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ORIGINAL RESEARCH ARTICLE

Genetic divergence and character significance in sweet potato genotypes for silage production

Alcinei Mistico Azevedo[1]*, Valter Carvalho de Andrade Júnior[2], José Altair Figueiredo[2], Carlos Enrrik Pedrosa[3], Daniel José Silva Viana[2], Vinícius Teixeira Lemos[3], Irã Pinheiro Neiva[4]

*[*1] Universidade Federal de Viçosa, Departamento de Fitotecnia, Brazil. E-mail: alcineimistico@hotmail.com*

[2] Universidade Federal dos Vales do Jequitinhonha e Mucuri, Campus JK, Departamento de Agronomia, Brazil.

[3] Universidade Federal de Lavras, Departamento de Agricultura, Brazil.

[4] Instituto Federal de Educação Ciência e Tecnologia do Norte de Minas Gerais, Campus Araçuaí, Brazil.

ABSTRACT

Considering the need to adopt more sustainable agricultural systems, it is important that sweet potato breeding programs seek to increase not only root productivity, but also the productivity and quality of branches for silage production. The objective was to evaluate the genetic divergence and the importance of traits associated with the production and quality of branch silage in sweet potato genotypes. The experiment was conducted on the JK Campus of the Federal University of Vales do Jequitinhonha and Mucuri Valleys in a randomized block design with 12 treatments and four repetitions. Twelve characteristics of branches and silage were evaluated. There was genetic variability between the genotypes, making it possible to select parents divergent for future breeding programs for silage production. The genotypes BD-54 and BD-31TO were the most divergent in relation to the others, being indicated its use in crossbreeding aiming the improvement of the culture for silage, once the high performance per se of all genotypes evaluated has already been verified in previous works. The characteristics Na, TDN and NDF were those that most contributed to the divergence.

Keywords: Animal Feed; Multivariate Analysis; Ipomoea Batatas; Genetic Improvement

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1. Introduction

Sweet potato (*Ipomoea batatas* L. (Lam.)) is native to Central and South America, being found from the Yucatan Peninsula in Mexico to Colombia. The crop belongs to the Convolvulaceae family, being the only species, whose individuals are hexaploid (2n = 6x = 90), being this ploidy level the most likely responsible for the high genetic variability found in the species. This genetic variability is amplified by self-incompatibility, which causes cross-pollination favoring the genotypic variability of this crop.

Given the great genetic variability of the species, the exploration in the various populations has been the focus of many works, enabling the selection of sweet potato genotypes for numerous purposes such as better nutritional quality and resistance to pests and diseases[1]; higher density and production of roots for human consumption[2]; higher dry matter content and biomass production[3]; greater suitability for ethanol production[4]; and higher production of branches for animal feed[1,5].

The cultivation of sweet potato is widespread among small farmers, who in most cases use it only for human food, without using the stalks and the waste roots, which can be used for animal feed[6].

Sweet potato branches are rich in starch, sugars and vitamins, have high percentages of crude protein and good digestibility, being a material of high nutritional value. In countries like China and Vietnam, the branches are used exclusively or in association with the roots for feeding pigs, either fresh or preserved as silage[7]. According to Viana *et al.*[5], sweet potato branch silage has protein and energy contents and fermentative profile suitable for animal feed.

Considering the need to adopt more sustainable agricultural systems, it is important that sweet potato breeding programs seek to increase, in addition to root productivity, the productivity and quality of branches for the production of silage. It is considered that any breeding program has genetic variability as a starting point, and that its characterization and evaluation are indispensable tools for plant breeding.

For the quantification of genetic variability, biometric characters are very accessible descriptors when compared to more advanced molecular techniques. This procedure has been used in the characterization and evaluation of the genetic divergence of germplasm through multivariate analysis, being used in sweet potato by several authors[8-11]. Among the multivariate techniques employed, the Euclidean distance, the generalized Mahalanobis distance, the canonical variables, the principal components and the hierarchical nearest neighbor method stand out[12,13]. Cruz *et al.*[14] stated that the choice of the analysis method to be employed is a function of the desired accuracy, the ease of analysis and how to obtain the data.

Thus, the objective of this work was to evaluate the genetic divergence and the importance of traits associated with the production of branch silage in sweet potato genotypes.

2. Material and methods

The experiment was conducted in the Olive Growing Sector, located on the JK Campus of the Federal University of Jequitinhonha and Mucuri Valleys in Diamantina, MG, at an altitude of 1,387 m and coordinates 18°12′01″ S and 43°34′20″ W. The soil is classified as typical Ortic Quartz Neosol. During the experiment period, the average maximum and minimum temperatures were 24.4 and 14.7 °C, respectively, and average annual rainfall of 1,082 mm. The experimental design was in randomized blocks, with 12 treatments (genotypes) and four repetitions, totaling 48 plots of 4.5 m^2 each. The spacing was 1.0 m between rows (beds) and 0.30 m between plants. The evaluated clones are part of the UFVJM germplasm: BD-06, BD-38, BD-45, BD-25, BD-31TO, BD-15, BD-67, BD-42, BD-54, Cambraia, and the cultivars Brazlândia Rosada and Brazlândia Branca. The origin of these genotypes is detailed by Andrade Júnior *et al.*[15], with the majority being obtained from collections in the Jequitinhonha Valley region.

Fertilization was made with 10 t ha^{-1} of tanned manure, 180 kg ha^{-1} of phosphorus, 45 kg ha^{-1} of potassium and 30 kg ha^{-1} of nitrogen, according to chemical analysis of the soil and recommendations for the crop[16]. The planting was performed using selected and standardized branches with eight nodes, burying 3 to 4 nodes, replanting the branches as soon as necessary until 20 days after planting. Sprinkler irrigation was used from planting until the seedlings took hold. Thirty days after planting, 45 kg ha^{-1} of potassium and 30 kg ha^{-1} of nitrogen were applied as top dressing.

The harvest was performed 163 days after planting, when the roots were developed. The green mass productivity was determined by weighing the branches harvested close to the ground in the plots of each treatment, and the results were expressed in t ha^{-1}. To calculate dry matter content, sub-samples of freshly harvested branches were taken, weighed, placed in paper bags and kept in an oven with forced ventilation at 60 °C until reaching constant mass. The dry mass productivity of the vines was obtained by the product between the green mass productivity and the dry matter content of the vines, and the results were expressed in t ha^{-1}. For the production of silage, the aerial part was cut close to the ground and subjected to withering in a shaded environment for four days. The branches were chopped in a disintegrator with particle sizes around 2 cm and ensiled in PVC silos, 50 cm high and 10 cm in diameter, fitted with a Bünsen valve

and sealed with adhesive tape. The silos were opened 46 days after ensiling, and silage samples were taken from the central portion of each silo, which were frozen for further analysis.

The crude protein content of the silage was determined by distillation in a Kjeldahl apparatus (semi-micro), and its values expressed as a percentage of dry matter[17]. The acid detergent fiber (ADF) and neutral detergent fiber (NDF) were determined by the method described by Silva & Queiroz[17]. The total digestible nutrients (TDN) were obtained as recommended by Sniffen *et al*.[18], and their values were expressed as a percentage of - dry matter. The pH was determined by potentiometry in a glass electrode, according to the technique of the Association of Official Analytical Chemists[19]. The minerals calcium, phosphorus and sodium were determined by atomic absorption spectrophotometry with acetylene flame, according to the methodology established by Sarruge & Haag[20].

The multivariate analyses were performed using the Genes program. For the application of the Tocher optimization clustering method, the generalized Mahalanobis distance (D^2) was used as a measure of dissimilarity. The hierarchical nearest neighbor method and canonical variable analysis were also used in the study of genetic diversity among the genotypes. To identify the most important characters for divergence, the relative contribution to genetic divergence was estimated by the method proposed by Singh.

2. Results and discussion

The genetic dissimilarity measures (**Table 1**), estimated from the generalized Mahalanobis distance (D^2), ranged from 13.03 to 2,083.86, which according to Benitez *et al*.[21]indicates the presence of wide genetic divergence among the genotypes studied. There was greater dissimilarity of the genotype BD-54 in relation to the genotypes BD-31TO and Cambraia, with distance estimates of 2,083.86 and 387.36, respectively. The dissimilarity between the BD-54 genotype and the BD-31TO and Cambraia genotypes was also verified by Neiva *et al*.[10] evaluating morphological characters. The dissimilarity found in this paper can be explained by the higher contents of branch dry matter, neutral detergent fiber, acid detergent fiber and lower contents of total digestible nutrients and phosphorus compared to the genotypes BD-31TO and Cambraia. As for the least dissimilar genotypes, there were lower dissimilarity estimates for the BD-25 genotype relative to BD-06 and BD-38 (13.03 and 14.63, respectively). These genotypes had very close values for dry matter content, total digestive nutrients, neutral detergent fiber, phosphorus and calcium.

It was observed that among all the possible combinations of each of the genotypes evaluated, most had maximum distance when combined with the genotypes BD-31TO and BD-54, indicating that these genotypes are the most divergent of the group of genotypes evaluated. This relevant information demonstrates that these genotypes can be used in crossbreeding, because according to Belete *et al*.[21], the crossing between genotypes with higher genetic divergence makes it possible to obtain highly segregating populations, with a higher probability of finding transgressive genotypes for multiple traits. Besides dissimilarity, for the choice of genitors it is important to have high performance per se, which has been confirmed for all genotypes in previous works[3,5,22,23] evaluating 65 sweet potato genotypes found that genotypes BD-06, BD-15, BD-38, Cambraia, BD-67, BD-45 and BD-42 were among the most productive, with an average of 4.19 t ha^{-1} of branches and 11.02 t ha^{-1} of commercial roots. The genotypes BD-54, BD-67 and Brasilândia Rosada stood out for the production of branches by Andrade Júnior *et al*.[1] with an average of 16.37 t ha^{-1} . Andrade Júnior *et al*.[22] found that the genotype BD-31TO stood out with 6.90 t/ha.

The grouping analysis by Tocher's method allowed the separation of the 12 genotypes into three groups. The first group was formed by the genotypes BD-06, BD-25, BD-38, BD-42, BD-15, BD-67, 'Braz. Branca', BD-45 and 'Braz. Rosada', totaling 75% of the genotypes evaluated. This indicates that although there are some genotypes with high genetic divergence among themselves, most are similar, which according to Silva *et al*.[12] evidences a restricted genetic base among the genotypes evaluated. The genotypes belonging to this

group present close values for dry matter content and sodium content. The second group was formed by the Cambraia and BD-31TO genotypes. These genotypes showed very close values for green matter productivity, dry matter productivity, ADF, TDN and calcium content. The third group was formed by the genotype BD-54. This genotype stood out from the others for its higher productivity of dry matter of branches and lower TDN content. The crossing of genotypes belonging to different groups of dissimilarity is desirable, providing greater genetic variability in the progenies.

Table 1. Estimates for the distance of the closest and most distant sweet potato genotypes, based on generalized Mahalanobis distances (D^2). Diamantina, UFVJM, 2009

Gen.	Smaller D^2	Gen. closest	Bigger D^2	Gen. furthest	D^2 Average
BD-06	13.03	BD-25	893.64	BD-31TO	221.439
BD-25	14.63	BD-38	804.00	BD-31TO	222.4689
BD-15	42.55	BD-42	1,180.12	BD-31TO	313.599
BD-38	14.63	BD-25	742.34	BD-31TO	214.9406
Cambraia	60.53	Braz. Rosada	1,387.36	BD-54	470.068
BD-31TO	344.03	Cambraia	2,083.86	BD-54	904.2498
BD-67	17.26	Braz. Branca	949.70	BD-31TO	240.8837
BD-45	50.35	Braz. Rosada	850.37	BD-54	258.5194
BD-42	23.59	BD-25	998.06	BD-31TO	256.3138
BD-54	162.23	BD-15	2,083.86	BD-31TO	713.0773
Braz. Branca	17.26	BD-67	1,012.56	BD-31TO	266.8121
Braz. Rosada	50.35	BD-45	962.39	BD-54	313.922

Figueiredo *et al*.[6], evaluating the same genotypes as in this study, stated that the silages produced are characterized as good quality bulks, with average values of 11.59% crude protein, low fiber content and TDN contents higher than 62.90%, with good potential for use of the branches as silage for animal feed. Gonçalves Neto *et al*.[4] evaluating 39 sweet potato genotypes for their suitability for human food, animal feed and production of ethanol found emphasis on the genotypes BD-06, BD-42 and BD-67 for animal feed. For human food, the genotypes BD-06, BD-38 and 'Brazlândia Rosada' stood out. The genotypes BD-06 and BD-67 were also suitable for ethanol production.

The first two canonical variables explained more than 80% of the total variance contained in the set of analyzed characteristics (92.02% of the total accumulated variance) (**Table 2**). Therefore, it was possible to explain the variability manifested among the genotypes evaluated and, in this way, represent the data in a two-dimensional graph[14].

From the analysis of the graphical dispersion of the scores (**Figure 1**), it was also possible to separate the genotypes into three groups, however, the genotype Cambraia that according to the Tocher method was part of group 2, was allocated to group 1, in the same way as observed in the illustrative dendrogram (**Figure 2**) considering the cut as the distance of 40%. Differences for the estimation of genetic divergence between the Tocher method and the dendrogram, were also observed by other authors[13,24], indicating the difference between the methods regarding accuracy and criterion. According to Azevedo *et al*.[13] differences between the results of different multivariate analysis methods is natural, since the methods are based on different clustering techniques. Thus, it is important to confront the results obtained by different multivariate analysis methodologies in order to obtain a more accurate interpretation of the results.

Table 2. Estimates of eigenvalues associated with the canonical variables, aiming to estimate the dissimilarity between sweet potato genotypes. Diamantina, UFVJM, 2009

Canonical variables	Estimates of the eigenvalues	
	λj (%)	λj (%)$_{Acum}$
Y1	80.88	80.88
Y2	11.14	92.02
Y3	5.11	97.13
Y4	1.22	98.34
Y5	0.64	98.99
Y6	0.45	99.44
Y7	0.30	99.73
Y8	0.15	99.88
Y9	0.09	99.97
Y10	0.02	100.00
Y11	0.00	100.00
Y12	0.00	100.00

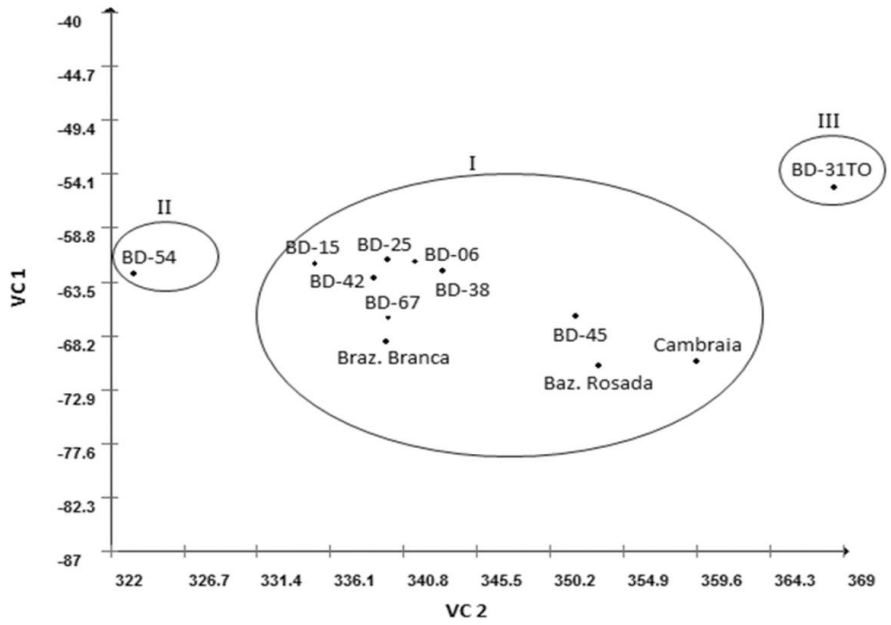

Figure 1. Graphical dispersion of scores in relation to the first two canonical variables (VC1 and VC2) in sweet potato genotypes. Diamantina, UFVJM, 2009.

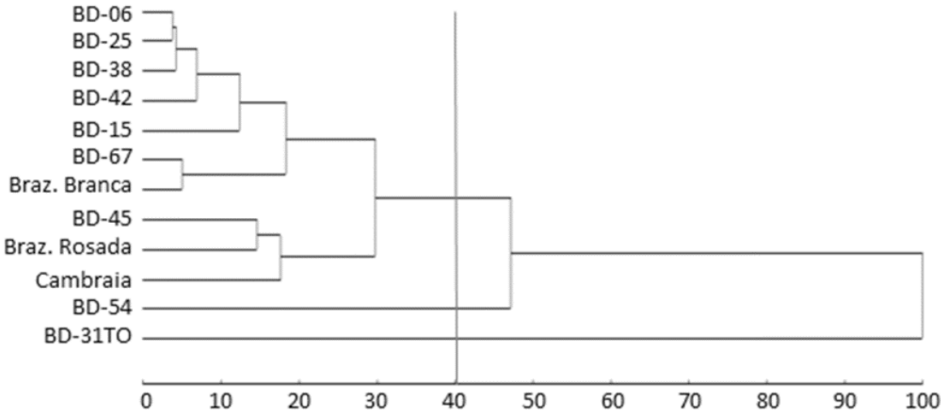

Figure 2. Dendrogram illustrating the dissimilarity pattern obtained by the nearest neighbor method, based on the generalized Mahalanobis distance in sweet potato genotypes. Diamantina, UFVJM, 2009.

Table 3. Relative contribution (%) of traits to genetic divergence in sweet potato genotypes, estimated by the method proposed by Singh[25]. Diamantina, UFVJM, 2009

Features	S.j	Value (%)
Na	7,543.30	39.11
TDN	2,691.46	13.95
NDF	2,029.03	10.52
%P	1,755.41	9.10
PMV	1,678.86	8.70
MS	1,180.51	6.12
PMS	1,026.58	5.32
ADF	631.06	3.27
MSS	426.77	2.21
PH	269.05	1.40
Ca%	49.49	0.26
PB%	5.57	0.03

PMV = green matter yield; DM = fruit dry matter content; PMS = fruit dry matter yield; MSS = dry matter content; NDF = neutral detergent fiber; ADF = acid detergent fiber; TDN = total digestible nutrients; pH = hydrogen potential; CP = crude protein; P = phosphorus; Ca = calcium; Na = sodium.

Among the advantages of using multivariate analysis techniques is the possibility to evaluate the importance of each characteristic studied on the total variation available among the genotypes evaluated. Thus, based on the criteria proposed by Singh[25], in terms of the relative contribution of each character evaluated for the genetic divergence between the genotypes (**Table 3**), we observed the highest relative contribution for the characteristics sodium content (39.11%), total digestible nutrients (13.95%) and neutral detergent fiber (10.52%), totaling 63.58%, which were the main determinants in the quantification of genetic divergence. The low relative importance of the characteristics pH (1.40%), calcium content (0.26%) and crude protein (0.03%) suggest that the analysis of these characteristics may be dispensable in future

studies, reducing expenditures of labor, cost and time.

3. Conclusion

The genotypes BD-54 and BD-31TO are recommended for crossbreeding with the other genotypes. The traits Na, TDN and NDF contributed the most to the divergence, while the traits pH, Ca% and PB% contributed the least, being dispensable in future work.

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Conflict of interest

The authors declare that they have no conflict of interest.

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