

## VARIABILITY OF CORN GENOTYPES IN THE BRAZILIAN AMAZON-CERRADO TRANSITION ZONE

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**Abstract** – The study of genotype divergence allows combinations of promising strains of hybrids aiming at higher productivity. Corn today has great importance and application for its prominence as a source of carbohydrates and vitamins in human food and in the formulation of animal feed. The geographic zone of transition between the Cerrado and the Brazilian Amazon Rainforest is a source of new corn genotypes that can be used at intersections. Thus, the genetic divergence of corn genotypes was estimated that allowed their combinations for greater grain yield and quality. The studies were conducted in the off-season of 2010.7 agronomic characteristics were used in a multivariate model in 6 genotype groups using the Tocher optimization method. Results were presented according to Mahalanobis (D2) distances, with combinations P13 x P17 and P9 x P17 the most promising for grain yield, diameter, and height of the spike.

### INTRODUCTION

Genetic divergence studies are important for the knowledge of genetic variability existing in germplasm banks, enabling monitoring, assisting in the identification of possible duplicates and providing parameters for choosing parents, who when crossed, allow greater heterosis effect, increasing the chances of obtaining higher genotypes in segregating generations (Cruz *et al.*, 2014). According to Fu *et al.* (2014) heterosis the superiority of vigor of hybrids in relation to their parents, varying according to the genetic distance of parents, and may provide increases of 15 to 50% in crop yield.

In the programs of improvement of corn heterosis and depression of inbreeding are phenomena of great importance. Thus, it is important to define heterotic groups which can lead to high performance and maximize corn production (Giraud *et al.*, 2017). In the USA, according to climatic aspects, the main hybrid lineages for corn production were defined, being known as heterotic

groups "Rigid Stalks" and the "Non-Rigid Stalks". While in Europe, the main heterotic groups are "Dent" and "Flint" Giraud *et al.* (2017).

In Brazil, specifically in the State of Tocantins, the average productivity of corn is low (4,517 kg ha<sup>-1</sup>) when compared to the national average (6,219 kg ha<sup>-1</sup>) De (2019) due, among other factors, the adverse climate conditions, combined with the low technological level employed by producers and the scarcity of cultivars improved for conditions of abiotic stress (Simon *et al.*, 2016); Santos *et al.* (2017). Thus, the employment and classification of heterotic groups in this Brazilian state is necessary for the adequacy of corn productivity due to climatic aspects and genetic divergence. The grouping techniques aim to divide an original group of genotypes into several homogeneous groups, following a similarity criterion. Among the most used grouping methods in plant breeding are the hierarchical and optimization methods. As an example of an optimization method, the one presented by Tocher Rao (1952), which has been extensively used in genetic divergence analyses of

various plant species (Paixão *et al.*, 2008; and Cruz *et al.*, 2014).

The use of multivariate techniques is also used to estimate genetic divergence in corn cultivars (Coimbra *et al.*, 2010; Dotto *et al.*, 2010; Carvalho *et al.*, 2011; Rotili *et al.*, 2012; Santos *et al.* (2014); Santos *et al.*, 2015; Silva *et al.* 2016; Santos *et al.*, 2017; Santos *et al.*, 2018). However, in the Brazilian amazon-cerradotr ansitionzone, there are still few studies on genetic divergence in corn genotypes. Therefore, the present study aimed to estimate the genetic divergence between corn genotypes to identify combinations of promising strains in obtaining superior hybrids and that can minimize the relationship of corn productivity in function of climatic aspects and genetic divergence.

## MATERIALS AND METHODS

The experiment was conducted at the experimental station of the Federal University of Tocantins–UFT on the Palmascampus, under dystrophic Yellow Red Latosol, with aw-type climate according to the Classification of Köppen Alvares *et al.*, (2013). The experimental design used was randomized blocks with 20 treatments and three replications. The treatments consisted of corn genotypes from the UFT breeding program, being named: P1, P2, P3, P4, P5, P6, P7, P8, P9, P10, P11, P12, P13, P14, P15, P16, P17, P18, P19, and P20.

The plot used consisted of four rows of five meters, spaced 0.9 m between lines. In the harvest, only the two central rows of each experimental unit were used, discarding 0.5 m from the ends of these rows. For soil preparation, grading was performed followed by the leveling of the area. Planting fertilization was performed manually, using 300 kg ha<sup>-1</sup> of N-P<sub>2</sub>O<sub>5</sub>-K<sub>2</sub> Formulation 5-25-15+0.5%Zn. Sowing was performed in the 2010 off season, manually in the groove at an average depth of 0.04 m. After emergence, thinning was performed leaving a spacing of 0.2 m between plants, to obtain a population of 55,555 plants ha<sup>-1</sup>.

Fertilization was performed in cover at stage V6, using urea nitrogen (45% N) as a source of nitrogen, at a dose of 333 kg ha<sup>-1</sup>. Cultural tracts, such as the control of infesting plants, diseases and pests were carried out according to the technical recommendations of the crop Borém *et al.*, (2015).

The harvest was performed when the plants reached stage R6 (physiological maturity). In the agricultural production laboratory - LPA of UFT, the

diameter, and length of an ear of 5 ears were measured by plots randomly using a digital caliper and the graduated ruler, respectively. To quantify the number of rows per ear and the number of grains per row, 5 ears were manually counted per plot spree randomly.

After harvested, the ears were trodden and the grains of each plot packed in a paper bag, which was identified by genotype and block. Productivity was determined per plot, corrected for 13% moisture and extrapolated to the hectare. The plant height and height of the ear were measured in stage R6 with the use of measuring tape, taking the distance from ground level to the last fully opened leaf, and until the insertion of the ear, respectively.

In order to study genetic divergence, the following characteristics were used as variables in the multivariate model: AP-plant height (cm), AE-spike height (cm), CE-ear length (mm), DE-spike diameter (mm), NFE - number of rows by ear, NGF - number of grains per row, RG - grain yield (kg ha<sup>-1</sup>).

The dissimilarities measures were determined according to the multivariate analysis model, which allowed the acquisition of matrices of dissimilarities and residual covariances and the means of populations. The Tocher grouping method was applied, using the generalized Mahalanobis distance (D2) Mahalanobis (1936), and Singh criterion (Singh, 1981) to quantify the relative contribution of the seven characteristics evaluated. Statistical analyses were performed using the Computational Genes program, version 2007.

## RESULTS AND DISCUSSION

Variance analysis revealed a significant difference by f test ( $p < 0.05$ ) between corn lines for all characteristics evaluated. The coefficient of variation (CV) for grain yield (5.10%) was classified as low, indicating good experimental accuracy Pimentel-Gomes (2009). For the variables, plant height (3.27%), spike height (7.37%) ear length (3.74%), spike diameter (4.39%) and number of rows per ear (4.91%) CV close to those found by Paixão *et al.*, (2008); Coimbra *et al.* (2010) and Dotto *et al.*, (2010).

Genetic dissimilarity measurements, estimated from Mahalanobis distance (Figure 1), showed high magnitude (1.83 to 144.24), and demonstrate the presence of genetic variability among the genotypes evaluated.

The combination P13 x P17 (Figure 1) was the

most divergent (D2 = 144.24), followed by the combination P9 x P17 (D2 = 130.87). The shortest distance was observed by genotypes P4 x P11 (D2 = 1.83), followed by pair P7 x P4 (D2 = 2.71).

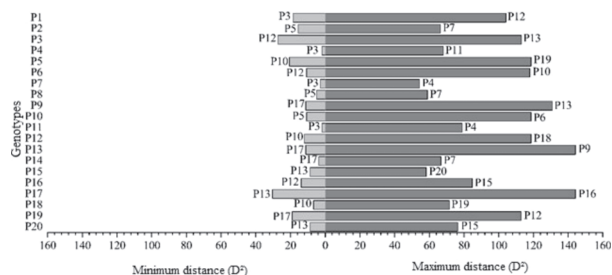


Fig. 1. Estimation of the maximum and minimum Mahalanobis (D2) distances of corn genotypes.

The shortest distance between P4 and P11 (Fig. 1) occurred probably due to the genotypes of these combinations from very close germplasms. In breeding programs, hybridization between genotypes with less genetic distance should be avoided, i.e., more similar, since it would decrease the success of hybrids with desirable characteristics. Since to achieve maximum heterosis it is necessary to combine genotypes that complement each other, i.e. on the loci where one has unfavorable alleles the other has favorable alleles.

The cluster analysis seeks the formation of different groups of genotypes, where the reishomogeneity with in and heterogeneity between them Cruz *et al.*, (2014). For this, first the dissimilarity measures are obtained (Figure 1), then a grouping technique is adopted. Using the Tocher optimization method, it was possible to classify genotypes into six groups (Figure 2).

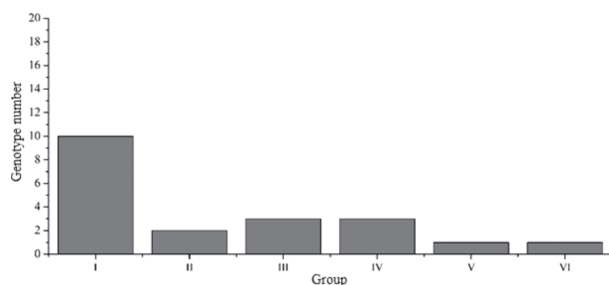


Fig. 2. Grouping by the tocher method, based on the dissimilarity expressed by the widespread Mahalanobis distance.

A large group consisted of 10 genotypes (50% of genotypes), a group with two genotypes, two groups with three genotypes and two groups consisting of only one genotype. According to Cruz

*et al.*, (2011) groups formed by only one genotype point in the direction that it is more divergent than the other.

It is noteworthy that the genotypes that constituted the most divergent pairs (Figure 1), based on a Mahalanobis distance matrix, were allocated in distinct groups by the Tocher optimization method (Figure 2). The differences presented in the composition of the groups (Figure 2) can be explained by the expression or non-expression of the favorable alleles present in the genotypes.

Estimates of the relative contribution of the five characteristics evaluated in the genetic dissimilarity of the 20 genotypes studied are presented in Figure 3. The characteristics that most contributed to divergence were grain yield (35.99%), followed by the height of the ear (17.71%) and spike diameter (14.00%). The characteristic that presented the lowest contribution was number of grains perrow (4.16%). Working with eight characters Rotili *et al.* (2012) also found grain yield, gas diameter and spike height as the most contributing.

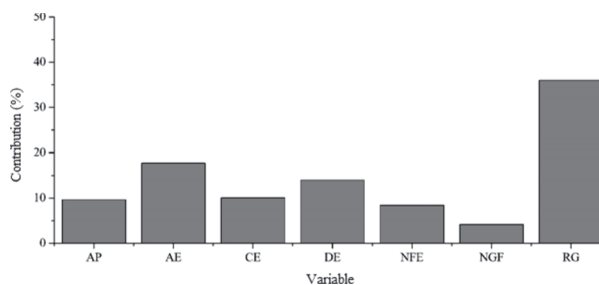


Fig. 3. The relative contribution of characteristics in the genetic dissimilarity of genotypes

According to Cruz *et al.*, (2014) the characteristics of lesser importance are those that have lower variability or are represented by others. Then variables with less importance, such as number of grains perrow, could be disregarded in future genetic divergence analyses, which would provide a reduction of theme, labor and costs in experimentation Oliveira *et al.*, (2006).

The analysis of Mahalanobis distances (Figure 1), together with the grouping established by the Tocher method (Figure 2), allowed the identification as promising genotypes P13 x P17 and P9 x P17.

CONCLUSION

1. Genotypes P13 x P17 and P9 x P17 are promising in obtaining higher hybrids.

2. The characteristics that most contributed to genetic divergence were grain yield, spike height and spike diameter.

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