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Prediction of genetic gains in sweet potato genotypes by polycross

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Abstract

Sweet potato crops present a wide genetic diversity, but genetic parameters of populations should be estimated in breeding programs, mainly when the selection is focused on multiple traits. Thus, the objective of this study was to estimate genetic parameters and select clones via a selection index in a sweet potato population obtained from uncontrolled crosses. The experiment was carried out in Ilha Solteira, Sao Paulo, Brazil, from June to November 2020, to evaluate 144 clones and three controls, totaling 147 treatments. A randomized block design was used, with two replications and three plants per plot. The data were analyzed through mixed modeling (REML/BLUP), and the selection index proposed by Mulamba & Mock was applied using a selection pressure of 17.3% for the selection of superior clones. The direct selection enabled a higher prediction of gains for each trait, but the joint analysis maximized the selection gains for all traits of interest. Clones 38, 63, 79, 77, and 5 are recommended, among the selected clones, for further stages of sweet potato breeding focused on improving traits for production and table consumption.

Keywords: Genetic parameters, Genetic diversity, *Ipomoea batatas* (L.) Lam, Selection index

Introduction

Sweet potato (*Ipomoea batatas* (L.) Lam.) is an important vegetable with characteristics that allow for its use for various purposes, such as human food, animal feed, and source of energy. China is the world's largest sweet potato producing country, but the crop is grown in many other countries. The estimated area with sweet potato crops in Brazil is approximately 59,790 hectares, with an estimated mean yield of 14,255 kg ha^{-1} in 2020 (Cavalcante et al., 2017; IBGE, 2022).

Sweet potato has a wide edaphoclimatic adaptation; plant deaths occur only under severe climate conditions, such as long drought or frost periods (Oliveira et al., 2015). Its wide genetic diversity enables the selection of genotypes for different purposes, such as improving nutritional quality and productivity. These purposes can be achieved in sweet potato breeding programs based on polycross or controlled cross (Ssali et al., 2019).

Biofortified foods were initially developed to fight hidden hunger, as the deficiency of specific micronutrients is considered a public health problem, resulting in disorders in the immune system and in diseases (Loureiro et al., 2018). Sweet potato is among vegetables with great potential for biofortified foods, as it contains polysaccharides with antimicrobial, antioxidant, anticancer, and anti-inflammatory activities, and has high contents of functional nutrients, such as beta-carotene, which contributes to the prevention of blindness in people with vitamin A deficiency (Wu et al., 2015; Lafia et al., 2020).

Currently, the demand for biofortified foods is high, which increases the need and interest in making foods more nutritious. This reinforces the need for selection of genotypes with better nutritional and commercial qualities than existing cultivars on the market, in addition

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to good adaptation and production. Thus, the use of selection methods that provide maximization of selective gains in all traits of interest is essential.

The success of breeding programs depends on establishing selection criteria that identify superior genotypes for all traits of interest simultaneously. Thus, the use of selection indices is an important strategy to select genotypes that accumulate favorable alleles in many traits. The index proposed by (Mulamba and Mock, 1978) has been used for several crop species, ordering the genotypes according to the evaluated trait, depending on the desired direction and sum of their classifications (Teixeira et al., 2012).

In this context, the objective of this study was to estimate genetic parameters and select genotypes in a sweet potato population obtained from uncontrolled crosses, for table consumption.

Material And Methods

The experiment was conducted in Ilha Solteira, state of Sao Paulo, Brazil (20°25'32"S and 51°21'12"W). The climate of the region is Aw, humid tropical, according to the Köppen classification, with two well-defined seasons: rainy in the summer and dry in the winter. The soil of the area was classified as a Typic Hapludult (Argissolo Vermelho Eutrófico; Santos et al., 2018).

The sweet potato clones evaluated in the present study (n = 144) were from an elite population developed by the breeding program of the International Potato Center (CIP) and the Agricultural Research Institute of Mozambique (IIAM), obtained through uncontrolled crosses (polycross).

The experiment was implemented in June 2020 with 144 new clones and three controls, totaling 147 treatments. A randomized block experimental design was used, with two replications and three plants per plot. The controls used consisted of three more adapted and stable sweet potato clones (CERAT25-27, CERAT25-23, and CERAT60-05), according to (Otoboni et al., 2020). The vines used for planting were collected from seminal seedlings that had been transplanted into pots. The experimental plot was arranged in rows with three plants, with spacings of 1 m between rows and 0.33 m between plants.

The experimental area was subjected to conventional soil tillage, with formation of ridges of approximately 40 cm in height, followed by soil fertilizer application using 357 Kg ha^{-1} of the 08-28-16 N-P-K formulation, supplemented with 105 Kg ha^{-1} of potassium chloride. The cultural practices used during the experiment were: topdressing using 24 Kg ha^{-1} of N 30 days after planting, weed control through herbicide applications and manual weeding as needed, and sprinkler irrigation when necessary.

Harvesting started 153 days after planting, in November 2020. The following quantitative traits were evaluated: total tuber yield (TY): weight of all tubers harvested in the plot, converted to Mg ha-^{1}; commercial tuber yield (CY): weight of tubers above 80 g in the plot (converted o Mg ha^{-1}); total number of tubers (TNT): number of tubers per plant harvested in the plot, converted to number of tubers per hectare; number of commercial tubers (NCT): number of tubers (above 80 g) per plant harvested in the plot, converted in number of tubers ha^{-1}; mean tuber weight (TW), obtained by TY/TNT; mean commercial tuber weight (CTW), obtained by CY/NCT; Total tuber dry weight yield (TDWY): tuber samples were dried in an oven at 65 °C for 72 hours until constant weight and the dry weight (%) was converted to Mg ha^{-1}; tuber dry weight content (TDW): obtained by (TDWY × 100) / Fresh Weight.

Traits related to tuber quality were evaluated visually, using a scale of grades varying according to the trait evaluated. The grades were assigned by two evaluators; each evaluator was considered a replication. The traits evaluated were: overall shape (OS): (1 = shape not suitable for commercialization, with deformations; 2 = poor shape for commercialization, with cracks; 3 = uneven shape; 4 = shape close to fusiform; 5 = fusiform shape); commercial standard (CS): (1 = worse commercial standard; 2 = standard that highly hinders commercialization; 3 = standard that moderately hinders commercialization; 4 = good commercial standard; 5 = best commercial standard); resistance to insects (RES): (1 = damages that completely affect the commercial appearance; 2 = damages that highly affect the commercial appearance; 3 = damages that moderately affect the commercial appearance; 4 = few damages; 5 = free of damages); eyes (EYE) (0 = many eyes; 1 = moderate presence of eyes; 2 = few eyes; 3 = absence of eyes); veins (VE): (0 = presence of veins; 1 = absence of veins); lenticels (LEN): (0 = many lenticels; 1 = moderate presence of lenticels; 2 = few and small lenticels; 3 = absence of lenticels); tuber skin color (SC): (1 = white; 2 = off white; 3 = yellow; 4 = brownish orange; 5 = pink; 6 = purplish red; 7 = dark purple); and flesh color (FC): (1 = white and purple; 2 = off white; 3 = yellow; 4 = orange; 5 = dark orange), according to the methodology adapted by (Costa, 2020).

The final data were subjected to homogeneity of residual variances and normality analysis, in which the traits that did not meet the basic assumptions for variance analysis were transformed into $\sqrt{x + 0.5}$. Subsequently, analysis of deviance was carried out for all traits through mixed models methodology (REML/BLUP), using the computational software Selegen (Resende, 2007), following the statistical model 20 (randomized blocks, test of unrelated clones, one evaluation per plot), represented by $y = Xr + Zg + e$, where *y* is the data vector, *r* is the vector of repetition effects (assumed to be fixed) added to the overall mean, *g* the vector of genotypic effects (assumed to be random), and *e* is the vector of errors or residuals (random). The uppercase letters (*X* and *Y*) represent the incidence matrices for the respective effects.

The following genetic parameters and variance components were estimated: genetic variance(σ_g^2); experimental error variance (σ_e^2); experimental and genotypiccoefficient of variations (CV_e%, CV_g%); broad-sense heritability based on clone means (h_{cm}^2); relative coefficient of variation (CV_r); overall mean and gain with direct selection (SG_d).

Subsequently, the genotypic values were used to calculate the selection index based on the sum of ranks proposed by (Mulamba and Mock, 1978), using a selection pressure of 17.3%, resulting in the selection of 25 clones. Considering the data on direct selection gain (SG_d) and index selection gain (SG_i), the efficiency of the index was calculated by determining the percentage of the direct gain relative to the index, using the following equation:

$$Efi = \frac{SG_i}{SG_d} x\ 100$$

Economic weights 2, 3, and 2 were attributed, respectively, to the traits CY, TDW, and FC, which have greater economic importance. Weight 1 was assigned to the other traits. The economic weights were used to maximize the efficiency of the index for the set of traits, establishing a minimum efficiency of 20% as a criterion.

Results And Discussion

The h_g^2 differed from zero, denoting significant genotypic variance for most evaluated traits; however, likelihood ratio test was applied and then significant differences were found for total tuber yield (TY), total number of tubers (TNT), number of commercial tubers (NCT), tuber dry weight (TDW), eyes (EYE), and veins (VE) (**Table 1**). However, selection was carried out for all traits, as the h_g^2 different from zero allowed for estimation of distinct genotypic values, thus preventing a regression due to selection of undesired genotypes for these traits and ensuring that the means of the selected genotypes

Table 1. Estimates of genetic parameters (GP) and components of variance (CoV) in agronomic and economic traits of sweet potatoe. Ilha Solteira, SP, Brazil, SAO PAULO STATE UNIVERSITY (UNESP), 2020

GP and CoV	Variables															
	TY[1]	CY[2]	TNT[3]	NCT[4]	TW[5]	CTW[6]	TDW[7]	TDWY[8]	OS[9]	CS[10]	RES[11]	EYE[12]	VE[13]	LEN[14]	CC[15]	FC[16]
σ_g^2	0.30*	0.24ns	3.34*	0.76**	0.0001ns	0.0002ns	0.04**	0.07ns	0.0005ns	0.01ns	0.001ns	0.03**	0.05**	0.001ns	0.001ns	0.01ns
σ_e^2	2.09	2.25	10.54	6.75	0.01	0.02	0.08	0.53	0.08	0.10	0.09	0.08	0.02	0.09	0.11	0.09
h_{mc}^2	0.22	0.18	0.39	0.18	0.02	0.02	0.53	0.21	0.09	0.02	0.01	0.45	0.84	0.02	0.02	0.11
CV_g(%)	16.19	16.27	19.93	15.24	1.08	1.63	3.95	13.78	5.13	2.16	1.85	16.82	25.93	2.56	2.07	5.61
CV_e (%)	42.74	49.67	35.39	45.42	11.90	15.17	5.27	38.04	21.97	22.52	22.20	26.23	15.72	23.48	23.10	22.10
CV_r(%)	0.38	0.33	0.56	0.33	0.09	0.11	0.75	0.36	0.23	0.09	0.08	0.64	1.65	0.11	0.09	0.25
Mean	3.38	3.02	9.17	5.72	0.81	0.87	5.39	1.91	1.33	1.42	1.38	1.09	0.85	1.28	1.47	1.37

[1]TY: total tuber yield (Mg ha^{-1}); [2]CY: commercial tuber yield (Mg ha^{-1}); [3]TNT: total number of tubers (ha^{-1}); [4]NCT: number of commercial tubers (ha^{-1}); [5]TW: mean tuber weight (kg); [6]CTW: mean commercial tuber weight (kg); [7]TDW: Tuber dry weight in %; [8]TDWY: total tuber dry weight yield (Mg ha^{-1}); [9]OS: overall shape; [10]CS: commercial standard; [11]RES: resistance to insects; [12]EYE: eyes; [13]VE: veins; [14]LEN: lenticels; [15]SC: tuber skin color; [16]FC: flesh color; σ^2_g: genotypic variance; σ^2_e: experimental error variance; h^2_{cm}: broad-sense heritability based on clone means; CV_g(%): genotypic coefficient of variation; CV_e(%): experimental coefficient of variation; CV_r= CVg to CVe ratio; *significant at 5% level by the likelihood ratio test (LRT); **significant at 1% by LRT. Values transformed by equation $\sqrt{x + 0.5}$.

were higher than zero. The estimate of genetic variance (σ_e^2) for all evaluated traits was higher than the estimates for experimental error variance (σ_g^2), except for VE (a trait related to sweet potato tuber quality) which presented σ_g^2 of 0.05 and σ_e^2 of 0.02. The combination of low to moderate estimates of genetic variance and high experimental variances resulted mostly in low estimates of broad-sense heritability based on clone means (h_{cm}^2). The estimates of h_{cm}^2 were mostly low and moderate, and only VE presented high h_{cm}^2, with 0.84. The other traits varied from 0.01 to 0.53, and 75% of them had h_{cm}^2 lower than 0.25; TDW, EYE, and TNT presented moderate estimates: 0.53, 0.45, and 0.39, respectively. This denotes that the effects of genetic origin had little control over these traits when compared to variations of environmental origin. (Cavalcante et al., 2009) studied production and genetic potentials of sweet potato clones for selection of more productive genetic materials and found higher estimates of genotypic variances and high heritability for tuber yield, with great possibilities of success for the selection for this trait; the other characters under study showed low to moderate heritability. (Vargas et al., 2020), found high magnitude of heritability for all the traits evaluated (total tuber yield, commercial tuber yield, total tuber dry weight yield, total yield of vines, and total dry weight yield of vines), with variations from 0.97 to 0.99.

Considering the traits evaluated in the 144 genotypes, 37.5% of these traits presented CV_g between 10% and 20%, one trait (VE) presented CV_g above 20%, and 56.25% presented CV_g below 10% (Table 1). VE presented the highest CV_g (25.93%).

The production-related traits presented CV_g between 10% and 20%, such as TY (16.19%), commercial tuber yield (CY; 16.27%), TNT (19.93%), NCT (15.24%), and total tuber dry weight yield (TDWY; 13.78%). (Otoboni et al., 2020) evaluated the presence of genetic variability and possibility of gains with selection in a sweet potato population and found higher CV_g for TY (58.19%) and CY (65.38%) compared to those found in the present study.

(Azevedo et al., 2015) studied agronomic performance of sweet potato genotypes and estimated genetic parameters for fresh weight yield of vines, total tuber yield, total mean tuber weight, commercial tuber yield, mean commercial tuber yield, tuber shape, and resistance to insects. They found coefficients of experimental variation above 20% for all traits, and commercial tuber yield was the only one that had variation index higher than 1.

CV_e estimates found for all traits were high and above those of CVg . The CV_r estimates were low for most of the traits and far from 1, although ranging from 0.08 (RES) to 1.65 (VE). VE (1.65) and TDW (0.75) were the only traits presenting CV_r indicative of greater probability of selection gains (Vencovsky and Barriga, 1992).

Ranking with indices, genotypic values, and original ranking of the clones for the studied traits are shown in (**Table 2**). However, the data were transformed and do not represent the actual gain in Mg ha^{-1}. According to the Mulamba and Mock index, clone 38 was ranked first considering all variables, but its performance in the ranking for each of the traits was as follows: 11th (TY); 14th (CY); 12th (TNT); 22nd (NCT); 30th (TW); 20th (CTW); 41st (TDW); 11th (TDWY) and (OS); 80th (CS); 4th (RES); 24th (EYE) and (LEN); 33rd (VE); 47th (SC); and 21st (FC). The direct selection resulted in gain estimates ranging from 0.002 (TW) to 1.74 (TNT); whereas, the selection gains by the index varied from 0.001 (TW) to 0.60 (TNT).

The lack of suitability for other purposes can emerge due to selection for only one use, and selection based on one trait may cause modifications in others (Gonçalves Neto et al., 2012). Different genotypes can exhibit one, multiple, or different agronomic aptitudes, such as food for humans and animals or as raw material for industrial production. Genetic materials with high potential require the identification of their suitability for other purposes, and the selection index is an efficient method to aid in this identification (Gonçalves Neto et al., 2011).

The trait TY had a selection gain of 0.27 through the index, which had and efficiency of 69.06% compared to the direct gain. Clone 25 had the highest genotypic value (0.78) among the 25 selected clones. (Azevedo et al., 2015), found selection gains of 4.26 for TY and 4.13 for CY.

CY had a selection gain of 0.22 through the index, which had an efficiency of 72.60% when compared to the direct gain (0.30). The selection for this trait resulted in clone 25 presenting the highest genotypic value (0.65). This clone was also ranked first for the trait TY. (Vargas et al., 2020) evaluated the selection gain in agronomic traits of sweet potato accessions for tuber production and dual-purpose and finding gains of 14.90 and 15.0 for TY and CY, respectively, using the same index.

TNT presented the highest selection gain (1.74) followed by NCT (0.54). The index resulted in gains of 0.60 (TNT) and 0.27 (NCT), with an efficiency of 34.26% and 49.63%, respectively. Clone 4 was selected due its highest genotypic values for TNT and NCT, but it was ranked 18th in the selection by the index. (Borges et al., 2010)

Table 2. Predicted genotypic values, overall ranking for the trait (between parentheses), direct selection gain (DSG), index selection gain (ISG), and efficiency of the Mulamba and Mock selection index (EFI%) for quantitative traits of 25 sweet potato genotypes. Ilha Solteira,SP, Brazil, SAO PAULO STATE UNIVERSITY (UNESP), 2020

Clone	Ranking by the index	Genotypic values (Overall Ranking of the Traits)							
		TY[1]	CY[2]	TNT[3]	NCT[4]	TW[5]	CTW[6]	TDW[7]	TDWY[8]
38	1	0.39(11)	0.26(14)	1.51(12)	0.36(22)	0.000(30)	0.002(20)	0.08(41)	0.20(11)
63	2	0.34(14)	0.31(10)	0.37(39)	0.38(17)	0.001(25)	0.001(27)	0.18(5)	0.20(12)
79	3	0.42(10)	0.37(8)	0.05(54)	0.38(19)	0.002(9)	0.002(16)	0.10(27)	0.22(8)
77	4	0.27(16)	0.27(13)	-0.42(80)	0.11(39)	0.002(8)	0.003(7)	0.16(11)	0.16(13)
5	5	0.25(18)	0.26(15)	-0.09(61)	0.43(12)	0.001(13)	0.001(25)	0.08(42)	0.13(16)
25	6	0.78(1)	0.65(1)	0.98(23)	0.85(5)	0.002(6)	0.002(13)	0.10(32)	0.40(1)
71	7	0.08(41)	0.08(39)	-0.31(72)	-0.03(71)	0.003(3)	0.004(6)	0.16(10)	0.06(33)
37	8	0.62(3)	0.47(3)	2.56(4)	0.97(3)	0.000(55)	0.000(59)	0.08(45)	0.32(2)
60	9	0.00(56)	0.02(52)	0.31(42)	-0.05(76)	-0.001(95)	0.001(36)	0.09(36)	0.01(49)
53	10	-0.08(73)	-0.02(64)	-1.69(131)	-0.45(119)	0.002(5)	0.006(3)	0.22(1)	-0.01(61)
132	11	0.10(39)	0.13(32)	-0.80(103)	0.05(52)	0.002(7)	0.002(19)	0.19(4)	0.08(27)
90	12	0.56(5)	0.46(4)	-0.07(59)	-0.03(66)	0.003(4)	0.009(1)	0.05(62)	0.28(4)
7	13	0.11(38)	0.09(37)	0.15(48)	0.12(36)	0.000(50)	0.001(39)	0.13(19)	0.07(31)
78	14	0.19(29)	0.19(19)	0.01(57)	0.38(18)	0.000(33)	0.000(50)	0.09(37)	0.10(23)
27	15	0.21(23)	0.16(22)	1.13(18)	0.43(13)	0.000(78)	-0.001(86)	-0.01(82)	0.11(22)
13	16	0.15(31)	0.15(25)	-0.38(74)	0.08(43)	0.001(23)	0.001(35)	0.10(29)	0.09(24)
108	17	0.47(9)	0.37(7)	0.97(24)	0.38(16)	0.001(21)	0.003(10)	-0.05(94)	0.20(10)
4	18	0.65(2)	0.47(2)	3.60(1)	1.06(1)	0.000(83)	0.000(60)	-0.03(87)	0.31(3)
65	19	0.28(15)	0.13(31)	2.51(6)	0.20(32)	-0.001(112)	0.002(11)	-0.14(111)	0.11(20)
1	20	-0.06(71)	-0.02(62)	-0.73(95)	-0.12(89)	0.000(41)	0.001(37)	0.16(12)	-0.01(59)
6	21	0.11(36)	0.14(29)	-0.03(58)	0.36(20)	0.000(31)	0.000(56)	-0.18(118)	0.03(44)
125	22	0.38(12)	0.24(16)	2.55(5)	0.59(8)	-0.001(105)	0.000(70)	-0.17(116)	0.15(14)
46	23	0.12(34)	0.12(33)	-0.73(96)	-0.27(107)	0.001(14)	0.001(34)	0.09(35)	0.08(26)
14	24	0.54(7)	0.34(9)	3.50(2)	0.89(4)	0.000(88)	-0.001(81)	-0.09(106)	0.24(5)
44	25	0.07(44)	0.00(58)	1.09(19)	0.19(33)	-0.001(111)	-0.001(93)	0.10(28)	0.04(37)
DSG		0.39	0.30	1.74	0.54	0.002	0.003	0.16	0.18
ISG		0.27	0.22	0.60	0.27	0.001	0.002	0.06	0.14
EFI%		69.06	72.60	34.26	49.63	55.13	59.68	39.85	75.48

[1]TY: total tuber yield; [2]CY: commercial tuber yield; [3]TNT: total number of tubers; [4]NCT: number of commercial tubers; [5]TW: mean tuber weight; [6]CTW: mean commercial tuber weight; [7]TDW: tuber dry weight, [8]TDWY: total tuber dry weight yield. Values transformed by equation . $\sqrt{x+0.5}$

classified and selected sweet potato clones using REML/ BLUP methodology and reported ordering of clones with genotypic values of 30.33 for TNT and 10.56 for NCT. Breeders should prioritize genotypic values, as these are the true values to be predicted (Borges et al., 2010).

Clone 71 exhibited the highest genotypic value for mean tuber weight (TW) among the 25 selected clones, despite being ranked third; this is because the top-ranked clone for TW was not selected by the index, therefore, clone 71 can be considered superior to the other selected clones for this trait. TW gain through the index was 0.001, with an index efficiency of 55.13%. Clone 90 presented the highest genotypic value for mean commercial tuber weight (CTW); however, it was ranked 12th by the selection index. The direct selection gain for CTW was 0.003 and the index selection gain was 0.002, with an index efficiency of 59.68%.

The direct selection gain for TDW was 0.16. Clone 53 presented the highest genotypic value for this trait (0.22), but it was ranked 10th by the index. The selection gain for TDW was of 0.06 by the index, with an index efficiency of 39.85%. Regarding TDWY, the selection gains were 0.18 (direct gain) and 0.14 (index), and the index efficiency was 75.48% when compared to direct selection gain. Clone 25 presented the highest genotypic value for TDWY (1st), but was ranked 6th by the selection index. (Otoboni et al., 2020) found higher selection gain for TDWY (4.74) through selection index, however, they found -0.09 for TDW.

Regarding traits related to tuber quality, grades were assigned to the traits, but the scale of grades varied according to the evaluated trait (**Table 3**). Clone 7 was ranked first among the selected clones for overall shape (OS), but it scored 13th in the index, which had an efficiency of 53.74%. According to the maximization of index efficiency across all traits and considering the 25 selected genetic materials, five clones (38, 63, 79, 77, and 5) were simultaneously identified and selected due to their superior performances for all traits evaluated; these clones presented good results in traits such as TY, CY, NCT, TW, CTW, and TDWY (Tables 2 and 3).

Clones 38 and 63 showed the most promising

Table 3. Predicted genotypic values, overall ranking for the trait (between parentheses), direct selection gain (DSG), index selection gain (ISG), and efficiency of the Mulamba and Mock selection index (EFI%) for quantitative characters of 25 sweet potato genotypes. Ilha Solteira,SP, Brazil, SAO PAULO STATE UNIVERSITY (UNESP), 2020

Clone	Ranking by the index	Genotypic values (Overall Ranking of the Traits)							
		OS[1]	CS[2]	RES[3]	EYE[4]	VE[5]	LEN[6]	SC[7]	FC[8]
38	1	0.03(11)	0.000(80)	0.0037(4)	0.13(24)	0.13(33)	0.005(24)	0.002(47)	0.028(21)
63	2	0.04(6)	0.002(62)	0.0033(11)	0.18(3)	-0.12(82)	0.005(27)	0.001(68)	0.008(59)
79	3	0.00(63)	0.004(10)	0.0033(13)	0.16(10)	-0.12(95)	0.006(6)	0.003(36)	0.001(72)
77	4	0.00(62)	0.004(31)	0.0027(29)	0.16(9)	0.39(14)	0.004(42)	0.003(35)	-0.007(87)
5	5	0.02(20)	0.003(42)	0.0033(8)	0.16(7)	-0.12(43)	0.005(17)	0.000(83)	0.008(52)
25	6	0.00(72)	0.005(1)	0.0008(60)	-0.01(57)	-0.12(53)	0.004(30)	0.000(84)	-0.007(81)
71	7	0.03(13)	0.002(64)	0.0033(12)	0.20(1)	-0.12(88)	0.004(40)	0.004(21)	0.008(60)
37	8	0.01(44)	0.003(46)	0.0027(23)	0.13(23)	-0.12(62)	0.005(23)	0.000(85)	-0.007(82)
60	9	0.02(27)	0.003(50)	0.0027(27)	0.15(15)	0.39(11)	0.005(26)	0.004(12)	0.036(5)
53	10	0.04(5)	-0.001(86)	0.0027(25)	0.15(14)	0.39(9)	0.004(39)	0.002(49)	0.036(3)
132	11	0.01(57)	0.004(41)	0.0025(33)	0.10(51)	-0.12(133)	0.006(15)	0.003(43)	0.028(32)
90	12	0.02(30)	0.001(73)	0.0015(54)	0.10(47)	0.39(16)	0.004(44)	0.003(37)	0.006(67)
7	13	0.04(1)	0.003(43)	0.0022(34)	-0.17(102)	0.39(3)	0.002(54)	0.001(67)	0.008(53)
78	14	0.00(77)	0.004(9)	0.0037(6)	-0.01(63)	-0.12(94)	0.006(5)	0.002(51)	0.008(62)
27	15	0.03(10)	0.000(79)	0.0008(61)	0.10(43)	0.39(7)	0.002(56)	0.004(16)	0.036(1)
13	16	0.01(41)	0.003(44)	0.0021(41)	-0.01(55)	0.39(5)	0.005(19)	0.000(77)	-0.007(79)
108	17	0.02(38)	0.002(68)	0.0027(31)	0.16(11)	-0.12(114)	0.005(29)	0.001(71)	0.024(36)
4	18	0.00(58)	0.004(15)	0.0000(75)	0.10(42)	0.39(1)	0.003(52)	0.001(66)	0.008(51)
65	19	0.03(12)	0.002(63)	0.0032(17)	0.13(29)	0.13(35)	0.005(28)	0.001(69)	0.036(6)
1	20	0.02(19)	0.001(74)	0.0015(49)	0.16(6)	-0.12(41)	0.005(16)	0.004(1)	0.008(50)
6	21	0.00(59)	0.004(16)	0.0027(20)	0.13(19)	0.39(2)	0.005(18)	0.002(44)	0.032(12)
125	22	0.00(67)	0.004(36)	0.0021(48)	0.13(38)	0.39(25)	0.006(13)	0.003(41)	0.032(19)
46	23	0.00(74)	0.004(23)	0.0042(1)	-0.04(81)	-0.12(70)	0.006(1)	0.002(63)	0.008(58)
14	24	0.02(31)	0.004(18)	0.0027(21)	0.13(20)	-0.12(46)	0.005(20)	0.000(78)	-0.007(80)
44	25	0.02(32)	0.003(45)	0.0022(36)	0.13(22)	-0.12(58)	0.004(32)	0.002(45)	0.008(55)
DSG		0.03	0.004	0.0033	0.15	0.39	0.006	0.004	0.033
ISG		0.02	0.003	0.0025	0.09	0.09	0.004	0.002	0.013
EFI%		53.74	67.02	76.11	59.55	24.03	81.40	51.87	39.72

[1]OS: Overall shape; [2]CS: commercial standard; [3]RES: resistance to insects; [4]EYE: Eyes; [5]VE: Veins; [6]LEN: Lenticels; [7]SC: tuber skin color, and [8]FC: flesh color. Values transformed by equation $\sqrt{x+0.5}$

results for OS and resistance to insects (RES) among these 5 superior clones. The index efficiency was 76.11% for RES, which was the second highest efficiency when compared to those found for the other tuber quality-related traits. Clone 79 stood out for commercial standard (CS) and lenticels (LEN), and the highest index efficiency (81.40%) was found for LEN. Tuber quality characteristics, such as CS, are essential for table consumption purposes, mainly when combined with resistance to pests and diseases.

Clones 63, 5, 77, and 79 are among the best clones regarding the trait EYE. Clone 77 also presented good results for SC, VE, and TDW. Sweet potatoes with higher dry weights are preferred for industrial purposes, as they result in higher yields during processing. TDW of sweet potatoes is directly connected to specific density of tubers (Otoboni et al., 2020).

Clone 38 presented the best results for flesh color (FC). Considering the 25 selected clones, 36% of them exhibited orange flesh, 32% off white, 24% white and purple, and 8% had yellow flesh. Flesh and skin color are highly important for marketing sweet potatoes for food consumption, mainly when considering the variety of shapes and colors of these vegetables (Cavalcante et al., 2009; Azevedo et al., 2015; Vizzotto et al., 2017). According to its characteristics, sweet potato can be suitable for production of processed food or other products such as ethanol.

Promoting the cultivation of orange-fleshed sweet potatoes can be a proactive strategy in combating malnutrition among populations with inadequate vitamin A intake. Yellow or orange-fleshed sweet potatoes have high levels of carotenoids (β-carotene) and a combination of phenolic acids, whereas purple-fleshed sweet potatoes contain high levels of anthocyanins and other phenolics with anti-inflammatory and antioxidant activities (Wang, Nie, Zhu, 2016; Grace et al., 2014).

Considering the varying results found for certain traits in the evaluated clones, incorporating missing traits or improving performance through selection may be necessary. Therefore, the different selected parents should be used for further breeding cycles, thereby ensuring productivity in the progenies.

Conclusions

The direct selection enabled a higher prediction of gains for each trait, but the joint analysis maximized the selection gains for all traits of interest. Clones 38, 63, 79, 77, and 5 are recommended, among the selected clones, for further stages of sweet potato breeding programs focused on improving traits for production and table consumption.

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