2 and 19.1 ºC, respectively.

The experimental design was randomized blocks with four replications. The area was divided into four blocks with a total of eighty-four plots, each with an area of 15.75 m² (3.15 x 5 m), with two meters spacing between blocks. Treatments consisted of 20 corn hybrids: XB6012, 2B655HX, A37HX, 2B5124, 2B433HX, 20A78HX, 30A95HX, AG 9010, MAXIMUS, P30F53, FÓRMULA TL, P3340, 2B604HX, XB6010, STATUS TL, 30A30HX, 2B587HX, XB7253, 30A91HX and 20A55HX.

In the preparation of the experimental area, desiccation was performed with the herbicide Roundup WG with glyphosate active ingredient in a dose of 1 kg ha^{-1}. After drying and complete plant death, the grooves were opened using a simple seeder, performing sowing manually under no-tillage on 02/02/2012, ten days after the desiccation, in which were distributed four seeds per meter within the row, spaced 0.45 m, to establishment of 55,556 plants ha^{-1}. The fertilizer at sowing consisted of 300 kg ha^{-1} formulation 4-20-20. The topdressing was performed at V5 stage using urea at a dose of 100 kg ha^{-1}.

At harvest, when the grains had around 18% moisture, it were taken the measurements of plant height (PH) and first ear height (EH), being carried out with graduated scale in five plants per plot. Stem diameter (SD) was evaluated above the third internode, with the aid of an analog caliper. In each experimental plot were randomly harvested five ears, which were numbered according to the evaluated plants, being determined ear diameter and ear length (ED and EL, respectively), number of rows per ear (NRE) and number of kernels per row (NKR).

The harvest and threshing of maize ears were manually performed in three central lines of 5 m in length, according to the cycle of each cultivar. The hundred grain weight (HGM) was determined by manual counting, weighing and moisture correction to 13%. Grain yield (YIE) was estimated in useful area with correction to 13% wet basis and extrapolating the values for one hectare.

Initially, to verify compliance of assumptions of normality of residues and homogeneity of variances were applied the Shapiro-Wilk and Bartlett tests, respectively. To verify the existence of variability among the genotypes, the data were submitted to analysis of variance and F-test for each trait. Means were compared by Scott and Knott's test at 5% probability of type I error. The following genetic parameters were estimated: environmental, phenotypic and genotypic variances; coefficients of experimental and genotypic variation; genotypic determination coefficient; heritability; b quotient; environmental, phenotypic and genotypic correlations represented, respectively, by the following estimators (JOHNSON et al., 1955):

$$\hat{\sigma}_E^2 = \frac{QM_r}{k} \tag{1}$$

$$\hat{\sigma}_F^2 = \frac{QM_g}{k} \tag{2}$$

$$\hat{\sigma}_G^2 = \frac{QM_g - QM_r}{k} \tag{3}$$

$$CV_g = \left(\frac{\sqrt{\hat{\sigma}_G^2}}{m} \right) \times 100 \tag{4}$$

$$CV_e = \left(\frac{\sqrt{QM_e}}{m} \right) \times 100 \tag{5}$$

$$\hat{h}^2 = \frac{\hat{\sigma}_G^2}{\hat{\sigma}_E^2} \tag{6}$$

$$b = \frac{CV_g}{CV_e} \tag{7}$$

$$r_E = \frac{COV_{E(xy)}}{\sqrt{\hat{\sigma}_{Ex}^2 \times \hat{\sigma}_{Ey}^2}} \tag{8}$$

$$r_F = \frac{COV_{F(xy)}}{\sqrt{\hat{\sigma}_{Fx}^2 \times \hat{\sigma}_{Fy}^2}} \tag{9}$$

$$r_G = \frac{COV_{G(xy)}}{\sqrt{\hat{\sigma}_{Gx}^2 \times \hat{\sigma}_{Gy}^2}} \tag{10}$$

Where: r_{xy} is correlation between traits X and Y; COV_{xy} is covariance between traits X and Y; S_x^2 and S_y^2 is variance of traits X e Y, respectively. All statistical analyzes

were performed with the application GENES (CRUZ, 2013) according to the procedures recommended by Cruz et al. (2014).

RESULTS AND DISCUSSION

There was attendance of assumptions of normality of residues and homogeneity of variances for all traits, indicating that the analysis of variance can be used safely. There were significant differences (p<0.01) among the hybrids for all evaluated traits (Table 1). Considering the existence

of genetic variability in a population as a decisive factor in any breeding program (CRUZ et al., 2004; LYNCH; WALSH, 1998; FALCONER; MACKAY, 1996; FALCONER et al., 1987; FALCONER; MACKAY et al., 1996), the population under study proved to be, in principle, promising to selection and crossing works aiming to improve the above traits. Similar results were obtained in other studies with maize hybrids (TORRES et al., 2013; TEODORO et al., 2014a; TEODORO et al., 2014b).

TABLE 1. P-value by Shapiro-Wilk (SW) and Bartlett (BT) tests, F calculated and genetic parameters from nine morphological traits in 20 maize hybrids grown in second harvest. Aquidauana, MS, 2014.

Parameter	EL	ED	SD	NRE	NKR	EH	PH	HGW	YIE
	-----------(cm)------------					-------(m)-------		(g)	(kg ha^1)
SW	0.12	0.22	0.54	0.61	0.33	0.19	0.78	0.28	0.09
BT	0.40	0.39	0.23	0.09	0.17	0.44	0.56	0.34	0.11
Fc	4.93*	4.62*	6.01*	4.10*	6.37*	5.41*	3.01*	16.44*	7.82*
CVg (%)	7.40	3.53	8.75	7.038	7.76	8.16	10.40	15.11	18.89
CVe (%)	7.46	3.70	7.82	7.99	6.70	7.77	14.68	7.69	14.46
b	0.992	0.9521	1.12	0.881	1.16	1.05	0.708	1.96	1.31
S²f	1.40	0.0347	2.33	5.38	0.0289	87.50	676.69	28.35	2434031.0
S²g	1.12	0.0272	1.95	4.066	0.0243	71.33	451.71	26.63	2123000.8
S²a	0.2846	0.0075	0.3886	1.31	0.0045	16.17	224.98	1.72	311030.2
h²	79.73	78.38	83.35	75.63	84.29	71.52	66.75	93.92	87.2

*: significant at 1% probability by F-test. CVg: coefficient of genotypic variation; CVe: coefficient of environmental variation; b: b quotient; S²f: phenotypic variance; S²g: genotypic variance; S²a: environmental variance; h²: heritability; EL: ear length; ED: ear diameter; SD: stem diameter; NRE: number of rows per ear; NKR: number of kernels per row; EH: first ear height; PH: plant height; HGW: hundred grains weight; YIE: grain yield.

Coefficientt of experimental variation (CVe) ranged between 3.7 (ED) and 14.7 (PH), which classifies according to Cruz et al. (2014) high experimental precision for polygenic traits and with continuous distribution. The coefficient of genotypic variation (CVg) ranged between 3.5 (ED) and 18.9 (YIE), which indicates that among the evaluated agronomic traits the YIE is which shows greater variability, being highly promising for selection. Whereas the existence of genetic variability in a population as a decisive factor in any breeding program, germplasm under study is, at first, promising for selection or hybridization works with potential to the development of new hybrids. The b quotient, except for the PH, was higher than 0.8 for all variables, indicating favorable conditions for selection for these traits, according to the interpretation of this value recommended by Cruz et al. (2014).

Following this trend, it were verified heritability values (h²) higher than 70%, except for PH (66.75%), being these values higher than those observed in the traits evaluated by Lemes et al. (1992) and Faluba et al. (2010) in maize crop. High estimates of h² are associated with greater genetic

variability, greater selective accuracy and greater chance of success in the selection of superior genotypes.

Significant (p<0.01) phenotypic correlations (r$_P$) were identified among ED x EL, ED x NRE, ED x NKR, EL x NRE, EL x NKR, SD x NKR, NKR x PH, NKR x HGW (Table 2). The trait YIE obtained r$_F$ significant negative (p <0.01) only with ED and NRE, which indicates that the plant selection based on other traits will result in more productive genotypes. Positive correlations indicate the occurrence of pleiotropism or gene linkage disequilibrium among the pairs of traits, and favors simultaneous selection of two or more traits by selection in a single trait (FALCONER, 1987; GOLDENBERG, 1968). Moreover, the selection of a trait may result in undesirable selection of another.

Genotypic correlations (r$_G$), in most cases, showed higher values than their corresponding r$_F$, reiterating that the phenotypic expression is reduced compared to environment influence. The genotype correlations were also, in most cases, higher than environmental correlations, which indicate that the r$_F$ were composed in large part by genetic portion of the correlation, confirming the results verified by

Lemes et al. (1992). Thus, the r_F can be useful in the absence of r_G estimates.

Table 2. Estimates of phenotypic (r_F), genotypic (r_G) and environmental (r_E) correlations.

Trait		EL	ED	SD	NRE	NKR	EH	PH	HGW
	r_F	0.3705	0.2533	0.6964*	-0.3037	-0.3322	-0.1802	-0.2704	0.0135
EL	r_G	0.4336	0.3389	0.6855*	-0.4080	-0.3850	-0.3146	-0.3313	-0.0771
	r_E	0.1323	-0.1251	0.7382**	0.1726	-0.1126	0.1899	0.1469	0.4837
	r_F	---	0.6950*	0.0965	-0.3335	-0.3914	-0.5647	-0.7089*	-0.5694
ED	r_G	---	0.7977**	0.0067	-0.4391	-0.4944	-0.8925**	-0.8327**	-0.7874**
	r_E	---	0.2645	0.3981	0.1270	0.0190	0.3016	0.0483	0.4913
	r_F		---	-0.3320	-0.5990	-0.3335	-0.5083	-0.7975**	-0.6597*
NRE	r_G		---	-0.3657	-0.6927*	-0.4089	-0.7052*	-0.9031**	-0.8498**
	r_E		---	-0.2069	-0.114	0.0204	0.0753	0.0158	0.4449
	r_F			---	0.1796	-0.1231	0.2096	0.2050	0.4514
NKR	r_G			---	0.1301	-0.1797	0.1899	0.2268	0.4297
	r_E			---	0.3868	0.0849	0.2623	0.1141	0.5800
	r_F				---	0.6429*	0.4745	0.6124	0.5350
SD	r_G				---	0.7026*	0.5401	0.6902*	0.5979
	r_E				---	0.3548	0.3032	-0.0172	0.1576
	r_F					---	0.2644	0.4044	0.3554
EH	r_G					---	0.2770	0.4478	0.3975
	r_E					---	0.2424	0.1192	0.1316
	r_F						---	0.5460	0.4952
PH	r_G						---	0.6193	0.5302
	r_E						---	0.3912	0.4395
	r_F							---	0.9111**
HGW	r_G							---	0.9458**
	r_E							---	0.6242

EL: ear length; ED: ear diameter; SD: stem diameter; NRE: number of rows per ear; NKR: number of kernels per row; EH: first ear height; PH: plant height; HGW: hundred grains weight; YIE: grain yield.

There was a negative phenotypic and genotypic correlation among NRE x HGW, which indicates antagonism among these traits (FANCELLI; DOURADO NETTO, 1999; TEODORO et al., 2014b). These correlations were also positively high among HGW x YIE, reiterating that the selection of genotypes based on the mass of hundred grains, besides result in a facility in the selection of genotypes, also leads to greater yield.

Environmental correlations (r_E) among traits with differences in magnitude and sign, regarding to their r_G correlations revealed that the environment favored one trait over the other and that the causes of genetic and environmental variation have different physiological mechanisms, hindering the indirect selection. The highest environmental correlations were observed among EL x NKR (0.74) and YIE x HGW (0.62), indicating a greater influence of the environment on these variables.

Differences in magnitude and direction of phenotypic, genotypic and environmental correlations estimates, among the various pairs of characters evaluated in the population, demonstrates the presence of distinct association trends. This show that the concept of correlation is similar to that of heritability and should be restricted to evaluated genetic constitution and environment under study (LYNCH; WALSH, 1998; FALCONER; MACKAY, 1996). This discrepancy may be attributed to environmental modifiers effects and to different physiological mechanisms controlling characters expression (FALCONER, 1987; GOLDENBERG, 1968) Johnson et al, 1955), as well as differences in combination capacity shown by parents (CRUZ et al., 2014).

Table 3 presents the agronomic traits of different hybrids. The hybrids XB9010, P30F53, 20A78HX, XB6012, P3340, AG9010 and XB7253 obtained the highest YIE by Scott-Knott's cluster (p <0.05). It was found that the group of hybrids with highest YIE was the same with the highest HGW, reiterating that this trait is directly correlated to YIE. The PH was another trait which showed high values in hybrids of greater YIE, except XB6012, P30F53 and AG9010. These results are in agreement with Lemes et al. (1992), which highlight plant height as

a trait that strongly affects YIE, because larger plants have high assimilates production, resulting, therefore, in an increase in PH.

Table 3. Agronomic traits of 20 maize hybrids grown in the agricultural year 2012. Aquidauana, MS, 2014.

Hybrids	EL	ED	SD	NRE	NKR	EH	PH	HGW	YIE
	-----------(cm)------------					-------(m)-------		(g)	(kg ha[1])
XB6012	14.1 b	47 a	2.2 b	15.0 b	29.9 b	1.21 a	1.82 b	37.3 a	9,285 a
2B655HX	14.5 b	4.7 a	1.8 c	18.0 a	27.8 c	1.00 c	1.87 b	32.2 b	7,243 c
30A37HX	14.4 b	4.7 a	1.9 c	15.0 b	29.8 b	0.96 c	1.86 b	30.7 b	6,050 d
2B5124	12.7 c	4.4 b	1.9 c	14.9 b	24.4 c	1.02 c	2.05 b	39.2 a	7,880 b
2B433HX	14.8 b	4.9 a	1.9 c	18.0 a	28.0 c	1.01 c	1.88 b	27.5 c	6,236 d
20A78HX	13.1 c	4.5 b	2.0 c	15.5 b	29.5 b	1.00 c	2.43 a	37.5 a	9,434 a
30A95HX	14.2 b	4.7 a	1.9 c	16.5 a	28.0 c	0.97 c	1.86 b	27.7 c	5,763 d
AG 9010	12.7 c	4.6 b	2.1 b	13.7 b	28.4 c	0.94 c	1.92b	42.1 a	8,997 a
Maximus	15.9 a	4.9 a	2.0 c	17.0 a	30.0 b	0.94 c	2.04 b	34.5 b	7,909 b
P30F53	15.6 a	4.5 b	1.9 c	16.4 a	29.0 b	1.01 c	1.78 b	37.9 a	9,951 a
Fórmula TL	15.6 a	4.9 a	2.1 b	16.5 a	32.0 a	0.91 c	2.08 b	31.7 b	7,408 c
P3340	15.3 a	4.4 b	2.1 b	13.2 b	32.2 a	1.09 b	2.54 a	39.3 a	9,151 a
2B604HX	14.2 b	4.7 a	1.8 c	17.5 a	27.5 c	1.05 c	1.84 b	26.2 c	5,662 d
XB6010	16.0 a	4.7 a	2.0 c	14.1 b	33.9 a	1.02 c	2.31 a	40.3 a	10,506 a
Status TL	15.1 a	4.9 a	2.0 c	17.5 a	29.8 b	1.08 b	2.01 b	31.9 b	7,530 c
30A30HX	12.8 c	4.6 a	2.5 a	14.2 b	27.9 c	1.22 a	1.92 b	38.3a	8,358 b
2B587HX	14.5 b	4.8 a	1.9 c	17.5 a	26.3 c	0.94 c	1.85 b	26.8 c	5,556 d
XB7253	14.3 b	4.3 b	2.3 b	14.1 b	29.0 b	1.17 a	2.50 a	39.7 a	8,898 a
30A91HX	14.6 b	4.8 a	1.8 c	17.5 a	26.8 c	1.10 b	1.82 b	30.3 b	6,395 d
20A55HX	14.2 b	4.8 a	2.0 c	17.0 a	27.5 c	0.94 c	1.97 b	26.2 c	5,512 d
Mean	14.3	4.7	2.0	15.9	28.7	103.5	2.04	34.1	7,714

Means followed by the same letter in the column do not differ by Scott-Knott's test at 5% probability. EL: ear length; ED: ear diameter; SD: stem diameter; NRE: number of rows per ear; NKR: number of kernels per row; EH: first ear height; PH: plant height; HGW: hundred grains weight; YIE: grain yield.

The other traits showed weak association when associated to the group of hybrids with higher YIE, indicating its absence or little influence on YIE of addition. Paixão et al. (2008), when analyzed the genetic diversity in maize populations under different environments reported that an important trait correlated with the increase in YIE is the SD. A plant storage organ, it acts as soluble solids storage structure that will be translocate to other plant organs if necessary, contributing to the grains formation, a fact that was not observed in this study. It is important to emphasize that the YIE obtained (7.7 t ha^{-1}) was higher than the national average yield for the same period, which was 2.6 t ha^{-1} (CONAB, 2013), highlighting the high yield potential and adaptability of evaluated hybrids in the region.

CONCLUSIONS

The hybrids XB9010, P30F53, 20A78HX, XB6012, P3340, AG9010 and XB7253, obtained the highest grain yield and mass of one hundred grains.

The population has a genetic variability and potential for selection of all traits.

Based on the evaluated genetic parameters, mass of one hundred grains can be used at the direct selection of genotypes with high grain yield.

RESUMO: O estudo do controle genético de caracteres agronômicos através de estimativas de parâmetros genéticos de uma população permite inferências sobre sua variabilidade genética e o ganho esperado com a seleção. Conhecer as correlações entre caracteres de interesse para a seleção permite ao melhorista saber o grau de associação entre os caracteres de importância econômica, uma vez que a seleção de determinado caráter altera o comportamento do outro. Com o objetivo de estimar os parâmetros genéticos e identificar quais caracteres agronômicos estão correlacionados com a produtividade de grãos de híbridos de milho, um experimento foi conduzido na Universidade Estadual de Mato Grosso do Sul - Unidade Universitária de Aquidauana (UEMS/UUA). O delineamento experimental utilizado foi o de blocos ao acaso com quatro repetições Os tratamentos consistiram de 20 híbridos de milho. Os caracteres avaliados foram: altura de

plantas, altura de inserção da primeira espiga, diâmetro do colmo, diâmetro da espiga, comprimento da espiga, número de fileiras por espiga, número de grãos por fileira, massa de cem grãos e produtividade de grãos. Os híbridos XB9010, P30F53, 20A78HX, XB6012, P3340, AG9010 e XB7253 obtiveram as maiores massa de cem grãos e produtividade. A população possui variabilidade genética e potencial para seleção de todos os caracteres. Com base nos parâmetros genéticos avaliados, a massa de cem grãos pode ser usada na seleção direta de genótipos com alta produtividade de grãos.

PALAVRAS-CHAVE: Caracteres morfoagronômicos. Componentes produtivos. *Zea mays* L.

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