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CHARACTERIZATION AND STUDIES OF GENETIC DIVERSITY OF SWEET POTATO FROM PARAGUAY

CARACTERIZACIÓN Y ESTUDIOS DE DIVERSIDAD GENÉTICA DE BATATA EN PARAGUAY

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ABSTRACT
The objective was to characterize the genotypes and obtain data on the genetic diversity of sweet potatoes. The experimental design was an RCBD with 26 treatments and three replications. It was evaluated total productivity, commercial and non-commercial root yield, number of roots per plant, biomass, root shape, and root color. The estimation of genetic diversity was obtained by the similar mean dissimilarity measure and, the delimitation group by the UPGMA dendogram. As a measure of proximity distances, the Euclidian Quadratic dissimilarity measure was used. and the number of clusters was determined using the Mojena Criterion. The collection was grouped into seven clusters. The highest number of accessions was grouped in cluster III, with nine accessions, cluster II with six accessions, cluster IV, with six accessions, cluster VII with two accessions and cluster I, V, and VII with one accession each. The greatest genetic distance was found between Morotí Guazú and Ib-019 with 40,443 and the most similar were Morado and Pyta guazú with a Euclidean dissimilarity measure value of 1098. Root productivity is the most important variable for genetic distance. The predominant skin color of the collection is cream and pale yellow flesh color.
Keywords: clusters; genetic distance; germplasm; *Ipomoea batatas L.;* production.

RESUMEN
El objetivo fue caracterizar genotipos y obtener datos sobre la diversidad genética de batata. El diseño fue en BCA con 26 tratamientos y tres repeticiones. Fueron evaluadas productividad total, rendimiento comercial y no comercial de raíz (t ha^{-1}), número de raíces por planta, biomasa aérea, forma y color de la raíz. La diversidad genética fue obtenida por la medida de disimilaridad media similares y para delimitación de grupos se utilizó el método de dendrograma UPGMA. Como medida de proximidad de distancias se utilizó la medida de disimilitud Euclidiana Cuadrática. La cantidad de clusters fue por el Criterio de Mojena. El mayor número de accesiones fue agrupado en el cluster III, con nueve accesiones, cluster II con seis accesiones, cluster IV, con seis accesiones, cluster VII con dos accesiones y cluster I, V y VII con una accesión cada una. La mayor distancia genética fue entre Morotí Guazú (6) e Ib-019 (23) con 40.443 y los más similares resultaron Morado (3) y Pyta guazú (9) con un valor de 1098. La productividad de raíces es la variable de mayor importancia para la distancia genética. El color predominante de la piel de la colección es crema y color de carne amarillo pálido.
Palabras clave: distancia genética; germoplasma; grupos; *Ipomoea batatas*; producción.

INTRODUCTION

The sweet potato (Ipomoea batatas L [LAM]), is a convolvulaceae from America[1], whose roots and leaves contain nutraceutical properties highly valued for consumption[2], and also for food security[3] [4]. It presents a wide range of root pigmentation[5], with orange pulp varieties having the highest content of beta-carotene and carotenoids[6].
It is tolerant to a wide range of edaphic and climatic conditions, making it one of the crops resilient to climate change[7] [8] [9] [10]. Traditional farmers have a fundamental role in the conservation and generation of diversity in cultivated species[11], alongside indigenous peoples[12]. Understanding the genetic diversity of this important crop is essential, given the continuous rise in food demand and the need to preserve plant genetic resources"[13].

The countries with the highest production of this item are Asia, Africa, and the USA[14] and to it occupies the fifth place in world production, after wheat, corn, cassava, and potatoes, which are the most used carbohydrate sources[15]. In Paraguay, it is called "batata" and "jety" (guaraní), and[13] other names in America such as "boniato", "camote", "batata doce" (portugués) and sweet potato.

The germplasm characterization determines the expression of highly heritable characters ranging from morphological, physiological, or agronomic characteristics, including agrobotanical traits such as plant height, leaf morphology, flower color, seed traits, phenology, and the overwintering capacity of perennial plants[16].

Sweet potato is a cross-pollinated and highly heterozygous crop that results in great variability for crop improvement; knowing about genetic diversity helps the breeder to choose desirable parents for use in breeding programs[17][16]. Studies of genetic divergence between genotypes in crops are used to analyze the genetic variability in the collection, identify closer or duplicate genetic materials, and generate parameters for the selection of genetically different parents that, when crossed, enable a greater heterotic effect, increasing the chances of obtaining maximum genetic variability and superior genotypes in generations[18].

For the analysis of genetic diversity, several multivariate statistical procedures are available, such as grouping analysis or clustering. The diversity study carried out by cluster analysis has the purpose of bringing together, by some criterion of similarity or dissimilarity, the parents of various groups, in such a way that there is greater homogeneity within the group and greater heterogeneity between groups[19]. Cluster analysis is a useful tool because it can group objects by the degree of similarity sufficient to bring them together in the same set[20].

There are other more specific and advanced methodologies for the analysis of genetic diversity[21] that can offer more detailed results, but are usually more expensive to execute, such as the use of molecular technology, which is a challenge for some institutions, as it requires advanced laboratory facilities and technical capacity[22].

To understand the genetic diversity of sweet potatoes, both morphological and molecular markers have been used [23] [24]. Morphological descriptors are potentially useful for clonal identification, due to their high variability and the estimation of genetic distances[25], and have been used as a first step to understanding both plant diversity and the conservation of plant genetic resources[26].

In genetic improvement programs, which include a selection of superior genotypes, it is necessary to have information about the germplasm to be used, its genetic potential and genetic parameters intrinsic to the characteristics that are to be improved[27].

In some Latin American countries, including Paraguay, some factors postpone in-situ and ex-situ conservation and study of this species, mainly resources for research, advancement of extensive agriculture, and migration of farmers and indigenous people. The objective of this work was to characterize the genotypes of a collection and obtain preliminary data on the genetic diversity of sweet potatoes, identifying those most promising for genetic improvement programs.

MATERIALS AND METHODS

The research was conducted at the Experimental Field of the Faculty of Agricultural Sciences (FCA) of the National University of Asunción (UNA), San Lorenzo (25°21'S and 57°27'W, 125 msnm). The place's average minimum and maximum temperature is 24°C and 32°C, respectively, with an average annual rainfall of 1,400 mm[28]. The results of the soil analysis indicate that the experimental area belongs to the order Ultisol and sandy loam texture with the following properties: pH= 6.28, organic matter= 0.47%, P= 9.03 (mg/kg), Ca -2= 1.30 cmolc/kg, Mg+2 = 0.54 cmolc/kg, K+= 0.16 cmolc/kg, Al+3 + H+ = 0.

Twenty-six sweet potato genotypes were evaluated, obtained from the sweet potato collection of the UNA/FCA Experimental Field and the Paraguayan Institute of Agrarian Technology (IPTA) collected from producer's farms.
The genotypes and corresponding numbering are: Moroti (1), Taiwanes (2), Morado (3), Pyta (4), Sa'y jú (5), Moroti Guazú (6), Boli (7), Pyta Uruguayo (8), Pyta Guazú (9), Yety Mandió (10), Taiwanes2 (11), Uruguayo (12), Dacosta (13), Yety Paraguay (14), Andai (15) and hybrid clones obtained by natural polycrossing: Ib-003 (16), Ib-005 (17), Ib-006 (18), Ib-010 (19), Ib-011 (20), Ib-012 (21), Ib-018 (22), Ib-019 (23), Ib-020 (24), Ib-022 (25) and Ib-023 (26) (Table 1, 3).

The experimental design was randomized complete block design, with 26 treatments, where each genotype corresponds to one treatment and three replicates, totaling 90 experimental units (EU). Each UE consisted of four rows of 3.0 m long and 3.0 m wide, separated from each other by 2 m streets, with a useful area of 6.0 m2 and 11 plants per row. Planting was done from branches with 6-8 nodes.

The harvest was carried out 150 days after planting and the following evaluations were made: total productivity, commercial and non-commercial root yield (t ha-1), the total number of roots per plant and biomass of the aerial part (stem, leaves and petioles) (t ha-1). A commercial root was considered as that with mass equal to or greater than 100 g, without damage or deformation[29]. In addition, the characterization of root shape and color was carried out according to the descriptors of Huaman[5].
For the grouping, the UPGMA (Unweighted Pair Group with Arithmetic Mean) hierarchical method where the agglomeration criterion is the average distance of all the individuals of a conglomerate with all the individuals of another[30].

The Mojena Criterion is a method used to determine the optimal number of clusters or groups in cluster analysis. It is based on the concept of the Quadratic Euclidean Distance[31], which measures the dissimilarity between data points within a cluster and measures the quality of the grouping using the Cophenetic correlation coefficient[32]. This value measures the correlation between the initial and final distances with which individuals have joined during the development of the method. Afterward, an analysis that explored and described each cluster in detail was conducted.

The study of the characters' relative importance in the genetic divergence prediction was carried out based on the method proposed by Singh[33] and the Scott and Knott method[34] for comparing the means of the significant variables. For statistical analyses, the software RStudio Team[35] was used.

RESULTS AND DISCUSSION

The UPGMA hierarchical method with Euclidean distances managed to group the genetic materials through their five agronomic characters into sevens (Figure 1) using the Mojena criterion[31]. The cophenetic correlation coefficient gave a value of 0.75, indicating an adequate adjustment in the grouping. Seven groups were defined and distributed according the genetic distance among 26 accessions (Figure 1).
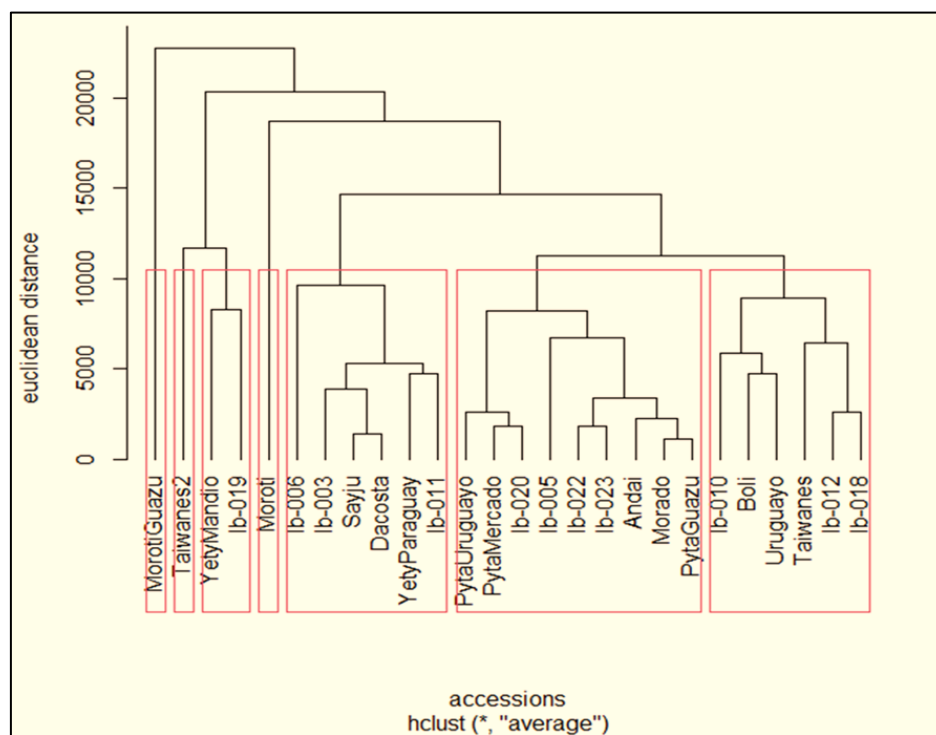

Figure 1 – Dendrogram of genetic distance of agronomic characters of sweet potato accessions. UNA-FCA, San Lorenzo, Paraguay. 2018

Seven distributed clusters were defined based on the genetic distance between 26 accessions. The largest number of accessions was grouped in Cluster III, with nine accessions, cluster II with six accessions, cluster IV, with six accessions, cluster VII with two accessions, and Clusters I, V, and VII with one accession each (Figure 1, Table 1). The genotypes grouped under the same cluster would have little genetic divergence from each other, which is why greater segregation is expected in crosses between different groups or clusters. The accessions grouped in Cluster III present superior characteristics in the variables studied and the accessions grouped in Cluster IV present characteristics of lower productivity. To obtain genetic variability, those accessions that are found with a greater Euclidean distance from each other should be considered.

On the other hand, accessions that present desirable productive characteristics in a collection can be directly selected by the plant breeder as promising.

The cultivars of a group have the same or almost the same characteristics that simplify the process of selecting crosses from a collection or germplasm bank[37].

The knowledge of genetic divergence generates parameters for the selection of parents that, when crossed, enable a greater heterotic effect in their descendants[18], increasing the possibilities of obtaining superior genotypes in segregating generations[37].

Cluster	Root productivity (t ha⁻¹)	Comercial root yield (t ha⁻¹)	Not commercial root yield (t ha⁻¹)	Comercial root number	Not comercial root number	Total number of root	Biomass (t ha⁻¹)
Cluster I	24,9	1,3	3,6	2,4	1,78	4,2	15,8
Cluster II	22,3	19,8	2,4	2,5	1,6	4,1	26,8
Cluster III	23,1	20,6	2,5	2,6	1,6	4,2	36,4
Cluster IV	9,1	7,3	1,8	1,57	1,6	3,2	32,8
CLuster V	10,6	9,2	1,4	1,3	0,9	2,3	50,5
Cluster VI	39,0	35,4	3,6	3,7	2,2	5,9	25,4
Cluster VII	37,9	34,5	3,4	2,4	2,4	4,8	36,6

Table 1. *Agronomic characteristics of four sweet potato clusters expressed as average. UNA-FCA, San Lorenzo, Paraguay. 2018. Cluster I: Moroti; Cluster II: Taiwanes, Boli, Uruguayo, Ib-010, Ib-012, Ib-018; Cluster III: Morado, Pyta, Pyta Uruguayo, Pyta Guazú, Andai, Ib005, Ib-020, Ib-022, Ib-023. Cluster IV: Sayju, Dacosta, Yety Paraguay, Ib-003, Ib-006, Ib-011; Cluster V: Moroti Guazu; Cluster VI: Yety mandio; Ib-019; Cluster VII: Taiwanes2.*

The proximity matrix of Euclidean distances (Figure 2), the proximities of the distances are observed that, when individuals with a greater Euclidean distance from each other are used as parents, greater genetic variability could be obtained.

Figure 2. *Matrix of dissimilarity or proximity measures of 26 sweet potato genotypes using Euclidean distances considering five agronomic characters. UNA-FCA San Lorenzo. Paraguay. 2018*

The most similar genotypes are Morado[3] and Pyta guazú[9] with a Euclidean dissimilarity measurement value of 1098, indicating the existence of little genetic variability between similar genotypes or those with lower Euclidean distance. The genotypes Moroti Guazú[6] and Ib-019[23] presented the greatest distance measurement equivalent to 40,443, indicating that they are the least similar among the 26 genotypes evaluated, therefore, to achieve heterozygous offspring it is necessary to choose parents with the greatest Euclidean distance.

Understanding the genetic diversity in a germplasm collection is of great importance, as it allows the identification of duplications of accessions, which can be eliminated and thus reduce space and operational costs in conservation. Among the characters studied in the diversity of the genotypes, it is observed that root productivity and total number of roots presented the highest percentage of relative contribution, with values of 48.32% and 14.61%, respectively, which indicates that the Groupings of genotypes were predominantly influenced by these characteristics and they differed on these variables (Table 2).

The interest in the evaluation of a smaller number of variables, which contribute to the discrimination of genotypes, enables savings in time and labor, both in data collection and in the management of the experiments, in addition to reducing costs in future analyses[18]. In this sense, biomass and commercial yield constitute the least important characteristics for the set of accessions characterized in this work (Table 2). The productivity of the green mass of branches does not influence the root format and the total and commercial productivity of roots, but it can interfere with the size of the roots, and larger branches, they tend to form larger roots[38].

Contribution of leaf size for genetic distance found higher[39], characters with lower contribution should be discarded for future studies[40]. It was found a lower contribution for the weight of non-commercial roots and a higher contribution for the total number of roots[41] also, it found a more significant contribution for the yield of roots and individual storage of roots, for the genetic distance in sweet potato[42].

For root productivity, genotypes 23 (Ib -019) and 11 (Yety Mandió) formed the cluster with the highest yield with values of 41.9 t ha-1 and 37.9 t ha-1, respectively. The high coefficient of variation for this parameter indicates the existence of variability (Table 3). Other authors, it found a total root yield of 43.0 t ha-1, a value higher than that of this research work[41] meanwhile, obtained root yields of 12.0 t ha-1 in the best genotype evaluated[42]; being this result lower than those obtained in this experiment.

Variables	S.J*	Valor (%)
Root Productivity	4268.2	48.3
Comercial root yield (t ha^{-1})	1098.3	12.4
No comercial root yield (t ha^{-1})	1235.9	14,0
Total root number	1290.4	14.6
Biomass (t ha^{-1})	939.7	10.6

Table 2. *The relative contribution of characters to the genetic distance of sweet potato clones. UNA/FCA, San Lorenzo, Paraguay. 2018*
*S. J. Estimated value of Singh's methodology (1981)

Under local conditions, on a producer's farm, productivity is less than 10 t ha-1[43], therefore, the values found in the accessions studied can be considered promising for the selection of parents with high productive potential. For productivity, all genotypes greater than 20 t ha-1 are considered to have high potential, and they are the genotypes Yety mandió[10], Pyta Uruguayo[8], Ib-020 (24), Moroti[1], Taiwanes[2], Boli[7], Uruguayan[12], Ib-005[17], Ib-023[26], Pyta[4], Ib-022[25], Morado[3], Ib-010[19] and Pyta Guazu[9]. [44]Although the variability of fresh weight is an intrinsic characteristic of the plant material, as well as the variety, climatic conditions, agronomic practices, and growth form of the storage root in a certain type of soil, it affects the acceptability and preference of the consumers.

In the analysis of commercial root yield, genotypes Ib-19[23], Taiwanes2[11], Yety mandió[10], Pyta uruguayo[8], and Ib -020[24] obtained values higher than the other genotypes between 38.6 and 30.7 t ha-1, and genotypes 6.18, and 20 between 12.41 and 10.7 t ha-1 presenting a high coefficient of variation (37.5%) (Table 3) so it is inferred that there is variability between the genotypes for this variable, also considering the environmental factor and cultural management that affect this feature. [45]Studies indicate that the amplitude of variation in productivity demonstrates that there is genetic variability, evidencing a situation favorable to improvement, when the objective is the selection of superior genotypes.

In relation to non-commercial root yield, the Taiwanes[2] and Moroti[1] genotypes present 4.7 and 4.5 t ha-1 of non-commercial roots and and genotype Pyta[4] presented the lowest value (Table 3). Other researchers[41] found an average yield of commercial and non-commercial roots of 23.0 t ha-1 and 19.0 t ha-1 respectively. On the other hand[46],

when evaluating sweet potato genotypes, obtained means of 31.2 t ha-1 and 6.2 t ha-1, for the same variables. For the number of roots per plant, the genotypes Ib-020[23], Pyta Guazu[8], Taiwanes[2], and (Morado [3] presented the greatest number of roots, with means of 6.97; 6.37; 6.11, and 5.81 roots plant-1 respectively, which are also among the most productive.

For biomass, 14 genotypes obtained statistically similar values, between 50.53 and 32.39 t ha-1, and eight genotypes obtained statistically similar biomass values between 31.1 and 27.4 (Table 3). In general, genotypes with high biomass values resulted in lower storage root values. [47]Biomass is an important indicator in terms of the efficiency of the species in the use of the environmental and genetic resources available to it. Likewise, it provides an idea of its potential, depending on the amount of fresh material it can provide for different uses.

Root productivity (t ha^{-1})		Comercial root yield (t ha^{-1})		No comercial root yield (t ha^{-1})		Total number of root per plant		Biomass (t ha^{-1})	
Genotype		Genotype		Genotype		Genotype		Genotype	
23	41,8 a	23	38,6 a	2	4,7 a	23	6,9 a	6	50,5 a
11	37,9 a	11	34,5 a	1	4,5 a	8	6,4 a	17	43,0 a
10	36,2 b	10	32,2 a	10	4,0 a	2	6,1 a	18	40,3 a
8	33,5 b	8	30,8 a	25	3,8 a	3	5,8 a	9	37,6 a
24	32,9 b	24	30,8 a	26	3,6 a	25	5,3 b	15	37,2 a
1	29,4 c	1	26,9 b	11	3,4 a	10	4,8 b	11	36,6 a
2	29,4 c	2	25,3 b	5	3,3 a	11	4,7 b	3	36,6 a
7	27,6 c	7	24,9 b	3	3,3 a	19	4,3 c	26	36,2 a
12	27,5 c	4	24,9 b	23	3,2 a	5	4,3 c	25	35,4 a
17	26,8 c	12	24,5 b	12	3,0 a	1	4,2 c	16	34,5 a
26	26,3 c	19	22,7 b	8	3,0 a	24	3,9 c	24	34,3 a
4	25,6 c	26	22,6 b	9	2,8 a	14	3,9 c	4	33,8 a
25	24,7 c	3	21,7 b	7	2,6 a	21	3,6 c	8	33,2 a
3	24,6 c	25	20,9 b	13	2,3 b	12	3,7 c	13	32,4 a
19	24,5 c	17	18,3 c	24	2,3 b	7	3,7 c	5	31,1 b
9	20,5 d	9	17,6 c	17	1,9 b	26	3,5 c	20	31,0 b
15	17,7 d	15	16,2 c	20	1,9 b	17	3,4 c	2	29,3 b
21	17,6 d	22	16,1 c	14	1,8 b	9	3,1 c	21	29,1 b
22	17,5 d	21	15,9 c	21	1,7 b	13	3,1 c	22	28,5 b
6	14,1 e	6	12,4 d	6	1,7 b	20	3,0 c	10	27,9 b
18	12,4 e	18	11,5 d	19	1,5 b	15	3,0 c	7	27,8 b
20	12,1 e	20	10,2 d	15	1,5 b	22	2,9 c	14	27,5 b
5	10,6 e	16	93,6 d	22	1,4 b	4	2,8 c	12	23,1 b
16	10,3 e	5	72,6 d	18	1,1 b	16	2,5 c	19	23,0 b
14	87,9 e	14	70,2 d	16	1,0 b	18	2,4 c	23	22,8 b
13	85,8 e	13	+62,9 d	4	0,7 b	6	2,3 c	1	15,8 b
C.V (%)	28,6		32,3		37,5		28,0		23,1

Tabla 3. *Agronomics characteristics of 26 sweet potato genotypes. UNA-FCA, San Lorenzo, Paraguay.*

Gen: Genotype. Means followed by the same letter in the column do not differ from each other according to the Test of Scott-Knott test (p= 0.05), C. V: Coefficient of variation. Moroti (1), Taiwanes (2), Morado (3), Pyta (4), Sa'y jú (5), Moroti Guazú (6), Boli (7), Pyta Uruguayo (8), Pyta Guazú (9), Yety Mandió (10), Taiwanes$_2$ (11), Uruguayo (12), Dacosta (13), Yety Paraguay (14), Andai (15) Ib-003 (16), Ib-005 (17), Ib -006 (18), Ib -010 (19), Ib -011 (20), Ib -012 (21), Ib -018 (22), Ib -019 (23), Ib -020 (24), Ib -022 (25) y Ib -023 (26).

In relation to the qualitative descriptors for root (Table 4), the elliptical shape is found in a higher percentage (46.2%) and the obovate shape in a lower percentage (3.8%). The local consumer generally prefers elongated shapes, and roots

of medium thickness, which stand out for culinary use in preparations preferably boiled. However, in gastronomy, there is a wide variety of preparations such as baked and fried. The characteristic, more elongated roots of elliptical shapes, rather than round or oblong, is another objective proposed for the selection of varieties. Those varieties[44] of various shapes can be used for agroindustry.

Descriptor		Porcentaje (%)
Root shape	Round	15,4
	Long eliptic	34,8
	Obovate	3,8
	Elíptic	46,2
Skin Color	Crem	53,8
	Yellow	7,7
Predominant colour	Dark purple	19,23
	Red-purple	15,38
	Orange	3,8
Predominant colour intensity	Pale	15,4
	Intermediate	38,4
	Dark	46,1
Flesh Colour	Cream	23,7
	Dark ream	11,5
Predominante colour	Pale yellow	46,1
Secundary flesh colour	Ausent	50,0
	White	7,6
	Cream	3,8
	Orange	19,2
	Yellow	15,3
	Red purple	3,8
	Dark purple	3,8

Table 4. *Participation of 26 sweet potato genotypes for qualitative root nominal scale descriptors. UNA-FCA, San Lorenzo, Paraguay. 2018*

The sweet potatoes collection consists mainly of cream-colored skin (53.8%) with dark purple (19.2%) and purplish red (15.4%) also present in significant amounts. Yellow (7.7%) and orange (3.8%) are present in smaller percentages. The predominant color has a higher percentage of dark shades (46.1%). The meat color is mainly pale yellow (46.1%), and the secondary color is absent in 50% of the samples, with other colors present in smaller percentages. These different shapes and colors highlight the variability in these descriptors (Table 4).

In marketing establishments, the purple-skinned sweet potato is prevalent, suggesting that it is the preferred pigment for local consumers. This characteristic should be taken into consideration for future improvement programs. The purple pigment has a higher content of beta-carotene and carotenoids[6].

CONCLUSION

The UNA/FCA collection presents sweet potato genotypes that can be used for genetic improvement programs. The genetic distances of the studied germplasm are grouped into seven clusters. Some characters, such as biomass, had less importance for diversity, with total root productivity being the variable that contributed the most to genetic distance.

There is variation in the studied population that can be used for genetic improvement related to productivity per hectare and per plant, root shape and color, since there is the possibility of generating variability between the studied clusters.

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Statement of authors Authors contribution	The authors declare that they have no conflicts of interest. VRSO carried out the conceptualization of the research and design of the methodology to be implemented, collected field data and measurements together with CREG and prepared the draft for publication. FPRS and ARMG worked on the different statistical evaluation methodologies of the research project and applied them to the results obtained in the field. They performed the interpretation of the statistical analyses. VRSO, AND CREG led the planning and execution of the field investigation. All authors reviewed and approved the final version of the manuscript.
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