








GENETIC DIVERSITY AMONG CASSAVA GENOTYPES (*Manihot esculenta crantz*) COLLECTED IN THE SOUTH-CENTRAL MESOREGION OF THE STATE OF MATO GROSSO-BRAZIL

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Abstract

The aim of this research was to evaluate the genetic divergence between 164 genotypes of *Manihot esculenta* from the South-Central mesoregion of the State of Mato Grosso. The genotypes are from projects conducted by the Laboratory of Genetic Resources & Biotechnology of the University of the State of Mato Grosso, Cáceres-Mato Grosso (UNEMAT), and the Brazilian Public Agricultural Research Corporation - Agrosilvopastoral (EMBRAPA). The agronomic descriptors evaluated were plant height, height of first branching, branching levels, weight of the aerial part of the plant, total weight of the plant, number of roots per plant, average weight of roots per plant, yield of commercial roots, yield of non-commercial roots, number of rotten roots per plant and harvest index. For the analysis of genetic divergence, multivariate analysis based on the standardized Euclidean mean distance was employed, later performing the Hierarchical UPGMA and Tocher Optimization agglomerative methods. The degree of preservation of the genetic distances in the dendrogram was verified using the Cophenetic Correlation Coefficient. The Singh criterion was used to quantify the relative contribution of characteristics to genetic divergence. The genotypes presented genetic dissimilarity for the evaluated characteristics and based on the results of the dissimilarity matrix and groupings, it is recommended the crossings between the genotypes allocated in group II with the genotype allocated in group V, for the development of segregated populations with high genetic variability.

Keywords: Agronomic Descriptors. Genetic Dissimilarity. Genetic Improvement.

1. Introduction

Cassava (*Manihot esculenta* Crantz) is of great importance for the survival of millions of people. This crop is considered one of the main sources of carbohydrates, being a staple food predominantly for people in Latin America and Africa (Alvarez et al. 2007), who use both tuberous roots as a rich source of starch and leaves as a source of proteins, minerals, and vitamins, mainly vitamin C (Ceballos 2012).

In Brazil, cassava is cultivated in practically all states, presenting a wide genetic variability with varieties adapted to different eco-geographical regions (Galera and Valle, 2007). The vast genetic diversity is because Brazil is the probable center of origin and diversification of cassava (Gulick et al. 1983; Allem 1994) and the central region of the country is the primary center of diversity of this culture (Lorenzi and Dias 1993;

Nassar 2000), considering the expressive number of species of the genus (38 out of 98 species) identified in this region.

It is estimated that in Brazil around 4,132 genotypes have already been cataloged, which are found in work collections and active germplasm banks distributed throughout the country (Fukuda and Alves 1997). However, for all this variability to be used continuously and efficiently, it is necessary that researchers know the variability of the available germplasm (Vieira et al. 2008).

The genetic diversity present in work collections and germplasm banks is of utmost importance because the success of any plant genetic improvement program is based on the presence of variability for characteristics that are desired to be improved. Thus, pre-improvement is essential to evaluate and characterize the available genetic resources, since it is through phenotypic expression that the presence and magnitude of diversity are inferred (Nick et al. 2010).

In general, pre-improvement surveys are performed using multivariate procedures based on dissimilarity measures, calculated from a set of characteristics, whether morphological, agronomic, molecular, or combined. In this context, this research aims to evaluate the genetic divergence of *M. esculenta* Crantz genotypes in the South-Central mesoregion of the State of Mato Grosso, based on agronomic characteristics.

2. Material and Methods

The experiment related to the evaluations of cassava genotypes was conducted on Red-Yellow Latosol soil, in the agricultural year 2014/2015, in the experimental area of the Laboratory of Genetic Resources & Biotechnology, belonging to the State University of Mato Grosso, Cáceres-MT (16°11'42" S and 57°40'51" O), approximately 118 m height. The climate of the region, according to Köppen's classification, is tropical, hot, humid, and dry winter (Awa), with a rainy season varying from October to April, and drought from May to September (Dallacort et al. 2014).

The 164 *M. esculenta* genotypes evaluated are from five municipalities located in the South-Central mesoregion of the State of Mato Grosso and belong to two projects. The genotypes collected in Cuiabá (EMCB), Jangada (EMJA) and Poconé (EMPO) belong to the project conducted by the Brazilian Public Agricultural Research Corporation - Agrosilvopastoral (EMBRAPA), the genotypes collected in Cáceres (UNCA) and Rosário Oeste (UNRO) belong to the project conducted by the Laboratory of Genetic Resources & Biotechnology, University of the State of Mato Grosso, Cáceres-MT.

For the planting, 10 "manivas" (cuttings) of approximately 20 cm of each genotype were placed into pits with 1.0 m x 1.0 m spacing to avoid competition among the clones. The cultural traits followed were those recommended for the Cerrado region by EMBRAPA - Cassava and Fruit-growing (Souza and Fialho 2003).

The agronomic characterization was carried out according to the descriptors proposed by Fukuda and Guevara (1998), evaluating characteristics of the aerial and root part at the time of harvest, established as 12 months after planting.

Eleven agronomic descriptors were evaluated:

Plant Height - Expressed in centimeters; considering the length that goes from the soil to the terminal branch.

Height of the first branch - Expressed in centimeters; the length that goes from the soil to the beginning of the first branch.

Branching levels - Number of times the plant branches counted before harvesting.

Weight of the aerial part of the plant - Expressed in kilograms (kg); weight of the aboveground parts of the cassava plant, excluding roots and the underground part of the cassava stem.

Total weight of the plant - Expressed in kilograms (kg), weight of all parts of the plant, except roots.

Number of roots per plant - Obtained from the average number of roots of five plants (commercial, non-commercial, and rotten).

Average weight of roots per plant - Expressed in kilograms (kg); obtained by the average weight of the roots (commercial, non-commercial, and rotten) of five plants.

Commercial root yield - Expressed in kg/ha⁻¹; result of the estimated productivity of the genotypes, considering only healthy roots and adequate to the commercial pattern.

Non-commercial root yield - Expressed in kg/ha^{-1} , considering only roots not suitable for commercial standard.

Number of rotten roots per plant - Obtained from the average number of rotten roots of five plants.

Harvest index - Quotient of the ratio of the weight of roots divided by the total weight of the aboveground plant.

To estimate genetic divergence between the genotypes were used the standardized Euclidean distance as a measure of dissimilarity. Based on the Euclidian matrix of dissimilarity were applied the Hierarchical UPGMA and Tocher Optimization agglomerative methods. The consistency of the dendrogram grouping was verified using the Cophenetic Correlation Coefficient (CCC) (Sokal and Rohlf 1962). The Singh (1981) criterion was also used to quantify the relative contribution of these characteristics to genetic divergence. All statistical analyses were performed on Genes software (Cruz 2013).

3. Results and Discussion

Based on the agronomic characterization performed on the 164 cassava genotypes, it was possible to highlight the variation amplitude of all evaluated characteristics. To the characteristic Plants' height, the amplitude variation was 3.5 m for the highest genotype (EMCB-11) and the lowest average height recorded was 0.70 m (EMPO-15). This wide variation for this characteristic was also evidenced by Afonso et al. (2020), evaluating 40 varieties of cassava in a survey carried out in Malanje, Angola, with values ranging from 113.82 to 325.65 cm.

It is possible that this variation is due to the influence of genotypic components expressed in varieties and environmental variations, as reported by Vitor et al. (2016) and Soares et al. (2017) when evaluating the effects on agronomic characteristics in cassava varieties at different harvest times. It is important to know that higher plants, as pointed by Fukuda et al. (2002) and Vieira et al. (2011a), exhibit easier cultural traits and less competition with weeds.

The average height of the first branch was 2.69 m, with the genotype EMCB-32 showing the higher height (2.76 m) and the genotype EMCB-27 the lowest (0.07 m). These average results are superior when compared to research carried out by Giles et al. (2018), evaluating 12 genotypes of *M. esculenta* in the state of Espírito Santo-Brasil, in which the average was 0.89 m.

Regarding the descriptor branch levels, two genotypes, UNCA-34 and EMCB-02 stood out among the others for presenting a high number of branches, 52 and 53 branches, respectively. The behavior of the genotype in relation to branching is an important indicator in the process of selection of genotypes in cassava genetic improvement programs. This characteristic is related to the ease of cultural traits, as mechanized planting, ease harvesting, and availability of cuttings. The preference is for genotypes that present greater height of the first branch or that do not present branching (Vidigal Filho et al. 2000; Fukuda et al. 2002; Vieira et al. 2011b). Barros et al. (2020) and Gomes et al. (2020), emphasize that the search for better adapted and productive genotypes is objective, paramount in breeding programs aimed at cassava culture.

The amplitude of variation for the descriptors weight of the aerial part of the plant and total weight of the plant was 19,800 kg and 23,280 kg, respectively. For both characteristics, four genotypes stood out with higher averages among the others, respectively for the weight of the aerial part of the plant and the total weight of the plant: EMPO-15 with 20,250 kg and 23,900 kg, EMCB-01 with 18,860 kg and 20,560 kg, EMCB-36 with 16,870 kg and 21,400 kg and EMCB-03 with 16,640 and 17,960 kg.

The production of the aerial part in cassava culture is important, since it is directly related to the supply of cuttings for new planting and soil cover, collaborating for erosion control, soil moisture maintenance, and weed control (Azevedo et al. 2006; Souza et al. 2011). Furthermore, the aerial part can be used as a source of protein in animal feed as silage, hay, or even fresh. The leaves are also used in human food, in the preparation of typical dishes of the North and Northeast regions of Brazil (Cardoso et al. 2006; Souza et al. 2011).

In relation to the descriptors that correspond to root yield, genotypes UNCA-21 and EMCB-03 stood out among the others, producing on average 21.4 and 18 roots per plant, respectively. As for the average number of rotten roots per plant, three genotypes stood out, UNRO-11 with an average of 3.6 rotten roots per plant, EMCB-08 with 3 rotten roots, and UNCA-23 with an average of 2.8 rotten roots per plant.

For the descriptors' average weight of roots per plant, two genotypes stood out - EMCB-16 and EMCB-35 – for presenting a greater average weight of roots per plant, producing 11.15 kg and 10.62 kg, respectively. For the estimated commercial roots yield, considering a density of 10.000 plants per hectare, the amplitude of variation was 0.406 t.ha⁻¹ to 111.5 t.ha⁻¹, with the genotype EMCB-16 being the most productive, obtaining approximately twice the productivity of the second most productive genotype - UNCA-38 (57.9 t.ha⁻¹). Although the genotype EMCB-35 had a great average number of roots per plant, it had the largest number of roots considered as non-commercial, with a yield of 106.2 t.ha⁻¹.

The average weight of roots per plant is a characteristic with great economic and marketing importance in cassava culture (Gomes et al. 2007). However, it is a character much influenced by the time of planting and environmental conditions, which makes it difficult to compare the results obtained (Silva et al. 2002; Kvitschal et al. 2003).

Under the experimental conditions that the genotypes of this research were submitted, approximately 40% of the genotypes obtained root yield (commercial and non-commercial) higher than the Brazilian average yield for cassava. In 2019, according to the Brazilian Institute of Geography and Statistics (IBGE), the average productivity of cassava was 15.14 t.ha⁻¹, and the projection of productivity for the year 2020 is lower, around 15.11 t.ha⁻¹.

The harvest index, a percentage obtained through the relationship between the total weight of the plant and the weight of roots produced by the plants, ranged from 2% (EMPO-15) to 82% (EMJA-12). The proportion of roots produced in relation to the weight of the plant is fundamental for cassava production since a high development of the aerial part can cause low root yields and high root yields can be obtained with lower development of the aerial part in relation to tuberous roots (Enyi 1972; Cock et al. 1977).

Significant differences in the harvest index have been recorded in cassava cultivars, with average values between 49% and 77% in 10-12 months after planting, indicating that this evaluation can be used as a selection criterion for genotypes with high production potential. Conceição (1987) states that harvest indexes above 60% are ideal for cassava cultivation, while Peixoto et al. (2005) consider a harvest index satisfactory for cassava production higher than 50%. It is worth noting that among the genotypes evaluated in this research, 22% had a harvest index equal to or higher than 50%.

The standardized Euclidean distance matrix revealed that the genotypes EMCB-01 and EMJA-07 are the most dissimilar (dii' 0.59). This dissimilarity is possibly due to the high yield of commercial roots (40.15 t.ha⁻¹) and high production of aerial part (18.86 kg) of the genotype EMCB-01, while the genotype EMJA-07 obtained low productivity of commercial roots (4.31 t.ha⁻¹) and low production of aerial part (0.450 kg).

The most similar genotypes based on the distance matrix were the EMCB-17 and EMJA-15 (dii' 0.28), both genotypes presented similarity in all the characteristics evaluated, as plant height (1.48m and 1.50m, respectively); average number of roots per plant (2 and 1.5, respectively); harvest index (24.76% and 21.72%, respectively); and branching levels (three branches for both genotypes).

Based on the standardized Euclidean distance matrix, the Tocher Optimization agglomerative method separated the genotypes into five groups, most of the genotypes (95.12%) were allocated in Group I, four genotypes were allocated in Group II, two genotypes in Group III and Group IV and Group V were composed by one genotype each (Table 1).

Table 1. Group of 164 *M. esculenta* genotypes with similar patterns, established by the Tocher method, using the standardized Euclidean mean distance as a dissimilarity measure.

Groups	No. of genotypes	Genotypes	Average intra-group distance
I	156	EMCB-17, EMJA-15, EMJA-44, EMJA-33, UNRO-23, EMJA-36, EMCB-38, EMCB16, EMJA-25, EMJA-34, EMJA-27, EMJA-48, EMJA-53, EMJA-26, EMJA-51, EMJA-28, EMCB-27, EMJA-38, EMJA-37, EMCB-22, EMCB-39, EMPO-08, EMJA-47, EMJA-52, UNCA-33, EMJA-50, UNRO-18, UNCA-44, EMJA-05, EMJA-18, EMCB-07, UNRO-19, EMCB-18, EMPO-03, EMCB-31, EMJA-09, EMPO-06, EMCB-04, EMJA-08, EMPO-01, EMJA-06, EMJA-31, UNRO-16, EMJA-32, EMJA-30, UNRO-22. EMJA-19, UNRO-21, EMCB-06, UNRO-08, EMCB-40, EMJA-04, EMJA-21, EMCB-26, EMJA-10, UNCA-22, EMCB-25, EMCB-24, EMJA-49, UNCA-07, EMCB-23, UNCA-11, EMCB-13, UNCA-15, EMJA-23, UNRO-14, EMJA-46, UNCA-31, UNRO-12, UNRO-01, EMJA-03, EMJA-35, UNRO-15, UNRO-20, UNCA-12, EMCB-15, EMJA-24, UNCA-25, EMCB-28, EMPO-07, UNCA-28, EMPO-16, UNCA-13, EMCB-05, UNCA-01, UNCA-19, EMCB-09, EMJA-29, UNRO-13, EMJA-22, EMCB-14, UNCA-40, EMCB-34, UNCA-29, UNCA-42, UNCA-18, UNCA-06, UNRO-17, EMPO-04, EMPO-05, EMPO-14, UNCA-36, UNCA-41, UNCA-09, UNCA-27, EMJA-01, EMJA-02, UNCA-24, UNCA-06, UNCA-02, UNCA-30, UNCA-20, EMJA-45, EMCB-19, EMJA-20, UNCA-08, UNCA-04, UNCA-35, UNCA-02, UNCA-03, EMPO-15, EMPO-02, UNCA-32, UNCA-09, UNCA-14, EMJA-17, EMCB-10, UNCA-26, UNRO-10, UNCA-16, EMJA-12, UNCA-05, UNRO-04, EMCB-30, EMJA-14, UNCA-39, UNRO-03, UNRO-05, EMCB-29, EMJA-11, EMCB-21, EMCB-11, EMCB-20, UNCA-10, EMJA-13, UNCA-23, UNCA-37, UNRO-07, UNCA-17, EMCB-08, EMCB-12, EMCB-32, UNCA-34, UNCA-38, UNCA-43, EMJA-07.	0.1935
II	4	EMCB-01, EMCB-36, EMCB-02, EMCB-03.	0.2833
III	2	UNCA-21, EMCB-16.	0.2932
IV	1	UNRO-11.	0
V	1	EMCB-35.	0

The inter-group distances were also calculated through Tocher Optimization agglomerative method, with the greatest distances established between Group II and Group V (0.5078), Group II and Group III (0.4833), and Group III and Group V (0.4706). The closest inter-group distance was between Group I and Group IV (0.3502), Groups II and Group IV (0.4113), and Group I and Group III (0.4135).

Inter-group distance analysis is a useful tool in choosing parents for a breeding program, in which more divergent genotypes can generate progenies with a greater heterotic effect (Zuin et al. 2009). Thus, the hybridization between the genotypes allocated in Group II with the genotype allocated in Group V would allow greater genetic gains. Thus, the hybridization between the genotypes allocated in Group II with the genotype allocated in Group V would allow higher genetic gains.

The hierarchical grouping of UPGMA, considering a cut line at 80% established by the t-test of significance, allowed the distinction of the genotypes into four groups. Group I allocated 96% of the genotypes; Group II allocated two genotypes; Group III one genotype; and Group IV allocated three

genotypes (Figure 1). The analysis of the Cophenetic Correlation Coefficient (CCC), applied to evaluate the consistency of the grouping pattern, showed a coefficient of high magnitude (0.85), revealing a good adjustment between the graphic representation with the numerical matrix (Rohlf 1993).

Although not identically, Hierarchical UPGMA and Tocher Optimization agglomerative methods were able to discriminate genotypes in a similar way. Genotypes UNCA-21 and EMCB-16 that were allocated in Group III on the Tocher analysis and the genotype EMCB-35 that was allocated individually in Group V, were also separated into distinct groups in the grouping of UPGMA analysis (Group II and Group III, respectively). Group II of Tocher analysis, in which the genotypes EMCB-01, EMCB-36, EMCB-02, and EMCB-03 were allocated, maintained a similar configuration in the grouping of UPGMA analysis, except for the genotype EMCB-02, which was grouped with the genotype UNRO-11, which was in an individual group in Tocher analysis.

The grouping of the genotypes UNCA-21 and EMCB-16 in both grouping methods was because the two genotypes are similar while the plant height (above 2.40 m), as well as the first branch height (above 1.40 m) and no rotten roots. The genotypes of Group II of Tocher analysis or IV of UPGMA analysis presented as tall plants (above 1.90m), with low first branch height (up to 0.40m) and similar harvest rates (on average 28%). The genotype EMCB-35, which was separated from the other genotypes in both agglomerative methods, presented a high average weight of roots, 10.65 kg of roots per plant, being the second-highest production among the genotypes evaluated. However, the roots of this genotype were not in accordance with the commercial pattern.

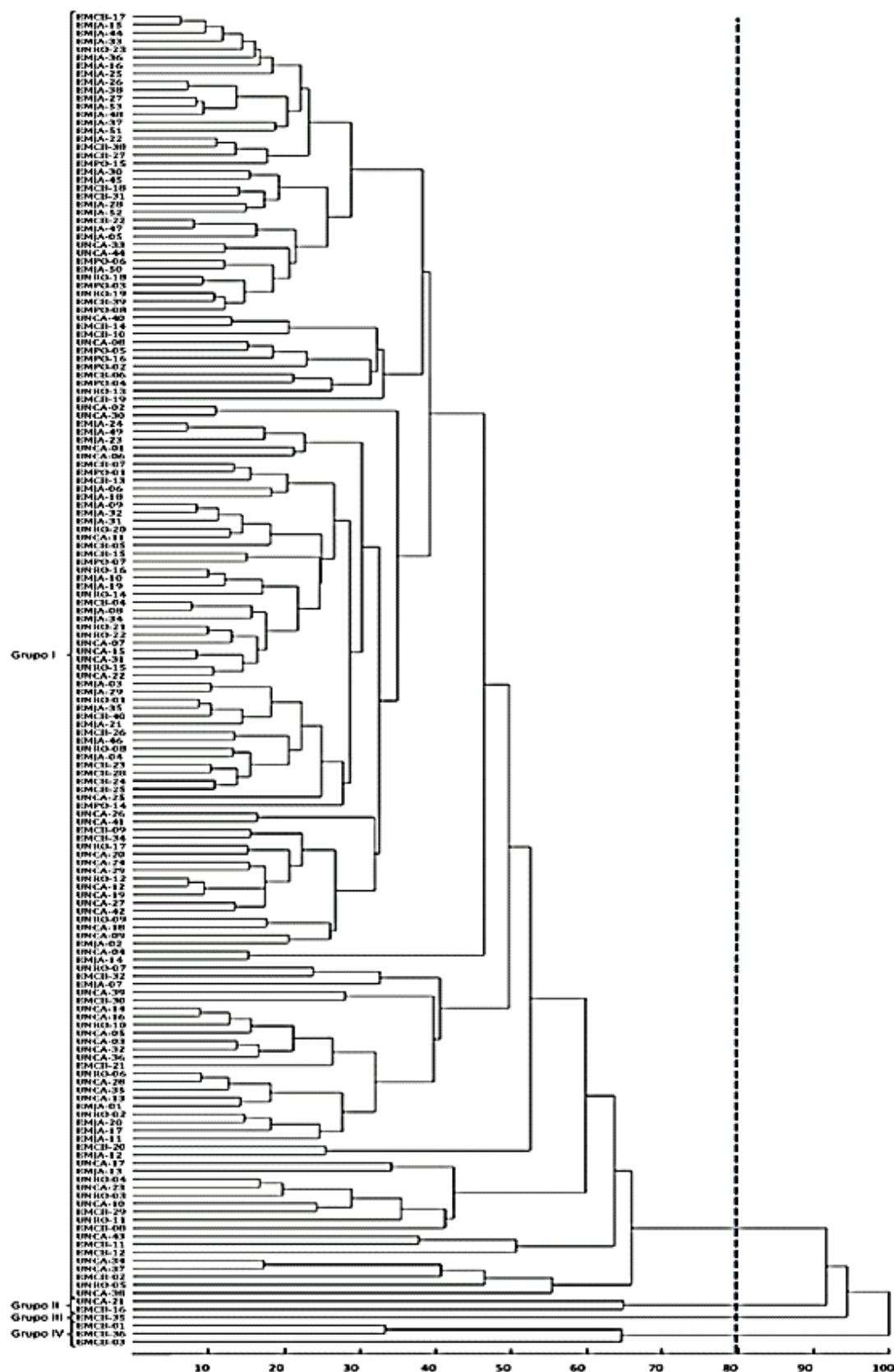


Figure 1. Representative dendrogram of the grouping of the 164 cassava genotypes from South Central mesoregion of the State of Mato Grosso, by the UPGMA Method, using the Standardized Euclidean distance matrix.

The genotype UNRO-11 was allocated into an individual group in the Tocher analysis (Group IV), which was not similar to the UPGMA analysis. Although genotypes allocated alone in a group are considered more divergent from the others (Vieira et al. 2005), it was not possible to observe in this genotype any characteristics where its performance stood out, presenting average values in all the descriptors evaluated, which justifies the divergence of the grouping of this genotype among both agglomerative methods.

Table 2 presents the relative importance of the characteristics. It is possible to notice that the characteristics harvest index, commercial root yield, branching levels, and non-commercial root yield contributed to 95% of the genetic divergence between the 164 cassava genotypes.

Table 2. Relative contribution of the eleven characteristics evaluated for the genetic divergence in 164 cassava genotypes in the South-Central mesoregion of the State of Mato Grosso, by the method proposed by Singh (1981).

VARIABLE	S.j *	Value (%)
Plant height	6319.89	0.03
Height of the first branch	9438.00	0.05
Number of rotten roots per plant	11278.48	0.06
Average weight of roots per plant	88157.79	0.49
Weight of the aerial part of the plant	179339.42	1.01
Total weight of the plant	232480.76	1.31
Number of roots per plant	378802.12	2.14
Non-commercial root yield	2176402.21	12.31
Branching levels	2362096.00	13.36
Commercial root yield	5493734.01	31.09
Harvest index	6731799.13	38.09

*Estimates of the contribution of each variable = (S.j).

This result suggests that these characteristics were efficient to explain the genetic dissimilarity between the genotypes and that they can be applied in the choice of genetic materials for improvement programs. It is also noted that the harvest index was the one with the highest contribution, reaching 38.09%. On the other side, the variables plant height, height of the first branch, and the number of rotten roots per plant were the characteristics that contributed less to explain the genetic diversity among the evaluated genotypes.

In a research conducted by Nick et al. (2008), evaluating 15 cassava clones through seven agronomic descriptors, it was observed that the harvest index was the third characteristics that most contributed to the genetic divergence with 14.01%, preceded by the root diameter (24.77%) and the total weight of the plant (24.36%). Contrary to what was obtained by Avijala et al. (2015), assessing the agronomic performance of 21 cassava genotypes. The authors observed that the total weight of the aerial part of the plant contributed 48.77% to the genetic divergence, while the average number of roots per plant contributed 16.93%. Commercial roots yield and harvest index had the lowest contribution to the genetic divergence among the characteristics evaluated, contributing respectively with 0.99% and 2.74%.

Cassava culture occupies a significant space in rural production in the State of Mato Grosso, with cultivation based mainly on small rural settlements. In these properties, several varieties are grown, be they commercial genotypes, traditional accessions, or even sexual reproduction plants. This genetic diversity present in these genotypes collected in the south-central region of the State of Mato Grosso can be widely used in breeding programs.

4. Conclusions

The cassava genotypes evaluated in this research showed genetic divergence for the agronomic descriptors evaluated.

The characteristics harvest index and commercial roots yield contributed the most to estimate the genetic divergence between the assessed genotypes and the height of the plant and the height of the first branch are the ones that have contributed least.

For greater heterotic effect in segregation populations, it is recommended to cross between the genotypes allocated in group II with the genotype allocated in group V.

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