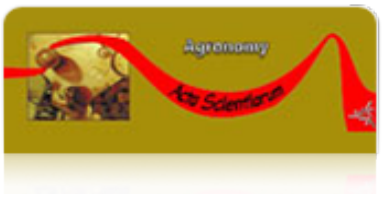

Acta Scientiarum. Agronomy
ISSN: 1679-9275
ISSN: 1807-8621
Editora da Universidade Estadual de Maringá - EDUEM

Otoboni, Maria Eduarda Facioli; Oliveira, Darllan Junior Luiz Santos Ferreira de; Pavan, Bruno Ettore; Andrade, Maria Isabel; Vargas, Pablo Forlan
Genotype × environment interaction for the agronomic performance of high #-carotene sweetpotato
Acta Scientiarum. Agronomy, vol. 44, e55766, 2022
Editora da Universidade Estadual de Maringá - EDUEM

DOI: https://doi.org/10.4025/actasciagron.v44i1.55766

Acta Scientiarum

http://www.periodicos.uem.br/ojs/
ISSN on-line: 1807-8621
Doi: 10.4025/actasciagron.v44i1.55766

Genotype × environment interaction for the agronomic performance of high β-carotene sweetpotato

Maria Eduarda Facioli Otoboni[1*], Darllan Junior Luiz Santos Ferreira de Oliveira[2], Bruno Ettore Pavan[1], Maria Isabel Andrade[3] and Pablo Forlan Vargas[4]

[1]Faculdade de Engenharia, Universidade Estadual Paulista, Rua Monção, Zona Norte, 15385-000, Ilha Solteira, São Paulo, Brazil. [2]Faculdade de Ciências Agrárias e Veterinárias, Universidade Estadual Paulista, Jaboticabal, São Paulo, Brazil. [3]International Potato Center, Maputo, Mozambique. [4]Universidade Estadual Paulista, Câmpus Experimental de Registro, Registro, São Paulo, Brazil. *Author for correspondence. E-mail: eduarda.otoboni@unesp.br

ABSTRACT. Sweetpotato (*Ipomoea batatas* L.) is an important tuber vegetable for human health worldwide owing to its nutritional value and productivity. Consumption of orange-fleshed sweetpotato is beneficial to combat vitamin A deficiency in the world, including Brazil, as these tubers are rich in β-carotene, a precursor of vitamin A. The genotype × environment interaction is one of the greatest challenges in plant breeding, specifically in the selection and approval of cultivars. In this context, adaptability and stability analyses are warranted to evaluate the performance of various genotypes in terms of general or specific adaptations to certain environments and to identify genotypes responsive to environmental variations. Thus, the objective of this study was to evaluate the genotype × environment interaction as well as to estimate the adaptability and stability of sweetpotato genotypes for identifying and selecting promising candidates for breeding. The experiments were performed in four environments: Vera Cruz in São Paulo, Selvíria in Mato Grosso do Sul, and one organic and another intercropped production system in Sete Barras in São Paulo. A randomized block design with two replicates was adopted. A total of 265 genotypes were tested, and the orange-fleshed sweetpotato cultivar 'Beauregard' was used as the control. The additive main effects and multiplicative interaction model was used to study environmental stratification, adaptability, and stability. The genotype × environment interaction was evident in all environments. The genotypes CERAT21-13 (marketable root yield, 22.30 t ha^{-1} in the four environments), CERAT29-26 (27.74 t ha^{-1}), and CERAT52-22 (20.24 t ha^{-1}) were the most adapted in general to the four environments. CERAT25-23, CERAT29-23, and CERAT29-26 were the most adapted to the environment in Vera Cruz; CERAT29-26, CERAT34-14, and CERAT56-32 to the environment in Selvíria; and CERAT31-10, CERAT35-19, and CERAT52-22 to the two environments in Sete Barras.

Keywords: adaptability; stability; environmental stratification; genetic variability; *Ipomoea batatas*.

Received on September 12, 2020.
Accepted on February 11, 2021.

Introduction

Sweetpotato (*Ipomoea batatas* L.) is economically important because of its high nutritional value; as such, it is an excellent source of vitamins, minerals, and carbohydrates. Its production has shown great prospects in recent years. In Brazil, 741,203 tons of sweetpotatoes were produced in an area under the cultivation of over 53,024 hectares in 2018, proving the economic importance of this crop in the country (Instituto Brasileiro de Geografia e Estatística [IBGE], 2020).

Sweet potato is an autohexaploid species, mostly propagated asexually; however, sexual propagation is performed for genetic improvement. Nonetheless, because of self-incompatibility and frequent introduction of plants from places far from its center of origin (Silva, Ponijaleki, & Suinaga, 2012), sweet potato shows a vast genotypic and phenotypic variability, resulting in a massive number of genotypes to be tested during the development of new cultivars.

Currently, sweetpotato breeding programs seek to explore the potential of the crop, including yield, root quality, adaptations to different productive regions, and generation and maintenance of genetic variability, in addition to the search for new highly productive and disease- or pest-resistant cultivars.

In Brazil, the Brazilian Agricultural Research Corporation, Federal University of Lavras, and Federal University of Tocantins are actively involved in sweetpotato genetic improvement programs. On a global

scale, the International Potato Center (CIP) is one of the largest institutions that conducts sweetpotato breeding programs. Currently, CIP has undertaken research projects in over 20 countries in Africa, Asia, and Latin America and part of the work on sweetpotatoes is aimed at the development and release of biofortified cultivars.

The selection and approval of highly productive genotypes are the main objectives of breeding programs for any crop. Typically, such programs aim at obtaining high-yielding genotypes in desired edaphoclimatic conditions. According to Cruz and Regazzi (2001), studies on the genotype × environment (G×E) interaction alone do not provide detailed information on the performance of each genotype under various environments. In this context, adaptability and stability analyses are essential to evaluate the performance of genotypes in terms of both general and specific adaptations to certain environments and to identify genotypes responsive to environmental variations (Cruz, Carneiro, & Regazzi, 2012). In addition to adaptability and stability, environmental stratification allows for the identification and approval of superior genotypes, thus enabling the selection and elimination of redundant loci in the experimental network. Furthermore, it reduces the experimental costs and increases efficiency (Pereira, Melo, Faria, Peloso, & Wendland, 2010).

There have been several studies on the adaptability and stability of sweetpotato genotypes. For instance, Daros and Amaral Júnior (2000) have reported the importance of releasing highly adaptive sweetpotato cultivars. In addition, according to Amaro, Talamini, Fernandes, Silva, and Madeira (2019), the national average sweetpotato yield is low due to the cultivation of varieties with inferior market traits, without prior evaluation and approval in a given region.

To this end, the objective of the present study was to evaluate the G×E interaction as well as to estimate the adaptability and stability of high β-carotene sweetpotato genotypes for identifying and selecting promising genotypes for breeding.

Material and methods

The experiments were conducted in four environments from December 2018 to June 2019: Vera Cruz in São Paulo State, Brazil (22°15′40.9″ S, 49°50'17.6″ W, 605 m a.s.l.; environment 1), Selvíria in Mato Grosso do Sul State, Brazil (20°20′39.40″ S, 51°23′51″ W, 335 m a.s.l.; environment 2), and two production systems [organic (24°17′51.1″ S, 48°05″48.0″ W, 32 m a.s.l.; environment 3), and intercropped (24°17′55.3″ S, 48°05′49.6″ W, 32 m a.s.l.; environment 4)] in Sete Barras in São Paulo State, Brazil.

A total of 265 sweetpotato genotypes from 15 half sib families were tested. These genotypes were obtained from the polycross seeds of an elite population and developed by the CIP and Mozambique Institute of Agricultural Research through recurrent selection for several years to achieve high β-carotene content and dry matter.

Additionally, the commercial cultivar 'Beauregard' was used as the control, because it is orange-fleshed and contains a significant amount of β-carotene (115 mg g^{-1} fresh roots) (Alves, Ito, Carvalho, Melo, & Godoy, 2012).

In all environments, a randomized block design with two replicates was adopted. Each experimental plot measured 1 m^2, with three plants arranged at 0.33 m spacing. A conventional production system was adopted in environments 1 and 2. In environment 1, 40-cm-high rows were constructed, spaced 1 m apart. In environment 2, the row height was the same as that in environment 1 but the spacing was 1.20 m.

In all environments, fertilization was applied together with soil preparation using 500 kg ha^{-1} of N-P-K formula (04-14-08), supplemented with 133 kg ha^{-1} of potassium chloride and 166 kg ha^{-1} of super simple phosphate, resulting in 20 kg ha^{-1} of nitrogen, 100 kg ha^{-1} of phosphorus, and 120 kg ha^{-1} of potassium.

In environments 1 and 2, all necessary farming practices were performed to explore the maximum productive potential of the crop. At 30 days after planting, top-dressing fertilization was applied with 30 kg ha^{-1} of nitrogen. For weed control, manual weeding was employed in the planting rows and chemical control with linurom (0.6 L ha^{-1}) and clethodim + alkylbenzene (0.20 L ha^{-1}) was employed between rows. In addition, irrigation was performed by a central pivot throughout the crop cycle, at an irrigation volume of 12 mm every 3 days, except in environment 1, where no irrigation was performed. Environment 1 was maintained unirrigated to explore the robustness of the genotypes and verify their true adaptation to the environment.

In environments 3 and 4, the basis participatory genetic improvement was adopted, which is advantageous over conventional breeding in terms of the involvement of farmers at all stages of cultivation, from planting to harvest, that follow the local practices. This allows for setting relevant criteria for farmers to guide the breeding objectives as well as adds value and generates jobs and income (Fonseca, 2014).

In environment 3, organic cultivation has been performed since the last 15 years. This area is mowed regularly, but there were residual trunks and roots. Thus, before the installation of the experiment, the area was cleaned and plant residues were removed; both procedures were performed by the local farmers. The planting rows were manually constructed with a spacing of 0.70 m. Alvorada phosphorite and shell limestone were applied at rate of 0.6 t ha^{-1} and rock powder at a rate of 3 t ha^{-1} to correct the acidity and meet the soil nutritional requirements of plants. Between rows, crotalaria (*Crotalaria juncea*) and pigeon pea (*Cajanus cajan*) were planted as green manure.

In the intercropping production system (environment 4), the sweetpotato vines were planted between the lines of 18-month-old pupunha and banana. Organic farming was also adopted, but with 0.50 m spacing between the planting rows of the main crops. Before planting the sweetpotatoes, thinning of pupunha and banana plants was conducted. In environment 4, all management practices, including fertilization, were the same as those in environment 3, except the spacing between planting lines. In environment 3 and 4, no irrigation system was used.

At 126 (environment 1), 127 (environment 2), and 140 (environments 3 and 4) days after planting, sweetpotato tubers were harvested, and the following characteristics were evaluated: total root yield (TRY) (total root weight of plants harvested from a plot, converted to tons per hectare); marketable root yield (MY) (roots with weights above 80 g in a plot, converted to tons per hectare); percent marketable root production (%MY) [(MY/TRY) × 100]; non-marketable root yield (NMY) (roots with weights below 80 g in a plot, converted to tons per hectare); number of total roots (TNR) (number of roots per plant harvested from a plot, converted to roots per hectare); number of marketable roots (NMR) (number of roots with weights above 80 g per plant harvested from a plot, converted to roots per hectare); number of non-marketable roots (NNMR) (number of roots with weights below 80 g per plant harvested from a plot, converted to roots per hectare); average root weight (MRW) (TRY/TNR); average marketable root weight (MMRW) (MY/NMR); total root dry weight (TRDW) [dry weight (%) of root samples oven dried at 65°C for 72h to a constant weight, converted to tons per hectare]; root dry mass (RDM) [(TRDW × 100)/fresh weight]; skin color; flesh color (FC); root damage; root shape; and root size.

For the analyses of G×E interaction, adaptability, and stability, only three characteristics, namely MY, RDM, and FC, were considered. For FC, scores from 1 to 5 were assigned by two evaluators, with 1 indicating white flesh (low β-carotene levels) and 5 indicating intense orange flesh (high β-carotene levels) (Figure 1).

For FC, which the primary trait-of-interest in the present study, 'Beauregard' was used as the control (score = 4). The genotypes that showed a more intense orange FC than 'Beauregard' received a score of 5. Scores were assigned sequentially: 1, white flesh; 2, cream flesh; 3, orangish but less intense than that of 'Beauregard'; 4, orange equal or close to that of 'Beauregard'; and 5, intense orange (Figure 1).

Figure 1. Grade scale for the classification of root flesh color in the tested sweetpotato genotypes. The scores were assigned as follows: 1, white; 2, cream; 3, orangish but less intense than that of 'Beauregard'; 4, orange equal or close to that of 'Beauregard'; and 5, intense Orange. Source: authors.

MY, RDM, and FC were considered the major characteristics of marketable roots, with FC representing the core trait-of-interest in the present study, which aimed at selecting high-yielding and highly adaptive genotypes with a high β-carotene content (indicated by orange flesh color). As this study focuses on household consumption, RDM was selected to meet the preferences of Brazilian consumers', who favor sweetpotatoes with a high dry matter content (Otoboni, Oliveira, Vargas, Pavan, & Andrade, 2020).

For analysis of variance (ANOVA), 97 of the 265 genotypes that produced marketable yield in the four evaluated environments were used individually or combined. The data were transformed using the following equation, because some results were null due to the loss of plots:

$\sqrt{(x + 0.5)}$ (1)

MY, RDM, and FC were subjected to individual ANOVA for each environment and subsequently to combined ANOVA across all four environments. The analyses were conducted using GENES (Cruz, 2006). The combined analysis was based on the following statistical model:

$$Y_{ijk} = \mu + G_i + E_j + GE_{ij} + B/E_{jk} + \varepsilon_{ijk} \quad (2)$$

where: Y_{ijk} is the observed value of the i^{th} genotype in the j^{th} environment and k^{th} block; μ is the general mean of the experiments; G_i is the effect of the i^{th} genotype; Ej is the effect of the j^{th} environment; GE_{ij} is the effect of the interaction of the i^{th} genotype with the j^{th} environment; B/E_{jk} is the random effect of the k^{th} block within the j^{th} environment; and ε_{ijk} is the random error.

In the combined analysis, the G×E interaction was assessed using the mean square expected values, considering the effect of genotypes as the fixed effect and the effects of the block, environment, residual, and G×E as the random effects.

Following individual and combined ANOVAs, adaptability, stability, and environmental stratification were assessed using the additive main effects and multiplicative interaction (AMMI) model, according to the equation proposed by Mandel (1971).

$$Y_{ij} = \mu + g_i + e_j + \sum_{k=1}^{n} \lambda_k \gamma_{ik} e_{jk} + p_{ij} + \varepsilon_{ij}, \quad (3)$$

where: Yij is the average response of the i^{th} genotype in the j^{th} environment, μ is the general mean; g_i is the fixed effect of the i^{th} genotype; e_j is the fixed effect of the j^{th} environment; λ_k is the square root of the k^{th} eigenvalue of the matrix $(\tau\upsilon)$ $(\tau\upsilon)'$ or $(\tau\upsilon)'$ $(\tau\upsilon)$ of equal non-zero eigenvalues, wherein $(\tau\upsilon) = [\tau\upsilon_{ij}]$ is the interaction matrix obtained as a residual of adjustment to the main effects by ANOVA applied to the matrix of means; γ_{ik} is the i^{th} element (related to factor τ) of the k^{th} eigenvector of $(\tau\upsilon)$ $(\tau\upsilon)'$; e_{jk} is the j^{th} element (related to the factor υ) of the k^{th} eigenvector of $(\tau\upsilon)'$ $(\tau\upsilon)$; p_{ij} is the noise present in the data; ε_{ij} is the average experimental error; i is the genotypic variation, i = (1, 2, ..., g); j is the environmental variation, j = (1, 2, ..., e); and p is the characteristic non-zero root, p = [1, 2, ..., min. (g^{-1}, e^{-1})].

Results and discussion

In the ANOVA for individual environments (Table 1), the coefficient of variation (CV%) ranged from 0.45% (environment 1) to 22.39% (environment 4), with an average of 8.78%, for MY; from 3.87% (environment 1) and 4.40% (environment 2), with an average of 4.14%, for RDM; and from 3.32% (environment 4) to 8.92% (environment 2), with an average of 6.09%, for FC. All values indicated good experimental precision. Only MY showed a CV% greater than 10% (Table 1). However, these variables are quantitative and therefore subject to environmental effects.

Average MY ranged from 0.66 (environment 4) to 21.49 t ha^{-1} (environment 2), with a total average of 9.78 t ha^{-1}, indicating the distinct performance of the genotypes under each environment. Average DRM ranged from 12% (environment 4) to 30.35% (environment 2) (Table 1).

In this study, a significant G×E interaction was observed, which affected the adaptability and stability of the tested genotypes.

The wide variation in commercial productivity found in this study may be related to the different environments and forms of cultivation. The average total MY across all environments was 9.78 t ha^{-1}. The result is similar to the value reported by Silva et al. (2018); they evaluated 45 sweetpotato clones and observed an average MY of 9.16 t ha^{-1}.

Genotypes showed different performances in the evaluated environments ($p \leqslant 0.01$) (Table 1). The significant effect of genotype on the three key characteristics in the four environments indicates the heterogeneity and genetic variability among the tested genotypes.

Average FC ranged from 1.26 (environment 4) to 2.79 (environment 2) (Table 1). Of note, this characteristic was based on a score from 1 to 5 attributed by visual observation; therefore, genotypes with higher scores (close to five) are better for selection, since they indicate the intense orange flesh color and, consequently, high β-carotene content.

The relationship between the smallest and largest mean squares of residuals from individual ANOVAs was studied (Table 1). For values exceeding the ratio of 7:1, the degree of freedom was adjusted such that it was not necessary to eliminate the discrepant environment, as proposed by Nass, Valois, Melo, and Valadares-Inglis (2001).

Table 1. Summary of individual analysis of variance for experiments in Vera Cruz (E1), Selvíria (E2), and organic (E3) and intercropped (E4) production systems in Sete Barras during 2018–2019.

FV		Mean square: E1		
	DF	MY	RDM	FC
Block	1	0.005**	0.053**	0.076**
Genotype	96	4,669.127**	0.177**	0.285**
Residual	96	0.232	0.042	0.013
Mean	-	13.67	27.35	2.73
CV%	-	0.45	3.87	6.52
FV		Mean square: E2		
	DF	MY	RDM	FC
Block	1	26.021**	0.029**	0.027**
Genotype	96	4,788.837**	0.223**	0.238**
Residual	96	6.433	0.059	0.025
Mean	-	21.49	30.35	2.79
CV%	-	1.83	4.40	8.92
FV		Mean square: E3		
	DF	MY	RDM	FC
Block	1	19.287**	0.142**	0.014**
Genotype	96	2,613.494**	0.137**	0.285**
Residual	96	22.247	0.052	0.009
Mean	-	3.32	28.29	2.66
CV%	-	10.48	4.25	5.61
FV		Mean square: E4		
	DF	MY	RDM	FC
Block	1	5.913**	0.010**	0.006**
Genotype	96	1,204.891**	10.512**	0.739**
Residual	96	4.549	0.012	0.001
Mean	-	0.66	12	1.26
CV%	-	22.39	4.05	3.32

MY: marketable yield (t ha^{-1}); RDM: root dry mass (%); FC: flesh color; CV%: coefficient of variation; **significant at 1% probability level by *F*-test. Source: authors.

As experiments were conducted in different environments, a combined ANOVA was performed to study the G×E interaction (Table 2).

CV% ranged from 4.30% (RDM) to 8.37% (FC), demonstrating high experimental precision in the test set. The general means obtained were 9.79 t ha^{-1} for MY, 24.50% for RDM, and 2.36 for FC. Combined ANOVA revealed significant effects ($p \leqslant 0.01$) of the sources of variation in environments and G×E interaction on all evaluated characteristics (Table 2), whereas the genotype effect was significant only for FC.

These results supported the findings of G×E interaction through adaptability and stability analyses, as genotypes performed differently in different environments.

One of the ways to mitigate the G×E interaction is to identify more productive genotypes with high adaptability and stability. As verified by our combined analysis (Table 2), the sources of variation in the G×E interaction were always significant, and the effect of genotype was significant for FC ($p \leqslant 0.01$). These results indicate that the genotypes performed differently under the evaluated environments, justifying the study of G×E interaction, adaptability, and stability.

Table 2. Summary of combined analysis of variance considering the 97 genotypes in experiments in Vera Cruz, Selvíria, and organic and intercropped production systems in Sete Barras during 2018–2019.

FV	Mean square		
	MY	RDM	FC
Block/environment	12.806	0.059	0.031
Environment	6,58,636.356**	353.092**	16.187**
Genotype	4,561.734^{ns}	2.547^{ns}	0.708**
G×E	4,835.855**	2.834**	0.368**
Residual	16.645	0.041	0.018
Mean	9.79	24.50	2.36
CV%	5.45	4.30	8.37

MY: marketable yield (t ha^{-1}); RDM: root dry mass (%); FC: flesh color; CV%: coefficient of variation; ^{ns}not significant by *F*-test; **significant at 1% probability level by *F*-test. Source: authors.

The adaptability and stability of MY using the AMMI model are graphically represented in Figure 2. The 97 genotypes and 4 environments are identified as G1 to G97 and E1 to E4, respectively (Figure 2).

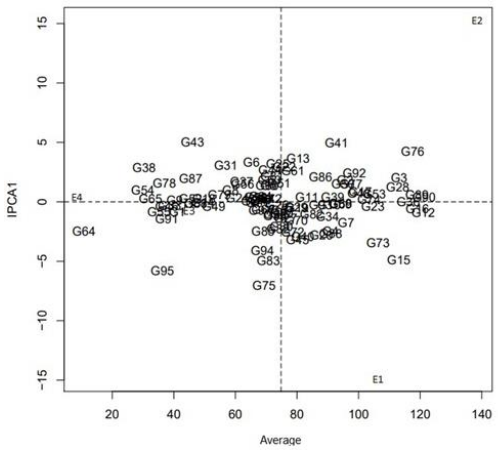

Figure 2. Graphical representation of marketable yield (MY) of the 97 sweetpotato genotypes evaluated in 4 environments: Vera Cruz (E1), Selvíria (E2), and organic (E3) and intercropped (E4) production systems in Sete Barras. [7.45 cm (H) × 8.50 (W)]. G: genotype; E: environment; IPCA1: first interaction axis.

In the present study, IPCA1 accounted for 47.85% and IPCA2 for 32.26% of the G×E interaction for MY. Overall, the AMMI model explained 80.11% of the total variation in the G×E interaction for MY.

The first principal component of the interaction (IPCA1) should accumulate variation from 27.20% to 72% in order to be represented in graphics (Duarte & Vencovsky, 1999). Therefore, in this study, two graphs were presented for MY, as opposed to one each for RDM and FC. According to Yokomizo, Dias, Dias, and Hongyu (2016), a non-significant IPCA2 may mostly constitute noise.

As stated in the Materials and Methods section, the data were adjusted. The values corresponding to means (Figures 2 and 3) are represented according to the already transformed data, not representing the values in tons per hectare.

In the AMMI graph, the genotypes and environments located close to the origin of the axes are considered to be more stable than the distant ones; therefore, they contribute less to the G×E interaction (Duarte & Vencovsky, 1999). Regarding adaptability, genotypes with specific adaptations to each environment are represented by the proximity of those genotypes and environments in any area of the graph.

The most promising genotypes in terms of MY, that is the most productive ones, in the four environments were G12 (CERAT21-05; general average in four environments, 22.54 t ha^{-1}), G16 (CERAT21-13; 20.24 t ha^{-1}), G36 (CERAT29-26; 22.16 t ha^{-1}), G76 (CERAT52-22; 17.64 t ha^{-1}), G89 (CERAT56-32; 21.39 t ha^{-1}), and G90 (CERAT60-05; 21.65 t ha^{-1}) (Figure 2). Among these genotypes, CERAT21-05 showed the highest average MY in the four environments (22.54 t ha^{-1}). Considering the most productive genotypes, the general average in all environments was 20.94 t ha^{-1}. Among the most promising genotypes in terms of MY, CERAT21-13, CERAT29-26, and CERAT60-05 were orange-fleshed, with FC scores of 5, 4, and 4, respectively, indicating a high β-carotene content.

The best productive performance of the evaluated genotypes was observed in environment 2. This may be the result of specific farming practices conduced in this environment alone, making it a high-yielding system.

Regarding MY, a relatively homogeneous distribution of genotypes relative to the central point of the graph was observed. The stability zone corresponds to the central region of the graph at the intersection of zero on IPCA1 and IPCA2. However, individual visualization of MY stability, albeit evident for most genotypes, was hampered by the sheer number of genotypes represented on the graph (Figure 3).

The approval of a cultivar for use in a given breeding program is typically based on a good productive performance and adaptability to the cropping region. In this context, the most adapted genotypes to environment 1 were G27 (CERAT25-23; 24.77 t ha^{-1}), G34 (CERAT29-23; 33.48 t ha^{-1}), G36 (CERAT29-26; 36.98 t ha^{-1}), and G72 (CERAT51-27; 32.33 t ha^{-1}) and those to environment 2 were G36 (CERAT29-26; 49.17 t ha^{-1}), G50 (CERAT34-14; 44.25 t ha^{-1}), G51 (CERAT34-15; 34.46 t ha^{-1}), G81 (CERAT55-20; 36.07 t ha^{-1}), and G89 (CERAT56-32; 49.19 t ha^{-1}). Therefore, CERAT21-05, CERAT29-23, and CERAT29-26 can be approved for both environments 1 and 2 (Figure 3). Among the genotypes approved for both environment 1 and 2, only CERAT29-26 had an FC score of 4, indicating a high β-carotene content.

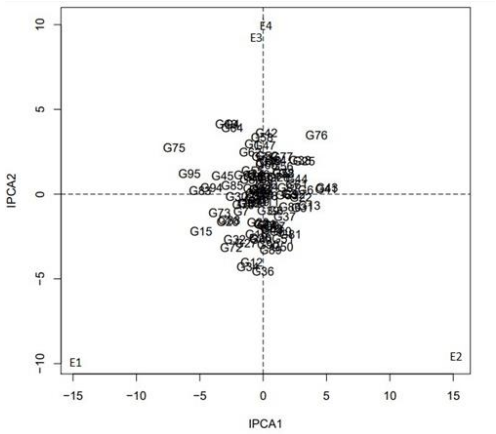

Figure 3. Graphical representation (AMMI2) of marketable yield (MY) of the 97 sweetpotato genotypes evaluated in 4 environments: Vera Cruz (E1), Selvíria (E2), and organic (E3) and intercropped (E4) production systems in Sete Barras. [7.55 cm (H) × 8.50 (W)]. G: genotype; E: environment; IPCA1: first interaction axis; IPCA2: second interaction axis.

Among the genotypes most adapted to environment 1, CERAT29-26 achieved the highest MY (37.00 t ha^{-1}), followed by CERAT29-23 (33.50 t ha^{-1}). Among the most adapted genotypes to environment 2, CERAT56-32 achieved the highest MY (49.19 t ha^{-1}), followed by CERAT29-26 (49.17 t ha^{-1}).

The best average in MY was achieved in environment 2. However, despite being the most productive, environment 2 was the most unstable, along with environment 1 (Figure 3).

The average MY of 'Beauregard' was 8.50 t ha^{-1} in the four environments, being highly inferior to that of the best genotypes in the respective environments. The best productive performance of 'Beauregard' was observed in environment 2 (17.50 t ha^{-1}).

MY was relatively more stable in environments 3 and 4 (Figure 3). Coincidentally, both environments presented the lowest average MY (E3: 3.32 t ha^{-1}; E4: 0.66 t ha^{-1}) (Table 1), indicating that this stability was not positively correlated to the productivity of the genotypes. As environments 3 and 4 were very close (Figure 3), the adapted and approved genotypes were similar for the two environments, indicating the possibility of environmental stratification and reducing the number of experiments required for the next evaluation cycle and, consequently, operational costs.

The most adapted genotypes to E3 and E4 were G4 (CERAT16-08), G40 (CERAT31-10), G42 (CERAT31-14), G58 (CERAT35-19), and G76 (CERAT52-22) (Figure 3). Although these genotypes were the most adapted, they achieved results below expectations, with CERAT52-22 being the most promising genotype (11.13 t ha^{-1}) in both environments.

The general average of MY for the six most productive genotypes in the four environments was 27.13 t ha^{-1}. Although some genotypes showed an excellent MY in environments 1 (Vera Cruz) and 2 (Selvíria), the opposite trends were observed in environments 3 (organic production system, Sete Barras) and 4 (intercropped production system, Sete Barras). For instance, CERAT21-05 obtained an MY of 41.89 and 43.32 t ha^{-1} in environments 1 and 2, respectively, but the value dropped to 4.96 t ha^{-1} in environment 3, indicating, once again, the heterogeneity of genotypes under diverse environments.

The general average of MY (20.94 t ha^{-1}) of the six most productive genotypes in the four environments in this study was higher than that reported in a previous study by Nasser et al. (2020); they evaluated the productivity and quality of sweetpotato roots propagated by different sizes of mini-cuttings in São Manuel (São Paulo State, Brazil) and obtained an average MY of 11.48 t ha^{-1}. However, the average MY in this study was close to that reported by Silva, Suinaga, Fonijaleki, and Amaro (2015); they evaluated the performance of six sweetpotato cultivars ('Princesa', 'BRS Amélia', 'BRS Cuia', 'Brazlândia Roxa', 'Beauregard', and 'BRS Rubisol') in Canoinhas (Santa Catarina) and observed the average MY of 21.21 t ha^{-1}. Similarly, Melo et al. (2020) evaluated six sweetpotato genotypes and two commercial cultivars in Brasilia and observed an average MY of 20.69 t ha^{-1}. Therefore, the general average MY of genotypes in this experiment was consistent with the previously reported values.

The average MY of 'Beauregard' (8.50 t ha^{-1}) in the four environments was much lower than that reported by Silva et al. (2015) (38.12 t ha^{-1}). Generally, 'Beauregard' has been reported to achieve a high average MY in the literature [37.91 t ha^{-1} by Amaro et al. (2019) or 28.18 and 35.68 t ha^{-1} by Melo et al. (2020)]. The low average

productivity of the cultivar in the present study may be due to the low yields obtained in the two production systems in Sete Barras (environments 3 and 4), which may have negatively affected the overall results.

The MY of all genotypes selected as the most adapted to environments 1 and 2 (environments with better performances) was highly superior to the Brazilian average (13.98 t ha^{-1}) (IBGE, 2020). Specifically, the MY of CERAT56-32 (49.21 t ha^{-1}) in environment 2 was 352% higher than the national average and 281% higher than that of 'Beauregard' in the same environment.

The adaptability and stability of RDM using the AMMI model are graphically represented in Figure 4. Only IPCA1 was significant, and represented 96.40% of the G×E interaction for RDM.

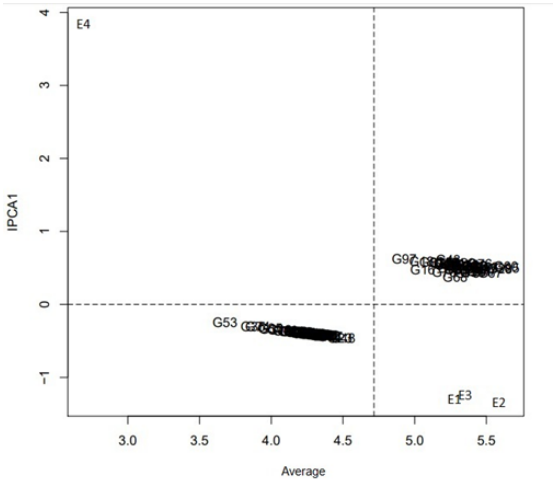

Figure 4. Graphical representation (AMMI1) of the root dry mass (RDM) of the 97 sweetpotato genotypes evaluated in 4 environments: Vera Cruz (E1), Selvíria (E2), and organic (E3) and intercropped (E4) production systems in Sete Barras. [7.48 cm (H) × 8.50 (W)]. G: genotype; E: environment; IPCA1: first interaction axis.

Environments 1, 2, and 3 were clustered in the same quadrant, indicating similarity among these environments. Unexpectedly, E4 made a greater contribution to the G×E interaction for RDM (Figure 4).

The most stable genotypes for RDM were G16 (CERAT21-13, general average, 25.13%), G30 (CERAT29-06; 27.45%), G35 (CERAT29-24; 24.13%), G67 (CERAT37-23; 28.91%), G74 (CERAT51-33; 24.29%), and G85 (CERAT56-15; 25.47%). Of these, CERAT21-13 (FC score = 4), CERAT29-06 (FC score = 5), CERAT29-24 (FC score = 4), CERAT37-23 (FC score = 3), and CERAT51-33 (FC score = 3) were orange-fleshed, indicating the presence of β-carotene.

No specific adaptation of the genotypes was observed to any environment; however, genotypes with the highest RDM were G28 (CERAT25-24; average, 30.18%), G36 (CERAT29-26; 31.80%), G60 (CERAT35-21; 32.75%), G67 (CERAT37-23; 29.52%), G71 (CERAT51-13; 28.44%), G76 (CERAT52-22; 28.71%), G77 (CERAT52-25; 30.27%), and G95 (CERAT60-22; 30.09%). Among these, CERAT25-24 (FC score = 3), CERAT29-26 (FC score = 4), CERAT35-21 (FC score = 4), and CERAT60-22 (FC score = 4) were orange-fleshed, indicating the presence of β-carotene.

Regarding RDM, environment 4 was discrepant from the remaining environments. It was highly unstable and presented values below the average, complicating genotype selection based on RDM in this environment. Although we identified the most stable genotypes in terms of RDM in the four evaluated environments, this stability provided an overall average below the expected value, as all six stable genotypes showed an average RDM below 30%. In contrast, the genotypes considered the most promising in terms of RDM showed excellent results, indicating the presence of a high dry mass content, corroborating one of the objectives of this study.

Among the genotypes with the highest RDM, CERAT35-21 (32.75%) was the most promising, followed by CERAT29-26 (31.80%). These values are higher than those reported by Andrade Júnior et al. (2012); they evaluated 12 sweetpotato clones in Diamantina (Minas Gerais) and observed an average RDM of 27.30%.

In addition, Oliveira et al. (2017) observed an average RDM of 31.87% in roots harvested 5 months after planting, and this value was lower than that of CERAT35-21 in the present study. Overall, however, the results of that previous study were superior to those of the present study (Tables 1 and 2). From an industrial viewpoint, to select genotypes suitable for the food or ethanol industries, a higher RDM is preferred, as this characteristic is directly related to the specific density of roots.

The adaptability and stability of FC using the AMMI model are graphically represented in Figure 5. IPCA1 accounted for 70.56% of the G×E interaction for FC.

Regarding FC, the genotypes were generally stable, indicating that FC does not change according to environmental variations. Therefore, once selected for FC, the genotypes will not undergo changes in this characteristic, thus facilitating the next selection cycle, reducing the number of tests required, and lowering the operational cost.

Environments 1, 2, and 3 were clustered in the same quadrant, suggesting little influence of the G×E interaction (Figure 5). Therefore, the genotypes approved for one environment can be approved for the remaining two environments. The most adapted genotypes to the three environments were G7 (CERAT16-18), G30 (CERAT29-06), G33 (CERAT29-22), and G42 (CERAT31-14), all with an FC score of 5, with the exception of CERAT29-22, which had a score of 4.

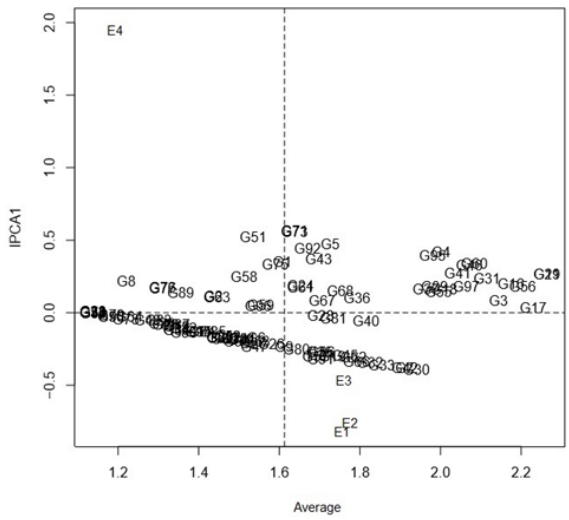

Figure 5. Graphical representation (AMMI1) of the flesh color (FC) of the 97 sweetpotato genotypes evaluated in 4 environments: Vera Cruz (E1), Selvíria (E2), and organic (E3) and intercropped (E4) production systems in Sete Barras. [7.46 cm (H) × 8.50 (W)]. G: genotype; E: environment; IPCA1: first interaction axis.

The most stable genotypes were G17 (CERAT21-21; FC score = 5), G28 (CERAT25-24; FC score = 4), G34 (CERAT29-23; FC score = 1), G48 (CERAT34-06; FC score = 1), G54 (CERAT34-26; FC score = 1), G64 (CERAT37-15; FC score = 1), G72 (CERAT51-27; FC score = 1), G79 (CERAT55-18; FC score = 1), and G81 (CERAT55-20; FC score = 3). The genotypes with a higher average FC score (intense orange) were G3 (CERAT16-03), G11 (CERAT21-04), G16 (CERAT21-13), G17 (CERAT21-21), G29 (CERAT25-27), and G56 (CERAT35-05). Among these, CERAT16-03 and CERAT21-13 received an FC score of 4, while the others received a score of 5. The averages represented in the graph represented data transformed as $\sqrt{(x + 0.5)}$.

Overall, the major traits affected by the G×E interaction were RDM (Figure 4) and FC (Figure 5) in environment 4 and MY (Figure 3) in environment 3.

Considering the low averages of the three major characteristics (MY, RDM, and FC), in environment 4 obtained by individual analyses (Table 2) and the AMMI model (Figures 2, 3, 4, and 5), intercropping with pupunha and banana in Sete Barras did not prove to be suitable for sweetpotato cultivation and negatively affected the results.

One of the benefits of using the AMMI model is the easy graphical interpretation of results. Nevertheless, due to the large set of evaluated genotypes, the interpretation was hindered. For reliable interpretation of the adaptability and stability, a previously selected genotype should be considered a single point. Thus, the best previously selected genotypes can be approved and further tested in other environments.

'Beauregard' was not selected for any characteristic based on the AMMI model, indicating the potential of the genotypes evaluated in the present study to become commercial sweetpotato cultivars in the future.

Conclusion

Analysis using the AMMI model facilitated the segregation of environments, consequently minimizing the number of necessary trials. The genotypes CERAT21-13, CERAT29-26, and CERAT52-22 were the most adapted in general to the four environments. CERAT25-23 and CERAT29-23 were the most adapted to Vera

Cruz; CERAT29-26 and CERAT56-32 to Selvíria; and CERAT31-10 and CERAT35-19 to Sete Barras. Our results indicated the presence of G×E interaction, suggesting that the set of tested genotypes shows genetic variability. These genotypes can be preserved in an active germplasm bank as the material for crossings and recombination in sweetpotato breeding programs aimed at developing new improved varieties.

Acknowledgements

The authors acknowledge the financial support of São Paulo Research Foundation (FAPESP): number 2017 / 08032-0; the Center for Tropical Roots and Starches (CERAT) of the UNESP for research support; and the International Potato Center for the support. This study was financed in part by the *Coordenação de Aperfeiçoamento de Pessoal de Nível Superior - Brasil* (CAPES) - Finance Code 001.

References

Alves, R. M. V., Ito, D., Carvalho, J. L. V., Melo, W. F., & Godoy, R. L. O. (2012). Stability of biofortified sweet potato flour. *Brazilian Journal of Food Technology*, *15*(1), 59-71. DOI: https://doi.org/10.1590/S1981-67232012000100007

Amaro, G. B., Talamini, V., Fernandes, F. R., Silva, G. O., & Madeira, N. R. (2019). Performance of sweet potato cultivars for yield and root quality in Sergipe, Brazil. *Revista Brasileira de Ciências Agrárias*, *14*(1), 1-6. DOI: https://doi.org/10.5039/agraria.v14i1a5628

Andrade Junior, V. C., Viana, D. J. S., Pinto, N. A. V. D., Ribeiro, K. G., Pereira, R. C., Neiva, I. P., ... Andrade, P. C. R. (2012). Productive and qualitative characteristics of the vines and roots of sweet potato. *Horticultura Brasileira*, *30*(4), 584-589. DOI: https://doi.org/10.1590/S0102-05362012000400004

Cruz, C. D. (2006). *Programa Genes: biometria*. Viçosa, MG: UFV.

Cruz, C. D., & Regazzi, A. J. (2001). *Biometric models applied to genetic improvement* (2nd ed.). Viçosa, MG: UFV.

Cruz, C. D., Carneiro, F. C. S., & Regazzi, A. J. (2012). *Biometric models applied to genetic improvement* (3rd ed.). Viçosa, MG: UFV.

Daros, M., & Amaral Júnior, A. T. (2000). Adaptabilidade e estabilidade de produção de *Ipomoea batatas*. *Acta Scientiarum*, *22*(4), 911-917.

Duarte, J. B., & Vencovsky, R. (1999). *Genotype x environment interaction: an introduction to "AMMI" analysis* (9th ed.). Ribeirão Preto, SP: Sociedade Brasileira de Genética.

Fonseca, M. A. J. (2014). Genetic resources and breeding of vegetables for and with family farming. *Horticultura Brasileira*, *32*(4), 1. DOI: https://dx.doi.org/10.1590/S0102-053620140000400023

Instituto Brasileiro de Geografia e Estatística [IBGE]. (2020). *Table 1612: planted area, harvested area, amount produced, average yield and value of temporary crop production*. Rio de Janeiro, RJ: IBGE. Retrieved on April 2, 2020 from https://sidra.ibge.gov.br/tabela/ 1612#resultado

Mandel, J. (1971). A new analysis of variance model non-additive data. *Technometrics 13*(1), 1-18. DOI: https://doi.org/10.1080/00401706.1971.10488751.

Melo, R. A. C., Silva, G. O., Vendrame, L. P. C., Pilon, L., Guimarães, J. A., & Amaro, G. B. (2020). Evaluation of purple-fleshed sweetpotato genotypes for root yield, quality and pest resistance. *Horticultura Brasileira*, *38*(4), 439-444. DOI: https://doi.org/10.1590/s0102-0536202004016

Nass, L. L., Valois, A. C. C, Melo, I. S., & Valadares-Inglis, M. C. (2001). *Genetic resources and breeding: plants*. Rondonópolis, MT: Fundação Mato Grosso.

Nasser, M. D., Cardoso, A. I. I., Rós, A. B., Mariano-Nasser, F. A. C., Colombari, L. F., Ramos, J. A., & Furlaneto, K. A. (2020). Productivity and quality of sweet potato roots propagated by different sizes of mini cuttings. *Scientia Plena*, *16*(7), 1-8. DOI: https://doi.org/10.14808/sci.plena.2020.070204

Oliveira, A. M. S, Blank, A. F., Alves, R. P., Arrigoni-Blank, M. F., Maluf, W. R., & Fernandes, R. P. M. (2017). Performance of sweet potato clones for bioethanol production in different cultivation periods. *Horticultura Brasileira*, *35*(1), 57-62. DOI: https://doi.org/10.1590/s0102-053620170109

Otoboni, M. E. F., Oliveira, D. J. L. S. F., Vargas, P. F., Pavan, B. E., & Andrade, M. I. (2020). Genetic parameters and gain from selection in sweet potato genotypes with high betacarotene content. *Crop Breeding and Applied Biotechnology*, *20*(3), 1-9. DOI: https://doi.org/10.1590/1984-70332020v20n3a42

Pereira, H. S., Melo, L. C., Faria, L. C., Peloso, M. J. D., & Wendland, A. (2010). Estratificação ambiental na avaliação de genótipos de feijoeiro-comum tipo carioca em Goiás e no Distrito Federal. *Pesquisa Agropecuária Brasileira, 45*(6), 554-562. DOI: https://doi.org/10.1590/S0100-204X2010000600004

Silva, G. O., Ponijaleki, R., & Suinaga, F. A. (2012). Genetic divergence among sweet potato accessions based on root traits. *Horticultura Brasileira*, *30*(4), 595-599. DOI: https://doi.org/10.1590/S0102-05362012000400006

Silva, G. O., Suinaga, F. A., Ponijaleki, R., & Amaro, G. B. (2015). Performance of root yield traits in sweet potato cultivars. *Revista Ceres*, *62*(4), 379-383. DOI: https://doi.org/10.1590/0034-737X201562040007

Silva, J., Ferreira, P. V., Oliveira, F. S., Teixeira, J. S., Silva, M. T. & Santos, D. G. (2018). Características de raízes tuberosas de clones de batata-doce por meio de técnicas multivariadas para seleção de genótipos superiores. *Revista Verde de Agroecologia e Desenvolvimento Sustentável*, 13(1), 33-38. DOI: http://dx.doi.org/10.18378/rvads.v13i1.5120

Yokomizo, G. K., Dias, J. S. A., Dias, C. T. S., & Hongyu, K. (2016). AMMI analysis on vegetative characters from banana genotypes in Amapá. *Revista de Ciências Agrárias*, *59*(1), 1-8. DOI: https://doi.org/10.4322/rca.1845