

RESEARCH ARTICLE

# Heritability estimates and genetic distance of S<sub>1</sub> progenies from landrace maize populations

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## ABSTRACT

The aim of study to estimate the broad sense heritability of S<sub>1</sub> progenies and to quantify the genetic variance through multivariate analyzes of S<sub>1</sub> progenies from landrace maize populations grown in the southern region of Rio Grande do Sul. The experimental design utilized was the augmented blocks, with ten S<sub>1</sub> progenies groups (Amarelão, Argentino Branco, Argentino Amarelo, Branco Vermelho Índio, Branco Oito Carreiras, Caiano Rajado, Cateto Branco, Criolão Dente de Ouro and BRS Planalto), and two commercial controls, the simple cross hybrids Pioneer 30F53 and Agroeste 1590, allocated in four repetitions. The traits grain depth and spike insertion height express the largest estimates of broad sense heritability. The S<sub>1</sub> progeny Argentino Amarelo provides the largest estimates of broad sense heritability for the set of evaluated traits. The S<sub>1</sub> progenies Caiano Rajado, Criolão, Branco Roxo Índio, BRS Planalto, Dente de Ouro, Amarelão and Branco Oito Carreiras have similar heritability patterns for the studied traits, allowing to employ a similar selection strategy in the next generations. The S<sub>1</sub> progenies from landrace maize populations present genetic variability for the agronomic traits studied.

## Highlighted Conclusions

1. The traits grain depth and spike insertion height express the largest estimates of broad sense heritability.
2. The S<sub>1</sub> progeny Argentino Amarelo provides the largest estimates of broad sense heritability for the set of evaluated traits.
3. The S<sub>1</sub> progenies Caiano Rajado, Criolão, Branco Roxo Índio, BRS Planalto, Dente de Ouro, Amarelão and Branco Oito Carreiras have similar heritability patterns for the studied traits, allowing to employ a similar selection strategy in the next generations.
4. The S<sub>1</sub> progenies from landrace maize populations present genetic variability for the agronomic traits studied.

## INTRODUCTION

Maize (*Zea mays* L.) is a diploid species (2n=2x=20 chromosomes), monoecious, cross-pollinated reproductive system and annual cycle (Paterniani and Viégas 1987). This species has been cultivated in a wide geographic extension that ranges between 58° North to 40° South latitudes, presenting high adaptation to the most varied edaphoclimatic conditions and growing systems (Fancelli and Dourado Neto 2000). Its wide cultivation and high nutritional value turn maize into the most produced cereal in the world. Large part of its production is destined to feed industry, ethanol production and utilization in the high technology industry. However, significant part is, directly or indirectly, destined to human consumption being the main ingredient for elaboration of cooked corn meal, couscous, hominy, breads, porridge, cakes, pastas and beverages (Dias Paes 2006).

In the 2015/2016 agricultural year, 177 million hectares were cultivated worldwide with production of 970 million tons of grains, and an average yield of 5.65 tons per hectare (USDA 2016). In Brazil, maize stands out as the second most cultivated agricultural species, becoming an important commodity, which moves the trade market and

generates economic resources to the country. In the last agricultural year, 84 million tons were produced, with most contribution of the states of Mato Grosso, Mato Grosso do Sul, Paraná and Rio Grande do Sul (CONAB 2016).

The increase in grain yield, tolerance to biotic and abiotic stresses, and improvements in grain nutritional composition are the classic objectives sought by maize breeding programs (Paterniani and Viégas 1987; Hallauer et al. 2010). Maize genetic breeding programs are based on the commercial exploitation of hybrids, which require plentiful labor and financial resources. The formation of base populations and improved inbred lines are fundamental for the breeding program success since they consist in the selection and achievement of agronomically desirable genetic constitutions, containing alleles of interest for the breeders (Paterniani and Campos 2005). In this context, populations with high genetic variability are searched, which are genetically distant and present favorable alleles for the agronomic traits of interest, being these heritable, thus enabling the formation of heterotic groups. A promising alternative for breeders is the exploitation of maize landrace populations since they present great genetic variability, genes of tolerance and/or resistance to biotic and abiotic factors, and did not went through intense cycles of selection (Araújo and Nass 2002).

The genetic variability present in populations and progenies refers to the divergence of different genetic forms in several genic loci of the species, being a primary source of genetic variability, potentiated by genetic recombination (Ramalho et al. 2012). Thus, it is possible to quantify the genetic variability present in a population or in a progeny group based on the genetic distance as it is associated with the degree of distancing between genotypes, for a set of common traits. In maize breeding programs, the knowledge of the genetic distance between progenies is fundamental to improve the efficiency of inbred lines selection for developing the next generations, and for hybrid formation (Amorim 2005).

The multivariate analyzes contribute in this sense with breeders, since they allow to evaluate a set of random traits related to each other, assigning the same degree of importance, resulting in the coefficients of genetic distance between genotypes (Cruz et al. 2012). The association of multivariate techniques is an efficient way of estimating the genetic distance, which involves analytical techniques such as measures of dissimilarity, clustering methods, main components and canonical variables (Cruz et al. 2004). The use of multivariate techniques to estimate genetic distance has become routine among plant breeders as evidenced by studies carried out by Costa Pinto et al. (2001), Moro et al. (2007), Paterniani et al. (2008) and Lamkey and Lorenz (2014).

In order to support selection strategies and maximize the success of breeding programs, breeders need to know the genetic parameters estimates of quantitative traits, such as heritability of progenies and inbred lines (Allard 1999; Hallauer et al. 2010). Heritability is one of the genetic parameters that most contribute in the selection process since it is the proportion of genetic variance present in the total phenotypic variation, in other words, it is associated with the similarities between individuals over the generations (Falconer and Mackay 1996). In addition, heritability has the function of predicting the phenotypic value, which is indicative of the genetic value (Falconer 1981). The study of genetic parameters in maize has been reported in the studies conducted by Churata and Ayala-Osuna (1996), Paterniani et al. (2004), Carvalho et al. (2005), Hallauer et al. (2010), Rovaris et al. (2011) and Ribeiro et al. (2016).

In maize breeding programs, selection in S1 progenies has been used to develop improved populations considering the fact that inbreeding increases genetic variance among progenies (Steola et al. 2006). Therefore, the present study aims to estimate the broad sense heritability of S1 progenies and to quantify the genetic variance through multivariate analyzes of S1 progenies from landrace maize populations grown in the southern region of Rio Grande do Sul.

## **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. According to Köppen, the climate is classified as subtropical Cfa, with rainfall annual average of 1,280 mm (Alvares et al. 2013). The soil is classified as Dystrophic Yellow Red Argisol, of clay texture and wavy relief (Santos et al. 2006).

The experimental design utilized 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 (OPV) BRS Planalto. 40 plants were evaluated in each S1 progeny.

The sowing occurred on 05/12/2014, with 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 to 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 were submitted to joint variance analysis by the F test at  $p \leq 0.05$  of probability in order to reveal significant differences between progenies. The individual variance analyzes were performed for each S1 progeny in order to verify the variance components for each progeny separately, which are estimated through the mathematical expectation of the variation sources mean products, similarly achieved to the mathematical expectations of the respective mean squares of each trait variance analysis (Cruz et al. 2004). The components of phenotypic and genotypic variance were obtained according to the methodology of Vencovsky and Barriga (1992), Cruz and Carneiro (2006) and Ramalho et al. (2012):

$$\sigma_{p(x)}^2 = MSPR_{(x)} / r$$

$$\sigma_{g(x)}^2 = (MSPR_{(x)} - MSR_{(x)}) / r$$

Where:  $\sigma_{p(x)}^2$  = Phenotypic variance of x;  $\sigma_{g(x)}^2$  = Genetic variance of x;

MSPR = Mean square of the progeny; MSR = Mean square of the residue;

r = number of repetitions.

The heritability in the broad sense ( $H^2$ ) was obtained by the ratio between the genetic variance and the phenotypic variance, according to Vencovsky and Barriga (1992) and Ramalho et al. (2012):

$$H^2 = \frac{\sigma_{g(x)}^2}{\sigma_{p(x)}^2}$$

Where:  $\sigma_{p(x)}^2$  = Phenotypic variance of x;  $\sigma_{g(x)}^2$  = genetic variance of x.

The heritability patterns of the progenies were obtained using the Mean Euclidean distance, and the UPGMA hierarchical clustering (*Unweighted Pair-Group Method using Arithmetic Averages*), according to Cruz and Carneiro (2006).

Based on the estimates of genetic variances for each trait in each S1 progeny, the genetic distance of the progenies was estimated, using the mean Euclidean distance obtained by the matrix:

$$d_{ij} = \sqrt{\frac{1}{n} \sum_j (X_{ij} - X_{i'j'})^2}$$

with the data standardized, as proposed by Cruz et al. (2004). For elaborating the dendrogram of the mean Euclidean distance, it was used the UPGMA clustering method. For the dendrogram cut-off point (CP), it was used the mean plus one standard deviation. The multivariate methods of Tocher's grouping were also performed, as described by Rao (1952), and graphic dispersion through the main components (Cruz et al. 2004).

In order to verify the relative importance of the traits, it was used the matrix of distances derived from the genetic variances between S1 progenies according to methodology proposed by Singh (1981). The analyzes were performed using the software Genes (Cruz 2013).

## RESULTS AND DISCUSSION

The joint variance analysis by the F test at  $p \leq 0.05$  of probability revealed significant differences among the S1 progenies of landrace maize populations for all studied traits. It allowed to infer that there is a genetic variation among progenies for the measured traits, which is a determining condition for a breeding program. Studies conducted by Carvalho et al. (2003) and Steola et al. (2006) revealed the importance of genetic variability for developing new selection cycles in maize half-siblings.

**Table 1. Broad sense heritability estimates (H<sup>2</sup>) of S1 progenies for spike insertion height (SH), plant height (PH), stem diameter (SD), tassel main stem length (TSL), number of ramifications of the tassel (NRT), number of days for flowering (NDF), spike diameter (SKD), spike length (SL), spike mass (SM) and grain depth (GD), in ten S1 progenies of landrace maize populations.**

PROGENIES	SH	PH	SD	TSL	NRT	NDF	SKD	SL	SM	GD
Amarelão	23.7	21.1	20.3	18.7	21.3	22.4	16.2	22.5	15.1	24.8
Argentino Amarelo	25.6	24.4	17.0	20.4	23.9	21.2	19.4	22.1	19.0	29.7
Argentino Branco	18.5	18.0	14.6	16.9	19.6	16.6	17.0	20.3	4.3	19.0
Branco Oito Carreira	23.8	23.4	17.6	18.3	21.1	22.6	20.0	21.4	11.3	24.7
Branco Roxo Índio	24.0	21.7	16.3	22.3	21.4	20.0	21.3	23.3	21.0	24.9
Caiano Rajado	24.0	22.7	17.2	19.3	23.1	22.4	21.7	23.3	17.2	24.9
Cateto Branco	24.2	21.5	11.8	16.9	20.8	3.74	14.3	21.6	11.9	24.8
Criolão	23.4	21.6	19.0	20.2	22.8	19.8	19.2	23.4	14.1	24.9
Dente de Ouro	24.0	23.9	18.1	22.9	20.5	20.7	18.8	22.5	14.2	24.7
BRS Plantalto	24.1	22.5	17.0	20.7	20.5	21.7	18.7	23.6	17.3	24.8
H <sup>2</sup> Média <sup>(1)</sup>	23.5	22.1	16.9	19.7	21.5	19.1	18.7	22.4	14.5	24.7

<sup>(1)</sup> H<sup>2</sup> mean = mean broad sense heritability.

Under the conditions of this study, it was generally verified that all S1 progenies showed low heritability estimates for the set of measured traits (Table 1). These results are probably related to the high participation of the environmental variation in the traits expression, as most of the phenotypic variation evidenced in the progenies is due to environment effects. According to Borém and Miranda (2009), heritability estimates are influenced by the method used to estimate the heritability value, the variability in the population, the population inbreeding degree, the size of the evaluated sample, the number and type of environments considered, the experimental unit considered, and the precision in conducting the experiment and data collecting. In addition, Hallauer et al. (2010) shows that open pollinated populations have lower heritability estimates compared to synthetic and progeny varieties derived from hybrids. In general, lower heritability traits are closely associated with reproductive adaptation, whereas higher heritability traits are less important in determining the natural selective value (Falconer 1981).

Estimates of heritability allow breeders to deduce the expected progress with selection, as well as they assist in choosing the most appropriate method to improve a group of progenies (Lamkey and Hallauer 1987). For the trait spike insertion height, it was evidenced a mean of 23.51%, being the highest heritability verified for the progeny Argentino Amarelo (25.61%) and lower for the progeny Argentino Branco (18.51%) (Table 1). Similar results were observed for plant height, where the progeny Argentino Amarelo had the highest heritability (24.36%), and the progeny Argentino Branco had the lowest heritability (18.03%). The mean heritability for these traits was 22.09%, and the progenies Branco Oito Carreiras, Caiano Rajado, Dente de Ouro and BRS Planalto presented heritability values above the average. These results corroborate with the studies carried out by Faluba et al. (2010), evaluating the genetic potential of the maize population UFV 7, which showed heritability estimates of 18.39% for plant height and 24.01% for spike height, in the three environments average.

According to Carvalho et al. (2003),

heritability values should be computed based on the type of selection unit, which is used to estimate the expected gain. The progeny Amarelão presented the highest heritability for stem diameter (20.31%); the other progenies showed a heritability of less than 20% for this trait; the lowest heritability was found in the progeny Cateto Branco (11.81%) (Table 1). Studying 35 maize experiments, Hallauer et al. (2010) obtained an average heritability for stem diameter of 36.1%.

According to Gomes et al. (2004), heritability is the best parameter to make any inference about the success of breeding a given trait. Heritability estimates for tassel-related traits are scarce in the literature, however, these traits are of great importance for breeders, and the knowledge of these estimates is essential. In this sense, the estimates of heritability for tassel main stem length ranged from 16.86% to 22.88%, in the progenies Cateto Branco and Dente de Ouro, respectively (Table 1). The average heritability for this trait was 19.65%. The trait number of ramifications of the tassel showed average heritability of 21.52%, being the highest verified for the progeny Argentino Amarelo (23.93%) and the lowest for the progeny Argentino Branco (19.61%).

The trait number of days for flowering had a mean heritability of 19.12%, ranging from 3.74% in the progeny Cateto Branco to 22.63% in the progeny Branco Oito Carreiras (Table 1). Thereby, it is observed that only the progenies Cateto Branco and Argentino Branco showed heritability values below the average. Studies by Hallauer et al. (2010) showed an average of 57.90% of heritability for number of days for flowering, analyzing the average of 48 experiments. It is noticed that the estimates verified in this experiment were far below the mean reported by these authors. According to Falconer (1981), different determinations of heritability for a same trait demonstrate a considerable range of variation, being attributed to samplings and real differences among populations or conditions under which they were studied.

Heritability estimates for spike diameter revealed values from 14.33% in the progeny Cateto Branco to 21.65% in the progeny Caiano Rajado. The average heritability observed for the trait was 18.64%, thus, the progenies Amarelão, Argentino Branco and Cateto Branco presented values below the average (Table 1). According to studies by Hallauer et al. (2010) the average heritability for this trait is 36.10%, higher than the results found in this study.

For the trait spike length, there was a small amplitude between the heritability estimates of the progenies, with values ranging from 20.26% to 23.60%, with a mean of 22.39% (Table 1). Works conducted by Hallauer et al. (2010) investigating 52 experiments, identified a heritability of 66.20% for this trait. Therefore, it is noticed that the estimates revealed in this study are inferior to those found by these authors. In small populations or in reduced sampling, the expected trend is that these heritabilities are lower than in large populations (Falconer 1981).

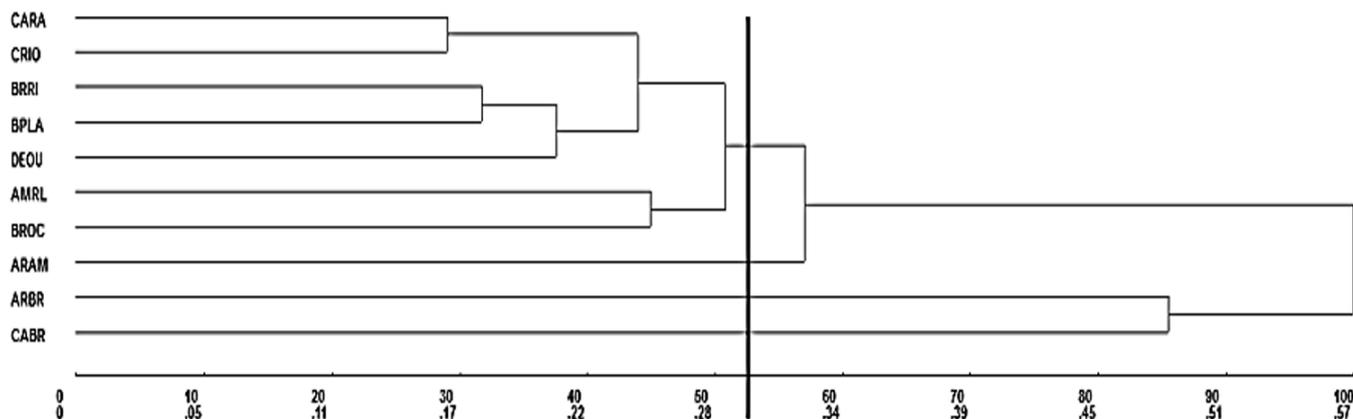
The progeny BrancoRoxo Índio presented the highest heritability estimate for spike mass (20.96%), whereas the lowest heritability estimate was found in the progeny Argentino Branco (4.27%), which was considerably different of the progenies average (14.52%) (Table 1). Studies conducted by Steola et al. (2006), in maize  $S_{0:1}$  progenies derived from a single cross hybrid, showed broad sense heritability from 70.82% to 71.30% for the trait yield of dehuskedspikes as a function of sowing density. Pinto et al. (2000), evaluating  $S_1$  progenies of the populations BR-105 and BR-10, observed an average heritability of 73.3% for the first population and 61.2% for the second. However, Carvalho et al. (2003), when estimating genetic parameters in the population CPATC-3, found heritability coefficients ranging from 40.02% to 48.59% for spike weight.

According to Marquez-Sanchez and Hallauer (1970) one of the ways to evaluate the intrinsic properties of a population or progeny is through the adequate estimation of their genetic parameters, which must be done according to the available resources and the variability in different populations. Grain depth revealed mean heritability of 24.70%, except for the progeny Argentino Amarelo, which presented the highest heritability (29.70%), and Argentino Branco, which had the lowest heritability (18.98%). The other progenies expressed heritability estimates very close to the average.

In a comprehensive way, the highest heritability estimates were evidenced in the progenies Argentino Amarelo, Caiano Rajado, Criolão and Branco Roxo Índio, thus, these progenies can be considered as potentially promising to be used in a breeding program. On the other hand, the progenies Argentino Branco and Cateto Branco expressed the lowest heritability estimates for the set of evaluated traits, and even though, they should be kept in the program because of their desirable agronomic traits. According to Falconer (1981) greater variation in environment conditions reduces heritability, as greater uniformity of this condition increases heritability.

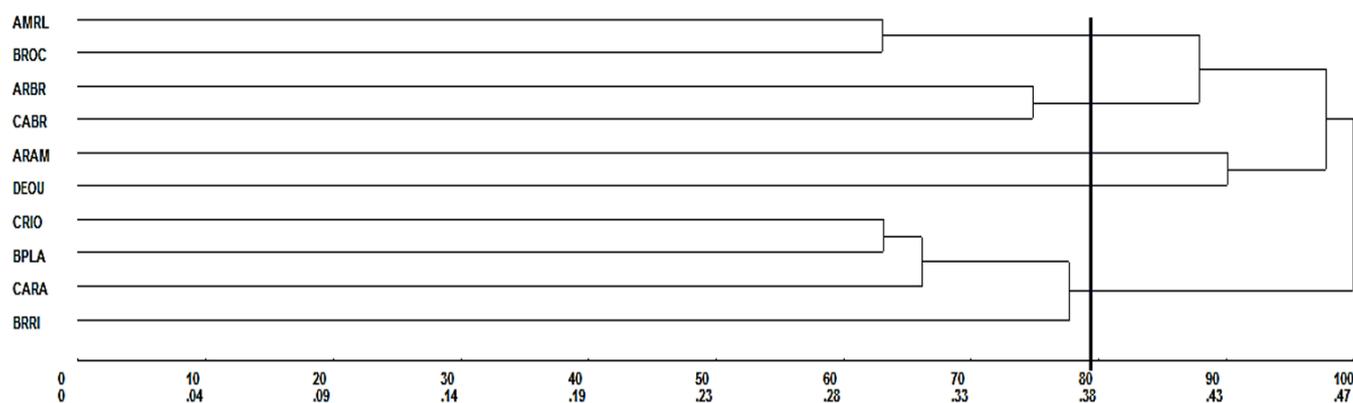
It is interesting for plant breeding to achieve great genetic variability in order to stablish selective processes that effectively result in significant gains (Bernardo 2002). Considering it, the determination of heritability patterns allows the breeder to accurately infer about selection and conduction of progenies and lineages in the next generations. In the progenies Caiano Rajado (CARA), Criolão (CRIO), Branco Roxo Índio (BRRI), BRS Planalto (BPLA), Dente de Ouro (DEOU), Amarelão (AMRA) and Branco Oito Carreiras (BROC), it was observed similar heritability patterns for the set of evaluated traits (Figure 1). In contrast, the progenies Argentino Amarelo (ARAM), Argentino Branco (ARBR) and Cateto Branco (CABR) present specific heritability patterns, since they constituted isolated groups. For the progeny Argentino Amarelo, it is possible to justify the formation of an isolated group due to this progeny evidencing the highest heritability estimates for the set of studied traits. However, in the progenies Argentino Branco and Cateto Branco, the selection of the traits spike mass and number of days for flowering,

respectively, should be carefully considered, as they were the traits that most influenced for separating these progenies. Falconer (1981) points out that all genetic components are influenced by genic frequencies and may differ from one population to another.



**Figure 1. Dendrogram of the broad sense heritability pattern established by the UPGMA hierarchical method, based on the mean Euclidean distance, for ten S1 progenies from landrace maize populations (AMRL: Amarelão; ARAM: Argentino Amarelo; ARBR: Argentino Branco; BROCC: Branco Oito Carreiras; BRR1: Branco Roxo Índio; CARA: Caiano Rajado; CABR: Cateto Branco; CRIO: Criolão; DEOU: Dente de Ouro; BPLA: BRS Planalto). The cutoff point (CP) consists of the mean distance plus one standard deviation.**

The analysis of genetic distance is related to the specific ability of the genitors to combine and demonstrate the importance of non-additive interactions, characterized by complementarity in relation to the frequency of alleles in loci with some dominance between genitors (Sprague and Tatum 1942). In addition, the genetic distance between genitors is indicative of the heterotic expression in the progenies (Falconer 1981). Thus, the genetic variation distance of S1 progenies from landrace maize populations estimated by the mean Euclidean distance and grouped by the UPGMA method, revealed the formation of five groups, being the group I formed by the progenies Amarelão (AMAR) and Branco Oito Carreiras (BROC), group II constituted by the progenies Argentino Branco (ARBR) and Cateto Branco (CABR), group III composed only by the progeny Amarelão (ARMA) (Figure 2). Group IV was also composed by only one progeny, Dente de Ouro (DEOU). Group V was composed by the largest number of progenies, being them Criolão (CRIO), BRS Planalto (BPLAN), Caiano Rajado (CARA) and Branco Roxo Índio (BRR1) (Figure 2).

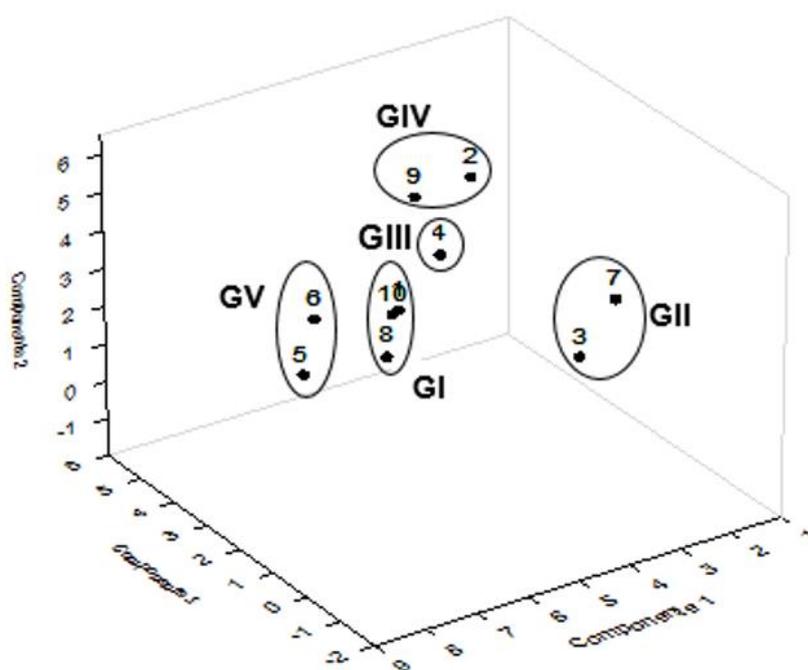


**Figure 2. Dendrogram of the broad sense heritability pattern established by the Unweighted Pair Group Method with Arithmetic Mean (UPGMA), based on the mean Euclidean distance, for ten S1 progenies from landrace maize populations (AMRL: Amarelão; ARAM: Argentino Amarelo; ARBR: Argentino Branco; BROCC: Branco Oito Carreiras; BRR1: Branco Roxo Índio; CARA: Caiano Rajado; CABR: Cateto Branco; CRIO: Criolão; DEOU: Dente de Ouro; BPLA: BRS Planalto). The cutoff point (CP) consists of the mean distance plus one standard deviation.**

For a satisfactory interpretation of the variability between genotypes or progenies, it is necessary that the three main components provide a minimum estimate of 70% of the total variation contained in the set of traits (Cruz et al. 2004). Three main components were required to explain 69.00%, thereby, it was necessary to represent the

graphic dispersion in three dimensions (3D) to expose the genetic variation between S1 progenies, being possible to satisfactorily explain the variability manifested between these progenies.

The main components provided a visual formation of five progeny groups. Group I was composed by the progenies Amarelão, Criolão and BRS Planalto, group II was constituted by the progenies Argentino Branco and Cateto Branco (Figure 3). Group III was formed only by progeny Branco Oito Carreiras. Group IV contemplated the progenies Argentino Amarelo and Dente de Ouro, and group V was composed by progenies Caiano Rajado and Branco Roxo Índio. The identification of the distance between group genetic variances of S1 progenies allows the breeder to predict selection strategies which can be applied according to each group. In addition, the greater the variability within the progenies, the greater is the possibility of extracting promising genetic constitutions from the traits of interest.



**Figure 3. Graphical dispersion of the genetic variance estimates verified by the principal componentes analysis in ten S1 progenies from landrace maize populations, being 1: Amarelão; 2: Argentino Amarelo; 3: Argentino Branco; 4: Branco Oito Carreiras; 5: Branco Roxo Índio; 6: Caiano Rajado; 7: Cateto Branco; 8: Criolão; 9: Dente de Ouro; 10: BRS Planalto.**

The identification of groups performed by the clustering method proposed by Tocher from the mean Euclidean distances created five distinct groups (Table 2), where the first group consisted of the progenies Argentino Branco, Branco Roxo Índio and Branco Oito Carreiras. Group two was composed of the progenies Argentino Amarelo, Criolão and Cateto Branco. The third group was formed by progenies Dente de Ouro and BRS Planalto. The fourth group contemplated only the progeny Amarelão. The fifth group consisted of the progeny Caiano Rajado (Table 2). Therefore, it is possible to indicate that the progeny Caiano Rajado has genetic variation distinguishable from the others, being this genetic variation composed of additive and nonadditive effects.

The groups formed by the three multivariate clustering methods using genetic variances presented specific results, with no concordant results among the methods. However, experimental evidence proves that the multivariate analyzes are efficient to discriminate individuals genetically, allowing them to be grouped in a way that there is homogeneity within the group and heterogeneity between groups, even though there are particularities in the formation of groups depending on the algorithm or the mathematical equation used by each method (Hair et al. 2005).

The relative contribution by Singh (1981) revealed that spike length (13.10%), grain depth (11.58%), plant height (11.39%), tassel main stem length (10.00%) and spike diameter (10.00%) were the traits that most contributed to explain the differences expressed by the genetic variation verified in the S1 progenies (Table 3). The importance of Singh's relative contribution lies in the possibility of discarding the traits that least contributed to explain the genetic variance, reducing time and cost of evaluations (Cruz et al. 2004). However, since all evaluated traits are important and of interest in the search for promising progenies, and no trait with low contribution were evidenced, the exclusion of traits is not recommended in this study.

**Table 2. Groups of S<sub>1</sub> progenies from landrace maize populations established by the Tocher method, based on the dissimilarity of the genetic variances expressed by the mean Euclidean distance.**

Group	S <sub>1</sub> Progenies
I	Argentino Branco; Branco Roxo Índio; Branco Oito Carreiras
II	Argentino Amarelo; Criolão; Cateto Branco
III	Dente de Ouro; BRS Planalto
IV	Amarelão
V	Caiano Rajado

**Table 3. Relative contribution of the genetic variances estimates of ten agronomic traits inferred in ten S<sub>1</sub> progenies derived from landrace maize populations by Singh's (1981) methodology.**

Agronomic trait	Relative Contribution (%)
SH <sup>(1)</sup>	9.48
PH	11.39
SD	7.21
TSL	10.01
NRT	9.89
NDF	9.88
SKD	10.00
SL	13.10
SM	7.44
GD	11.57

<sup>(1)</sup> 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.

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