



PHENOTYPIC, GENETIC, AND ENVIRONMENTAL CORRELATIONS IN S₁ PROGENIES OF LANDRACE MAIZE

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Abstract: Maize (*Zea mays* L.) belongs to the Poaceae family and stands out among the most cultivated cereals worldwide because of its great economic and social importance. This study aims to estimate and identify phenotypic, genetic, and environmental associations in S₁ maize progenies from the southern Rio Grande do Sul landrace populations. The experimental design was the augmented blocks, with ten S₁ progenies groups, and two commercial controls, the simple cross hybrids Pioneer 30F53 and Agroeste 1590, allocated in four repetitions. The S₁ progenies were obtained after self-fertilization of random plants in the maize landrace populations, being them: Amarelão, Argentino Branco, Argentino Amarelo, Branco Vermelho Índio, Branco Oito Carreiras, Caiano Rajado, Cateto Branco, Criolão and Dente de Ouro, and the open pollinated variety BRS Planalto. The S₁ progenies present specific genetic and phenotypic correlations in both senses and magnitudes, becoming difficult to define strategies for indirect selection based on correlation between traits. Spike length presents strong and positive genetic and phenotypic correlation with spike mass and may be used for indirect selection of S₁ progenies with greater spike mass, regardless of the origin of the progeny. Positive phenotypic and genotypic correlations of intermediate magnitudes were verified between spike diameter and grain depth, which are similar for all progenies. Plant height reveals strong and positive phenotypic and genetic associations with spike insertion height, however, this trait did not steadily correlate with grain yield. The environmental correlations present significant effects of the phenotypes expression of S₁ progenies produced in the southern Rio Grande do Sul.

Keywords: *Zea mays* L., phenotypic, genetic and environmental correlation, landrace population, plant breeding, food security, sustainable development

Introduction

Maize (*Zea mays* L.) belongs to the Poaceae family and stands out among the most cultivated cereals worldwide because of its great economic and social

importance. Brazil is the third largest producer, behind the United States and China, with a production of approximately 84.0 million tons in the 2015/2016 agricultural year (USDA, 2016). In the southern region, Paraná state is the main producer,



followed by Rio Grande do Sul. In the last harvest, an area of 823 thousand hectares was grown in Rio Grande do Sul, with a total production of 5.8 million tons and average yield of 7.16 tons per hectare (Conab, 2016).

Genetic breeding seeks to yield increments of cultivated species in order to increase the availability of food sources to the world's growing population (Allard, 1971). The success of a breeding program is conditioned by the existence of genetic variability, which allows the breeder to perform selection and achieve superior genetic constitutions (Cruz, 2012). In this context, landrace maize populations are important for crop genetic breeding, since they are potential sources of genetic variability. These populations are mostly cultivated in communities, indigenous folks, and by family farmers, where they satisfactorily perform under local environmental conditions (Teixeira et al., 2005), and stand out because they contemplate unexplored genetic properties, and are possible sources of favorable alleles for disease resistance, hydric stress and grain yield (Paterniani et al., 2000; Araújo and Nass, 2002).

The study of associations between traits is of great importance for genetic breeding programs because it provides an indicative of how to act in the indirect selection of individuals. Thus, the associations quantify the possibility of gains with selection of correlated traits, as characters of low heritability and hard measurement may be selected with greater efficiency when the selection is based on higher heritability traits, once they present high correlation magnitudes (Cruz and Regazzi, 1997). According to Paterniani and Campos (2005), the efficiency of a trait selection is increased when the correlation between traits is considered.

The two traits association verified by direct measurement is called phenotypic correlation (Falconer, 1981) and it measures the genetic and non-genetic degree of association between two or more traits (Hallauer et al., 2010). For the purposes of more precise inferences about correlation between traits, it is necessary to distinguish genetic and environmental causes, since the phenotypic correlation has little practical value and may induce

selection mistakes (Falconer and Mackay, 1996). Genetic correlation is mainly caused by pleiotropy and linkage. Pleiotropism is the ability of a gene to simultaneously control two or more traits, and linkage is a transitory cause, as genes located on the same chromosome are transferred together, depending on the distance between them. Environmental correlation refers to two traits influenced by the same environmental conditions (Falconer, 1981; González et al., 1994; Churata and Ayala-Osuma, 1996).

Studies of phenotypic, genetic, and environmental correlation estimates involving maize morphological and grain yield traits are abundant in the literature, including the works of Churata and Ayala-Osuma (1996), Carvalho et al. (2001), Carpentieri-Pípolo et al. (2002), Barros et al. (2010), Cargnellutti et al. (2010), Mahesh et al. (2013) and Nardino et al. (2016). However, studies on genetic, phenotypic, and environmental correlation estimates in early maize lineages (S_1) are still scarce. Therefore, the study of correlations between traits in early lineages is relevant, since they allow the breeder to obtain faster progress than only by direct selection of the desired trait.

This study aims to estimate and identify phenotypic, genetic, and environmental associations in S_1 maize progenies from the southern Rio Grande do Sul landrace populations.

Material and methods

The experiment was conducted in the experimental area of the Genomic and Plant Breeding Center of the Federal University of Pelotas, located at the Palma Agricultural Center, in the city of Capão do Leão – RS, Brazil, under geographic coordinates: 31° 45'S latitude, 52° 29'W longitude, average altitude of 13 meters. The soil is classified as Dystrophic Yellow Red Argisol, of clay texture and wavy relief (Santos et al., 2006). According to Köppen, the climate is classified as subtropical Cfa, with rainfall annual average of 1,280 mm (Alvares et al., 2013).

The experimental design utilized was the augmented blocks, with ten S_1 progenies groups, and two commercial controls, the

simple cross hybrids Pioneer 30F53 and Agroeste 1590, allocated in four repetitions. The S_1 progenies were obtained after self-fertilization of random plants in the maize landrace populations, being them: Amarelão, Argentino Branco, Argentino Amarelo, Branco Vermelho Indio, Branco Oito Carreiras, Caiano Rajado, Cateto Branco, Criolão and Dente de Ouro, and the open pollinated variety (OPV) BRS Planalto. 40 plants were evaluated in each S_1 progeny.

The sowing occurred on 05/12/2014, using spacing of 0.70 meters between rows and population density adjusted for 60,000 plants per hectare through manual thinning. The base fertilization occurred at the groove opening, using the tractor-sowing set in no-tillage system, incorporating 300 kg of the N-P-K formulation (05-20-20). Subsequent management and cultural practices were carried out in accordance with the crop technical recommendations (RTAM, 2013).

The evaluated traits were: spike insertion height (SH), measured in centimeters (cm); Plant height (PH), measured in centimeters; Stem diameter (SD), measured in millimeters (mm); tassel main stem length (TSL), measured in centimeters; Number of ramifications of the tassel (NRT), in units (un.); Number of days for flowering (NDF), in units; spike length (SL), measured in centimeters; Spike diameter (SKD), measured in millimeters; Spike mass (SM), measured in grams (g); and grain depth (GD), measured in millimeters.

The data obtained for each trait in all populations were subjected to joint and individual variance analysis, including the Z variable, which consists of the sum of two X and Y characters, necessary to estimate the average product between the X and Y character, both for progenies and experimental error. The variance and covariance estimates of the mathematical expectations components were obtained through the mean squares and mean products of the variance and covariance analysis.

The covariance components for each pair of characters (X and Y) were obtained by the mean products of the progeny (Pro) and res-

idue (R) variation source, through $MP_{xy} = [(MS_{xy} - MS_x - MS_y)/2]$, which equals to $Cov_{xy} = [(\sigma_{x+y} - \sigma_x - \sigma_y)/2]$ and the estimators $\sigma_{xy}^2 = [(MPPro - MPR)/r]$,

$\sigma_x^2 = [(MSPro_{(x)} - MSR_{(x)})/r]$ and $\sigma_y^2 = [(MSPro_{(y)} - MSR_{(y)})/r]$ obtained through the progeny (Pro) and residue (R) Mean Square for the X and Y characters.

The phenotypic (r_p), genotypic (r_g), and environmental (r_e) correlation estimates were achieved through the method proposed by Cruz and Regazzi (1997).

$$(Eq. 1) \quad r_{p(XY)} = \frac{Cov_{p(xy)}}{\sqrt{\sigma_{p(X)}^2 \times \sigma_{p(Y)}^2}}$$

$$(Eq. 2) \quad r_{g(XY)} = \frac{Cov_{g(xy)}}{\sqrt{\sigma_{g(X)}^2 \times \sigma_{g(Y)}^2}}$$

$$(Eq. 3) \quad r_{e(XY)} = \frac{Cov_{e(xy)}}{\sqrt{\sigma_{e(X)}^2 \times \sigma_{e(Y)}^2}}$$

Where: $Cov_{p(XY)}$, $Cov_{g(XY)}$, and $Cov_{e(XY)}$ respectively correspond to phenotypic, genotypic and environmental covariances between X and Y characters; $\sigma_{p(X)}^2$, $\sigma_{g(X)}^2$, and $\sigma_{e(X)}^2$ correspond to phenotypic, genotypic and environmental variances of the X character, and $\sigma_{p(Y)}^2$, $\sigma_{g(Y)}^2$, and $\sigma_{e(Y)}^2$ correspond to phenotypic, genotypic and environmental variances of the Y character.

The significance of the phenotypic, genotypic and environmental correlation coefficients was tested by the t-test at 0.05 and 0.01 of significance, obtained from the formula

$$t = \frac{r}{\sqrt{1-r^2}} \sqrt{n-2} \quad (\text{Steel and Torrie, 1980}).$$

The correlation coefficients were classified according to their magnitude, following the model proposed by Carvalho et al. (2004), where $r = 0.00 =$ null; from $r = 0.00$ to $r = 0.30 =$ weak; $r = 0.30$ to $r = 0.60 =$ intermediate; $r = 0.60$ to $r = 0.90 =$ strong; $r = 0.90$ to $r = 1 =$ very strong; and $r = 1 =$ perfect.

Results and discussion

The phenotypic, genetic, and environmental correlation analysis performed for morphological and grain yield traits in S_1 progenies from landrace maize populations revealed a total of 45 pairs of phenotypic, genetic, and environmental correlations, of which, 29 phenotypic correlations, 39 genetic correlations, and 41 environmental correlations presented significant effects by the t-test (Table 1).

Genetic correlations, in their majority, had higher magnitudes than phenotypic correlations and smaller than environmental correla-

tions. The superiority of environmental correlations is related to edaphoclimatic conditions, and part is due to non-additive genetic deviations, considering that, in the S_1 generation, there is a large proportion of heterozygotic loci, prevailing the dominance and epistatic effects, inflating the environmental correlations (Falconer, 1981). However, genetic correlations are more relevant than phenotypic and environmental correlations, especially when the traits involved present complex inheritance, controlled by several genes, and with high environmental effect (Vencovsky and Barriga, 1992).

Table 1. Phenotypic (r_p), genetic (r_g), and environmental (r_e) correlations among ten morphological and grain yield traits, resulting from the joint analysis of ten S_1 progenies from ten landrace maize populations.

		SH ⁽¹⁾	PH	SD	TSL	NRT	NDF	SKD	SL	SM	GD
SH	r_p	-									
	r_g	-									
	r_e	-									
PH	r_p	0.716**	-								
	r_g	0.702**	-								
	r_e	0.842**	-								
SD	r_p	0.144**	0.220**	-							
	r_g	-0.364**	-0.409**	-							
	r_e	0.871**	0.817**	-							
TSL	r_p	0.120**	0.403**	0.023	-						
	r_g	0.322**	0.832**	1.465**	-						
	r_e	-0.423**	-0.387**	-0.562**	-						
NRT	r_p	0.042	0.062	0.066	0.199**	-					
	r_g	0.082	-0.012	0.850**	0.090*	-					
	r_e	-0.115*	0.266**	-0.360**	0.369**	-					
NDF	r_p	-0.183**	-0.205**	-0.269**	0.123**	0.049	-				
	r_g	-0.294**	-0.412**	-0.892**	-0.413**	-0.230**	-				
	r_e	0.138**	0.247**	-0.029	0.785**	0.528**	-				
SKD	r_p	0.083*	0.223**	0.103*	0.061	-0.037	-0.172**	-			
	r_g	0.215**	0.337**	1.389**	0.353**	-0.431**	-0.034	-			
	r_e	-0.304**	0.004	-0.445**	-0.276**	0.597**	-0.354**	-			
SL	r_p	0.102*	0.136**	-0.036	0.120**	-0.021	0.060	0.117**	-		
	r_g	0.162**	0.158**	0.604**	-0.127**	-0.380**	-0.198**	-0.045	-		
	r_e	-0.207**	0.057	-0.533**	0.616**	0.957**	0.644**	0.469**	-		
SM	r_p	0.075	0.159**	-0.001	0.116**	0.011	0.018	0.359**	0.764**	-	
	r_g	-0.294**	-0.503**	-2.758**	0.491**	-0.523**	-0.700**	1.024**	1.428**	-	
	r_e	0.749**	0.962**	0.642**	-0.104*	0.468**	0.524**	-0.049	0.304**	-	
GD	r_p	0.117**	0.205**	0.083*	0.095*	-0.004	-0.079	0.553**	0.151**	0.426**	-
	r_g	0.091*	0.171**	0.000	0.148**	-0.036	-0.160**	0.767**	0.157**	0.639**	-
	r_e	0.730**	0.899**	0.685**	-0.110*	0.346**	0.500**	-0.149**	0.219**	0.920**	-

** significant at 1% of probability by the t-test. * Significant at 5% of probability by the t-test. For all traits, the value of the number of observations (n) was 400. ⁽¹⁾ SH: spike insertion height; PH: plant height; SD: Stem diameter; TSL: Tassel main stem length; NRT: number of ramifications of the tassel; NDF: number of days for flowering; SKD: Spike diameter; SL: Spike length; SM: spike mass; and GD: grain depth.

The trait spike insertion height revealed strong and positive phenotypic and genetic correlation with plant height for most S₁ progenies, except for the genetic correlation of the population Argentino Branco. In general, as plant height increases, the height of spike insertion increases as well, corroborating with results found by Andrade and Miranda Filho (2008) and Barros et al. (2010), which showed strong and positive phenotypic and genetic correlations between these traits.

The absence of genetic correlation in the Argentino Branco progeny allows to explore lineages with lower plant height, without overly reducing spike insertion height. This trait is desired by breeders, since the tendency is to develop short stature hybrids, with spike insertion height between 90 and 110 centimeters (Paterniani and Campos, 2005).

The pairs of correlation between spike length and spike mass, and spike diameter and grain

depth revealed strong and positive genetic and phenotypic correlations for all S₁ progenies (Table 1, Table 2, Table 3, Table 4, Table 5, and Table 6).

Liao et al. (2014) indicated that, among the most important studied traits, spike mass stands out for positively contributing to grain yield. The identification of traits that present stable correlations with spike mass is of great importance for breeding and achieving superior lines, since the production of a single-cross hybrid depends on the lineages performance, in other words, the ability of the lineage to contribute with alleles for hybrid formation (Vencovsky, 1987). The consistency of these pairs of correlations allows to infer that these traits are genetically associated, allowing indirect selection to obtain the greater mass of spike, when selecting longer spikes, and increasing grain depth by selecting spikes of larger diameter. For He et al. (2014), spike

Table 2. Phenotypic (r_p) and genetic (r_g) correlations among ten morphological and grain yield traits in S₁ progenies from the landrace maize populations Argentino Amarelo (higher diagonal) and Amarelão (bottom diagonal).

		Argentino Amarelo									
		SH ⁽¹⁾	PH	SD	TSL	NRT	NDF	SKD	SL	SM	GD
SH	r_p	-	0.692**	0.122	0.161	0.026	-0.070	0.263	0.218	0.199	0.301*
	r_g	-	0.686**	0.038	0.223	0.032	-0.091	0.372**	0.255	0.149	0.295*
PH	r_p	0.499**	-	0.236	0.468**	0.102	0.066	0.451**	0.092	0.129	0.309*
	r_g	0.471**	-	0.165	0.583**	0.094	0.048	0.573**	0.097	-0.004	0.299*
SD	r_p	0.443**	0.355*	-	0.088	-0.344*	-0.278*	0.054	0.075	0.102	0.120
	r_g	0.405**	0.261	-	0.326*	-0.376**	-0.368**	0.317*	0.259	-0.206	0.103
TSL	r_p	-0.101	0.113	-0.131	-	0.420**	0.366*	0.260	-0.149	-0.051	-0.127
	r_g	-0.061	0.239	-0.010	-	0.440**	0.267*	0.463**	-0.309*	-0.031	-0.138
NRT	r_p	0.330*	0.020	0.504**	-0.092	-	0.446**	-0.122	-0.189	-0.056	-0.151
	r_g	0.379**	-0.024	0.677**	-0.204	-	0.449**	-0.253	-0.297*	-0.156	-0.163
NDF	r_p	-0.283*	-0.211	-0.376**	0.372**	-0.427**	-	-0.093	-0.273*	-0.255	-0.058
	r_g	-0.318*	-0.278*	-0.436**	0.300*	-0.562**	-	-0.006	-0.449**	-0.552**	-0.085
SKD	r_p	-0.081	0.228	0.085	0.107	-0.011	-0.210	-	0.235	0.516**	0.639**
	r_g	-0.050	0.307*	0.274*	0.273*	-0.197	-0.186	-	0.173	0.846**	0.805**
SL	r_p	0.135	0.063	-0.076	0.086	0.019	0.008	0.109	-	0.858**	0.353*
	r_g	0.162	0.065	-0.003	-0.014	-0.110	-0.064	0.028	-	1.086**	0.375*
SM	r_p	-0.025	0.134	-0.048	0.027	-0.156	-0.096	0.458**	0.772**	-	0.550**
	r_g	-0.178	-0.147	-0.318*	0.090	-0.375**	-0.275*	0.764**	0.966**	-	0.638**
GD	r_p	-0.234	-0.016	0.161	-0.048	0.194	-0.258	0.493**	0.105	0.344*	-
	r_g	-0.257	-0.053	0.149	-0.050	0.198	-0.289*	0.626**	0.105	0.376**	-

Amarelão

** significant at 1% of probability by the t-test. * Significant at 5% of probability by the t-test. For all traits, the value of the number of observations (n) was 40. ⁽¹⁾ SH: spike insertion height; PH: plant height; SD: Stem diameter; TSL: Tassel main stem length; NRT: number of ramifications of the tassel; NDF: number of days for flowering; SKD: Spike diameter; SL: Spike length; SM: spike mass; and GD: grain depth.

Table 3: Phenotypic (r_p) and genetic (r_g) correlations among ten morphological and grain yield traits in S_1 progenies from the landrace maize populations Branco Oito Carreiras (higher diagonal) and Argentino Branco (bottom diagonal).

		Branco Oito Carreiras									
		SH ⁽¹⁾	PH	SD	TSL	NRT	NDF	SKD	SL	SM	GD
SH	r_p	-	0.884**	0.165	0.218	-0.352*	-0.505**	0.187	0.264*	0.282*	0.231
	r_g	-	0.887**	0.074	0.318*	-0.381**	-0.554**	0.248	0.311*	0.245	0.219
PH	r_p	0.277*	-	0.180	0.334*	-0.335*	-0.579**	0.099	0.414**	0.386**	0.230
	r_g	0.176	-	0.084	0.465**	-0.406**	-0.649**	0.114	0.456**	0.320*	0.212
SD	r_p	-0.300*	-0.080	-	0.022	0.008	-0.330*	-0.298*	0.029	0.290*	0.113
	r_g	-0.664**	-0.452**	-	0.251	0.111	-0.408**	-0.254	0.178	0.058	0.084
TSL	r_p	0.269*	0.391**	0.047	-	-0.027	0.009	-0.050	0.277*	0.106	-0.024
	r_g	0.440**	0.652**	0.367**	-	-0.131	-0.142	0.018	0.198	0.254	-0.020
NRT	r_p	0.091	0.102	0.239	0.040	-	0.416**	-0.365*	-0.496**	-0.198	-0.340*
	r_g	0.129	0.061	0.487**	-0.065	-	0.403**	-0.573**	-0.749**	-0.540**	-0.389**
NDF	r_p	0.455**	-0.410**	-0.157	0.172	-0.286*	-	-0.150	-0.376**	-0.516**	-0.422**
	r_g	0.546**	-0.632**	-0.227	-0.089	-0.554**	-	-0.119	-0.512**	-0.992**	-0.465**
SKD	r_p	-0.215	-0.077	-0.034	-0.227	0.136	-0.310*	-	-0.025	-0.171	0.376**
	r_g	-0.200	-0.100	0.154	-0.210	0.007	-0.295*	-	-0.126	-0.257	0.433**
SL	r_p	0.296*	-0.248	-0.079	-0.113	-0.283*	0.143	0.162	-	0.575**	0.076
	r_g	0.376**	-0.316*	0.078	-0.321*	-0.552**	0.003	0.087	-	0.787**	0.072
SM	r_p	0.041	-0.247	0.124	-0.2873*	-0.223	-0.138	0.262	0.740**	-	0.258
	r_g	-0.395**	-1.455**	-0.608**	-0.584**	-0.931**	-0.959**	0.671**	1.425**	-	0.267*
GD	r_p	-0.101	0.037	0.125	-0.201	0.247	-0.428**	0.623**	-0.075	0.123	-
	r_g	-0.141	-0.015	0.093	-0.233	0.257	-0.556**	0.732**	-0.094	0.050	-

Argentino Branco

** significant at 1% of probability by the t-test. * Significant at 5% of probability by the t-test. For all traits, the value of the number of observations (n) was 40. ⁽¹⁾ SH: spike insertion height; PH: plant height; SD: Stem diameter; TSL: Tassel main stem length; NRP: number of ramifications of the tassel; NDF: number of days for flowering; SKD: Spike diameter; SL: Spike length; SM: spike mass; and GD: grain depth.

Table 4: Phenotypic (r_p) and genetic (r_g) correlations among ten morphological and grain yield traits in S_1 progenies from the landrace maize populations Caiano Rajado (higher diagonal) and Branco Roxo Índio (bottom diagonal).

		Caiano Rajado									
		SH ⁽¹⁾	PH	SD	TSL	NRT	NDF	SKD	SL	SM	GD
SH	r_p	-	0.746**	0.271*	0.010	0.163	-0.268*	0.393**	-0.517**	-0.209	0.207
	r_g	-	0.744**	0.213	0.060	0.180	-0.299*	0.456**	-0.536**	-0.361*	0.202
PH	r_p	0.608**	-	0.405**	0.319*	0.253	-0.205	0.382**	-0.485**	-0.123	0.274*
	r_g	0.598**	-	0.338*	0.447**	0.252	-0.254	0.431**	-0.532**	-0.360*	0.269*
SD	r_p	0.326*	0.229	-	0.128	0.163	0.010	0.341*	-0.222	-0.096	0.082
	r_g	0.281*	0.071	-	0.381**	0.274*	0.020	0.560**	-0.180	-0.430**	0.066
TSL	r_p	-0.476**	0.066	-0.441**	-	0.116	-0.110	0.024	-0.193	-0.057	0.152
	r_g	-0.485**	0.129	-0.434**	-	0.080	-0.278*	0.088	-0.317*	-0.040	0.177
NRT	r_p	0.377**	0.165	0.040	0.033	-	0.023	-0.147	-0.053	0.021	0.178
	r_g	0.426**	0.149	0.161	-0.015	-	-0.026	-0.231	-0.131	-0.063	0.179
NDF	r_p	-0.352*	-0.016	-0.409**	0.715**	0.097	-	-0.011	0.499**	0.332*	0.087
	r_g	-0.416**	-0.068	-0.555**	0.709**	0.009	-	0.035	0.486**	0.302*	0.080
SKD	r_p	0.380**	0.468**	0.114	-0.106	0.213	0.025	-	-0.025	0.465**	0.610**
	r_g	0.448**	0.545**	0.289*	-0.081	0.146	0.105	-	-0.078	0.614**	0.661**
SL	r_p	-0.623**	-0.222	-0.312*	0.517**	0.090	0.301*	-0.027	-	0.714**	-0.039
	r_g	-0.647**	-0.253	-0.295*	0.509**	-0.005	0.262	-0.083	-	0.835**	-0.045
SM	r_p	-0.325*	-0.094	-0.300*	0.267*	0.123	0.162	0.303*	0.652**	-	0.451**
	r_g	-0.430**	-0.275*	-0.612**	0.325*	0.060	0.083	0.368**	0.701**	-	0.501**
GD	r_p	0.367**	0.314*	0.144	-0.153	0.160	-0.264*	0.287*	0.016	0.326*	-
	r_g	0.366*	0.316*	0.147	-0.160	0.164	-0.311*	0.315*	0.013	0.331*	-

Branco Roxo Índio

** significant at 1% of probability by the t-test. * Significant at 5% of probability by the t-test. For all traits, the value of the number of observations (n) was 40. ⁽¹⁾ SH: spike insertion height; PH: plant height; SD: Stem diameter; TSL: Tassel main stem length; NRP: number of ramifications of the tassel; NDF: number of days for flowering; SKD: Spike diameter; SL: Spike length; SM: spike mass; and GD: grain depth.

Table 5: Phenotypic (r_p) and genetic (r_g) correlations among ten morphological and grain yield traits in S_1 progenies from the landrace maize populations Criolão (higher diagonal) and Cateto Branco (bottom diagonal).

		Criolão									
		SH ⁽¹⁾	PH	SD	TSL	NRT	NDF	SKD	SL	SM	GD
SH	r_p	-	0.567**	0.144	-0.131	0.165	0.038	0.087	0.333*	0.132	-0.001
	r_g	-	0.542**	0.040	-0.096	0.188	0.026	0.147	0.371**	0.008	-0.014
PH	r_p	0.695**	-	0.088	0.449**	0.131	0.063	0.422**	0.216	0.331*	0.438**
	r_g	0.699**	-	-0.073	0.613**	0.115	0.026	0.517**	0.235	0.140	0.448**
SD	r_p	-0.106	0.135	-	-0.185	-0.162	-0.276*	0.185	-0.063	0.015	0.202
	r_g	-0.324*	-0.134	-	-0.081	-0.131	-0.347*	0.381**	0.005	-0.294*	0.206
TSL	r_p	0.319*	0.466**	0.324*	-	0.307*	-0.259	0.195	0.024	0.239	0.459**
	r_g	0.449**	0.719**	0.987**	-	0.302*	-0.520**	0.323*	-0.052	0.399**	0.516**
NRT	r_p	-0.304*	-0.158	0.379**	0.248	-	0.032	0.080	0.323*	0.343*	0.047
	r_g	-0.330*	-0.235	0.777**	0.215	-	-0.045	-0.006	0.271*	0.350*	0.042
NDF	r_p	0.127	0.129	0.026	-0.217	0.079	-	-0.230	0.349*	0.307*	-0.440**
	r_g	0.272*	0.122	0.173	-1.983**	-0.345*	-	-0.196	0.318*	0.224	-0.513**
SKD	r_p	-0.123	0.103	0.115	0.055	0.052	-0.149	-	0.001	0.145	0.557**
	r_g	-0.118	0.144	0.626**	0.254	-0.157	0.220	-	-0.067	0.244	0.643**
SL	r_p	-0.083	0.038	-0.211	-0.354*	-0.140	0.496**	-0.279*	-	0.578**	-0.106
	r_g	-0.076	0.035	-0.107	-0.633**	-0.337*	0.770**	-0.558**	-	0.724**	-0.114
SM	r_p	-0.249	0.017	-0.100	-0.319*	0.079	0.379**	0.146	0.729**	-	0.046
	r_g	-0.511**	-0.378**	-0.925**	-0.489**	-0.098	0.110	0.325*	1.012**	-	0.007
GD	r_p	0.185	0.105	-0.299*	-0.023	-0.281*	0.166	0.540**	0.007	0.055	-
	r_g	0.176	0.078	-0.511**	-0.021	-0.326*	0.312*	0.730**	-0.001	-0.017	-

Cateto Branco

** significant at 1% of probability by the t-test. * Significant at 5% of probability by the t-test. For all traits, the value of the number of observations (n) was 40. ⁽¹⁾ SH: spike insertion height; PH: plant height; SD: Stem diameter; TSL: Tassel main stem length; NRP: number of ramifications of the tassel; NDF: number of days for flowering; SKD: Spike diameter; SL: Spike length; SM: spike mass; and GD: grain depth.

Table 6: Phenotypic (r_p) and genetic (r_g) correlations among ten morphological and grain yield traits in S_1 progenies from the open pollinated variety BRS Planalto (higher diagonal) and the landrace maize population Dente de Ouro (bottom diagonal).

		BRS Planalto									
		SH ⁽¹⁾	PH	SD	TSL	NRT	NDF	SKD	SL	SM	GD
SH	r_p	-	0.676**	-0.037	0.082	0.120	-0.360*	-0.185	0.148	0.137	-0.035
	r_g	-	0.671**	-0.163	0.130	0.146	-0.405**	-0.183	0.166	0.069	-0.049
PH	r_p	0.845**	-	0.155	0.327*	-0.026	-0.074	-0.066	-0.052	-0.082	0.119
	r_g	0.845**	-	0.010	0.440**	-0.072	-0.117	-0.082	-0.061	-0.319*	0.099
SD	r_p	0.166	0.204	-	-0.098	0.074	-0.337*	-0.037	0.207	0.125	-0.174
	r_g	0.089	0.139	-	0.046	0.215	-0.430**	0.125	0.346*	-0.110	-0.254
TSL	r_p	0.300*	0.453**	0.207	-	0.074	0.382**	0.017	-0.276*	-0.222	0.430**
	r_g	0.346*	0.508**	0.359*	-	0.010	0.311*	0.095	-0.381**	-0.262	0.480**
NRT	r_p	0.000	0.044	-0.038	0.379**	-	-0.032	-0.055	0.167	0.036	-0.214
	r_g	0.010	0.024	0.055	0.385**	-	-0.136	-0.233	0.080	-0.099	-0.252
NDF	r_p	-0.367**	-0.328*	0.172	0.273*	0.207	-	0.029	-0.200	-0.137	0.361*
	r_g	-0.425**	-0.392**	0.231	0.205	0.139	-	0.118	-0.283*	-0.313*	0.372**
SKD	r_p	-0.005	-0.137	-0.160	-0.243	-0.246	-0.130	-	-0.080	0.267*	0.352*
	r_g	0.030	-0.162	-0.059	-0.245	-0.472**	-0.072	-	-0.161	0.391**	0.417**
SL	r_p	0.611**	0.600**	0.059	0.249	0.084	-0.085	-0.247	-	0.812**	-0.104
	r_g	0.672**	0.642**	0.184	0.211	-0.053	-0.197	-0.391**	-	0.955**	-0.112
SM	r_p	0.633**	0.536**	0.049	0.112	-0.080	-0.188	0.074	0.803**	-	0.193
	r_g	0.724**	0.550**	-0.270*	0.183	-0.308*	-0.482**	0.138	1.036**	-	0.178
GD	r_p	0.068	0.060	0.113	-0.153	0.037	-0.243	0.632**	-0.177	0.147	-
	r_g	0.053	0.040	0.086	-0.157	0.022	-0.294*	0.744**	-0.196	0.105	-

Dente de Ouro

** significant at 1% of probability by the t-test. * Significant at 5% of probability by the t-test. For all traits, the value of the number of observations (n) was 40. ⁽¹⁾ SH: spike insertion height; PH: plant height; SD: Stem diameter; TSL: Tassel main stem length; NRP: number of ramifications of the tassel; NDF: number of days for flowering; SKD: Spike diameter; SL: Spike length; SM: spike mass; and GD: grain depth.

insertion height and spike diameter are fundamental characteristics to be considered during selection of lineages, in order to explore genotypes with higher grain yield.

Spike length is mainly determined by the number of grains per row in the spike. Thus, larger spikes present higher number of grains and consequently bigger spike mass. These results corroborate with the studies of Munawar et al. (2013) and Nardino et al. (2016) which revealed the existence of a positive effect of spike length with spike mass and consequently grain yield.

Spike diameter is constituted by grain depth and cob diameter. In lineages breeding, as in hybrids development, the tendency is to reduce cob diameter and to increase length of grains, thereby, grain depth represents the most important portion in the constitution of spike diameter. Lopes et al. (2007) studying the phenotypic associations in maize spikes related to the types of hybrids observed a correlation of 0.63 between spike diameter and grain length.

Phenotypic and genetic correlations were significant, however, with opposite signs in the associations between spike insertion height and stem diameter ($r_p = 0.14$ and $r_g = -0.36$), plant height and stem diameter ($r_p = 0.22$ and $r_g = -0.40$), tassel main stem length and number of days for flowering ($r_p = 0.12$ and $r_g = -0.41$), spike length and tassel main stem length ($r_p = 0.12$ and $r_g = -0.12$), plant height and spike mass ($r_p = 0.15$ and $r_g = -0.50$) in the joint analysis of the ten progenies (Table1). In these circumstances, where the phenotypic and genetic correlation coefficients do not present the same signal, this inconvenience is attributed to sampling errors (Cruz et al., 2004) or due to great heterogeneity among progenies, since no situation of this kind was observed in individual analyzes by progeny (Table2, Table3, Table4, Table 5, and Table6).

Magnitudes of correlations greater than +1 and smaller than -1 were evidenced in the genetic correlations between stem diameter and tassel length ($r_g = 1.46$), stem diameter and spike diameter ($r_g = 1.38$), stem diameter and spike mass ($r_g = -2.75$) spike diame-

ter and spike mass ($r_g = 1.42$) (Table1), spike length and spike mass ($r_g = 1.08$) (Table2), plant height and spike mass ($r_g = -1.45$), spike length and spike mass ($r_g = 1.42$) (Table3), tassel main stem length and number of days for flowering ($r_g = -1.98$), spike length and spike mass ($r_g = 1.01$) (Table5) and spike length and spike mass ($r_g = 1.03$) (Table6). The occurrence of genetic correlations outside the unit is mainly due to overestimated values and data sampling problems. According to Moro et al. (1992) and Cavassim and Borém (1998), when these estimates are near the interval, they can be considered as true associations between traits, and magnitudes more distant from the unit can be used to guide other correlation studies in breeding programs.

Genetic and environmental correlations between spike insertion height and plant height ($r_g = 0.70$ and $r_e = 0.84$), spike insertion height and grain depth ($r_g = 0.09$ and $r_e = 0.73$), number of ramifications of the tassel and tassel length ($r_g = 0.09$ and $r_e = 0.36$), plant height and grain depth ($r_g = 0.17$, $r_e = 0.88$), spike length and grain depth ($r_g = 0.15$ and $r_e = 0.21$), and spike mass and grain depth ($r_g = 0.63$ and $r_e = 0.92$), showed the same sense (Table1).

The results expected in correlation studies indicate that the genetic correlation and environmental correlation usually have the same sense (González et al., 1994; Churata and Ayala-Osuna, 1996; Marchioro et al., 2003). The other associations between traits revealed opposite sense in relation to significant genetic and environmental correlation. When it occurs, there is an indication that the causes of genetic and environmental variation influence traits through different physiological mechanisms (Falconer, 1981; Cruz, 2012).

In the environmental correlations (Table 1), strong and positive magnitudes were verified for spike insertion height with plant height ($r_e = 0.84$), stem diameter ($r_e = 0.87$), spike mass ($r_e = 0.74$) and grain depth ($r_e = 0.73$); for plant height with stem diameter ($r_e = 0.81$), spike mass ($r_e = 0.96$), grain depth ($r_e = 0.89$); for stem diameter with spike mass ($r_e = 0.642$) and grain depth ($r_e = 0.68$); for tassel main stem length and number of days

for flowering ($r_e = 0.78$) and spike length ($r_e = 0.61$), for number of ramifications of the tassel and spike length ($r_e = 0.95$); for number of days for flowering and spike length ($r_e = 0.64$); between spike mass and grain depth ($r_e = 0.92$). Environmental correlations with intermediate and negative magnitudes were evidenced for the trait spike insertion height with tassel main stem length ($r_e = -0.42$) and spike diameter ($r_e = -0.30$), for the trait plant height and tassel main stem length ($r_e = -0.38$), between number of days for flowering and spike diameter ($r_e = -0.35$). Negative environmental correlations indicate that the environment benefits one trait to the detriment of other, and positive values indicate that the two traits are benefited or harmed by the same causes of environmental variations (Cruz and Regazzi, 1994).

On S_1 progenies of the population Amarelão, the association between the ten morphological traits and grain yield revealed 45 phenotypic and genetic associations, of which 13 phenotypic and 20 genetic correlations were significant (Table 2). For the progeny of the population Argentino Amarelo, 16 phenotypic correlations and 23 genetic correlations with significant effects were evidenced (Table 2). The phenotypic and genetic correlations of the ArgentinoBranco progeny revealed 14 phenotypic correlations and 24 significant genetic correlations (Table 3). In the progenies of the population Branco Oito Carreiras, 19 phenotypic correlations and 26 genetic correlations were evidenced with significant effects (Table 3). The phenotypic and genetic correlations of the progenies Branco Roxo Índio revealed that 23 phenotypic correlations and 26 genetic correlations were significant (Table 4). For the progenies of the population CaianoRajado, 17 phenotypic correlations and 23 genetic correlations with significant effects were evidenced (Table 4). In the progenies of the population Cateto Branco, 26 phenotypic correlations and 26 genetic correlations with significant effects were evidenced (Table 5). The phenotypic and genetic correlations of the progeny of Criolão revealed 14 phenotypic correlations and 21 genetic correlations with significant effects (Table 5). In the progenies of

the population Dente de Ouro, 13 phenotypic correlations and 19 genetic correlations with significant effects were evidenced (Table 6). For the progeny of BRS Planalto open pollinated variety, 11 phenotypic correlations and 15 genetic correlations with significant effects were evidenced (Table 6).

The results shown in Table 2, Table 3, Table 4, Table 5, and Table 6 show that great majority of pairs of correlation did not constantly keep their significant effects for all populations S_1 progenies. Specific correlations were evidenced in certain progenies or group of progenies. These results reveal the need for differential exploitation of the progenies, thus, it is necessary to consider the correlations of each progeny in order to avoid selection mistakes, when it is based on indirect selection through correlated traits. According to Falconer (1981) in populations with low intensity of artificial selection, the genetic characteristics of a trait are initially determined by the relationship between a metric characteristic and adaptive capacity, therefore, the associations between traits may assume specific parameters according to the adaptive need that each population was submitted.

The phenotypic and genetic correlations between spike insertion height and the morphological traits stem diameter, tassel main stem length, and number of ramifications of the tassel presents inconsistent sense and magnitude in the S_1 progenies, therefore, there is a great difficulty for breeders to apply an indirect selection strategy to all progenies. However, it is possible to exploit the population progenies in differential ways, achieving genetic constitutions that express favorable alleles to the formation of elite lineages. Generally, when analyzing progenies, there is a greater tendency for positive phenotypic and genetic associations between spike insertion height and tassel main stem length. These results corroborate with Andrade and Miranda Filho (2008), who showed positive genetic correlations between spike insertion height and tassel length, and opposite to those found by Coimbra et al. (2001), where negative correlations between spike insertion height and number of ramifications of the tassel were verified.

The trait spike insertion height revealed phenotypic and genetic correlations of intermediate and negative magnitudes with number of days for flowering in the progenies of the populations Amarelão ($r_p = -0.28$ and $r_g = -0.31$), Branco Oito Carreiras ($r_p = -0.50$ and $r_g = -0.55$), Branco Roxo Índio ($r_p = -0.35$ and $r_g = -0.41$), Caiano Rajado ($r_p = -0.26$ and $r_g = -0.29$), Dente de Ouro ($r_p = -0.36$ and $r_g = -0.42$) and BRS Planalto ($r_p = -0.36$ and $r_g = -0.40$). For these progenies, the increase in number of days for flowering tends to reduce spike insertion height. However, in the progenies of Argentino Branco and Cateto Branco, the genetic correlation between these traits was positive ($r_g = 0.54$ and $r_p = 0.27$), and the higher number of days for flowering tended to increase spike insertion height, since the plant remains for a longer period carrying out photosynthesis, and tends to produce greater amount of photoassimilates and/or energy for its development. This result is in agreement with Barros et al. (2010) who verified a genetic and phenotypic correlation of 0.32 and 0.59, respectively, between the traits spike insertion height and number of days for flowering.

Regarding spike insertion height, estimates of genetic and phenotypic correlation were significant and positive with spike length in the progenies of Argentino Branco ($r_p = 0.29$ and $r_g = 0.37$), Branco Oito Carreiras ($r_p = 0.26$ and $r_g = 0.31$), Criolão ($r_p = 0.33$ and $r_g = 0.37$) and Dente de Ouro ($r_p = 0.61$ and $r_g = 0.67$), and strong and negative in the progenies of Branco Roxo Índio ($r_p = -0.62$ and $r_g = -0.64$) and Caiano Rajado ($r_p = -0.51$ and $r_g = -0.53$). Studies performed by Coimbra et al. (2001) found negative phenotypic and genetic correlations between spike insertion height and spike length.

The S_1 progenies of the populations Argentino Branco, Branco Roxo Índio, Caiano Rajado, and Cateto Branco revealed genetic correlations of intermediate and negative magnitudes between spike insertion height and spike mass. A strong and positive genetic correlation between these traits was observed only in the progenies of the population Dente de Ouro. However, similar tendencies were observed for the association be-

tween plant height and spike mass. The progenies of Branco Oito Carreiras and Dente de Ouro presented correlations of intermediate and positive magnitudes. Studies carried out by Churata and Ayala-Osuna (1996) and Coimbra et al. (2001) reveal genetic and phenotypic correlations of high magnitude and in the same sense between spike insertion height and spike grains mass.

The trait plant height revealed negative phenotypic and genetic correlations of intermediate to strong magnitude with number of days for flowering in the progenies of Argentino Branco, Branco Oito Carreiras, and Dente de Ouro. The estimates indicate that the loci involved in the control of these traits may be connected or have pleiotropic action (Falconer, 1981).

The trait plant height revealed significant phenotypic and genetic correlations with tassel main stem length, for most progenies, except for the progeny of Amarelão and Branco Roxo Índio. The correlations observed were positive with magnitudes ranging from intermediate to strong. Therefore, plants with larger stature have greater tassel main stem length, in addition, tassel length significantly contributes to plant height increases. These results corroborate with Andrade and Miranda Filho (2008), who verified positive phenotypic and genetic correlations between plant height and tassel length.

The phenotypic and genetic correlations between the trait plant height and the grain yield traits spike diameter and grain depth, revealed positive effects of intermediate to strong magnitude in the progenies of Argentino Amarelo ($r_p = 0.45$, $r_g = 0.57$, $r_p = 0.30$, and $r_g = 0.29$), Branco Roxo Índio ($r_p = 0.46$, $r_g = 0.54$, $r_p = 0.31$, and $r_g = 0.31$), Caiano Rajado ($r_p = 0.38$, $r_g = 0.43$, $r_p = 0.27$, and $r_g = 0.26$) and Criolão ($r_p = 0.42$, $r_g = 0.51$, $r_p = 0.43$ and $r_g = 0.48$). Thus, in the lineages of Caiano Rajado S_1 progeny, plants with higher stature tend to increase spike length and diameter, and provide longer grains. However, estimates of genetic correlation between plant height and spike length revealed intermediate and negative magnitudes for the progenies of Argentino Branco ($r_g = -0.31$) and Caiano Rajado ($r_g = -0.53$), and positive magnitudes

in the progenies of Branco Oito Carreiras ($r_g = 0.45$) and Dente de Ouro ($r_g = 0.64$). Studies conducted by Andrade and Miranda Filho (2008) in ESALQ-PB1, evidenced negative genetic and phenotypic correlations ($r_g = -0.26$ and $r_p = -0.11$) between plant height and spike diameter.

The trait stem diameter presented negative phenotypic and genetic correlations of intermediate magnitudes with number of days for flowering for the progenies of Amarelão, Argentino Amarelo, Branco Oito Carreiras, Branco Roxo Índio, Criolão, and BRS Plantalto. Therefore, plants with larger stem diameter tend to have lower vegetative cycle, since they are more efficient in accumulating reserves in these structures during shorter period of time. The accumulation of reserves in the stem is related to the greater growth of this structure.

The phenotypic and genetic correlations between stem diameter and the traits tassel main stem length, number of ramifications of the tassel and spike diameter showed a tendency of positive associations for the progenies Amarelão, Argentino Branco, Caiano Rajado, and Cateto Branco. In the Argentino Amarelo, and Branco Roxo Índio progenies, the correlations showed opposite effects, evidencing negative correlations between stem diameter and number of ramifications of the tassel, and tassel main stem length, respectively.

Regarding the trait tassel main stem length, positive phenotypic and genetic correlations of intermediate magnitude with number of ramifications of the tassel were evidenced, in the progenies of Argentino Amarelo ($r_p = 0.42$ and $r_g = 0.44$), Criolão ($r_p = 0.30$ and $r_g = 0.30$), and Dente de Ouro ($r_p = 0.39$ and $r_g = 0.38$). Correlations of the same sense and magnitude were observed in the association between tassel main stem length and grain depth, however, only for progenies of Criolão ($r_p = 0.45$ and $r_g = 0.51$) and BRS Plantalto ($r_p = 0.43$ and $r_g = 0.48$). In the S_1 progeny of the population Criolão, plants with higher tassel length are associated with higher number of ramifications of the tassel, spike diameter, spike mass and grain depth, and fewer days for flowering (Table 5).

Similar results were observed in the progeny of BrancoRoxoÍndio, however, the phenotypic and genetic correlation were positive between tassel main stem length and number of days for flowering ($r_p = 0.71$ and $r_g = 0.70$). Phenotypic and genetic correlations among these traits were also positive in the progenies of Amarelão ($r_p = 0.37$ and $r_g = 0.30$), Argentino Amarelo ($r_p = 0.36$ and $r_g = 0.26$) and BRS Planalto ($r_p = 0.38$ and $r_g = 0.31$). On the other hand, in the progeny of Cateto Branco, genetic correlations reveal that tassel main stem length is negatively associated with number of days for flowering, spike length, and spike mass. Therefore, the selection of longer tassel plants in this progeny increases precocity and reduces grain yield traits. Negative correlations between tassel size and yield components are evidenced by Geraldi (1977) and by Nardino et al. (2016) studying single-cross maize hybrids. The progeny of Argentino Branco also revealed negative phenotypic and genetic correlations between tassel main stem length and spike mass (Table 3).

The progenies of the populations Amarelão, Argentino Branco, and Cateto Branco revealed negative genetic correlations of intermediate magnitudes between number of ramifications of the tassel and number of days for flowering. In contrast, the progenies of Argentino Amarelo and Branco Oito Carreiras presented positive phenotypic and genetic correlations between these traits. Positive genetic and phenotypic correlations of intermediate magnitude were observed between number of ramifications of the tassel and the traits spike length ($r_p = 0.32$ and $r_g = 0.27$) and spike mass ($r_p = 0.34$ and $r_g = 0.35$) in the progeny of Criolão. In the other progenies that evidenced significant effects for genetic and phenotypic correlations between number of ramifications of the tassel and the traits spike diameter, spike length, spike mass and grain depth, negative and intermediate to strong magnitudes were verified. Thus, for most S_1 progenies, the high number of ramifications of the tassel is associated with a reduction in grain yield traits, considering that the plant energy reserves are invested in male reproductive structure growth, and are not di-

rected towards female structures in which the primary grain yield components are concentrated (Munaro et al., 2011).

The trait number of days for flowering revealed negative genetic correlations of weak to strong magnitudes with spike mass and grain depth in the progenies of Amarelão ($r_g = -0.27$ and $r_g = -0.28$), Argentino Branco ($r_g = -0.95$ and $r_g = -0.55$), Branco Oito Carreiras ($r_g = -0.99$ and $r_g = -0.46$), and Dente de Ouro ($r_g = -0.48$ and $r_g = -0.29$). Negative genetic correlations were also evidenced between this trait and spike length in the progenies of Argentino Amarelo ($r_g = -0.44$), Branco Oito Carreiras ($r_g = -0.51$) and BRS Planalto ($r_g = -0.28$). Therefore, reduction of vegetative period for these progenies results in the increase of spike mass and grain depth, being sources of alleles of interest regarding early lineages for hybrids formation. However, in the progenies of Caiano Rajado, Cateto Branco, and Criolão, the trait number of days for flowering revealed phenotypic and genetic correlations of positive and intermediate magnitudes with the traits spike length and spike mass.

The genetic correlations between spike diameter and spike mass were positive with intermediate to strong magnitudes in the progenies of the populations Amarelão ($r_g = 0.76$), Argentino Amarelo ($r_g = 0.84$), Argentino Branco ($r_g = 0.67$), Branco Roxo Índio ($r_g = 0.36$), Caiano Rajado ($r_g = 0.61$), Cateto Branco ($r_g = 0.32$), and BRS Planalto ($r_g = 0.39$). Estimates of positive phenotypic correlations between these traits were evidenced in studies conducted by Lopes et al. (2007).

The increase in spike diameter promotes an increment in spike mass in S_1 progenies from landrace maize populations.

The trait grain depth showed positive phenotypic and genetic correlations of intermediate magnitude with spike mass in the progenies of Amarelão ($r_p = 0.34$; $r_g = 0.37$), Argentino Amarelo ($r_p = 0.55$, $r_g = 0.63$), Branco Roxo Índio ($r_p = 0.32$; $r_g = 0.33$), Caiano Rajado ($r_p = 0.45$; $r_g = 0.50$) and genetic correlation only with the progeny of Branco Oito Carreiras ($r_g = -0.23$).

Conclusion

S_1 progenies from different landrace maize populations present specific genetic and phenotypic correlations in both senses and magnitudes, becoming difficult to define strategies for indirect selection based on correlation between traits. The trait spike length presents strong and positive genetic and phenotypic correlation with spike mass and may be used for indirect selection of S_1 progenies with greater spike mass, regardless of the origin of the progeny. Positive phenotypic and genotypic correlations of intermediate magnitudes were verified between spike diameter and grain depth, which are similar for all progenies. The trait plant height reveals strong and positive phenotypic and genetic associations with spike insertion height, however, this trait did not steadily correlate with grain yield characters. The environmental correlations present significant effects on the expression of the phenotype of S_1 progenies produced in the southern Rio Grande do Sul.

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