

MORPHOAGRONOMIC CHARACTERIZATION OF SWEET POTATO ACCESSIONS FROM THE GERMPLASM BANK OF EMBRAPA HORTALIÇAS

CARACTERIZAÇÃO MORFOLÓGICA DE ACESSOS DE BATATA-DOCE MANTIDOS NO BANCO DE GERMOPLASMA DA EMBRAPA HORTALIÇAS

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ABSTRACT: Studies on the determination of genetic divergence among genotypes are important tools in breeding programs, contributing to the identification of parents with considerable productive potential. However, little is known about the combinatorial capacity of sweet potato (*Ipomoea batatas*) accessions and its adaptation to the different regions of Brazil. The objective of this study was to evaluate the morpho-agronomic traits from 102 sweet potato accessions from the Germplasm Bank of Embrapa Hortaliças. The experiment was laid out as an augmented block design comprised of 102 treatments. Nineteen above ground traits were measured using descriptors for the respective parts. Estimated values of broad sense heritability were high for the traits mean branch length (95.75%), immature leaf color (85.06%), and predominant branch color (90.57%). Coefficients of environmental variation were below 30.00% for all variables, except for branch weight (51.62%). The 102 clones analyzed presented broad genetic variability for the different traits evaluated, especially for branch weight, and branch length, and mature leaf color.

KEYWORDS: Genetic parameters. Genotypes. Sweet potato vegetative organs.

INTRODUCTION

In Brazil, sweet potato (*Ipomoea batatas* L.) is cultivated mainly by small farmers and can be considered as one of the oldest crops used as human food, especially by low-income populations (CARMONA et al., 2015). Due to its high level of ploidy, the sweet potato grown in the Brazilian territory show high phenotypic and genotypic diversity, which needs to be preserved and studied to contribute to future breeding programs (DAROS et al., 2002; BORGES et al., 2010).

Genetic divergence studies among accessions are essential to analyze the genetic

identify duplicated or genetically similar materials. These studies also provide means for selecting genetically different parents aiming to obtain a higher heterotic effect (OLIVEIRA et al., 2000; PAIXÃO et al., 2008).

Sweet potato has high nutritive value and is considered an energetic food due to its elevated starch content. It provides considerable amounts of mineral salts, mainly calcium and iron, and vitamins from the B and C complexes, in addition to vitamin

E, which is essential for skin health. Some cultivars are rich in carotenoids (NASCIMENTO, 2013).

This rustic crop presents few insect and disease problems. Although it responds well to fertilizers, sweet potato can be grown even in low fertility and often degraded soils. Therefore, knowledge of existing genetic diversity within accessions is of great economic importance for sweet potato management. It also enables the use of plant materials within germplasm banks, contributing to the genetic improvement of the species (GUEDES, 2004; MANTOVANI et al., 2013; SOBRAL et al., 2012).

The morphological characterization of accessions is usually the most accessible tool for quantification of genetic diversity. Hence, increased species collection, characterization, and evaluation of plant materials must be a priority among the approach and management strategies of the genetic resources of the species in Brazil (DAROS et al., 2002; RITSCHER; HUAMÁN, 2002; CAVALCANTE et al., 2009; MOULIN et al., 2014).

This study aimed to characterize and to evaluate the genetic variability of 102 sweet potato accessions from the Germplasm Bank of Embrapa

Hortaliças, in Brasília-DF, based on 15 morphological descriptors.

MATERIAL AND METHODS

The experiment was performed from September 2014, when cuttings were planted in polystyrene trays (72 cells), to October 2015, when plants were field transplanted. The field experiments were carried out at Embrapa Hortaliças (CNPq), located at BR-060 Km 09 (15°56'31" S and 48°8'55" W, 997 m asl), in Brasília, DF. The plants were cultivated in a dark red latosol at a spacing of 0.90 (between-rows) by 0.30 m (within-rows). The cultivar Beauregard was used as an external border for each plot.

A total of 102 accessions (Table 1) and 10 plants per accession were characterized. At 45 days after field planting, 19 above ground morphological traits were evaluated, based on standard descriptors used for the registration of sweet potato cultivars (HUAMÁN, 1991, 1992 end 1999).

Plant type (PT), plant vigor (PV), leaf lobe type (LLT), leaf lobe number (LLN), shape of central leaf lobe (SCLL), petiole length (PL; cm), petiole pigmentation (PP), branch internode length (VIL; cm), vine internode diameter (BID; cm), predominant vine color (PBC), secondary branch color (SBC), branch tip pubescence (BTP), abaxial leaf vein pigmentation (ALBP), immature leaf color (ILC), mature leaf size (MLS), mature leaf color (MLC), and leaf shape (LS).

In addition, vine weight (BW; t h⁻¹) was recorded by cutting all vines from each plot, six months after planting. The branches were individually weighed in an analytical scale. Branch length (VL; cm) was a measure of three plants per plot.

Soil analysis presented the following results: pH (H₂O) = 4.8; H⁺ + Al⁺⁺⁺ = 4.2 cmol_c dm⁻³; Ca⁺⁺ = 1.8 cmol_c dm⁻³; Mg⁺⁺ = 1.1 cmol_c dm⁻³; P (Mehlich) = 1.1 mg dm⁻³; K⁺ = 122 mg dm⁻³ or 0.31 cmol_c dm⁻³; organic matter = 26 g dm⁻³; CEC = 7.43 cmol_c dm⁻³; and V = 43.5 %. Liming was applied (1.8 t ha⁻¹ of dolomitic limestone) three months before planting and incorporated by plowing. The soil was harrowed twice and lines of 0.60 m width and 0.40 high were organized prior to planting. An equivalent to 600 kg ha⁻¹ of NPK 4-30-16 was incorporated to the lines as pre-planting fertilization.

The mean score for each morphological descriptor was considered for statistical analyses. Estimated values of broad sense heritability (h_a²) and coefficients of genetic (CGV) and

environmental variation (CEV) were calculated using the software Genes (CRUZ, 2013).

A dendrogram was generated with the unweighted pair group method with arithmetic mean (UPGMA). Quantitative traits were used for diversity analyses among accessions based on the Euclidean distance measurement. For hierarchical clustering (HCA), a dendrogram was generated for the pairs ordered by the UPGMA.

Pearson's correlation coefficient was calculated for each combination of traits. Correlation intensity was classified according to the magnitude of the values, as suggested by Shimakura and Ribeiro Júnior (2009): 0.00 ≤ |r| < 0.20 (very weak); 0.20 ≤ |r| < 0.40 (weak); 0.40 ≤ |r| < 0.70 (moderate); 0.70 ≤ |r| < 0.90 (strong); and 0.90 ≤ |r| ≤ 1 (very strong).

Table 1. Sweet potato (*Ipomea batata*) Accessions from the Germoplasm Bank of Embrapa Hortaliças (CNPH), Brasília-DF, 2018.

Nº	Acesseccion	Origin	Nº	Acesseccion	Origin	Nº	Acesseccion	Origin	Nº	Acesseccion	Origin			
1	CNPH 768	Içara-SC	21	CNPH 1262	Brasília - DF	41	CNPH 872	Caçador-SC	61	CNPH 904	Videira-SC	82	CNPH1277	Porto Alegre - RS
2	CNPH 769	Contenda-PR	22	CNPH 901	Caçador-SC	42	CNPH 1132	Macatuba - SP Embrapa Hortaliças	62	CNPH906	Maravilha-SC	83	CNPH1282	Presidente Prudente - SP
3	CNPH 773	Pomerode-SC	23	CNPH 813	Videira-SC	43	CNPH 962		63	CNPH908	Agronômica-SC	84	CNPH1284	
4	CNPH 774	Morro da Fumça-SC	24	CNPH 817	Caçador-SC	44	CNPH 874	Corupá-SC	64	CNPH909	Corupá-SC	85	CNPH1285	Lagoa dourada - MG
5	CNPH 777	Taió-SC	25	CNPH 825	Rio Fortuna-SC	45	CNPH 876	Ilhota-SC	65	CNPH916	Caçador-SC	86	CNPH1366	Tibo indígena Krahô
6	CNPH 785	Caçador-SC	26	CNPH 823	Ituporanga-SC	46	CNPH 877	Biguaçu-SC	66	CNPH871	Pelotas-RS	87	CNPH1369	Tribo indígena Krahô
7	CNPH 786	Caçador-SC	27	CNPH 832	Embrapa Hortaliças	47	CNPH 878	Viçosa-MG	67	CNPH942	Campos Novos-SC	88	CNPH1370	Tribo indígena Krahô
8	CNPH 787	Xanxerê-SC	28	CNPH 834	Nova Erechim-SC	48	CNPH 824	Joinville-SC	68	CNPH895	Rio Fortuna-SC	89	CNPH1377	Itabaiana - SE
9	CNPH 789	Pomerode-SC	29	CNPH 845	Videira-SC	49	CNPH 886	Florianópolis-SC	69	CNPH932	Concórdia-SC	90	CNPH1403	Embrapa Hortaliças
10	CNPH 790	Angelina-SC	30	CNPH 848	Embrapa Hortaliças	50	CNPH 887	Pelotas-RS	70	CNPH936	Herval do Oeste-SC	91	CNPH 1387	Embrapa Hortaliças
11	CNPH1401	Embrapa Hortaliças	31	CNPH 1261	Viçosa -MG	51	CNPH 888	Nova Veneza-SC	71	CNPH 947	Laurentino-SC	92	CNPH 1390	Embrapa Hortaliças
12	CNPH796	Maravilha-SC	32	CNPH 1163	Japão	52	CNPH889	Taió-SC	72	CNPH 948	Herval do Oeste-SC	92	CNPH 1395	Embrapa Hortaliças
13	CNPH797	Dionísio Cerqueira-SC	33	CNPH 850	Embrapa Hortaliças	53	CNPH 896	Ilhota-SC	73	CNPH 949	Abelardo Luz-PR	94	CNPH 837	Laurentino-SC
14	CNPH798	Ponte Serrada-SC	34	CNPH 852	Blumenau-SC	54	CNPH 1027	Limeira - SP	74	CNPH 952	Embrapa Hortaliças	95	CNPH 1283	Presidente Prudente - SP
15	CNPH799	Abelardo Luz-PR	35	CNPH 857	Petrolândia-SC	55	CNPH 1010	S. Luis - MA	75	CNPH 953	Embrapa Hortaliças	96	CNPH 964	Embrapa Hortaliças
16	CNPH801	São Miguel do Oeste-SC	36	CNPH 858	Treze Tilias-SC	56	CNPH893	Mafra-SC	76	CNPH 959	Embrapa Hortaliças	97	CNPH 965	Embrapa Hortaliças
17	CNPH803	São Carlos-SC	37	CNPH 865	Anitápolis-SC	57	CNPH894	Ituporanga-SC	77	CNPH 980	Embrapa Hortaliças	98	CNPH 829	Joinville SC.
18	CNPH804	São Bonifácio-SC	38	CNPH 867	Agrolândia-SC	58	CNPH826	Taió-SC	78	CNPH 983	Embrapa Hortaliças	99	CNPH 1389	Embrapa Hortaliças
19	CNPH806	Caçador-SC	39	CNPH 869	Blumenau-SC	59	CNPH899	Concórdia-SC	79	CNPH 961	Embrapa Hortaliças	100	CNPH 1397	Embrapa Hortaliças
20	CNPH809	Treze Tilias-SC	40	CNPH 969	Embrapa Hortaliças	60	CNPH 900	Treze Tilias-SC	80	CNPH 946	Concórdia-SC	101	Trat. Comum 1	Embrapa Hortaliças
									81	CNPH 1265	Espanha	102	Trat. Comum 2	Brazlândia - DF

Source: Embrapa Hortaliças. Brasília, DF, 201

RESULTS AND DISCUSSION

Estimated values of broad sense heritability were high for the traits LLN (100.00%), VL (95.75%), PBC (90.57%), ILC (85.06%), MLC (76.06%), and PV (68.12%) (Table 2). These results highlight that most of the phenotypic variability was due to genetic effects. These findings are corroborated by Marchese et al. (2010) and Kalkmann et al. (2013), who also reported similar heritability values for sweet potato. High heritability values indicate a possibility of successful selection of superior plants for the traits evaluated.

According to Vencovsky (1978), the selection of genetic material is favored by CGV/CEV values above the unit, as observed in this study. Moreover, minimum heritability values of 80.00% are necessary for satisfactory genetic gains with selection (FALCONER, 1987). Therefore, the results here reported for the genetic parameters indicate the possibility to obtain genetic progress even with simple selection methods.

Coefficients of environmental variation lower than 30.0% were observed for all variables, except for BW (51.62%) (Table 2), indicating medium to high experimental precision. The estimated coefficients of genetic variation were 29.63 and 28.24% for PB and SBC, respectively. These estimates were higher than the estimated coefficient of environmental variation, indicating a greater expression of the genetic variation as compared to environmental effects (Table 2).

The highest CGV/CEV values were verified for BTP (47.38), BIL (39.32), BW (30.01), SBC (26.44), and SCLL (22.09) (Table 2). However, PV, BL, MLS, ILC, ILM, PBC, LLT, BID, LS, and LLN presented CGV/CEV values below 18.22 (Table 2). Analyses of estimated genetic parameters are of great importance in genetic breeding programs. Studies on the genetic control and inheritance of agronomic traits by the estimation of genetic parameters of a population allow inferences about the existing genetic variability in this population and the expected gains with selection (BORGES et al 2007).

Table 2. Estimates of broad sense heritability (h_a^2), coefficient of genetic variation (CGV), coefficient of environmental variation (CEV), and CGV/CEV ratio for morphological traits evaluated in 102 sweet potato (*Ipomoea batatas* L.) accessions from the Germplasm Bank of Embrapa Hortaliças. Brasília-DF, 2018.

Genetic parameters	PV	BL	BIL	MLS	ILC	MLC	PBC	LLT
h_a^2 (%)	68.12	95.75	37.65	64.36	85.06	76.06	90.57	0
CGV (%)	10.42	18.67	16.12	10.03	21.21	27.59	28.25	0.99
CEV (%)	1.47	4.75	0.41	1.34	2.39	1.78	3.09	0.99
CGV/CEV	7.09	3.93	39.32	7.49	8.84	15.5	9.14	1

Genetic parameters	SBC	BID	SCLL	LS	LLN	BW	BTP
h_a^2 (%)	55.85	0	38.45	59.71	100.00	74.83	1.56
CGV (%)	29.63	0.99	17.45	9.77	28.24	51.62	6.18
CEV (%)	1.12	0.99	0.79	1.22	1.55	1.72	0.13
CGV/CEV	26.44	1	22.09	8.01	18.22	30.01	47.38

ILC - immature leaf color; LLN - leaf lobe number; LS - leaf shape; LLT - leaf lobe type; MLC - mature leaf color; MLS - mature leaf size; PV - plant vigor; PBC - predominant branch color; SCLL - shape of central leaf lobe; SVC - secondary vine color; BID - branch internode diameter (cm); BIL - branch internode length (cm); BL - branch length (cm); BTP - branch tip pubescence; VW - branch weight ($t h^{-1}$).

ILC and MLC indicated the existence of variability among accessions of the Germplasm Bank of Embrapa Hortaliças. The following distribution was verified for ILC: 35% of the clones were classified as green leaves with purple edges; 33% mostly purple; 8% slightly purple. A greater variation was observed for MLC: 22% slightly purple; 17% mostly purple; 17% green upper and

purple lower; and the remaining clones with MLC distributed among the categories yellow-green, green, and green with purple edge. These traits are of great importance for selection in genetic breeding programs, especially with focus on the ornamental use.

The accessions also showed great variability for LLN, the following distribution was verified:

33% (5 lobes per leaf); 31% (1 lobe per leaf); 25% (3 lobes per leaf); and 11% with 2 or 7 lobes per leaf.

Most clones (86%) showed PL within the expected values for sweet potato. Clone CNPH774 presented the highest BL (1.3 m). BL analysis is essential in a breeding program aiming to select clones for cutting propagation.

BW varied from 0.6 (CNPH1027) to 10.6 t h⁻¹ (CNPH959). Six clones had BW greater than 6.0 t h⁻¹ (CNPH895, CNPH768, CNPH964, CNPH1390, CNPH001, and CNPH953). Clones of sweet potato with high branch production can be used in animal feed and the leaves used as an enriching source in preparations for human consumption.

Most of the accessions (80%) had green with few purple spots PVC while 20% presented green or mostly purple PVC. SBC allowed better distinction of the accessions as compared to PBC since 50% of the accessions showed green base, 40% had no SBC, and 10% presented green tip or green base. BTP was also a good descriptor for accession characterization. Forty one percent of the accessions showed no BTP while sparse (33%) and heavy (26%) BTP were also recorded.

A total of 17 groups were formed for the 102 clones evaluated. According to Dias (1980), the criteria used to establish groups in plant materials using characteristics of interest to the species, starting from the analysis of dendrograms, have been used by many researchers successfully to investigate the similarities between accessions, clones and or cultivars.

The largest group (group 17) comprised more than 50% of the clones (CNPH824, CNPH845, CNPH1366, CNPH942, CNPH1369, CNPH895, CNPH886, CNPH848, CNPH909, CNPH876, CNPH823, CNPH899, CNPH969, CNPH1262, CNPH1261, CNPH1132, CNPH813, CNPH832, CNPH834, CNPH858, CNPH803, CNPH817, CNPH825, CNPH901, CNPH804, CNPH801, CNPH799, CNPH1401, CNPH809, CNPH796, CNPH797, CNPH787, CNPH798, CNPH 790, CNPH777, CNPH789, CNPH773, CNPH785, CNPH774, CNPH768, CNPH786,

CNPH959, CNPH769, CNPH867, CNPH806, CNPH1283, CNPH894). Formation of large groups may indicate existing duplicates in the collection (HALCOMB et al., 1977; HUAMÁN, 1992). Sweet potato is vegetatively propagated commercially using branch cuttings from production fields or sprouted storage roots (LOEBENSTEIN; THOTTAPPILLY, 2009). Although the accessions from the Germplasm Bank were collected at different sites, they may have the same genotype due to the specific propagation type of the species.

Groups 1 (CNPH 1277, T2) and 2 (CNPH 983, CNPH965) had two clones each. Each of the groups from 3 to 7 were comprised of three clones: group 3 (CNPH 904, CNPH946, CNPH1389), group 4 (CNPH1010, CNPH952, CNPH1395), group 5 (CNPH887, CNPH932, CNPH370), group 6 (CNPH878, CNPH871, CNPH1285), and group 7 (CNPH 877, CNPH916, CNPH1284). The remaining groups presented four clones each: group 8 (CNPH962, CNPH906, CNPH1265, CNPH1397), group 9 (CNPH874, CNPH908, CNPH1277, T1), group 10 (CNPH872, CNPH900, CNPH961, CNPH829), group 11 (CNPH893, CNPH953, CNPH865, CNPH837), group 12 (CNPH826, CNPH980, CNPH869, CNPH964), group 13 (CNPH949, CNPH1390, CNPH857, CNPH1027), group 14 (CNPH948, CNPH1387, CNPH852, CNPH896), group 15 (CNPH888, CNPH936, CNPH1163, CNPH1377), and group 16 (CNPH1403, CNPH 947, CNPH889, CNPH858) (Figure 1). Some authors report that the groups should be subjectively established based on the accentuated changes in the dendrogram levels and the previous experience of the researcher with the material under evaluation (CRUZ; REGAZZI, 1997).

Clones in more distant groups are dissimilar and may be considered as a promising artificial cross to obtain superior segregating populations. However, in addition to genetic divergence, the selected clones must present gene complementation associated with high variability for the evaluated traits (MARTINS et al., 2012).

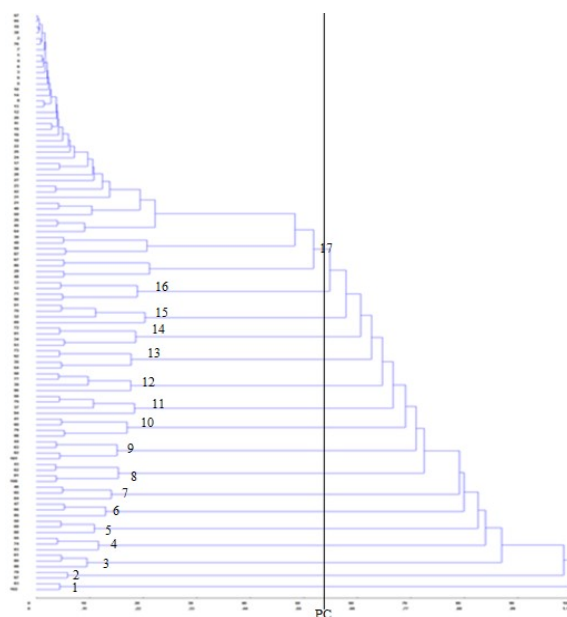


Figure 1. Dissimilarity dendrogram of 102 sweet potato (*Ipomoea batatas* L.) clones, established by the UPGMA method, using the Euclidian distance, and based on 15 above ground morphological descriptors.

Embrapa Hortaliças, Brasília-DF, 2018. PC= Cut point.

Heritability is very important in plant breeding since it estimates the inheritable portion of the phenotypic variation. Therefore, for successful genetic improvement, the trait under selection must be inheritable, and variation is required in the population where selection will occur (CRUZ; CARNEIRO, 2006). Since heritability influences correlations, if correlated traits have low heritability values, the phenotypic correlation will be determined mainly by the environmental correlations. However, if high heritability values are observed, then genetic correlations will be the most important (FALCONER, 1987).

Thus, knowledge on the genetic parameters and the association between the traits studied may allow efficient breeding strategies to select superior sweet potato clones that meet the consumer market demands.

Table 3 shows the values of the Pearson correlation matrix generated for morphological characteristics of sweet potatoes.

LLN was positively and moderately correlated to LLT (0.68) (Table 3). Positive and moderate correlations were also found between BID and BIL (0.48); LLT and LS (0.66); LLN and LS (0.65); SCLL and LS (0.51); SCLL and LLT (0.52); MLC and PBC (0.41).

Among the various tools used in genetic breeding programs, correlation analyses provide an identity for each plant material and allow studies of the genetic variability of each trait (DAROS et al.,

2002). When a morphological characterization is performed, the quantification of the diversity among accessions will only be meaningful if the phenotypic divergence expresses the genetic divergence (BUZAR et al., 2007)

Table 3. Pearson correlation matrix generated for sweet potato (*Ipomoea batatas* L.) above ground morphological traits. Embrapa Hortaliças, Brasília-DF, 2018.

	PT	BIL	BID	PBC	SBC	BTP	LS	LLT	LLN	SCLL	MLS	MLC	ILC	BL	BW	Vigor
PT	1	0.05	-0.11	-0.06	0.34	0.18	-0.18	-0.26	-0.17	-0.23	-0.01	-0.18	0.01	0.16	-0.15	-0.01
BIL		1	0.48*	0.03	0.01	0.13	0.08	0.06	0.09	-0.07	0.3	0.01	-0.03	0.35	0.37*	0.22
BID			1	-0.27	0.19	0.19	-0.05	0.05	0.03	-0.04	0.28	0.09	-0.01	0.13	0.08	0.15
PBC				1	-0.13	-0.09	0.27	0.02	0.04	0.24	-0.1	0.17	0.41*	-0.05	0.1	-0.05
SBC					1	0.12	-0.3	-0.36	-0.24	-0.34	0.18	-0.06	0.02	-0.01	-0.18	-0.03
BTP						1	-0.02	0.02	0.15	-0.23	0.22	0.02	0.13	0.16	-0.01	-0.07
LS							1	0.66*	0.65*	0.51*	0.02	0.37	0.1	-0.14	0.25	-0.05
LLT								1	0.68*	0.52*	-0.06	0.28	-0.02	-0.02	0.18	-0.09
LLN									1	0.29	0.11	0.16	0.13	-0.07	0.2	-0.05
SCLL										1	0.02	0.2	0.08	-0.01	0.07	-0.05
MLS											1	-0.13	0.05	0.18	0.21	0.07
MLC												1	0.1	-0.01	0.15	0.11
ILC													1	-0.01	0.01	-0.14
BL														1	0.2	0.09
BW															1	0.23
Vigor																1

*Significant at 5% level. PT = plant type; BIL - branch internode length; BID - branch internode diameter; PBC - predominant branch color; SBC - secondary branch color; BTP - branch tip pubescence; LS - leaf shape; LLT - leaf lobe type; LLN - leaf lobe number; SCLL - shape of central leaf lobe; MLS - mature leaf size; MLC - mature leaf color; ILC - immature leaf color; BL - branch length; BW - branch weight.

CONCLUSIONS

The qualitative and quantitative morphoagronomic characterization was efficient to estimate the existing genetic diversity among the sweet potato accessions from the Germplasm Bank of Embrapa Hortaliças.

The traits PVC and LS allowed good discrimination of the accessions and were considered good descriptors for the morphoagronomic characterization. Since 41% of the clones had green SVC, this trait was a good

indicator of variability in this study. Clone CNPH959 had the greatest branch weight.

Broad genetic variability was verified for the different traits evaluated, despite the occurrence of some genetically very close clones probably due to the existence of duplicates in the collection.

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RESUMO: Estudos de determinação de divergência genética entre genótipos são ferramentas de grande importância em programas de melhoramento, auxiliando na identificação de genitores com considerável potencial produtivo. No entanto, pouco ainda se sabe sobre a capacidade combinatória de acessos de batata-doce (*Ipomoea batatas*) e sobre a adaptação a diferentes regiões do Brasil. O objetivo deste trabalho foi avaliar características agrônomicas de 102 acessos de batata-doce mantidos no Banco de Germoplasma da Embrapa Hortaliças. O experimento foi instalado utilizando o delineamento em blocos aumentados, com 102 tratamentos. Foram mensuradas 19 características da parte aérea utilizando-se descritores das respectivas partes. Os valores das estimativas de herdabilidade no sentido amplo foram altos para as características comprimento médio das ramas (95,75%), cor da folha imatura (85,06%) e cor predominante da rama (90,57%). Os coeficientes de variação foram inferiores a 30 % para todas as variáveis, exceto para peso das ramas (51,62%). Os 102 clones analisados apresentaram ampla variabilidade genética para as diferentes características avaliadas, principalmente para peso das ramas, comprimento das ramas e cor da folha madura.

PALAVRAS-CHAVE: Parâmetros genéticos. Genótipos. Órgãos vegetativos de batata-doce.

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