RESEARCH ARTICLE

GENETIC PARAMETERS IN MAIZE HYBRIDS ANALYSIS IN DIFFERENT ENVIRONMENTS

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ABSTRACT

Penetrance and expressivity are phenomena that interfere the trait-gene relationship and tend to modify the correspondence between genotype and phenotype, difficulting the breeder's task. The aim of this study was to determine the penetrance and expressivity of following traits in cornhybrids (*Zea mays* L.): tassel length, distance from the last node of the stem to the first branch of the tassel, distance from flag leaf to the first branch of the tassel, number of branches on the main stem of the tassel, thousand-kernel weight and grain yield of corn as the magnitude of genetic parameters in different growth sites for single hybrid selection (HS). The crosses were performed in Clevelândia-PR, Brazil, which afforded 25 HS, the seeds were sown in five different environments. The experimental design was a randomized complete block design with three replications. The results reveal that the length of the tassel and the thousand-grain weight are the traits with high genetic variance, indicating variable penetrance and expressivity.

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INTRODUCTION

Estimates of variance components and genetic parameters are extremely important for plant breeding, because they allow inferences about the nature of trait. The variability in traits is caused by genetic differences and environment in which the plants grow (Allard, 1971; Ramalho *et al*., 2012). Estimates of parameters allow express the magnitude of the component parts of the phenotype. The characterization of the biological variation is the basis for the work of geneticists and plant breeders where that to distinguish and understand the hereditary basis of the traits, the distinguish of two components is required: genetic and nongenetic (environmental) and the magnitude of its effects. In this context, the genetic-statistics models had been contributed to elucidate this change, especially for quantitative traits. The efficiency and clarification of the models has brought a significant contribution to the work of plant breeders (Bueno *et al*., 2006). The study of heritability is important for decision-practical taken as to which breeding method, according to the breeding program goal. According to Fehr (1987), the heritability is conceived in broad and narrow sense. The heritability in the

broad sense is provided by the total genetic variance, including additivity, dominance and epistasis in relation to the phenotypic variance. The heritability in the narrow sense is the proportion of additive variance in relation to phenotypic variance. The concepts of heritability are important for the analysis and identification of traits that are floating according to different environments, this because it allows us to foresee the possibility to selection, reflecting the proportion of phenotypic variation that can be inherited. Estimates of heritability of a trait is not immutable, due occur trait change regarding the proportion of genetic variation present and with the effect of the environment (Ramalho *et al*., 2012). In this context, one can increase the heritability estimates using population with highestgenetic variation and controlling the environmental effects through improved experimental conditions in order to reduce the environmental contribution to the total phenotypic variation. Due to the complex nature of the trait-gene relationship, it is expected that environmental factors can modify certain inheritance models, even if these factors are subtle and trivial. Most genes are expressed in fairly uniform and predictable manner, considering normal environmental conditions to which they are exposed. The expression of a gene can be significantly altered by genetic factors and or environment. The expression of a gene refers to expression mode, generally ranging for different environmental conditions. The penetrance refers to the

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expression or non-expression of a gene. Thus, penetrance and expressivity are phenomena that mask the relative trait-gene and tend to modify the correlation between genotype and phenotype, making difficult the breeder's task, especially for traits that have incomplete penetrance and variable expressivity (Allard, 1971). In this context, we aimed to assess the penetrance and expressivity of corn traits to the magnitude of genetic parameters in identifying growth sites for the selection of superior hybrids.

MATERIALS AND METHODS

The crossing of homozygous lines was conducted in the municipality of Clevelândia - PR in the 2010/2011 growing season. The inbred lines came from the breeding program of KSP Seeds Ltd. company, based in PatoBranco, PR, Brazil. The crossings for formation of hybrids was carried out in a partial diallel, using 15 (female lines) and eight (male lines), the lines were in the ninth self-pollination generation (S_9). After completion of directed crossings, we obtained the F_1's seeds that were sown in the 2011/2012 growing season. Sowing of hybrids derived from crosses was carried out in five environments of the three southern states of Brazil: Ampére, PatoBranco, and Clevelândia in Paraná state, Itapiranga in the Santa Catarina state and Frederico Westphalen in the Rio Grande do Sul state (Figure 1).
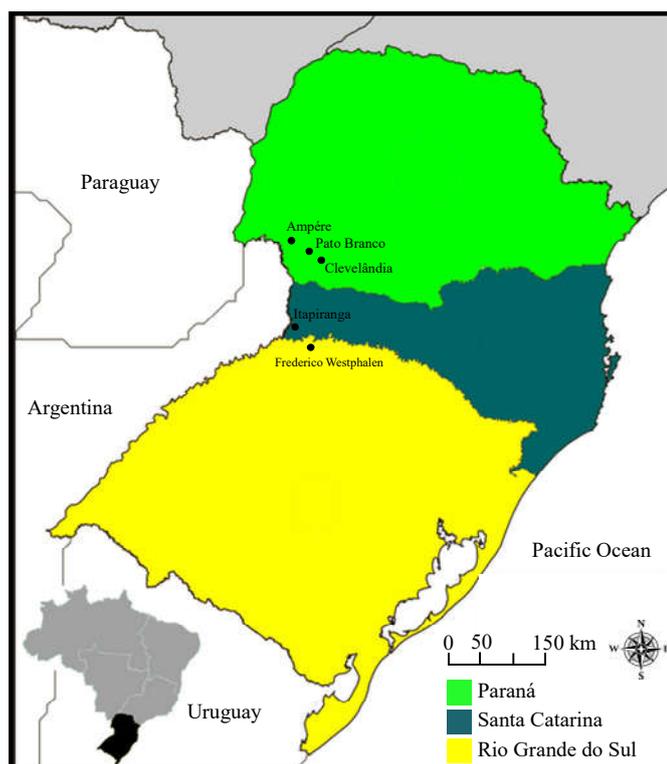

Figure 1. Geographical location of environments where the trial were conducted. You can observe the southern region of Brazil, highlighted in black on the bottom map and the three states where the trials were conducted highlighted in colors on the main map

Table 1 shows the locations of driving tests with geographical coordinates and the level of each experimental area. Also are present the classification and characteristics of climate.

Prior the installation of the trials was carried out verification and survey of potentially disruptive characteristics, thus, in all environments, a randomized complete block design with three replications per location was used in order to ensure uniformity within the block and heterogeneity between the blocks. The experimental units were composed of two 5-m long cultivar rows, spaced by 0.70 meters. The seeding rows were marked with no-tillage seeder system, after, the hybrid seeds were manually sown. Sowing was carried out according to the agricultural zoning of each site. Soil management and cultural practices were the same for the five sites obeying the phenological stages and the need for culture. After emergence and crop establishment, we adjusted the plant density to 42 plants per experimental unit, equivalent to 60 000 plants ha^{-1}. The assessed traits were tassel length (TL) in centimeters; distance from the last node of the stem to the first branch of the tassel (DLN) in centimeters; distance of the flag leaf to the first branch of the tassel (DFL) measured in the collar of flag leaf to the insertion of the first branch in the tassel, in centimeters; number of branches on the main stem of the tassel (NBT); thousand-kernel weight (TKW), measured by manual counting of 8 replicates of 100 seeds, in grams; and grain yield (GY), conducted by manual harvesting of all experimental units and extrapolated to kg ha^{-1}Previously the analysis of genetic parameters, we verified the effects of homogeneity of variances and the data normality. After, the data were subjected to individual analysis of variance, to prove the absence of correlation among errors. Meeting the assumptions, we performed the genetic parameters estimates.

Aiming to identify the variation of the progenies, in each environment we estimate the genetic variance and heritability in the broad sense with their respective confidence intervals, as proposed by Knapp *et al*. (1985):

$$\hat{\sigma}_G^2 = \frac{MST - RMS}{R}$$

Were $\hat{\sigma}_G^2$ = Genetic variance; MST = Mean square for treatments; RMS: Residual mean square and R = number of replicates each treatment.

$$h^2 = \frac{\hat{\sigma}_G^2}{MST/R}$$

h^2: heritability in the broad sense; $\hat{\sigma}_G^2$ = genetic variance; MST = mean square for treatment; R = number of replicates.

$$CI = 1 - \left[\frac{MST}{RMS}(F\ DF_1, DF_2)\right]$$

CI = confidence interval to heritability of trait; DF: degrees freedom, 1 (Treatment/environment)and 2 (residual degree of freedom); $F_{0.05:120:240}$= 0.7652997 e $F_{0.95:120:240}$= 1.289621, where F is the tabulated value at a specified probability level with respect to specific number of degrees of freedom of treatments (Crossings) varying inside of environments and residual.

Statistical procedures were carried out in Genes (Cruz, 2013) and SAS (SAS, 2013) softwares.

Table 1. Location and climate characteristics of experimental areas

State	City	South LAT	West LONG	MASL	Climate[+]	Average temperature[+,*] (ºC)		Annual rainfall[+] (mm)
						T_{cold}	T_{hot}	
Rio Grande do Sul	FredericoWestphalen	27°23'80"	53°25'26"	480	Cfa	14.8	23.6	1881
Santa Catarina	Itapiranga	27°10'10"	53°42'44"	206	Cfa			1760
Paraná	Ampére	25°54'65"	53°25'39"	580	Cfa			1960
	PatoBranco	26°13′44″	52°40′15″	760	Cfa			1947
	Clevelândia	26°21'52"	52°28'22"	860	Cfb	13.4	20.0	2243

[+] The climate classification is according to Alvarez *et al.* (2014).
* Average air temperature for the two climate classifications presented in the trial places. T_{hot}= average air temperature in the hottest month of the year, T_{cold}= Average air temperature in the coldest month of the year.

Table 2. Estimates of genetic variance (σ^2_G), heritability in sense broad coefficients and their respective confidence intervals (Upper Limit - UP, Low Limit - LL), and coefficient of variation for six traits of F_1's hybrids maize growing in five environments of south region of Brazil

Traits		Ampére	Clevelândia	Itapiranga	PatoBranco	FredericoWestphalen
DLF	σ^2_G	2.260	1.297	1.230	2.837	2.168
	Heritability UP	0.909	0.777	0.456	0.962	0.903
	Heritability	0.883	0.713	0.299	0.951	0.875
	Heritability LL	0.847	0.625	0.083	0.936	0.837
	CV (%)	6.509	8.189	19.929	4.522	6.412
DLN	σ^2_G	2.559	4.146	2.977	1.323	3.986
	Heritability UP	0.859	0.543	0.708	0.550	0.837
	Heritability	0.819	0.410	0.623	0.420	0.790
	Heritability LL	0.763	0.230	0.508	0.242	0.726
	CV (%)	6.103	18.396	10.802	10.918	7.481
TL	σ^2_G	6.893	5.880	0.236	12.743	16.858
	Heritability UP	0.851	0.717	0.243	0.892	0.920
	Heritability	0.808	0.635	0.024	0.860	0.897
	Heritability LL	0.749	0.524	-0.276	0.817	0.865
	CV (%)	3.637	5.215	9.442	4.148	3.854
NBT	σ^2_G	10.201	2.564	3.178	10.244	2.675
	Heritability UP	0.892	0.539	0.797	0.929	0.696
	Heritability	0.861	0.405	0.739	0.909	0.608
	Heritability LL	0.818	0.223	0.659	0.881	0.488
	CV (%)	14.814	21.271	11.439	10.472	15.477
TKW	σ^2_G	671.700	192.789	386.050	586.902	46.866
	Heritability UP	0.699	0.767	0.605	0.665	0.355
	Heritability	0.612	0.701	0.491	0.567	0.168
	Heritability LL	0.493	0.607	0.335	0.435	-0.088
	CV (%)	11.834	4.168	11.086	10.622	8.055
GY	σ^2_G	944367.22	1653325.56	1462500.96	1040344.34	1065751.78
	Heritability UP	0.775	0.899	0.919	0.848	0.914
	Heritability	0.709	0.870	0.896	0.803	0.888
	Heritability LL	0.620	0.831	0.863	0.744	0.854
	CV (%)	10.004	5.809	6.506	6.953	8.813

TL - tassel length, DLN - distance from the last node of the stem to the first branch of the tassel, DFL - distance of the flag leaf to the first branch of the tassel, NBT - number of branches on the main stem of the tassel, TKW -thousand-kernel weight and GY - grain yield.

RESULTS AND DISCUSSION

The genetic variance for the DLF trait showed variations in environments from 1.29 to 2.83 (cm) for DLN from 1.32 to 4.14 (cm) and for the TL from 0.23 to 16.85 (cm). Among these traits, the TL shows greater genetic variance among the analyzed environments. The NBT had variance from 2.56 to 10.24, however, TKW had magnitudes from 46.86 to 671.70 (g). The GY presented most genetic fluctuation between Ampere and Clevelândia, with the smaller variation in Ampere (Table 2). The determination of the genetic variation is the basis for the plant breeder's work, which aim understanding the hereditary basis of the traits. Thus, to dismember the phenotypic component in genetic and environmental components is necessary (Bueno *et al.*, 2006). The determination of a variance component as a parameter as heritability are important in breeding programs for the quantification of genetic variation in the number of individuals seeking future genetic gains. This point is considered the best form to allocate the necessary resources during the process of selecting a trait of interest, especially to reduce the selection time (Smalley *et al.*, 2004).

The different estimates for the traits reveled that the effects of growing environments provide changes in expression of the trait, where the environment is the main element for increased phenotypic variation. These oscillations between estimates of genetic varianceare attributed to the contrasting effects and environmental modifiers, influencing the physiological mechanisms and controlling the expression of the traits (Falconer, 1996; Carvalho *et al.*, 2004). These results demand caution of breeders since the environment is not hereditary component, so the presence of phenotypic variation inflated primarily by environmental component may to implicate in the

no-selection of superior genotypes to certain traits. Confidence intervals for the heritability in the broad sense are different from zero in Ampere, Clevelândia and PatoBranco environments for all analyzed traits. We can see that some traits shown estimates of broad heritability close to zero, such as the DLF and TL in Itapiranga environment. Heritability estimates close to zero indicate low expression of the character to the environmental conditions, and/or the need for a greater number of replications and plant sampling in the conditions of this environment. According to Pinto *et al*. (2000), the occurrences of low parameter estimation, indicate an increase in population sample of work. Components and heritability estimates are important parameters for breeding programs in determining the allocation of resources necessary for the selection of a trait of interest and thus increase the genetic gain using less time and resources (Smalley *et al*., 2004). Heritability for DLF and TL traits was high, revealing high penetrance and expressivity of the traits for Ampere, Clevelândia, PatoBranco and FredericoWestphalen, 70-95% and 63-89%, respectively, however, Itapiranga shows low heritability for these traits (29.9% and 2.24%, respectively). These estimates were lower than in other environments, demonstrating that the expressiveness of these traits is reduced in this environment condition (Hallauer *et al*., 2010). The mechanisms that acted in this sites, e.g., temperature, humidity and solar radiation, increased the phenotypic variance of the hybrids and thus reduced the expressiveness of the traits. Possibly, with greater plants sampling, the effects of environment would be minimized, raising the representation for this specific site. The heritability of DLN and NBT traits reveal their expressiveness by median and high estimates. Lower heritability coefficients are observed for Clevelândia (41 and 40%, respectively). Thus, we proved that the expressiveness is specific to each environment, and type of progeny (stepbrothers, brothers complete, S_1, S_2) of each population, findings similar to found by Hallauer (2007). The TKW shows high variations of heritability coefficients in the five environments studied (0.16 to 0.70 for Frederico Westphalen and Clevelândia, respectively), indicating that this trait has a complex action with its expression being controlled by a larger number of genes, having greater variations in expressiveness when subjected to differing conditions, where the action of the interaction above the genotype is more impactful. This is grounded once that high heritability estimates, indicate greater stability to environmental variations and by the traits present a less complex (Hall *et al*., 2007). Thus, the penetrance and expressivity of the trait under stable conditions is higher. The DLF and TL traits had low expressiveness in Itapiranga and together with Frederico Westphalen for TKW, due the magnitude of heritability coefficients be lower than those other environments. For GY the heritability estimates show little variation and its values were considered high. We believe that due the heritability be obtained by the ratio between genotypic and phenotypic variance in each environment, their estimates remained high due the adequate experimental conditions, since the variation coefficients were low. Another point that can be highlighted in our results is that the main traits of interest to the breeder, as TKW and GY had high heritability estimates in Clevelândia. The driving segregant inbred lines in an environment tends to provide better aclimatation of these to certain ambient

conditions in which were selected. As breeding program KSP seed was conducted at this location, hybrids resulting from these crosses tend to have less influence of environment in Clevelândia, there for, the contribution of environmental variation in phenotypic variation is smaller, which increases the estimate of heritability, as observed in this study. The accuracy in predicting the responses of the traits is very important for achieving success in plant breeding programs, where the goal is to get reliable estimates of traits' mean (Fritsche-Neto *et al*., 2012). The technologies and aggregate planning on experiments have been positively contributing to the increase of experimental accuracy in maize trials. For Pimentel Gomes (2000), this dimensionless statistics enables you to compare the accuracy of the experiments. The CV (%) of the individual analysis in each place had low to median values (Table 2), indicating good accuracy in taking the data in each environment for traits (PimentelGomes, 1985). However it is noteworthy that the CV is given by the ratio between the residual standard deviation with the percentage of general average of the trial, thus, the comparison with different trials and traits may not be suitable because of the different conditions of planning and execution of trial, and also the specific magnitudes of traits for the specie under study.

Conclusions

The tassel length and the thousand-grain weight are the traits with high genetic variance. For the yield traits, Clevelândia environment is indicated for selection due the high estimates of heritability. Itapiranga and Frederico Westphalen environments has the lowest expression for the traits tassel length, distance from the flag leaf to the first branch of the tassel and thousand-grain weight.

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