

# Selection of superior sweet potato genotypes for human consumption via mixed models

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**ABSTRACT:** The growing consumer demand for sweet potato roots results in the need for genotypes with higher yields and better root quality. Thus, the objective of this study was to agronomically evaluate sweet potato genotypes via mixed models to select superior genotypes for human consumption and predict their selection gains. The study had a partially balanced triple lattice design with three replicates. As treatments, 92 sweet potato genotypes from the Universidade Federal de Lavras germplasm bank selected in the first selection cycle were evaluated along with eight controls, namely, Brazlândia Roxa, Princesa, Uruguiana, BRS Amélia, Beauregard, UFVJM-57, UFVJM-58, and UFVJM-61. The treatments were ranked by the mixed linear model via restricted maximum likelihood (REML) and best linear unbiased prediction (BLUP). We highlighted the 15 best genotypes for each agronomic trait, then identified the best ones overall considering all quantitative and qualitative traits. High heritability was found for the trait commercial root yield (56.31%). For all traits, there were selection gains relative to the population mean. The use of mixed models was efficient for the selection of superior sweet potato genotypes. The genotypes 2018-19-464, 2018-72-1409, 2018-72-1428, 2018-19-443, 2018-36-807, 2018-72-1418, 2018-19-455, 2018-72-1376, 2018-54-1137, 2018-54-1114, 2018-65-1249, and 2018-28-556 have good traits related to commercial root yield and root quality and may be recommended for human consumption.

**Key words:** *Ipomoea batatas* L., quality, REML/BLUP, roots, yield.

## INTRODUCTION

Sweet potato (*Ipomoea batatas* (L.) Lam) is a crop of economic and social importance in Brazil that is widespread and mainly cultivated by small farmers, especially for subsistence (Azevedo et al. 2014). In recent years, the demand for sweet potato has increased significantly, as evidenced by the increase in its Brazilian production (FAO 2021). This increase in consumption is mainly related to the search for healthier diets. This has changed the profile of producers, who have increasingly improved their crops by introducing technologies such as fertilization, irrigation, and, especially, high-performance cultivars to meet this demand.

Constant genetic improvement of sweet potato is essential for the development of cultivars with greater agronomic potential and root quality. The basis for the improvement provided by genetic breeding is the presence of genetic variability, which allows significant gains to be obtained by the selection of superior genotypes. Sweet potato is a hexaploid ( $2n = 6x = 90$ ), allogamous, self-incompatible species with multiple allelisms (Ramalho et al. 2012, Isobe et al. 2019, Donato et al. 2020). These traits confer a broad genetic diversity on the species. Thus, each seed has the potential to originate a commercial genotype (Grüneberg et al. 2009).

In genetic improvement of sweet potato, hybridization and subsequent selection cycles are responsible for generating genotypes with traits of interest (Baafi et al. 2016). Therefore, the agronomic evaluation of these genotypes is of paramount importance for selecting the best individuals with different use purposes, such as for human and animal consumption or ethanol production (Ritschel et al. 1999, Torquato-Tavares et al. 2016, Lestari et al. 2019). Among these purposes, use for human consumption has been the main objective of breeding research, and there are few studies on the other purposes.

For human consumption, in addition to yield-related traits, a sweet potato genotype should also have good qualitative traits, such as shape and insect resistance (Gonçalves Neto et al. 2012). The bioactive compounds contained in sweet potato, such as carotenoids and anthocyanins, have also attracted consumer interest (Tanaka et al. 2017). These bioactive compounds can be identified by their different colors, such as cream, yellow, orange, pink, and purple. Few studies have been done on the selection of sweet potato genotypes for quantitative and qualitative traits or on evaluating and characterizing different color groups.

A problem in the selection of materials for breeding programs is how to predict the genetic value of an accession (Borges et al. 2010). This prediction is important to infer future means when cultivars are commercially planted (Borges et al. 2010). Genotype selection methods based on analysis of variance are marred by such limitations as inaccuracy in the presence of experimental imbalance (Resende 2016). Thus, methods using mixed models, with restricted maximum likelihood (REML) and best linear unbiased prediction (BLUP) estimates, are the best for genotype selection (Borges et al. 2010, Silva et al. 2022). Despite its efficiency in genotype selection, few studies have explored the technique in sweet potato. The simultaneous use of these methods has advantages such as allowing the comparison of individuals or varieties over time and space and simultaneously allowing correction for environmental effects, estimation of variance components, and prediction of genetic value (Resende 2016).

This study aimed to agronomically evaluate sweet potato genotypes via mixed models to select the best genotypes for human consumption and to predict their selection gains.

## MATERIAL AND METHODS

The experiment was conducted at the Center for Development and Technology Transfer of the Universidade Federal de Lavras (UFLA), located at Palmital Farm, in the municipality of Ijaci, Minas Gerais, Brazil (altitude: 918 m; latitude: 21°14'16"S; longitude: 45°08'00"W), from April 2 to October 4, 2019. During the experiment, the mean temperature was 19.69°C, with a minimum mean of 14.51°C, and a maximum mean of 26.89°C. The cumulative rainfall was 195.1 mm, and the mean relative humidity was 67.16%.

The experimental design used a partially balanced triple lattice design, with 100 treatments in each of the three replicates, allowing greater local control. The kinship between close plots was restricted in the randomization of rows and columns as recommended by Bueno Filho and Gilmour (2003). The treatments consisted of 92 sweet potato genotypes from the UFLA germplasm bank, which were obtained from polycrosses between 55 genotypes. Eight controls were evaluated, including five commercial cultivars – Brazlândia Roxa, Princesa, Uruguaiana, BRS Amélia, and Beauregard – and three genotypes from the Universidade Federal dos Vales do Jequitinhonha e Mucuri (UFVJM) – UFVJM-57, UFVJM-58, and UFVJM-61.

The soil was prepared by plowing and harrowing, and 0.35-m-high beds were then raised. Each experimental plot consisted of 10 plants, with a spacing of 1 m between rows and 0.30 m between plants. The useful area of the plots was composed of the eight central plants. Planting was performed on April 2, 2019, using segments of sweet potato stems collected from the germplasm bank of UFLA. Each stem segment was approximately 30-cm long, with six to eight buds, and three of these buds were buried in the soil for rooting. Fifteen days after planting, the plants were checked and replanted in the plots to ensure the presence of 10 plants per plot. Nutritional management was based on the recommendation for sweet potato (Ribeiro et al. 1999). Crop treatments such as weeding, topdressing, and phytosanitary management were performed manually and according to the needs of the crop. Irrigation was performed by drip irrigation based on the crop requirements and water balance.

The crops were harvested 180 days after planting, starting on September 23 and ending on October 4. Immediately after harvest, in the useful area of each plot, the following agronomic variables were evaluated for the 100 genotypes:

- Commercial root yield: we weighed tuberous roots with a weight between 100 and 800 g, free of damage and with good commercial appearance in each plot. The results were converted to  $\text{mg}\cdot\text{ha}^{-1}$  (Azevedo et al. 2014);

- General shape: the roots were visually analyzed and then scored by two evaluators according to the method proposed by Azevedo et al. (2002) with adaptations:
  - score 1 = fusiform shape;
  - score 2 = near-fusiform shape;
  - score 3 = uneven shape;
  - score 4 = poor shape for commercialization, with cracks;
  - score 5 = unmarketable shape with many deformations.

Thus, score 1 was most desirable;

- Commercial standard: the roots in the plot were visually analyzed, and then scores were assigned by two evaluators according to the method proposed by Silva et al. (2022) with adaptations:
  - score 1 = best commercial standard;
  - score 2 = good commercial standard;
  - score 3 = standard that moderately hindered commercialization;
  - score 4 = standard that greatly hindered commercialization;
  - score 5 = worst commercial standard

Score 1 was more desirable;

- Insect resistance: two evaluators measured the occurrence of galleries and/or holes in the roots using the following scoring scale:
  - 1 = damage free;
  - 2 = little damage;
  - 3 = damage that moderately affected the commercial aspect;
  - 4 = damage that greatly affected the commercial aspect;
  - 5 = damage that totally affected the commercial aspect (Azevedo et al. 2002).

Score 1 was most desirable;

- Root clustering: after digging the bed, the roots were exposed without detaching them, and their clustering was evaluated by two evaluators as:
  - 3 = closed;
  - 5 = open;
  - 7 = disperse;
  - 9 = very disperse (Huamán 1999)

Scores 3 and 5 were desirable;

- Veins: the roots were visually observed and assigned scores by two evaluators, with 0 = absence of veins and 1 = presence of veins (score 0 was desirable);
- Enzymatic browning: two roots from each plot were cut and after 1 minute they were analyzed by two evaluators:
  - 1 = no browning;
  - 2 = slight browning;
  - 3 = moderate browning;
  - 4 = extensive browning;
  - 5 = complete browning (Gonçalves Neto et al. 2011).

Score 1 was most desirable;

- Root skin color: two evaluators visually defined the color according to the scores proposed by Huamán (1999) with adaptations:
  - 1 = white;
  - 2 = cream;
  - 3 = yellow;
  - 4 = brownish orange;
  - 5 = pink;

- 6 = reddish purple;
- 7 = dark purple.
- Root flesh color: two evaluators visually defined the predominant color and the secondary color (lower proportion), when present, according to the scores proposed by Huamán (1999) with adaptations:
  - 1 = white;
  - 2 = cream;
  - 3 = yellow;
  - 4 = orange;
  - 5 = purple.

For the traits evaluated by scoring scales, the correlation between the scores from the two evaluators and the confidence intervals were analyzed by the Pearson's method.

The Box and Cox (1964) method was used to seek the transformation that would best describe the normal approximation. A likelihood-based confidence limit for each estimated lambda was also used as a normality test (considered normal if includes 1 after transformation). A likelihood ratio test was carried out to compare models with and without variance component to genotypes. This yielded the following values for each trait:

- Commercial root yield:  $\lambda = 0.41$ ;
- General shape:  $\lambda = 0.66$ ;
- Commercial standard:  $\lambda = 0.77$ ;
- Insect resistance:  $\lambda = -0.45$ ;
- Root clustering:  $\lambda = 0.53$ ;
- Veins:  $\lambda = -3$ ;
- Enzymatic browning:  $\lambda = -0.79$ .

The trait presence of veins ( $\lambda < -3$ ) was disregarded in the analysis. To calculate the mean value obtained in the evaluation of each agronomic trait for the treatments, as well as to estimate the population mean, the inverse transformation of the Box and Cox's formula (1964) was used (Eq. 1):

$$y = (1 + \lambda y^t)^{\frac{1}{\lambda}} \quad (1)$$

in which:  $\lambda$  = the parametric transformation;  $y^t$  = the vector of transformed observations.

Analysis of variance was performed only to determine the efficiency of local control (blocks, rows, and columns). For each agronomic trait, a mixed model was fitted to estimate the genotypic variance ( $\hat{\sigma}_g^2$ ) and the residual variance ( $\hat{\sigma}_e^2$ ). The REML/BLUP estimates (Patterson and Thompson 1971, Henderson 1984) are considered the most adequate for the incomplete block model and lattice design (Bueno Filho and Vencovsky 2000) (Eq. 2):

$$y_{ijk} = m + b_j + c_k + g_i + e_{ijk} \quad (2)$$

in which:  $y_{ijk}$  = the realization of the random variable in study, taken in the  $j^{\text{th}}$  block (row), and  $k^{\text{th}}$  column from the  $i^{\text{th}}$  genotype;  $b_j$  and  $c_k$  = assumed to be fixed effects;  $g_i$  = assumed to be a random effect.

The genotypes under study were ranked for each trait, and a selection intensity of 15% (15 genotypes from the UFLA germplasm bank) was simulated. Vectors  $g$  and  $e$  of genetic and error effects = assumed to be multivariate normally distributed with zero means and respective covariances given by  $G = I_{100}$  and  $R = I_{300}$ .

Based on the estimates of the variance components, the broad-sense heritability was calculated for the selection between clones by the Eq. 3:

$$h^2(\%) = \frac{\hat{\sigma}_g^2}{\hat{\sigma}_f^2} = \frac{\hat{\sigma}_g^2}{\hat{\sigma}_g^2 + \frac{\hat{\sigma}_e^2}{r}} \times 100 \quad (3)$$

in which:  $h^2$  = the broad-sense heritability;  $\hat{\sigma}_g^2$  = the estimated genotypic variance;  $\hat{\sigma}_e^2$  = the estimated variance of the experimental error;  $\hat{\sigma}_f^2$  = the estimated phenotypic variance between means of clones;  $r$  = the number of treatment replicates.

Heritability values lower than 20% will be considered low heritability, between 20 and 50% will be of moderate heritability, and higher than 50% will be of high heritability (Santos et al. 2018).

Confidence limits for variance components were worked out using  $\chi^2$  scaled distributions. Confidence limits for heritability estimates were approximated from Monte Carlo samples of the distributions for variance components. We used 10,000 independent samples for each variance parameter in each trait.

The selection gain was calculated directly by the mean BLUP for the selected genotypes. The traits that showed low heritability and whose gain for the selection intensity did not differ from 0 were not included in the results.

The data were analyzed with the statistical software R (R Core Team 2018). The linear mixed-effects models were fit with function *lmer* from the *lme4* library (Bates et al. 2015). Confidence limits for  $\lambda$  in Box-Cox transformation were evaluated with *boxcox* function of library MASS (Ripley et al. 2022).

## RESULTS AND DISCUSSION

### Analysis of variance and variance components

The analysis of variance showed that the F test was significant ( $P \leq 0.05$ ) for the block, column, and row sources of variation in at least one agronomic trait (Table 1). This indicated that there were significant variations in these sources of variation.

**Table 1.** Probability of significance in the F test of the analysis of variance for the effects of local control, namely, blocks, rows, and columns.

Trait	p-value		
	Source of variation		
	Block	Column	Row
Commercial root yield	0.072 <sup>ns</sup>	0.171 <sup>ns</sup>	0.000 <sup>***</sup>
General shape	0.014 <sup>*</sup>	0.310 <sup>ns</sup>	0.000 <sup>***</sup>
Commercial standard	0.551 <sup>ns</sup>	0.133 <sup>ns</sup>	0.639 <sup>ns</sup>
Insect resistance	0.370 <sup>ns</sup>	0.789 <sup>ns</sup>	0.096 <sup>ns</sup>
Root clustering	0.107 <sup>ns</sup>	0.962 <sup>ns</sup>	0.009 <sup>**</sup>
Veins	0.000 <sup>***</sup>	0.000 <sup>***</sup>	0.000 <sup>***</sup>
Enzymatic browning	0.319 <sup>ns</sup>	0.662 <sup>ns</sup>	0.015 <sup>*</sup>

p-value: P value of the F test at 5% probability; \*\*\*significant at  $P \leq 0.001$ ; \*\*significant at  $P \leq 0.01$ ; \*significant at  $P \leq 0.05$ ; <sup>ns</sup>not significant.

The trait with the highest broad-sense heritability was commercial root yield ( $h^2 = 80.19\%$  [73.94%; 85.10%]) (Table 2). This indicates that this trait showed a higher genetic variance than environmental variance, i.e., it was the trait under the greatest influence of genes.

The vein trait was disregarded from the other analyses because it did present neither significant genetic nor environmental variance ( $h^2 \approx 0\%$ , [0%; 0%]) (Table 2). The other traits related to root quality, including general shape ( $h^2 = 62.52\%$ , [53.72%; 69.92%]), commercial standard ( $h^2 = 58.20\%$ ), insect resistance ( $h^2 = 36.26\%$ , [28.57%; 44.54%]), root clustering ( $h^2 = 57.32\%$ , [48.64%; 65.32%]), and enzymatic browning ( $h^2 = 56.16\%$ , [47.41%; 64.38%]), showed higher residual variance than genetic variance. Therefore, environmental conditions have greater control over these traits than genetic effects. However, the veins trait showed low heritability, and the insect resistance showed moderate heritability, while the other traits showed high heritability.

**Table 2.** Genetic and residual variance, broad-sense heritability and their confidence limits for the agronomic traits evaluated in sweet potato (*Ipomoea batatas* L.) genotypes.

Trait	Genetic variance			Residual variance			Broad-sense heritability (%)		
	Estimate	Lower limit	Upper limit	Estimate	Lower limit	Upper limit	Estimate	Lower limit	Upper limit
Commercial root yield	1.609	1.240	2.171	1.192	0.981	1.481	80.19	73.94	85.10
General shape	0.138	0.107	0.187	0.249	0.205	0.309	62.52	53.72	69.92
Commercial standard	0.182	0.140	0.245	0.391	0.322	0.486	58.20	49.51	66.13
Insect resistance	0.013	0.010	0.017	0.068	0.056	0.085	36.26	28.57	44.54
Root clustering	0.193	0.148	0.260	0.430	0.354	0.534	57.32	48.64	65.32
Enzymatic browning	0.003	0.003	0.005	0.008	0.007	0.010	56.16	47.41	64.38

The design used in the study was efficient for estimating the genetic parameters. Fixed effects for blocks were estimated as relevant and contributed to greater accuracy in the selection of sweet potato genotypes. Genetic variance parameters for most traits were also relevant.

In sweet potato, the estimation of heritability in the broad sense is highly important, since the effects of dominance and epistasis can be fixed to the genotypes through vegetative propagation (Gonçalves Neto et al. 2012). Nóbrega et al. (2019) found a broad-sense heritability of commercial root yield equal to 91.87%, a value higher than that observed in this study. This could be related to the fact that genetic parameters depend on the studied population and environmental conditions. Therefore, it is important that genotypes should be tested in other locations.

The qualitative traits were influenced by environment-dependent factors, such as the presence of insects, soil types, nutrition, and moisture (Silva et al. 2015), which resulted in low to high heritability. Low heritability may be a limitation for the efficient selection of these genotypes. Thus, for the introduction of this trait in genotypes that do not have it, recurrent selection cycles should be performed to seek a greater heterotic effect and increase the number of possibly superior individuals available for selection.

Variance components were relevant for all traits with moderate and high heritability, as can be verified in the  $\chi^2$  approximation of the likelihood ratio test for models with and without respective variance components (Table 3). However, only a few traits of high heritability and economic relevance were considered for selection. For the traits commercial root yield, general shape, commercial standard, and root clustering, genotypic values were estimated.

**Table 3.** Likelihood-ratio test using  $\chi^2$  approximation for comparing the model with variance components vs. the model without it. Agronomic traits evaluated in sweet potato (*Ipomoea batatas* L.) genotypes.

Trait	$\chi^2$	p-value
Commercial root yield	82.739	$9.363 \cdot 10^{-20}$
General shape	27.189	$1.844 \cdot 10^{-7}$
Commercial standard	26.496	$2.641 \cdot 10^{-7}$
Insect resistance	6.586	$1.028 \cdot 10^{-2}$
Root clustering	21.710	$3.171 \cdot 10^{-6}$
Enzymatic browning	14.346	$1.520 \cdot 10^{-4}$

## Estimated genotypic values for each trait

Considering the selection intensity of 15% of the sweet potato genotypes from the UFLA germplasm bank, the highest commercial root yields varied between 11.01 and 18.68 mg·ha<sup>-1</sup> (Table 4). These genotypes showed an increase in yield of 70.79 to 190.51% relative to the overall population mean, corresponding to selection gains of between 4.58 and 12.25 mg·ha<sup>-1</sup>, which are considered good for the trait.

**Table 4.** Ranking of the estimated genotypic values of the 15 best sweet potato (*Ipomoea batatas* L.) genotypes from the Universidade Federal de Lavras germplasm bank and the commercial cultivars for the traits commercial root yield, general shape, commercial standard, and root clustering, with the best genotype represented by rank 1, and correlation of the scores of the two evaluators and corresponding confidence interval by the Pearson's method for qualitative traits.

Rank	Commercial root yield						General shape						
	Genotype	Skin color	Flesh color	Estimate	Average Mg·ha <sup>-1</sup>	SG	Rank	Genotype	Skin color	Flesh color	Estimate	Average Score	SG
1	2018-19-464	Pink	Cream	2.87	18.68	12.25	1	Beauregard	Pink	Orange	-0.77	2.21	-1.08
2	2018-72-1409	Purple	Purple/White	2.21	15.18	8.75	2	2018-19-443	Pink	Cream	-0.63	2.39	-0.90
3	2018-72-1428	Pink	Cream	1.98	14.09	7.66	3	2018-19-464	Pink	Cream	-0.60	2.44	-0.85
4	2018-19-443	Pink	Cream	1.82	13.32	6.88	4	2018-36-807	Cream	Cream	-0.58	2.46	-0.83
5	2018-72-1408	Pink	White/Purple	1.81	13.28	6.85	5	2018-54-1137	Pink	White/Purple	-0.54	2.52	-0.77
6	2018-36-807	Cream	Cream	1.74	12.98	6.54	6	2018-72-1376	Pink	White/Purple	-0.49	2.58	-0.71
7	Beauregard	Pink	Orange	1.74	12.96	6.53	7	2018-31-671	Pink	Cream	-0.48	2.60	-0.69
8	2018-72-1418	Purple	Purple/White	1.72	12.87	6.43	8	2018-31-666	Pink	Cream/Purple	-0.44	2.65	-0.64
9	2018-19-455	Cream	White/Purple	1.67	12.64	6.21	9	2018-54-1114	Pink	Cream	-0.38	2.74	-0.55
10	2018-74-1507	Cream	Cream	1.57	12.22	5.79	10	2018-55-1156	Brownish orange	Cream/Purple	-0.36	2.77	-0.52
11	2018-67-1321	Pink	Cream	1.47	11.75	5.32	11	2018-14-259	Pink	Yellow	-0.35	2.78	-0.51
12	2018-72-1376	Pink	White/Purple	1.44	11.64	5.20	12	2018-72-1418	Purple	Purple/White	-0.32	2.82	-0.47
13	2018-54-1137	Pink	White/Purple	1.38	11.37	4.93	13	2018-72-1409	Purple	Purple/White	-0.32	2.83	-0.46
14	2018-54-1114	Pink	Cream	1.33	11.18	4.75	14	2018-72-1428	Pink	Cream	-0.31	2.84	-0.45
15	2018-65-1249	Pink	White	1.30	11.05	4.62	15	2018-19-455	Cream	White/Purple	-0.30	2.86	-0.43
16	2018-28-556	Cream	Cream	1.29	11.01	4.58	16	2018-72-1381	Pink	Cream/Purple	-0.28	2.87	-0.42
17	Brazlândia Roxa	Pink	Cream	1.24	10.81	4.37	21	BRS Amélia	Pink	Orange	-0.20	3.00	-0.29
36	BRS Amélia	Pink	Orange	0.39	7.66	1.23	22	Uruguaiana	Pink	Yellow	-0.19	3.00	-0.28
44	Uruguaiana	Pink	Yellow	0.26	7.23	0.80	23	Brazlândia Roxa	Pink	Cream	-0.19	3.01	-0.28
71	Princesa	Cream	Cream	-0.55	4.91	-1.52	53	Princesa	Cream	Cream	-0.00	3.29	-0.00
	Mean			2.79	6.43						1.81	3.29	
	Standard deviation			0.60							0.23		
	Correlation of scores										0.85		
	Confidence interval										0.82 - 0.88		

continue...

**Table 4.** Continuation...

Commercial standard							Root clustering						
Rank	Genotype	Skin color	Flesh color	Estimate	Average	SG	Rank	Genotype	Skin color	Flesh color	Estimate	Average	SG
					Score							Score	
1	Beauregard	Pink	Orange	-0.70	2.39	-0.88	1	2018-65-1249	Pink	White	-0.67	4.25	-1.41
2	2018-54-1137	Pink	White/ Purple	-0.66	2.43	-0.84	2	2018-54-1137	Pink	White/ Purple	-0.60	4.38	-1.28
3	2018-19-464	Pink	Cream	-0.61	2.50	-0.77	3	Beauregard	Pink	Orange	-0.59	4.41	-1.25
4	2018-72-1428	Pink	Cream	-0.58	2.53	-0.75	4	2018-15-276	Cream	Cream	-0.57	4.44	-1.23
5	2018-36-807	Cream	Cream	-0.55	2.58	-0.70	5	Brazlândia Roxa	Pink	Cream	-0.53	4.53	-1.14
6	2018-28-556	Cream	Cream	-0.47	2.67	-0.61	6	2018-72-1448	Purple	Purple/ White	-0.51	4.58	-1.09
7	2018-65-1249	Pink	White	-0.45	2.69	-0.58	7	2018-28-556	Cream	Cream	-0.49	4.60	-1.06
8	2018-72-1418	Purple	Purple/ White	-0.41	2.75	-0.53	8	2018-36-807	Cream	Cream	-0.48	4.63	-1.03
9	2018-19-443	Pink	Cream	-0.41	2.75	-0.52	9	2018-67-1323	Cream	Cream	-0.46	4.67	-1.00
10	2018-15-276	Cream	Cream	-0.40	2.75	-0.52	10	2018-72-1429	Pink	Purple/ White	-0.45	4.68	-0.98
11	2018-72-1376	Pink	White/ Purple	-0.40	2.76	-0.51	11	2018-14-260	Cream	Cream	-0.44	4.72	-0.95
12	2018-31-666	Pink	Cream/ purple	-0.40	2.77	-0.51	12	2018-72-1388	Pink	White/ Purple	-0.41	4.77	-0.89
13	2018-72-1388	Pink	White/ Purple	-0.39	2.78	-0.50	13	2018-19-464	Pink	Cream	-0.40	4.79	-0.87
14	2018-19-435	Pink	White/ Purple	-0.36	2.81	-0.47	14	2018-72-1432	Purple	Purple/ White	-0.39	4.81	-0.86
15	2018-14-260	Cream	Cream	-0.35	2.82	-0.45	15	2018-19-445	Cream	Cream	-0.39	4.81	-0.85
16	2018-74-1507	Cream	Cream	-0.35	2.83	-0.45	16	2018-28-543	Cream	Yellow	-0.38	4.83	-0.83
37	BRS Amélia	Pink	Orange	-0.10	3.15	-0.13	17	2018-54-1082	Cream	Cream	-0.37	4.85	-0.81
55	Uruguaiana	Pink	Yellow	0.02	3.31	0.03	18	Uruguaiana	Pink	Yellow	-0.34	4.92	-0.74
59	Princesa	Cream	Cream	0.04	3.33	0.05	25	Princesa	Cream	Cream	-0.24	5.14	-0.52
60	Brazlândia Roxa	Pink	Cream	0.04	3.34	0.06	35	BRS Amélia	Pink	Orange	-0.09	5.45	-0.21
Mean				1.94	3.28						2.84	5.66	
Standard deviation				0.28						0.29			
Correlation of scores			0.82						0.88				
Confidence interval			0.77 - 0.85						0.85 - 0.90				

Genotype: the name consists of the year the genotype was obtained followed by the family it belongs to and the plot where the genotype was in the experiment in which it was tested; Flesh color: when two colors are described, the first is the predominant color and the second is the secondary color; REML/BLUP: mixed model estimate; Score: estimated mean score for the genotype; SG: selection gain; Mean: population mean.

The average commercial root yield of commercial cultivars was 8.71 mg·ha<sup>-1</sup> (Table 4). Of the 15 best genotypes under study, six of them were superior to the commercial cultivar Beauregard, which showed commercial root yield of 12.96 mg·ha<sup>-1</sup> and selection gain of 6.53 mg·ha<sup>-1</sup>. The other commercial cultivars were lower than the 15 best genotypes.

The mean commercial root yield of the 100 genotypes studied was 6.43 mg·ha<sup>-1</sup>, which represents reduction of 73.79% relative to the mean total root yield (24.53 mg·ha<sup>-1</sup>). This reduction occurred due to the strong interference of the soil structure on the development of commercial roots, as more clayey soils like those found in the present study favor root deformations (Valadares et al. 2022).

Andrade Júnior et al. (2018) evaluated genotypes belonging to the germplasm bank of UFVJM. The authors reported that 64.50% of the roots were commercial, while in the present study the mean value was only 26.21%. Even though different genotypes were studied, these differences in the proportion of commercial roots might be related to other environmental factors, such as soil type and tillage practice, that affected the good development and commercial standard of the roots. Therefore, to confirm the performance of these genotypes, new studies should be conducted in other locations. Silva et al. (2012) noticed that the performance of sweet potato cultivars and clones in terms of root yield-related traits may vary according to the environment, as they are traits with quantitative heritability under strong environmental influence. Azevedo et al. (2014), in a study of sweet potato in two locations, observed that the commercial root yield of the same genotypes ranged from 5.09 to 12.96 mg·ha<sup>-1</sup> in one location and from 7.04 to 44.82 mg·ha<sup>-1</sup> in another, showing the importance of testing genotypes in different environments.

Another important aspect is the variability in the flesh and skin color of the study genotypes. Regarding the skin color, 13.33% of the best genotypes for commercial root yield were purple, 26.67% cream, and 60% pink (Table 4). These genotypes showed different flesh colors: 13.33% purple with white secondary color; 33.33% white, of which 80% had purple as the secondary color; and 53.33% cream.

Another important factor in the selection of sweet potato genotypes for human consumption is the root color, as it allows the development of new sweet potato varieties for different needs (Nóbrega et al. 2019). These varieties have different nutritional compositions and bioactive compounds (Tanaka et al. 2017). In Minas Gerais, considering the scoring scales established in this study, the sweet potato with the highest demand had cream and pink skin colors with white or cream flesh.

Regarding the qualitative traits, the 15 best sweet potato genotypes from the UFLA germplasm bank for general shape had scores between 2.39 and 2.87, i.e., they had near-fusiform roots to roots tending to a nonuniform shape (Table 4). Only the three best genotypes had near-fusiform roots, because the highest score was 2.46. These three genotypes showed selection gains between -0.90 and -0.83 relative to the population mean (3.29). The correlation between the evaluators' scores was 0.85, with confidence interval of 0.82 to 0.88.

The commercial cultivar Beaugard showed the highest average score for the general shape, being superior to all the genotypes from the UFLA germplasm bank, with the score of 2.21 and the selection gain of -1.08 in relation to the overall population mean (Table 4). The other commercial cultivars were lower to the 15 best genotypes with average score of 3.08; they had roots tending to a nonuniform shape, and selection gain of between -0.42 and -0.

For human consumption, the most important trait is commercial root yield (Gonçalves Neto et al. 2012). This is because of the market demand for better-quality roots. Thus, a higher commercial root yield is important to reduce waste if the goal is exclusively human consumption. In addition to the commercial root yield, fusiform-shaped roots are desired for the human consumption market (Azevedo et al. 2002), but no genotype with this predominant trait was found in the present study. Gonçalves Neto et al. (2011) studied 39 sweet potato genotypes and did not find any with optimal shape. This variation in shape may be associated with different growing conditions.

For the commercial standard trait, the 15 best genotypes from the UFLA germplasm bank had scores between 2.43 and 2.83. Thus, the two best genotypes had roots with good commercial standard, while the other genotypes tended to have roots that would moderately hinder commercialization (Table 4). The population mean (3.28) also corresponded to a standard that would moderately hinder commercialization. These best genotypes showed a selection gain between -0.45 and -0.84, i.e., less than one unit on the scoring scale. The correlation between the evaluators' scores was 0.82, with confidence interval of 0.77 to 0.85.

Considering the commercial cultivars, only Beaugard was superior to the 15 best genotypes, showed roots with good commercial standard, with the score of 2.39 and the selection gain of -0.88 in relation to the general average of the population (Table 4). However, the other commercial cultivars had the average score of 3.28 and selection gain between -0.13 and 0.06. Thus, these commercial cultivars have roots that would moderately hinder commercialization.

The commercialization standard influences root quality in terms of yield, shelf life, presence of pest damage, and commercial acceptance (Azevedo et al. 2014). According to Melo et al. (2020), knowledge of the adaptation of sweet potato genotypes to the environment and their production efficiency in various farming systems is essential for the identification

of genotypes with better performance. This reinforces the need for further evaluations of the genotypes selected in this study under other environmental conditions.

The 15 best genotypes from the UFLA germplasm bank for root clustering had scores between 4.25 and 4.85, tending to open clustering (Table 4). These scores were better than the population mean (5.66), indicating a selection gain between -1.41 and -0.85. This gain was beneficial because it indicated that, overall, the genotypes had open to disperse roots. The scores showed good agreement, since the correlation between the evaluators' scores was high (0.88), with a confidence interval of 0.85 to 0.90.

Of the 15 best genotypes, two of these were superior to the commercial cultivar Beaugard, which presented the score of 4.41 and the selection gain of -1.25 in relation to the general average of the population (Table 4). Another outstanding commercial cultivar was Brazlândia Roxa, with the average score of 4.53 and gain of -1.14, being inferior only to the three genotypes and the commercial cultivar Beaugard. The other commercial cultivars were inferior to the 15 best genotypes with the average score of 5.17 and selection gain between -0.74 and -0.21. All commercial cultivars showed roots tending to open clustering.

It is considered best to select roots with a clustering between closed and open, since it facilitates mechanized harvesting, so these patterns were prioritized in this genetic improvement program. Conversely, when the root clustering is dispersed or very dispersed, the genotypes can be used for other purposes, such as animal feeding, by using the stems (Silva et al. 2022).

## REML/BLUP estimates and joint evaluation of genotypes

For commercial root yield, since high yields are ideal, higher REML/BLUP estimates were desirable. Thus, genotypes with positive estimates, above 0, were important for selection (Table 4). Among the 15 best genotypes from the UFLA germplasm bank, the estimates for this trait ranged from 1.29 to 2.87 for 2018-28-556 and 2018-19-464, respectively. The standard deviation of the 100 genotypes for commercial root yield was 0.60.

For the qualitative traits, it is desired to select genotypes with the lowest REML/BLUP estimates, e.g., with better root quality. Thus, the genotypes with negative estimates, below 0, were ideal for selection (Table 4).

The best genotypes for yield also had a good general shape, except for 2018-72-1408, 2018-74-1507, 2018-67-1321, 2018-65-1249, and 2018-28-556 (Table 4). The lowest estimate was found for the commercial cultivar Beaugard. The standard deviation for general shape was 0.23.

The estimates the 15 best genotypes from the UFLA germplasm bank for commercial standard ranged between -0.70 and -0.35 for Beaugard and 2018-74-1507, respectively (Table 4). The standard deviation for this trait was 0.28.

The genotypes 2018-65-1249 (-0.67) and 2018-54-1137 (-0.60) had lower estimates for root clustering. These genotypes were superior to the commercial cultivar Beaugard (-0.59). The standard deviation among the 100 genotypes was 0.29.

In addition to separately describing the root yield and root quality traits, the joint evaluation of these sets of traits is important for meeting market needs. Desirable genotypes for human consumption must have a good commercial root yield linked to good root quality.

The genotypes 2018-19-464, 2018-36-807, Beaugard, and 2018-54-1137 were the only genotypes to present good performance on all traits, being commercial root yield, general shape, commercial standard, and root clustering (Table 4). These genotypes showed commercial root yields of 18.68, 12.98, 12.96, and 11.37 mg·ha<sup>-1</sup>, respectively. Furthermore, Beaugard (score 2.21), 2018-19-464 (score 2.44), and 2018-36-807 (score 2.46) presented a near-fusiform general shape, while 2018-54-1137 (score 2.52) had roots tending to a nonuniform shape. Good commercial standards were observed for the Beaugard (score 2.39) and 2018-54-1137 genotypes (score 2.43), while 2018-19-464 (score 2.50) and 2018-36-807 (score 2.58) had roots with a standard that would moderately hinder commercialization. These four genotypes had roots with open clustering, with scores of 4.79 (2018-19-464), 4.63 (2018-36-807), 4.41 (Beaugard), and 4.38 (2018-54-1137).

The 2018-72-1428, 2018-19-443, 2018-72-1418, and 2018-72-1376 stood out for commercial root yield, general shape, and commercialization standard (Table 4). Their commercial root yield ranged from 11.64 (2018-72-1376) to 14.09 mg·ha<sup>-1</sup> (2018-72-1428). The genotype 2018-19-443 (score 2.39) showed near-fusiform shape, while 2018-72-1376

(score 2.58), 2018-72-1418 (score 2.82), and 2018-72-1428 (score 2.84) had nonuniform roots. These four genotypes showed commercial standards that would moderately hinder commercialization, with scores between 2.53 (2018-72-1428) and 2.76 (2018-72-1376).

In addition, the genotypes 2018-65-1249 and 2018-28-556 are among the 15 best genotypes for commercial root yield (11.05 and 11.01 mg·ha<sup>-1</sup>, respectively), commercial standard (scores 2.69 and 2.67, respectively, that would moderately hinder commercialization), and root clustering (scores 4.25 and 4.60, respectively, grouping of open roots) (Table 4).

The genotypes 2018-54-1114, 2018-19-455, and 2018-72-1409 stood out for commercial root yield and general shape (Table 4). These yields were 11.18, 12.64, and 15.18 mg·ha<sup>-1</sup>, respectively. In addition, these genotypes had a nonuniform shape (scores between 2.74 and 2.86).

Last, genotypes 2018-67-1321, 2018-74-1507, and 2018-72-1408 had commercial root yield of 11.75, 12.22, and 13.28 mg·ha<sup>-1</sup>, respectively (Table 4). It did not stand out in terms of root quality traits.

It is important to highlight that only two control treatments, Beaugard and Brazlândia Roxa, stood out among the best genotypes in at least one trait, although the commercial cultivars Princesa, Uruguiana and BRS Amélia, and the three genotypes from UFVJM did not perform well.

## CONCLUSION

For all studied traits, there were selection gains in relation to the population mean. The use of mixed models was efficient for the selection of superior sweet potato genotypes. The genotypes 2018-19-464, 2018-72-1409, 2018-72-1428, 2018-19-443, 2018-36-807, 2018-72-1418, 2018-19-455, 2018-72-1376, 2018-54-1137, 2018-54-1114, 2018-65-1249, and 2018-28-556 had good traits related to commercial root yield and root quality and can be recommended for human consumption. These first five genotypes were superior to the performance of the best commercial cultivar for the commercial root yield trait. For the traits general shape and commercial standard, although the best average score was of the commercial cultivar Beaugard, the genotypes 2018-19-443, 2018-19-464, and 2018-36-807 showed a similar general shape, as well as the genotypes 2018-54-1137 and 2018-19-464 in commercial standard. The 2018-65-1249 and 2018-54-1137 genotypes were superior to the best commercial cultivar for the root clustering trait.

## AUTHORS' CONTRIBUTION

**Conceptualization:** Costa, A. L. and Andrade Júnior, V. C.; **Methodology:** Costa, A. L., Andrade Júnior, V. C. and Bueno Filho, J. S. S.; **Supervision:** Andrade Júnior, V. C.; **Investigation:** Costa, A. L., Gama, A. B. N., Silva, E. A., Brito, O. G. and Silva, J. C. O.; **Formal analysis:** Bueno Filho, J. S. S.; **Visualization:** Costa, A. L. and Bueno Filho, J. S. S.; **Writing – Original Draft:** Costa, A. L.; **Writing – Review and Editing:** Costa, A. L., Andrade Júnior, V. C., Brito, O. G. and Bueno Filho, J. S. S.

## DATA AVAILABILITY STATEMENT

All dataset were generated and analyzed in the current study.

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