ISSN: 2230-9926

Available online at http://www.journalijdr.com

IJDR

International Journal of Development Research
Vol. 10, Issue, 10, pp. 41084-41088, October, 2020
https://doi.org/10.37118/ijdr.20145.10.2020

RESEARCH ARTICLE OPEN ACCESS

GENETIC DIVERGENCE OF SWEET SORGHUM GENOTYPES BASED ON MORPHOAGRONOMIC CHARACTERS BY MULTIVARIATE TECHNIQUES

Taniele Carvalho de Oliveira[1]*, Marco Antonio Aparecido Barelli[1], Rafhael Felipin Azevedo[1], Danilo de Lima Gonçalves[1], Paulo Ricardo Junges dos Santos[1], Valvenarg Pereira da Silva[1], Altacis Junior de Oliveira[1], Flávio Dessaune Tardin[2], Rafael Augusto da Costa Parrella[2]

[1]Laboratório de Recursos Genéticos & Biotecnologia, Departamento de Agronomia, Universidade do Estado de Mato Grosso, Cáceres, Mato Grosso, Brasil; [2]Empresa Brasileira de Pesquisa Agropecuária, Centro Nacional de Pesquisa em Milho e Sorgo. Sete Lagoas, Minas Gerais, Brasil

ARTICLE INFO

Article History:
Received 07th July, 2020
Received in revised form
14th August, 2020
Accepted 15th September, 2020
Published online 24th October, 2020

Key Words:
Genetic diversity, Morphoagronomic Characteristics, *Sorghum bicolor* (L.) Moench.

Corresponding author:
Taniele Carvalho de Oliveira

ABSTRACT

The sweet sorghum apart from being used as food, feed and fiber, is also an excellent source for production of alcohol biofuel due to its high content of soluble sugars in the plant stalk sap), little has been researched about genetic diversity. The objective of this research was to evaluate the genetic divergence of sweet sorghum genotypes based on morphoagronomics characteristics. Twenty-five genotypes of sweet sorghum were evaluated in a randomized blocks design and the variables analyzed were: number of days to flowering; plant height; number of stalks per hectare; green mass production; dry mass production; number of leaves; diameter of stalks; volume of extracted juice and percentage of total soluble solids. The genetic diversity of genotypes was estimated based on the *Mahalanobis* distance as dissimilarity measure for the clustering structure we used the method of Tocher, UPGMA and canonical variate analysis. Groups generated demonstrated similarity in clustering genotypes, with more similar combinations remained in the same group in both clustering methods and most dissimilar combinations were isolated. The genotypes CMSXS644 and 201027018 were most are dissimilar the genetically and the characters that contribute most to the genetic diversity among the genotypes analyzed were PH and FLOWER.

Citation: ***Taniele Carvalho de Oliveira, Marco Antonio Aparecido Barelli, Rafhael Felipin Azevedo, Danilo de Lima Gonçalves, Paulo Ricardo Junges dos Santos et al., 2020.*** "Genetic divergence of sweet sorghum genotypes based on morphoagronomic characters by multivariate techniques", *International Journal of Development Research*, 10, (10), 41084-41088.

INTRODUCTION

Sweet sorghum (*Sorghum bicolor* L.) Moench belongs to the Poaceae´s family, resembles sugarcane because it has succulent stems and high levels of fermentable sugars, as well as potential for use in forage production (ASIKIN *et al*., 2018). Sorghum culture has been standing out nationally in the agricultural context for its excellent productivity and its energy components (FEITOSA, 2019). There are studies that indicate the feasibility of using S. bicolor in sugarcane harvesting in Brazil, providing the plants with anticipation and expansion during the milling period (GIACOMINI *et al*., 2013; WILLIS *et al*., 2013). The crop is a renewable source capable of contributing to the increase in the production of ethanol, and can be used as a complementary crop to sugarcane in areas of reform, areas considered marginal to sugarcane or areas that have not been contemplated in the zoning of climate risks (EMYGDIO *et al*., 2011; ASIKIN *et al*., 2018). The sweet sorghum has wide genetic variability (HUD *et al*., 2016), and this variability is essential in the breeding programs of practically all the characters of economic importance. In general, the selection of parents should take into account populations that associate high average and broad genetic variability for the characters of interest (COSTA *et al*., 2008). Among the different measures of dissimilarity proposed for the quantification of distances between genotypes, the generalized distance of *Mahalanobis* has been widely used when experiments with repetitions are available, since this one differs from the other techniques by taking into account the correlations between the evaluated characters (CRUZ and REGAZZI, 2001; MEENA *et al*., 2016).The use of multivariate techniques to estimate genetic

divergence has become common in different species, such as in research aimed at breeding sorghum (GELETA *et al*., 2006; SÁVIO *et al*., 2008; QUINTERO *et al*., 2012; ILYAS *et al*., 2018). Currently, sugar sorghum is one of the most promising species to increase ethanol production in Brazil. Besides presenting such characteristics, the culture has a wide genetic diversity, being important for the maintenance of genetic improvement programs, and speed up the process of generating a new cultivar. Therefore, the objective of this work was to evaluate the genetic divergence of sweet sorghum genotypes based on morphoagronomic characters, using multivariate techniques.

MATERIAL AND METHODS

The experiment was conducted in the experimental area of the Laboratory of Genetic Resources & Biotechnology (LRG&B), of the Universidade do Estado de Mato Grosso (UNEMAT), county of Cáceres, state of Mato Grosso (latitude of 16°04'59" South and longitude of 57°39'01" West), with an altitude of 118 m, in a dystrophic yellow red Latosol. The climate of the region according to classification of Köppen is tropical hot and humid, with dry winter (Awa). The highest average temperatures occur in the wet season and the lowest in the dry period, configuring the local climate in two defined seasons, with period of rains varying from October to March, and drought from April to September. Twenty five sweet sorghum genotypes were evaluated assigned by the Genetic Improvement Program of the Embrapa Corn and Sorghum: 1-BR501, 2-BR505, 3-BRS506, 4-BRS509, 5-CMSXS630, 6-CMSXS634, 7-CMSXS642, 8-CMSXS643, 9-CMSXS644, 10-CMSXS646, 11-CMSXS647, 12-CMSXS648, 13-201027013, 14-201027014, 15-201027015, 16-201027016, 17-201027017, 18-201027018, 19-201027019, 20-201027020, 21-BRS601, 22-Sugargraze, 23-V82391, 24-V82392 and 25-V82393. Planting was carried out under no-tillage conditions, using a randomized blocks design, with three replications, where each plot was composed of four rows with 5 m with spacing of 0.7 m between rows, with only the two central rows considered as useful area. For the preparation of the area, harrowing was performed and the fertilization was done based on the soil analysis and according to the recommendation of the crop, applying 150 kg ha^{-1} of the mineral formulation 20-05-20 N-P_20_5-K_2O and 375 kg ha^{-1} of P_20_5 for planting and cover fertilization was applied at 45 days using 89 kg ha^{-1} of N. The genotypes were harvested when the grains presented in the hard/farinaceous stage, approximately 113 days after planting.

The characteristics evaluated were: number of days elapsed from sowing until the date when 50% of the plants of the plot were with at least the flowers of the upper third of the panicle releasing pollen (FLOWER); average height of ten plants (PH) in m; number of stems per hectare (NS); production of green mass of five whole plants, without panicle (PGM) in kg; production of dry mass of five whole plants, without panicle (PDM) in kg, dehydrated in a forced aeration oven at 65 °C for 72 hours; average number of leaves of ten plants (NL); average stem diameter of ten plants (SD) in mm; average broth volume extracted from eight whole plants, without panicles (VB) in one ha^{-1} and total soluble solids (BRIX) determining the percentage of total soluble solids. Genetic divergence of genotypes was estimated from the generalized distance of *Mahalanobis* as a measure of dissimilarity. For the grouping of genotypes, the Tocher method of optimization and analysis of canonical variables were used, using the computational resource GENES (CRUZ, 2013) and the clustering analysis by Unweighted pair-group method with arithmetic averaging (UPGMA) used the computational program R.

RESULTS AND DISCUSSION

The measures of genetic dissimilarity, estimated from the Generalized Distance of *Mahalanobis* ($D^2_{ii'}$) showed a magnitude of 2.37 to 249.82, indicating the presence of wide genetic variability for the evaluated genotypes. The combination between CMSXS644 and 201027015 ($D^2_{ii'}$ = 249.82) was the most divergent, followed by the combination between CMSXS644 and 201027017 ($D^2_{ii'}$ = 221.53), since these pairs of genotypes showed the highest estimates. SINGH *et al*. (2008) found similar results when studying 32 genotypes of sorghum, where they obtained Generalized Distance of *Mahalanobis* from 14.31 to 125.10, being the lowest divergence observed among the pairs CMSXS630 and CMSXS643 ($D^2_{ii'}$ = 2.37) and between genotypes BR505 and V82392 ($D^2_{ii'}$ = 4.09). The clustering of genotypes performed by the Tocher optimization method allowed the formation of eight groups (Table 1). Group I was the most numerous, accounting for 56.0% of the genotypes, with the greatest dissimilarity in this group represented between genotypes BRS506 and V82392 (39.41) and the less dissimilarity in this group among the genotypes CMSXS630 and CMSXS643 (2.37).

Group II collected only three genotypes of the total evaluated (12.0%), showing less genetic dissimilarity between the genotypes 201027015 and 201027017 (5.06) and greater dissimilarity between 201027015 and 201027016 (16.31). Groups III and VI presented formation with only two genotypes (8.0%), in which the genotypes 201027014 and 201027019 (23.96), CMSXS646 and CMSXS642 (24.17) respectively, thus characterizing a good degree of divergence.

Table 1. Representation of the cluster generated by the Tocher optimization method based on dissimilarity among 25 sweet sorghum (*Sorghum bicolor* L.) genotypes

Groups	Genotypes	% of Genotypes
I	CMSXS630, CMSXS643, CMSXS648, BR505, 201027020, BRS506, BRS509, CMSXS634, Sugargraze, CMSXS647, BRS601, V82391, V82392 e V82393	56.0
II	201027015, 201027016 e 201027017	12.0
III	201027014 e 201027019	8.0
IV	CMSXS642 e CMSXS646	8.0
V	CMSXS644	4.0
VI	201027018	4.0
VII	201027013	4.0
VIII	BR501	4.0
Total	25	100.0

The groups V, VI, VII and VIII were the least expressive, formed by only one genotype, CMSXS644, 201027018, 201027013 and BR501 respectively, suggesting that these genotypes are the most divergent of the total analyzed. Benitez *et al*. (2011) a ocorrência de grupos com apenas um genótipo evidencia ampla divergência, já que os genótipos em grupos unitários são mais dissimilares em relação ao conjunto.

MOHAMMADI and PRASANNA (2003) highlight that, through grouping analysis, genetically more dissimilar genotypes can be identified by reducing the number of combinations required in a breeding program. Similar results were found by FAGUNDES *et al*. (2013), where evaluating 45 sweet sorghum genotypes in the county of Lavras, state of Minas Gerais, obtained the formation of four distinct groups, where the first group collected 86.6% of the evaluated genotypes. The results obtained from the Tocher optimization method, with which intra and intergroup dissimilarity were determined, showed that the largest average intragroup distance was observed in group III (d_{III} = 24.75), while the lowest intragroup distance was verified in group II (d_{II} = 9.64). The intragroup distances were lower than any intergroup distance, corroborating with the criteria established for the Tocher optimization method (CRUZ and CARNEIRO, 2003). The greatest intergroup distances were observed between groups II and V ($d_{II;V}$ = 226.98), II and VII ($d_{II;VII}$ = 168.07), III and V ($d_{III;V}$ = 144.50), corresponding the major divergences between groups and indicating possibly the best combinations for crossing. On the other hand, the smaller intergroup distances were obtained between groups I and VIII ($d_{I;VIII}$ = 31.43), I and VII ($d_{I;VII}$ = 36.02) and between V and VII ($d_{V;VII}$ = 36.98). The smaller intergroup distances indicate that the cross between genotypes of these groups should not be indicated to obtain superior genotypes because they present low genetic dissimilarity (RAJARAJAN*et al*., 2016). Based on the UPGMA grouping method, submitted to a significant cut of 30% genetic distance, it allowed the division of genotypes into seven distinct groups (Figure 01). The Cophenetic Correlation Coefficient (CCC), applied to the clustering method by the t-test presented satisfactory adjustment, with significant values ($P \leq 0.01$) for the UPGMA method ($r \geq 0.72$), demonstrating reliability in the relationship between the dissimilarity matrix and the dendrogram generated by UPGMA.

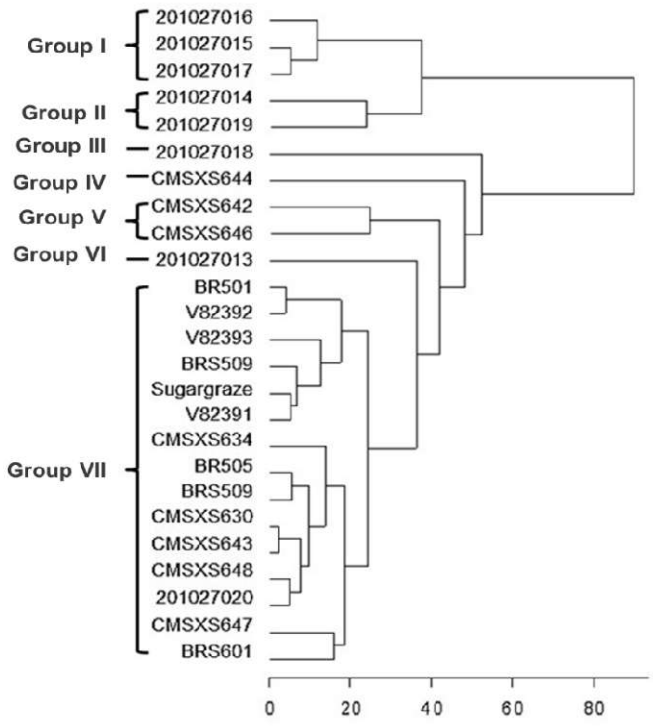

Figure 1. Dendrogram representative of the grouping of twenty-five genotypes of sweet sorghum (*Sorghum bicolor* L.), by UPGMA Method, based on the dissimilarity estimated from nine morphoagronomic characteristics

This grouping formed more groups, compared with BERTAN *et al*. (2006), comparing grouping methods in the representation of the morphological distance genotypes, where the UPGMA method constituted five groups for the 19 evaluated genotypes. Work conducted by KOLLING *et al*. (2014), also presented lower number of groups generated, four, when evaluating eight morphoagronomic characteristics for sorghum. In the present study, there was a greater number of groups produced indicating high dissimilarity among the evaluated genotypes. Among the groups formed by the dendrogram, group I consists of two of the twenty-five genotypes analyzed, allocating the genotypes 201027016, 201027015 and 201027017 for showed fewer days for flowering. Group II is constituído by genotypes 201027014 and 201027019 because they have a smaller DS. Groups III and IV are generated by only one genotype each, 201027018 and CMSXS644, respectively. Where the group III having as main characteristic greater percentage of Brix, and group IV greater NS. The group V was formed by only two of the twenty-five genotypes evaluated (CMSXS642 and CMSXS646) because they had higher PH. The group VI is constituídoby only one genotype (201027013) having as main characteristic greater NL and greater PDM. The group VII was considered the most numerous, allocating sixteen of the twenty-five genotypes, allocating the genotypes BR501, V82392, V82393, BRS509, Sugargraze, V82391, CMSXS634, BR505, BRS509, CMSXS630, CMSXS643, CMSXS648, 201027020, CMSXS647 and BRS601 because they present higher PGM and higher VB.

Both methods showed similarity in the clustering of genotypes, however, the composition was somewhat different in the Tocher method. This difference in the groups formed by the two methods was in relation to the genotypes of group VIII, generated by the Tocher method, which incorporated the group VII of the UPGMA method, which brings together fifteen of the twenty-five evaluated genotypes. CASTRILLON *et al.* (2017) also found in both methods composition partially concordant in the grouping of genotypes. The other groups formed showed similarity in the clustering of the genotypes. These results corroborate with CAMPOS *et al*. (2010) where they characterized the genetic divergence in cassava (*Manihot esculenta* L.) accesses, in the county of Cáceres, state of Mato Grosso, concluding that the clustering methods of Tocher and Hierarchical Optimization UPGMA, presented close results in the formation of groups. SIMON *et al*. (2012), evaluating the genetic divergence among 19 simple corn (*Zea mays* L.) hybrids grown in the summer and in the outcrop season in the county of Rio Verde, state of Goiás, observed that both grouping methods similarly allocated the hybrids in groups with greater genetic equivalents. As for the analysis by canonical variables (CV), the first three (CV1, CV2 and CV3) were sufficient to represent 85.67% of the total variance of the genotypes, 60.09% for the first, 17.78% for the second and 7.80% for the third, so that genetic divergence can be evaluated in a three-dimensional space facilitating the geometric interpretation. In the graph of dispersion of genotypes, based on the first three canonical variables, arranged in three-dimensional space (Figure 2), it is observed the formation of seven groups. The groups I, formed by the genotypes: 15, 17 and 16 (201027015, 201027017, 201027016, respectively), groups II, IV and VI were composed by only two genotypes each (19: 201027019 and 14: 201027014), (3: BRS506 and 11: CMSXS647) and (10: CMSXS646 and 17: 201027017), respectively.

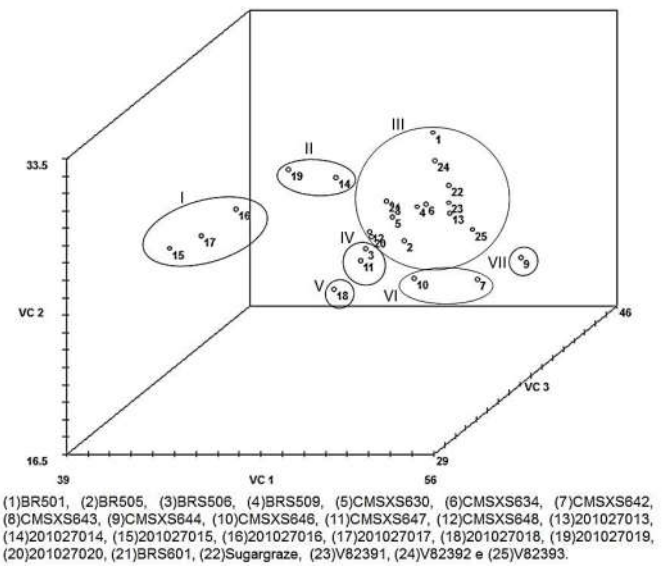

Figure 2. 3D graphic dispersion of twenty-five sweet sorghum (*Sorghum bicolor* L.) genotypes in relation to the first three canonical variables established by the combination of nine morphoagronomic characteristics

Group III was the most numerous, composed of genotypes 1, 24, 22, 23, 13, 25, 4, 6, 2, 5, 12, 8, 20 and 21 (BR501, V82392, Sugargraze, V82391, 201027013, V82393, BRS509, CMSXS634, BR505, CMSXS630, CMSXS648, CMSXS643, 201027020 and BRS601, respectively). Groups V and VII were formed by only one genotype each (18: 201027018) and (9: CMSXS644), respectively. Similar genotypes were ordered in similar groups, identifying and isolating the most divergent in distinct groups, indicating great genetic divergence among the twenty-five genotypes of sweet sorghum. Similar to results found by CASTRILLON *et al*. (2017), regarding the formation of the groups, it was observed agreement with the previous groupings, the groups constituted through the graphic dispersion of the scores were similar to the groups generated in the clustering analyzes, using the hierarchical method (UPGMA) (Figure 01) and the distribution of groups with similar patterns of behavior by the Tocher´s Method (Table 01). With the exception of the genotypes of group IV produced in the graphic dispersion (3: BRS506 and 11: CMSXS647) that in both Tocher and UPGMA clustering methods were part of group I and V, respectively, forming in this case an isolated group. And the genotype group VII and VI of the Tocher and UPGMA grouping methods, respectively, were incorporated into group III of the graphic dispersion.

The analysis to estimate the relative contribution of each character to the expression of genetic divergence according to the method of SINGH (1981) indicated that the characters PH (48.73%) and FLOWER (26.86%) contributed the most total divergence among the twenty-five sweet sorghum genotypes evaluated. These results evidenced the importance of PH and FLOWER in discriminating genotypes, indicating that these characters should not be discarded from future evaluations. These results demonstrate the importance of plant height and flowering in the discrimination of genotypes, indicating that these characters should not be discarded from future evaluations. VOGT *et al*. (2010) evaluating the genetic divergence among seventeen sunflower cultivars based on morphological and physiological characters in the northern of the state of the Santa Catarina, Brazil, observed that the PH and FLOWER characters contributed most to the total divergence. According to the results of genetic divergence of the sweet sorghum genotypes analyzed in this research it is suggested for combinations for hybridizations with the following materials: CMSXS642 x CMSXS644; CMSXS642 x 201027018; CMSXS646 x CMSXS644; CMSXS646 x 201027018; CMSXS647 x CMSXS644 and CMSXS647 x 201027018.

Conclusions

There is genetic variability among sweet sorghum genotypes for the morphoagronomic characteristics and the established clusters can help the breeder to choose the crosses to be made in breeding programs that see the generation of segregant populations with higher characteristics. The genotypes CMSXS644 and 201027018 were most are dissimilar the genetically and the characters that contribute most to the genetic diversity among the genotypes analyzed were PH and FLOWER.

Acknowledgements

The authors are grateful to Fundação de Amparo à Pesquisa do Estado de Mato Grosso (FAPEMAT) and Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq) for granting a scholarship and to Embrapa Milho e Sorgo for support in conducting the experiments.

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