

Productive performance and multivariate interrelations of open-pollinated and hybrid maize in Brazil

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ABSTRACT. Corn is considered one of the most important crops in the world agricultural scenario. In order to improve production, it is crucial to understand and quantify the genetic variation involved in the phenotypic manifestation of this species. We evaluated the agronomic performance of open pollinated genotypes, used by small scale family farmers, compared to commercial hybrid genotypes in various growing environments. The experimental design was a randomized block and the treatments were arranged in four replicates. Eight maize genotypes were used: three open-pollinated varieties and five simple hybrids. The following characters were measured plant height, ear insertion height, stem diameter, ear length, number of seed rows of the ear, number of seeds per row of ear, thousand seed weight and seed yield. The best yields of seeds were obtained in Entre-Ijuís, RS. Seed yield varied according to the genotype and growing environment; in Pelotas, RS the highest yields were obtained with the HC2 and HC1 genotypes (9090 and 9002 kg.ha⁻¹, respectively). Genotypes with a narrow genetic base express less variation in their responses to the environments, in contrasting

environments. Under limiting conditions the open pollinated varieties responded favorably. The use of biometric approaches allows us to reveal patterns in the grouping of genotypes.

Key words: *Zea mays*; biometric models; trait associations

INTRODUCTION

Maize (*Zea mays*) plays an important agricultural, economic and social role due to the multiplicity of uses, from human and animal feeding, to the production of bioproducts to obtaining biofuels (Ferreira Júnior et al., 2014; Szareski et al., 2018). It is cultivated both as an agricultural commodity in high-level management systems (Argenta et al., 2003; Demari et al., 2018) and in family agriculture, aiming at the subsistence and sustainability of rural properties (Sandri and Tofanelli, 2008).

One of the important components in the definition of maize yield is the genetic base used, distinct technological levels, being a necessary tool for decision making in the management and breeding. The combination of these factors will allow the maximum obtainment of the resources of the environment, seeking to optimize the productivity of the species of agricultural importance in a sustainable way (Argenta et al., 2003; Nardino et al., 2016; Baretta et al., 2017).

In maize crop, genotypes based on open pollinated varieties and simple, modified, double and triple hybrids are commonly used. The choice of genotype is linked to the management practices used, which depend on the farmer's investment capacity. According to Bisognin et al. (1997), the use of open pollinated varieties is economically advantageous for farmers who use low technology investment in their property.

This advantage is due to the lower price of the seeds, the possibility of using the own seeds in subsequent harvests, greater tolerance to biotic and abiotic stresses. According to Tokatlidis and Koutroubas (2004), the superiority of the hybrids can occur in relation to the varieties of open pollination due to the processes of breeding, hybrid vigor and selection.

In spite of the low genetic potential, open-pollinated varieties, under some specific growing conditions, may present superior performance to some maize hybrids (Carvalho et al., 2005; Rosa et al., 2018). The increase in grain yield and the economic return of maize in Brazil depends on the genetic characteristics of the genotype, the management system used by the farmer and the peculiar characteristics of the growing environment. In this way this work had the objective of evaluating the agronomic performance and the positioning of the genotypes of open pollination against normal commercial hybrids in various growing environments.

MATERIAL AND METHODS

The experiments were conducted in the municipalities of Pelotas (31°52'19" S and 52°21'33" W) and Entre-Ijuís (28°21'32" S and 54°16'04" W), located at six and 215 m of altitude, respectively in Rio Grande do Sul state. Seeds from family farmers and from the Research Center of EMBRAPA Temperate Climate - Pelotas were used.

The experimental design was a randomized block and the treatments were arranged in four replicates. Eight maize genotypes were used: three open-pollinated varieties (PL1, PL2 and PL3) and five simple hybrids (HP1, HP2, HP3, CD1 and CD2). Seeding was done manually, with spacing between rows and plants of 45 and 36 cm, respectively, population density of 55,000 ha⁻¹ plants (Borghi and Crusciol, 2007). Each experimental unit consisted of six rows 4 m long, and useful plot area of 5.4 m².

Seeding of the genotypes was done manually in December 2016, with previously corrected and fertilized experimental area (CQFS RS/SC, 2004). The meteorological attributes based on maximum and minimum air temperature and stratified rainfall for the study environments were recorded (Figure 1). The evaluations were conducted after the physiological maturity of the seeds, based on the following attributes:

- Plant height (PHE): measured by the distance between the soil level to the last fully expanded leaf, results in centimeters.
- Ear insertion height (EHE): distance between ground level and the insertion node of the first viable ear, results in centimeters.
- Stem diameter (SDI): obtained with the aid of a digital caliper where the measurements were standardized, where the equipment was perpendicular to the sowing line, results in millimeters.
- Ear length (ELE): extension between the basal and apical end of the ear, results in centimeters.
- Number of seed rows of the ear (NRE): counting the number of rows with whole seeds in the ear, results in units.
- Number of seeds per row of ear (NSE): of the magnitude of seeds arranged longitudinally in row of ear, results in units.
- Thousand seed weight (TSW): determined according to the Rules of Seed Analysis (Brasil, 2009), results in grams.
- Seed yield (YEI): obtained through the harvest and track of the useful area of each experimental unit, adjusted to 13% moisture and yield per hectare, results in kg.ha⁻¹.

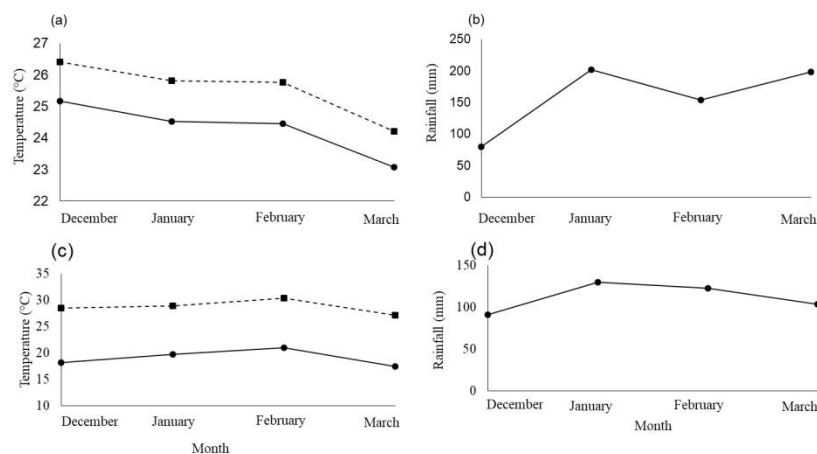


Figure 1. A- monthly averages for the maximum (---) and minimum (—) air temperature of Entre-Ijuís. C - monthly averages for the maximum (---) and minimum (—) air temperature of Pelotas. B-Rainfall of Entre-Ijuís. D - Pelotas rainfall during the months of December 2016 to March 2017. Source: São Luiz Gonzaga Meteorological Station and Pelotas Agrometeorology Station.

In order to identify the multivariate patterns for the selection of the most similar genotypes, an Artificial Neural Networks (ANNs) approach was used, based on estimates through unsupervised computational learning. The topological definition of centroids and associated neurons was obtained by the Kohonen Mapping method. The experimental design was a randomized block in which the treatments were arranged in four replications, being organized in a factorial scheme, being: eight maize genotypes x two growing environments. The data were submitted to analysis of variance, when the interaction was significant at 5% probability by the F test, decomposed into the simple effects; when there was no interaction, the complementary analyses were carried out with a Duncan test at 5% probability.

RESULTS

The variance analysis revealed significance for the interaction between maize genotypes x growing environments at 5% probability for PHE, ear EHE, SDI, ELE, NRE, NSE, TSW and YEI.

In Pelotas the genotypes HP1, PL1, PL2, HP2 and HC1 had similar performances; the shortest plant heights were found for PL3 and HC2 with magnitudes between 197.5 and 206.4 cm, respectively (Table 1). In Entre-Ijuís the genotypes PL1, HP1, HP3 and HC1 were superior. Among growing environments, Entre-Ijuís, was superior for PHE through the PL1, HP3 and HC1 and HC2 genotypes. According to Gorgulho and Miranda Filho (2001), the height and the insertion of the ear are highly dependent on the characteristics of the genotypes and growing environments. Plant height is determined genetically (Souza et al., 2003; Nardino et al., 2018), influenced by plant population (Brachtvogel et al., 2012) and soil nutrient availability (Paterniani, 1997; Cortez et al., 2009; Repke et al., 2013).

Table 1. Plant height (PHE), stem diameter (SDI), ear insertion height (EHE), number of seed rows per ear (NRE) and number of seeds per row (NSE) measured in different genotypes grown in two environments.

Genotype	PHE (cm)		SDI (cm)		EHE (cm)		NRE		NSE	
	Pelotas-RS	E. Ijuís-RS	Pelotas-RS	E. Ijuís-RS	Pelotas-RS	E. Ijuís-RS	Pelotas-RS	E. Ijuís-RS	Pelotas-RS	E. Ijuís-RS
PL1	226.2abB*	248.0aA	3.6abc	3.6bcd	120.8aA	122.0aA	15.0ab	16.0abc	26.3b	28.5a
PL2	228.8abA	234.9bA	3.2c	3.1de	122.8aA	120.0abA	13.5b	14.5bc	33.3a	34.0a
PL3	197.5cA	201.5dA	3.3bc	2.9e	96.5dA	94.0dA	13.5b	14.0c	30.5ab	29.2a
HP1	234.5aA	237.4abA	4.0a	3.7abc	121.8aA	113.8bcB	16.5a	17.5a	32.5ab	33.7a
HP2	223.2abA	217.6cA	3.8ab	4.2a	118.5abA	119.0abA	16ab	17.5a	30.8ab	29.0a
HP3	222.6bB	239.7abA	3.7abc	3.4abc	120.8aA	122.3aA	14.5ab	15.0abc	31.0ab	29.7a
HC1	230.0abB	242.3abA	3.7abc	3.9ab	110.0cA	110.8cA	16.0ab	17.0ab	28.7ab	31.0a
HC2	206.4cB	221.2cA	3.5abc	3.3cde	111.5bcA	118.5abA	15.0ab	15.5abc	32.7ab	34.5a
CV (%)	3.2		8.99		4.37		10.69		13.15	

* Averages followed by the same lowercase letter in the column and upper case in the row do not differ statistically by 5% probability.

The EHE varied according to the genotype and growing environment; for Pelotas there was superiority for the PL1, PL2, HP1, HP2 and HP3 genotypes, in contrast, Entre-Ijuís showed higher magnitudes for this character through the PL1, HP3, PL2, HP2 and HC2 genotypes. Research by Miranda et al. (2003) define that extremely high plants can increase the probability of lodging. For Cadore (2008), the ear insertion height consists of a characteristic of importance, since smaller distances between the level of the ground and the

point of ear insertion add the balance of the plant (Santos et al., 2010; Kappes et al., 2013; Rodrigues et al., 2014).

The SDI in Pelotas was higher for the genotypes HP1, HP2, HP3, HC1, HC2 and PL1, however, in Entre-Ijuís larger magnitudes were expressed through genotypes HP1, HP2, HP3 and HC1. The number of seed rows of the ear (NRE) was superior for HP1 genotype in Pelotas. For Entre-Ijuís - RS, this character was superior by genotypes HP1 and HP2. This character is determined by genetic effects (Neto et al., 2003; Valderrama et al., 2011), nutritional levels (Carmo et al., 2012), management (Albuquerque et al., 2013).

Researches define that this attribute is largely influenced by the intrinsic characteristics of the genotype (Fernandes et al., 2005; Valderrama et al., 2011), mineral nutrition (Carmo et al., 2012), ear dimensions (Kappes et al., 2013; Carvalho et al., 2017). The number of seeds per row of the ear did not express great influence of the growing environment, because these environments were in nutritional balance and the magnitude of genotypes studied was not elevated. Research by Freitas et al., (2013), define that this character shows high control of the effects.

The thousand seed weight (TSW) in Pelotas was higher for HC1 and HP3 with 297.86 and 297.45 g, respectively. The smallest magnitudes were obtained through the genotypes PL1, PL2 and PL3. For Entre-Ijuís-RS, it was observed that HC1 was the most productive cultivar (Table 2). Highly agronomic characters based on large numbers of genes and highly influenced by the environment are extremely dependent on the genetic base in the genotype used, the smaller efforts to improve open pollinated varieties result in lower performance of these in relation to high-performance and narrow genetic base hybrids (Sangoi et al., 2006; Cruz et al., 2011; Nardino et al., 2016).

Table 2. Ear length (ELE), thousand seed weight (TSW) and yield (YEI) measured in different genotypes grown in two environments.

Genotype	ELE (cm)		TSW (g)		YEI (kg ha ⁻¹)	
	Pelotas-RS	E. Ijuís-RS	Pelotas-RS	E. Ijuís-RS	Pelotas-RS	E. Ijuís-RS
PL1	16.98	17.70	234.04 cB*	270.59 dA	6277.5 eB	7391.5 dA
PL2	16.99	17.70	252.50 cA	269.76 dA	6705.0 dA	6962.5 eA
PL3	16.33	17.02	239.65 cB	265.37 dA	6120.0 eA	6349.0 fA
HP1	16.41	16.12	275.17 bA	280.16 cdA	8057.5 bcA	8380.0 bA
HP2	17.65	16.12	294.45 abA	297.37 bcA	7697.5 cA	7857.0 cA
HP3	16.98	16.60	297.45 aA	305.70 bA	8327.5 bB	9327.0 aA
HC1	19.78	17.76	297.86 aB	326.45 aA	9090.0 aA	9195.0 aA
HC2	18.74	18.30	286.64 abA	287.36 bcdA	9001.7 aB	9533.7 aA
CV (%)	12.81		5.12		3.75	

* Averages followed by the same lowercase letter in the column and upper case in the row do not differ statistically by 5% probability.

In general, the best performances were obtained in Entre-Ijuís - RS, being dependent on the fertility levels (Velooso et al., 2006) and the production system used (Castoldi et al., 2011), climatic conditions in the seed filling stage and temperature (Figure 1) of the air (Floss, 2004). Seed yield (YEI) varied according to the genotype and growing environment, because in Pelotas the highest yields were obtained through the HC2 and HC1 genotypes (9090 and 9002 kg.ha⁻¹, respectively). Only the open pollinated genotypes were found in Pelotas through the PL2 genotype, yielding 6705 kg.ha⁻¹. The great variation expressed for this character is due to the phenotypic plasticity that the genotypes present

due to their broad or narrow genetic base (Emyde et al., 2013; Baretta et al., 2017; Carvalho et al., 2017).

The analysis of the linear correlations between the agronomic characteristics measured was established to establish trends among these characters, with significance based on a probability of 5% by the t test. Eight characters measured in maize genotypes grown under growth environment were used (Figure 2). In this way, the analysis of the linear correlations was carried out in order to establish trends among these characters, with significance based on a 5% probability by the t test. Eight characters measured in maize genotypes grown in the growing environment were used (Figure 2).

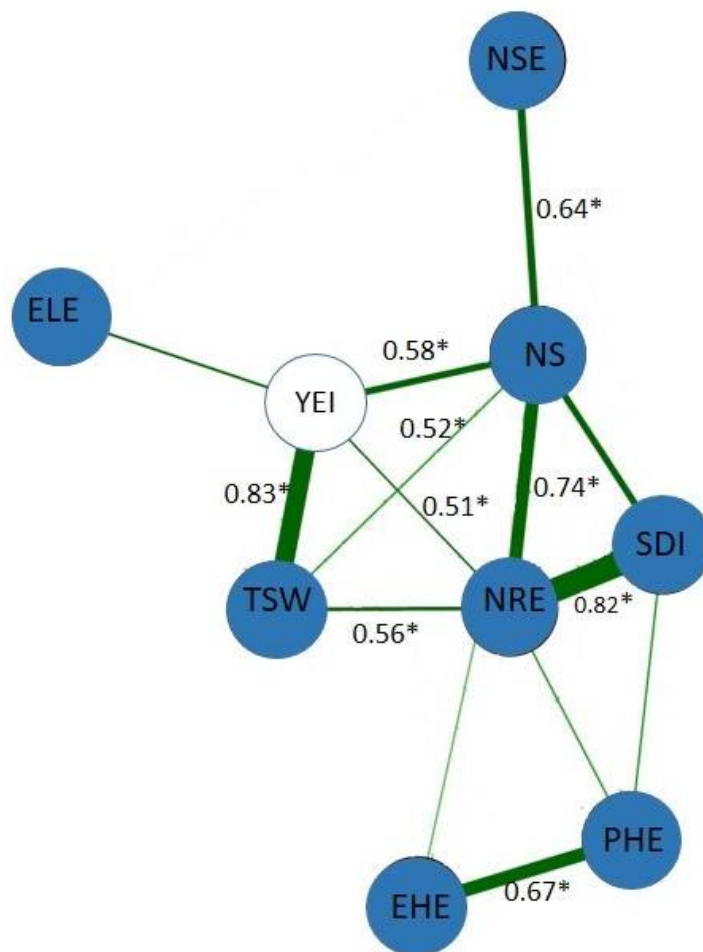


Figure 2. Linear correlation network elaborated for characters plant height (PHE), ear insertion height (EHE), stem diameter (SDI), ear length (ELE), number of seed rows of the ear (NRE), number of seeds per row (NSE), number of seeds per ear (NS), thousand seed weight (TSW) and seed yield (YEI), measured in maize genotypes grown in two environments of Rio Grande do Sul.

The correlation network defined that YEI is strongly associated with TSW, NS and NRE, and the NRE correlates with SDI, NS and TSW. Based on the correlations between

these attributes, it was defined that the ideal genotype to raise corn seed yields in these growing conditions should be based on the identification of plants that maximize the components of the crop yield.

The use of ANNs is essential to define mathematical patterns through nonlinear stochastic phenomena. In this way, the definition of the network topology is defined by an unsupervised iterative computational process, where the magnitude of network inputs corresponds to the number of neurons associated with the explicability of the model, these neurons when related allow the definition of a centroid that corresponds to the midpoint between the existing associations (Nascimento et al., 2013; Teodoro et al., 2015; Carvalho, 2018). For this study, the use of the Kohonen Mapping method, where the phenotypic matrix was submitted to iterative procedures, defined a neural network with eight centroids that establish associative patterns among the environments and genotypes tested, being necessary 10 synaptic connections to interconnect the centroids (Figure 3).

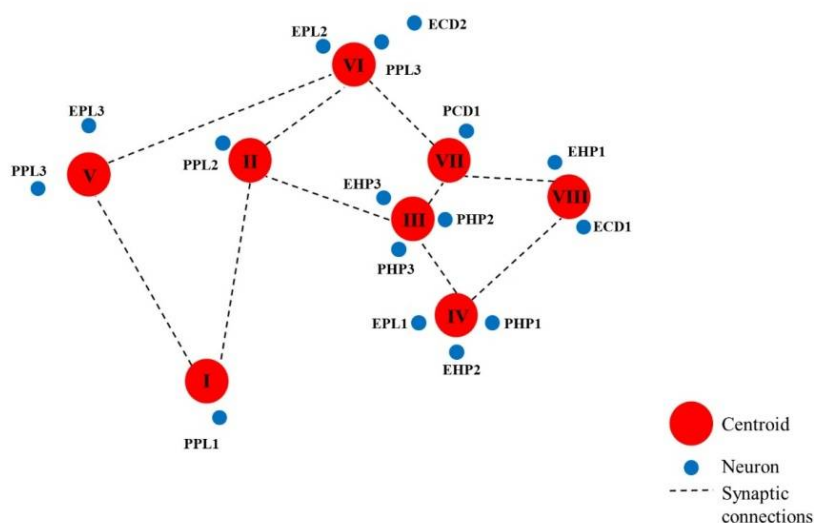


Figure 3. Artificial Neural Networks (ANNs) obtained by the Kohonen Map defining the centroids (red) and the neurons of interest (blue) and the synaptic connections (black dashed lines), these being EPL1, PPL1, EPL2, PPL2, EPL3, PPL3, EHP1, PHP1, EPH2, PHP2, EHP3, PHP3, ECD1, PCD1, ECD2 and PCD2.

The patterns established through the genotypes and their respective growing environment were defined: PPL1 (centroid 1); PPL2 (centroid 2); EHP3, PHP2 and PHP3 (centroid 3); PHP1, EPL1 and EHP2 (centroid 4); PPL3 and EPL3 (centroid 5); EPL2, PPL3 and ECD2 (centroid 6); PCD1 (centroid 7); EHP1 and ECD1 (centroid 8). The clusters maintain genotypes grouped in the same centroid due to their similarities of characteristics that establish their proximity, which serves as a tool for the selection of distinct characteristics among genotypes or the choice of genotypes with phenotypic similarity. Based on the computational learning approach, these eight genetic patterns are defined, so the selections can be directed to certain agronomic aspects, with the possibility of identifying the centroid of interest and consequently the group of corresponding genotypes or neurons.

CONCLUSIONS

There was variability in the genotypes studied, with higher seed yields in Entre-Ijuís. Among the open-pollinated genotypes studied, PL2 showed superiority in the Pelotas environment, with an average yield of 6705 kg.ha⁻¹, while PL1 genotype was superior in the Entre-Ijuís environment, with a productive average of 7391.5 kg.ha⁻¹. Among the hybrids, HC1 and HC2 presented superiority in the Pelotas culture environment, whereas in the Entre-Ijuís environment the hybrids HC1, HC2 and HP3 were superior.

Genotypes with a narrow genetic base express less variation in their responses to the environments, in contrasting environments and under limiting conditions the open pollinated varieties respond favorably. The use of biometric approaches allows one to reveal patterns regarding the grouping of genotypes, and the sizes of the groups depend on the intrinsic premises of the genetic variability studied.

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