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AGRONOMIC CHARACTERIZATION OF SWEET POTATO GENOTYPES OBTAINED THROUGH CROSSBREEDING[1]

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ABSTRACT - The average national sweet potato yield of Brazil falls below the productive potential of the crop because of the cultivation of local and unimproved varieties. To improve this, more productive cultivars must be adopted along with adequate culture treatments. This study was conducted between January and May 2019 in Selvíria, Mato Grosso do Sul, Brazil, to characterize sweet potato genotypes obtained through crossbreeding. The experimental design consisted of randomized blocks containing 264 genotypes, the control ('Beauregard'), and two replicates. Plant harvesting began 127 d after planting. After harvesting, the roots were washed and dried in a covered area ready for evaluation. The total, commercial, and non-commercial yield; total, commercial, and non-commercial root number; root dry matter content; and dry matter productivity were evaluated. The genotypes CERAT16-20, CERAT31-1, and CERAT21-2 are promising in terms of root production for household consumption because of their high productivity of commercial roots. In contrast, genotypes CERAT16-20, CERAT31-1, CERAT25-17, CERAT25-12, CERAT21-2, CERAT29-26, CERAT34-4, CERAT31-11, and CERAT24-8 are promising for industry because of the high production of dry mass per hectare. The main components, total number of commercial roots, production of non-commercial roots, mass of commercial roots, total production of dry mass of roots, mass of roots, and total production of roots have a low contribution to the discrimination of the genotypes; therefore, their analysis can be discarded in future studies, under the same soil and climate conditions, thus reducing workload, expense, and time.

Keywords: *Ipomoea batatas* L. Genetic enhancement. Productivity.

CARACTERIZAÇÃO AGRONÔMICA DE GENÓTIPOS DE BATATA-DOCE OBTIDOS POR MEIO DE POLICRUZAMENTOS

RESUMO - O rendimento médio nacional da batata-doce está abaixo do potencial produtivo da cultura, principalmente devido ao cultivo de variedades locais e não melhoradas que apresentam baixos rendimentos. Para melhorar essa condição, junto com tratamentos culturais adequados, deve-se buscar cultivares mais produtivas. Assim, objetivou-se caracterizar genótipos de batata-doce obtidos por meio de cruzamentos. O experimento foi conduzido de janeiro a maio de 2019 em Selvíria, Mato Grosso do Sul, Brasil. O delineamento experimental foi em blocos casualizados com 264 (genótipos) + Controle ('Beauregard'), com duas repetições. A colheita de todas as plantas começou 127 dias após o plantio dos propágulos. Após a colheita, as raízes foram lavadas e colocadas para secar em área coberta para avaliação. Foram avaliados: rendimento total, comercial e não comercial; número total, comercial e não comercial da raiz; teor de matéria seca de raízes; e a produtividade de matéria seca. Os genótipos CERAT16-20, CERAT31-1 e CERAT21-2 são promissores para a produção de raízes para consumo doméstico devido à alta produtividade das raízes comerciais. Os acessos CERAT16-20, CERAT31-1, CERAT25-17, CERAT25-12, CERAT21-2, CERAT29-26, CERAT34-4, CERAT31-11 e CERAT24-8 são promissores para a indústria devido à alta produção de massa seca por hectare. Os componentes principais, número total de raízes comerciais, produção de raízes não comerciais, massa de raízes comerciais, produção total de massa seca de raízes, massa de raízes e produção total de raízes têm baixa contribuição para discriminação dos genótipos, portanto, sua análise pode ser descartada em trabalhos futuros, sob mesmas condições edafoclimáticas, reduzindo o trabalho, despesas e tempo.

Palavras-chave: *Ipomoea batatas* L. Melhoramento genético. Produtividade.

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INTRODUCTION

Sweet potatoes (*Ipomoea batatas* L.) are among the ten most consumed and the fourth most cultivated vegetable in Brazil, with a productivity of 14.5 t ha^{-1} (IBGE, 2019). They could potentially be used to ensure food security, especially in low-income populations, because of the number of roots produced per unit area and their nutritional quality (VARGAS et al., 2016), for example, their carbohydrate content, minerals, and precursors of vitamin A, C, and B complexes. They also have good sensory versatility in terms of pulp color, taste, texture, and sugars (VIZZOTTO et al., 2018). Sweet potatoes with orange flesh are an excellent source of provitamin A, particularly for people in developing countries (KOUROUMA et al., 2019).

In addition, sweet potato starch is an important industrial commodity that is used to manufacture various industrial products. Fresh sweet potato roots contain 80–90% dry weight carbohydrates, 50–80% of which takes the form of starch (HARAHAP; JULIANTI; SINAGA, 2020). For example, in Southeast Asia, sweet potato starch is an important ingredient in regional foods, such as noodles and vermicelli (BACH et al., 2021). China is the leading country in the commercial production of sweet potato starch, producing 120,000 tons of starch, 70,000 tons of noodles and 10,000 tons of vermicelli (WANG et al., 2020). Sweet potato can also be used as an alternative to sugar cane, beetroot, or sweet sorghum in sugar and ethanol production. The cultivar BRS Cuia, with an average yield of 50 t ha^{-1}, needs just 0.15 ha to produce 1 t of ethanol (RIZZOLO et al., 2021).

Despite the importance of sweet potato as a source of minerals, carbohydrates, and bioactive compounds, studies are scarce, indicating that it has been neglected by the agricultural sector in terms of both public research and private enterprises.

The results of this study show that almost all commercial sweet potatoes come from local genotypes of producers or materials of unknown origin, rather than from cultivars registered with the Brazilian Ministry of Agriculture, Livestock, and Food Supply (MAPA). This is one of the factors responsible for low yield, resulting in low productivity of approximately 13.5 t ha^{-1}, which is below the potential of the crop (ANDRADE JÚNIOR et al., 2009; ANDRADE JÚNIOR et al., 2012; SILVA et al., 2015).

Thirty sweet potato cultivars are registered in Brazil, many of which are obsolete, and others are used for ethanol production (MAPA, 2018). Thus, the search for new cultivars is essential for boosting the production of this vegetable, especially for genotypes with high yields. In 2017, the sweet potato genetic improvement program was started at the Universidad Estadual Paulista ¨ Júlio de Mesquita Filho-UNESP. Hence, our objective was to characterize sweet potato genotypes obtained through crossbreeding.

MATERIAL AND METHODS

The research was conducted in an experimental area at the Teaching, Research, and Extension Farm of the School of Engineering of UNESP, Ilha Solteira Campus, Selvíria, MS (51º 22 'W, 20º 22' S, 335 masl), from January to May 2019. According to the Köppen climate classification system, this region is classified as humid subtropical, CWa, with an average annual rainfall of 1261 mm, air temperature between 21.4 and 26.9 °C, and an average relative humidity of 62.4% (PORTUGAL; PERES; RODRIGUES, 2015). The soil was classified as clayey dystroferric red latosol (SANTOS, 2013). Soil samples (0–0.20 m) were sent to the Soil Laboratory of UNESP, Ilha Solteira Campus, for chemical characterization. The results were as follows: P (resin), 23 mg dm^{-3}; MO, 20 g dm^{-3}; pH ($CaCl_2$), 5.0; K, 2.3 $mmol_c dm^{-3}$; Ca, 20 $mmol_c dm^{-3}$; Mg, 17 $mmol_c dm^{-3}$; H + Al, 34 $mmol_c dm^{-3}$; SB, 39.3 $mmol_c dm^{-3}$; CTC, 73.3 $mmol_c dm^{-3}$, and V%, 54.

The experimental design consisted of randomized blocks with 264 genotypes, a control (‘Beauregard’), and two replicates. Each experimental plot contained three plants with 1.20 m between rows and 0.33 m between plants. Sixteen genotypes from 15 families with uncontrolled crossings (polycrosses) were used. These families were obtained from the genetic improvement program of the International Potato Center (CIP), which is in partnership with the Sweet Potato Genetic Improvement Program of UNESP. This partnership was established for the development of new cultivars from genotypes advanced by the CIP, and to increase the genetic variability of sweet potatoes in the UNESP program, which will provide subsidies for the development of future cultivars.

The study area was plowed then harrowed twice. Subsequently, mounds 1.2 meters apart and 40 cm high were mechanically raised. Simultaneously, 500 kg ha^{-1} planting fertilizer with the formulation 04 -14-08, 133 kg ha^{-1} of potassium chloride, and 166 kg ha^{-1} of simple superphosphate, corresponding to 20, 100, and 120 kg ha^{-1} of nitrogen, phosphorus, and potassium was incorporated into the soil (MONTEIRO; PERESSIN, 1997).

Propagules were obtained from a production field of genotype mother plants, with each propagule containing 8–10 buds. These were planted by burying 1/4 of the propagule in holes specifically made by a hoe for this purpose. Thirty days after planting, 30 kg ha^{-1} nitrogen fertilizer was added (MONTEIRO; PERESSIN, 1997). Weeds were controlled mechanically with a hoe and chemically with 0.6 L ha^{-1} Linurom and 0.20 L ha^{-1} Clethodim +

alkylbenzene. The plants were irrigated using a central pivot, a 12 mm nozzle, and a three-day watering schedule. Pests and disease were not controlled because they did not reach a level that constitutes economic damage.

Harvesting began 127 d after planting, after which the roots were washed and dried in a covered area. The following aspects were then evaluated: total root production (TRP), the mass of all roots harvested from the plot, kg ha^{-1}; commercial root production (CRP), mass of roots weighing > 80 g, kg ha^{-1}; non-commercial root yield (PNC), mass of roots weighing < 80 g, kg ha^{-1}; percentage of commercial root production (PCRP), PCRP = (CRP/ TRP) × 100; total number of roots (TNR), number of roots per plant, number of plants ha^{-1}; total number of commercial roots (TNCR), number of roots per plant weighing > 80 g, plants ha^{-1}; total number of non-commercial roots (NNCR), number of roots per plant weighing < 80 g, plants ha^{-1}; average root mass (ARM), ARM = TRP/TNR; average commercial root mass (ACRM), ACRM = CRP/NCR; average non-commercial root mass (ANRM), ANRM = PNC/ NNCR; root dry matter content (DM), root samples were dried in an oven at 65 °C until they reached a constant mass to determine the dry matter content (%); and total production of dry root mass (TDM), TDM = (TRP×DM)/100. Measurements were performed using a digital electronic balance with a capacity of 15 ± 5 g and a semi-analytical electronic scale with a capacity of 3,200 ± 0.01 g.

Data were transformed using the equation $\sqrt{X + 0.5}$. Analysis of variance with F tests and grouping of the means using the 5% Skott-Knott test were performed on the mean of each characteristic using SISVAR software (FERREIRA, 2019). Subsequently, analyses were conducted using mixed models to obtain the genotype values using Selegen software (RESENDE, 2016), to which the mean was added. A multivariate analysis of the principal components was performed to standardize the variables. This procedure evaluates the genotypic distances between materials and it benefits from the graphic efficiency of the principal component model. After analysis, the importance of the characteristics was evaluated, eliminating those that were not significant, contributed little, or were redundant.

Analysis of the relative contribution of each characteristic to genetic divergence was conducted according to the method proposed by Singh (1981). In addition, genotypic and phenotypic correlations were observed. The magnitudes of the correlation coefficients were classified according to the criteria proposed by Carvalho, Lorencetti, and Benin (2004): null = 0; weak = 0.1–0.30; mean = 0.31–0.60; strong = 0.61–0.90; and very strong = 0.91–1. Statistical analyses were performed using Genes (CRUZ, 2013).

Table 1 shows only the results of the genotypes relevant to this discussion.

RESULTS AND DISCUSSION

For all variables, except MRNC and DM, heritability ranged from medium to high, indicating that genetics had the greatest impact on the results (Table 1). In terms of PNC, MRNC, and DM, environmental variance was greater than genetic variance.

High heritability is essential for successful selection, allowing breeders to use the most appropriate selection strategies (OTOBONI et al., 2020). Heritability in sweet potatoes is important because dominance and epistatic effects are maintained by vegetative propagation (GONÇALVES NETO et al., 2012). As shown in Table 1, genetics had the greatest impact on the majority of variables, indicating that these characteristics are heritable between generations. This provides greater security for breeders as they can select sweet potato genotypes based on these variables.

Table 1. Variance Components: productivity (PT), commercial production (PC), non-commercial production (PNC), commercial percentage (% PC), total number of roots (TNR), number of commercial roots (NCR), number of non-commercial roots (NNCR), mean root mass (MR), mean mass of commercial roots (MRC), mean mass of non-commercial roots (MRNC), root dry matter content (DM), total dry matter production (TDM) of different sweet potato genotypes.

CV	PT	PC	PNC	PPC	TNR	NCR	NNCR	MR	MRC	MRNC	DM	TDM
σ_e^2	82.79	71.37	1845	0.14	3080	1928	8676	0.002	0.005	0.002	13.93	8.36
σ_g^2	85.23	75.7	866	0.08	6916	3022	9404	0.032	0.1	0.0001	3.4	6.9
h_g^2 %	50.7± 16.34	51.47 ± 16.46	31.95± 12.97	37.52± 15.05	69.18± 19.08	61.05± 17.93	52.01± 16.55	93.15± 22.14	5.24± 22.39	6.83± 6.00	19.63± 10.17	45.20± 15.43
h_m^2 %	67.3	67.97	48.43	54.57	81.78	75.81	68.43	96.45	97.56	12.8	32.82	62.26
CVe%	24.61	26.01	124.69	4.06	13.76	14.7	97.42	18.9	6.03	79.79	12.87	27.08

*Variance components (CV), residual variance (σ_e^2), genotypic variance (σ_g^2), individual heritability in the broad sense (h_g^2), heritability of genotype mean (h_m^2), and residual coefficient of variation (CVe%).

The genotypes CERAT31-1 and CERAT16-20 presented the best yields of 76.17 and 71.99 t ha^{-1}, respectively (Table 2). These values are 525 and 496% higher than the national average of 14.5 t ha^{-1}, respectively (IBGE, 2019). CERAT60-22 had the lowest productivity of just 1.11 t ha^{-1}.

In contrast to previous studies, the commercial cultivar Beauregard yielded 19.59 t ha^{-1} (Table 1); other studies obtained higher yields, for example, Amaro et al. (2019) verified a yield of 44,54 t ha^{-1} in Umbaúba, SE, in summer 2013/2014, while Silva et al. (2015) reported yields of 52.88 and 46.45 t ha^{-1} in 2012 and 2013, respectively. Yield differences can be associated with a number of factors, such as the growing season, soil type, watering regime, and health of propagating material.

In the four groups with the highest average yields, 49 genotypes produced > 33 t ha^{-1} and > 168.47% that of the commercial Beauregard cultivar. Thus, these genotypes could potentially be used for commercial production, and may constitute a base population for future programs for the genetic improvement of sweet potatoes.

The genotypes CERAT31-1, CERAT 16-20 and CERAT21-1 had the highest commercial yields of 71.44, 70.41, and 62.52 t ha^{-1}, respectively (Table 2). These are greater than those reported by Amaro et al. (2019), who obtained an average of 29.70 t ha^{-1} commercial root yield for eight sweet potato cultivars: BRS Amelia, Beauregard, Brazlândia Rosada, Brazlândia Roxa, BRS Cuia, Princesa, and BRS Rubissol in Umbauba, SE, in summer 2013/2014. These results reinforce the agronomic potential of the genotypes evaluated in this study. However, CERAT52-1, CERAT37-15, CERAT60-27, and CERAT60-22 had no commercial yield (> 80 g per root).

In terms of non-commercial productivity, CERAT51-30 and CERAT51-31 produced 13.83 and 15.45 t ha^{-1}, respectively. Among the studied genotypes, 173 had lower production of non-commercial roots, 0–4.72 t ha^{-1}, which would be of interest to producers or breeders.

For the commercialization of fresh roots, the total production of roots is as important as the production of commercial roots > 80 g. Hence, 49 genotypes that performed well were grouped, ranging from 95.07 to 100% commercial sweet potato roots. Vargas et al. (2016) found 56 genotypes with commercial production potential ranging from 93.92–99.85% within a population of 97 genotypes; therefore, it may be reasonable to use genotypes to set the commercial standard.

In terms of the total root number ha^{-1}, the 26 genotypes with the highest number of total roots had between 252,51 and 401,42 roots ha^{-1}, while CERAT51-16 and CERAT26-18 had the lowest values at 8,417 and 12,625, respectively (Table 2). Amaro et al. (2019) reported lower total root numbers for 26 genotypes of eight sweet potato cultivars, BRS Amelia, Beauregard, Brazlândia Rosada, Brazlândia Roxa, BRS Cuia, Princesa, and BRS Rubissol, in Umbaúba-SE in summer 2013/2014, ranging from 66 to 119.50. This difference may be because of the genetic diversity of the genotypes analyzed, soil characteristics, water management, and health of propagating materials.

The CERAT31-11 genotype had the highest number of commercial roots, followed by that of the other six genotypes, between 168,378 and 200,550 (Table 2). CERAT52-1, CERAT37-15, CERAT60-27, and CERAT60-22 had no commercial roots. The highest average commercial root mass was from CERAT52-25 at 1.58 kg, while CERAT29-17 and CERAT51-9 had the lowest mean root mass, 20 and 40 g, respectively (Table 2). However, high root mass is suboptimal for the fresh market, which prefers roots < 400 g. Twenty-nine of the genotypes studied presented commercial root mass > 500 g, which is preferable for the industrial and animal feed markets.

In terms of average non-commercial root mass, no statistical difference was observed between the genotypes. This shows that the differences in commercial yield did not occur due to variations in average root size, but due to root yield (AMARO et al., 2019). In addition, a high coefficient of variation was common owing to several zero values obtained by certain genotypes.

Considering the percentage of dry matter, 50% of the genotypes contained 17.90–29.62%, while the remaining 50% ranged from 29.70–46.42% (Table 2). Vieira et al. (2015) reported dry matter values ranging from 25.12–37.67%, with an average production value of 33.05%. The percentage of dry matter in sweet potato roots is directly correlated with starch levels, which are important in the starch extraction industry (VIEIRA et al., 2015). On average, a sweet potato has 30% dry matter in its roots, 85% of which is carbohydrate, the main component of which is starch (SILVA; LOPES; MAGALHÃES, 2008).

The genotypes CERAT31-1, CERAT24-8, CERAT16-20, CERAT31-11, CERAT34-4, CERAT29-26, CERAT21-2, CERAT25-12, and CERAT25-17 produced the most dry matter: 21.14, 19.47, 19.25, 18.08, 17.65, 17.64, 17.45, 16.57, and 16.51 t ha^{-1}, respectively (Table 1). Elsayed et al. (2018) evaluated 40 sweet potato genotypes from the UFVJM germplasm bank, including the genotypes Batata Mandioca, Brazlândia Branca, Brazlândia Rosada, Cambraia, Cariru Vermelha, Espanhola, Licuri, Palmas, Tomba Carro1, and UFVJM in Diamantina, MG, and reported an average yield of 13.0 t ha^{-1}.

Table 2. Means of characteristics: productivity (PT), commercial production (PC), non-commercial production (PNC), commercial percentage (% PC), total number of roots (TNR), number of commercial roots (NCR), number of non-commercial roots (NNCR), mean root mass (MR), mean mass of commercial roots (MRC), mean mass of non-commercial roots (MRNC), root dry matter content (DM), and total dry matter production (TDM) for different sweet potato genotypes.

Code[#]	Genotype	PT	PC	PNC	%PC	TNR	NCR	NNCR	MR	MRC	MRNC	DM	TDM
		t ha^{-1}	t ha^{-1}	t ha^{-1}	%	Root ha^{-1}	Root ha^{-1}	Root ha^{-1}	Kg	Kg	Kg	%	t ha^{-1}
6	CERAT16-13	10.45g	9.10 f	1.35 a	86.99 a	63.127 d	37.876 f	25.251 a	0.172 e	0.250 f	0.056 a	27.66 b	2.85 e
9	CERAT16-19	11.29 g	10.05 f	1.24 a	88.49 a	58.919 d	33.668 f	25.251 a	0.196 e	0.298 e	0.040 a	28.86 b	3.24 e
11	CERAT16-20	71.99 a	70.41 a	1.58 a	97.79 a	1.466 c	116.838 d	29.168 a	0.493 d	0.602 f	0.058 a	26.76 b	19.29 a
14	CERAT16-25	33.83 d	26.67 d	7.16 b	78.79 a	248.301 b	122.046 d	126.255 b	0.136 e	0.218 f	0.057 a	27.59 b	9.29 c
18	CERAT21-2	62.62 b	62.52 a	0.10 a	99.83 a	137.587 c	92.077 d	510 a	0.193 e	0.243 e	0.058 a	27.88 b	17.45 a
20	CERAT21-5	42.79 c	39.08 c	3.70 a	91.27 a	105.212 c	102.295 d	53.419 a	0.292 e	0.321 e	0.007 a	30.34 a	13.05 c
23	CERAT21-7	14.02 f	14.02 e	0.00 a	100.00 a	84.170 d	21.042 f	0.00 a	0.385 d	0.596 d	0.000 a	26.45 b	3.72 e
25	CERAT21-10	16.43 f	11.87 e	4.56 a	73.77 a	126.255 c	54.710 e	71.544 a	0.129 e	0.219 f	0.060 a	29.28 b	4.79 d
32	CERAT21-27	21.87 f	21.12 e	0.75 a	96.53 a	502 d	29.459 f	21.042 a	0.445 d	0.188 f	0.018 a	24.85 b	5.44 d
33	CERAT23-25	23.89 f	10.73 e	13.15 c	45.13 b	309.846 a	64.836 e	245.010 d	0.077 e	0.166 f	0.053 a	28.85 b	6.88 d
42	CERAT24-8	60.08 b	53.41 b	6.66 b	88.78 a	200.425 b	108.338 d	92.087 b	0.299 e	0.493 f	0.072 a	32.45 a	19.47 a
41	CERAT24-17	25.87 e	16.47 e	9.40 c	66.45 a	332.471 a	138.880 c	193.591 c	0.078 e	0.129 f	0.046 a	17.90 b	4.69 d
48	CERAT24-28	22.29 f	11.58 e	10.70 c	50.26 b	273.552 a	71.544 e	202.008 c	0.081 e	0.158 e	0.053 a	26.50 b	5.87 d
49	CERAT24-30	26.62 e	19.35 e	7.27 b	73.00 a	401.429 a	125.212 d	276.216 d	0.066 e	0.155 f	0.026 a	27.80 b	7.39 d
52	CERAT25-1	29.70 e	27.70 d	19.99 a	93.22 a	397.259 a	140.085 c	257.174 d	0.074 e	0.197 f	0.750 a	28.09 b	8.37 c
51	CERAT25-7	21.54 f	14.35 e	7.18 b	67.62 a	214.633 b	79.961 d	134.672 b	0.111 e	0.181 f	0.048 a	29.07 b	6.29 d
55	CERAT25-12	53.04 b	44.71 b	8.33 b	84.27 a	191.256 b	85.038 d	106.218 c	0.277 e	0.528 f	0.078 a	31.25 a	16.57 c
56	CERAT25-17	45.77 c	34.95 d	10.78 c	76.43 a	324.785 a	177.323 b	147.462 b	0.140 e	0.197 e	0.073 a	36.09 a	16.51 a
58	CERAT25-28	12.70 g	4.89 f	7.89 b	38.78 b	218.842 b	33.668 f	185.174 c	0.070 e	0.072 f	0.004 a	23.21 b	2.95 e
63	CERAT26-12	8.95 g	6.31 f	2.64 a	75.00 a	79.961 d	29.459 f	502 a	0.151 e	0.214 f	0.026 a	33.14 a	2.94 e
70	CERAT26-18	3.60 g	3.60 f	0.00 a	100.00 a	12.625 d	12.625 f	0.00 a	0.304 e	0.304 e	0.000 a	30.67 a	1.076 e
80	CERAT29-17	6.93 g	1.04 f	5.89 b	16.34 c	269,344 a	4.208 f	265.135 d	0.025 e	0.124 f	0.022 a	26.32 b	1.82 e
85	CERAT29-26	55.35 b	45.87 b	9.47 c	82.77 a	323.012 a	200.550 b	122.461 b	0.171 e	0.230 e	0.077 a	31.79 a	17.64 a
87	CERAT31-1	76.17 a	71.44 a	4.72 a	93.37 a	277.761 a	185.174 b	92.587 b	0.275 e	0.383 f	0.049 a	27.62 b	21.14 a
91	CERAT31-11	52.90 c	50.09 b	28.47 c	94.60 a	291.837 a	231.732 a	60.104 d	0.18 e	0.210 e	0.05 a	34.15 a	18.08 a
99	CERAT34-4	62.87 b	52.28 b	10.58 c	83.77 a	319.846 a	176.757 b	143.089 b	0.196 e	0.305 f	0.067 a	28.06 b	17.65 a
116	CERAT35-4	11.22 g	11.22 e	0.00 a	100.00 a	25.251 d	25.251 f	0.00 a	0.550 d	0.550 e	0.000 a	34.21 a	3.84 e
131	CERAT37-15	1.64 g	0.00 f	1.64 a	0.00 c	32.177 d	0.00 f	32.177 a	0.057 e	0.000 f	0.057 a	33.84 a	0.55 e
133	CERAT37-19	14.14 f	14.14 e	0.00 a	100.00 a	42.085 d	42.085 f	0.00 a	0.342 d	0.342 e	0.000 a	32.24 a	4.52 d
144	CERAT51-9	9.94 g	6.14 f	3.79 a	61.86 b	145.475 c	40.987 f	104.488 b	0.042 e	0.242 f	0.036 a	27.20 b	1.67 e
148	CERAT51-16	1.41 g	1.41 f	0.00 a	100.00 a	8.417 d	8.417 f	0.00 a	0.168 e	0.168 f	0.000 a	32.36 a	0.47 e
152	CERAT51-30	59.33 b	45.50 b	13.83 c	76.58 a	320.927 a	144.546 c	176.380 c	0.184 e	0.315 f	0.078 a	26.27 b	15.59 b
153	CERAT51-31	30.01 e	14.56 e	15.48 c	49.84 b	328.263 a	67.336 e	260.927 d	0.092 e	0.223 f	0.058 a	26.99 b	8.12 c
155	CERAT52-1	2.969 g	0.00 f	2.96 a	0.00 c	50.168 d	0.00 f	50.168 a	0.059 e	0.000 f	0.059 a	42.14 a	1.25 e
160	CERAT52-9	19.70 f	19.70 e	0.00 a	100.00 a	40.251 d	40.251 f	12.625 a	0.484 d	0.484 e	0.000 a	34.02 a	6.63 d
171	CERAT52-25	25.65 e	25.30 d	0.35 a	98.57 a	16,210 d	15,923 f	33,668 a	1.582 a	1.589 b	0.000 a	31.71 a	8.13 c
173	CERAT52-28	8.06 g	8.06 f	0.00 a	100.00 a	37.876 d	37.876 f	46.293 a	0.206 e	0.206 f	0.000 a	26.94 b	2.16 e
207	CERAT60-22	1.09 g	0.00 f	1.09 a	0.00 c	24.353 d	0.00 f	19.353 a	0.045 e	0.000 f	0.060 a	33.36 a	0.36 e
210	CERAT60-27	1.17 g	0.00 f	1.17 a	0.00 c	16.261 d	0.00 f	16.261 a	0.072 e	0.000 f	0.072 a	30.03 a	0.33 e
	TEST	19.58 f	14.00 e	5.58 b	52.15 b	171.320 b	70.694 e	100.626 b	0.105 e	0.183 a	0.052 a	22.14 b	0.05 d
	CV	14.84	18.68	36.15	19.66	17.17	20.9	32.85	17.35	20.15	45.18	6.65	16.31
	Amount F	10.017**	8.96**	3.91**	2.45**	7.20**	5.33**	4.74**	6.77**	5.47**	1.24^{ns}	2.02**	8.32**

#Code for verification of the principal component graph in Figure 1. ** Significant at the 1% level; ns not significant; CV = coefficient of variation. Means followed by the same letter were grouped using the Skott-Knott method at the 5% level.

For genotypic correction between the productivity characteristics, the estimates produced by Carvalho, Lorencetti, and Benin (2004) were used to verify the strong positive correlation between total productivity, commercial productivity (0.96), and dry mass productivity (0.93); the greater the total production, the greater the commercial and dry mass production (Table 3). A strong positive correlation was observed between commercial productivity and dry mass productivity (0.89), while there was a strong negative correlation between non-commercial productivity and the percentage of commercial roots (-0.82), as a greater number of non-commercial roots led to a lower percentage of commercial roots (Table 3).

The total number of roots correlated with the number of commercial and non-commercial roots, which had a strong positive correlation with both and a strong negative correlation with average root mass. This correlation was expected because when the number of roots increased, the average mass per root decreased. A strong negative correlation was observed between the number of commercial roots and average mass of commercial roots (Table 3). There was also a strong positive correlation between the average root mass and the average commercial root mass (0.80).

The phenotypic correlation between productive characteristics was verified using estimates. Total productivity had a strong positive correlation with the total number of roots (0.77) and with dry mass content (0.92, Table 3). This was also expected because the higher the number of roots per plant or per unit area, the greater the productivity. Amaro et al. (2019) also found that an increase in the number of roots per plant was directly related to increased commercial productivity.

Commercial productivity had a strong positive correlation with the commercial percentage (0.78) and commercial root number (0.83). The percentage of commercial productivity had a strong positive correlation with the total number of roots (0.67) and number of commercial roots (0.90). Carmona et al. (2015) found significant strong correlations between several pairs of characteristics, including the number of commercial roots per plant and total productivity (0.89), number of commercial roots per plant and percentage of commercial roots (0.82), as well as commercial productivity and percentage of roots (0.81). Andrade Junior et al. (2018) evaluated 40 sweet potato genotypes from the germplasm bank of UFVJM and found strong correlations between total root productivity, commercial root productivity, root dry matter productivity, crude protein productivity in the roots, and total dry mass productivity.

In this study, the total number of roots had a strong positive correlation with the dry mass content (0.76), while the number of non-commercial roots had a strong positive correlation with the root mass (0.76). In terms of the correlation between productivity and dry mass content, the higher the productivity, the greater the dry mass content.

Table 3. Phenotypic and genotypic correlations between sweet potato productivity characteristics. Genotypic correlations are shown on the upper transverse axis and phenotypic correlation on the lower transverse axis.

	PT	PC	PNC	PPC	TNR	NCR	NNCR	MR	MRC	MRNC	TDM	DM
PT	1.00	0.96	0.33	-0.03	0.45	0.54	0.15	0.04	-0.02	0.26	0.93	-0.06
PC	0.16	1.00	0.08	0.23	0.28	0.49	-0.01	0.15	0.04	0.21	0.89	-0.07
PNC	0.46	-0.39	1.00	-0.82	0.59	0.29	0.61	-0.27	-0.16	0.17	0.02	0.33
PPC	0.41	0.78	-0.13	1.00	-0.52	-0.12	-0.52	0.39	0.23	-0.24	-0.10	-0.08
TNR	0.78	0.31	0.37	0.67	1.00	0.78	0.76	-0.65	-0.51	-0.06	-0.03	0.45
NCR	0.08	0.83	-0.39	0.90	0.29	1.00	0.32	-0.48	-0.61	0.04	0.01	0.56
NNCR	0.39	-0.31	0.46	-0.36	0.00	-0.40	1.00	-0.38	-0.18	-0.18	-0.02	0.15
MR	0.46	-0.12	0.47	-0.13	0.02	-0.20	0.76	1.00	0.85	0.03	0.07	0.04
MRC	-0.03	0.12	-0.10	-0.00	0.00	-0.01	-0.09	-0.08	1.00	-0.11	-0.02	-0.06
MRNC	-0.12	-0.04	-0.06	-0.10	-0.08	-0.10	-0.07	-0.12	-0.02	1.00	0.08	0.28
TDM	0.93	0.39	0.31	0.56	0.76	0.27	0.26	0.35	0.01	0.11	1.00	0.28
DM	-0.07	0.18	-0.14	0.19	0.06	0.21	-0.12	-0.09	-0.05	-0.16	0.05	1.00

PT, productivity; PC, commercial productivity; PNC, non-commercial productivity; PPC, percentage of commercial productivity; TNR, total number of roots; NCR, number of commercial roots; NNCR, number of non-commercial roots; MR, root mass; MRC, commercial root mass; MRNC, non-commercial root mass; DM, dry mass content; TDM, dry mass productivity.

The principal components with the greatest levels of variance were TNR (37.06%), PC (23.47%), PPC (13.45%), MRNC (10.42%), and DM (8.48%). NCR, PNC, MRC, TDM, MR, and PT exhibited low levels of variance. Carmona et al. (2015), who morphologically characterized 23 sweet potato genotypes from the active germplasm bank at Embrapa Hortaliças, found that commercial productivity and the total number of roots were the principal components in the variance between genotypes. In principal component analysis, the variance of the principal components decreases from the first to the last, so the latter components explain a very small part of the total variance. Thus, the variable with the highest coefficient in the component with the lowest eigenvalue can be eliminated because it is the least discriminating variable and is already correlated with the other variables (DAHER; MORAES; CRUZ, 1997).

Figure 1 shows the principal components and illustrates that CERAT26-12 was distant from the other genotypes. CERTAT16-19 and CERAT16-13 are similar to each other but isolated from the others, indicating genetic variability. Meanwhile, CERAT21 -10, CERAT25-07, CERAT16-25, and CERAT21-05 are isolated from the other genotypes in the upper-right part of the graph, demonstrating genetic variability (Figure 1). CERAT25-28, CERAT21-27, CERAT24-17, CERAT21-02, and CERAT23-25 form a similar group; however, they are allocated in isolation, showing genetic variability.

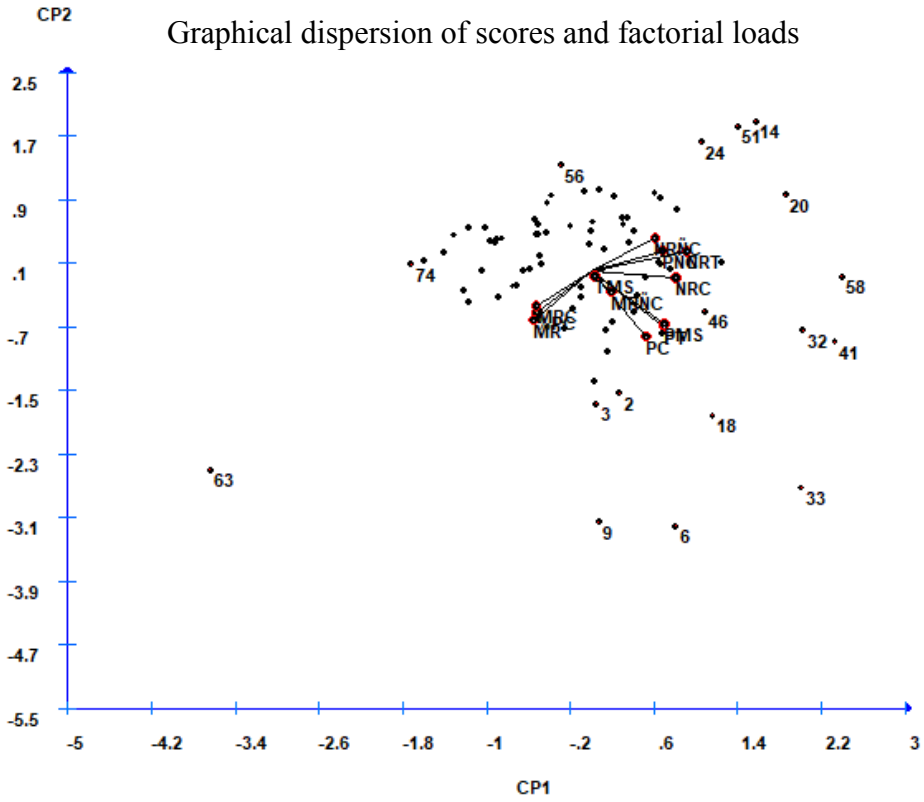

Figure 1. Principal components of sweet potato genotypes.

CONCLUSION

Under the edaphoclimatic conditions of this study, the genotypes CERAT16-20, CERAT31-1, and CERAT21-2 are promising for root production for domestic consumption because of their high productivity of commercial roots.

The CERAT16-20, CERAT31-1, CERAT25-17, CERAT25-12, CERAT21-2, CERAT29-26, CERAT34-4, CERAT31-11, and CERAT24-8 genotypes are promising for industry because of their high production of dry mass per hectare.

The principal components NCR, PNC, MRC, TDM, MR, and PT have low levels of contribution; therefore, their analysis may be dispensable in future studies to reduce labor, expense, and time.

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