Journal of Crop Science and Biotechnology (2021) 24:349–360
https://doi.org/10.1007/s12892-020-00083-0

ORIGINAL RESEARCH

Selection of new sweet potato genotypes based on production parameters, physical root characteristics and resistance to *Euscepes postfasciatus*

Murilo Henrique Souza Leal[1] · André Ricardo Zeist[1] · Nilson Rodrigues Júnior[1] · André Dutra Silva Júnior[1] · José Henrique Verhalem Arantes[1] · Jair Garcia Neto[1] · Julia Roberta Sanches de Pieri[1] · Amanda Carvalho Perrud[1]

Accepted: 31 December 2020 / Published online: 26 January 2021

Abstract

Sweet potato (*Ipomoea batatas* L.) is a root that allows healthy eating and combats malnutrition. There is a need for more productive sweet potato genotypes displaying good resistance and a favorable appearance and shape. New genotypes that are more productive, resistant to the main soil pests and with good physical characteristics would contribute to meet the needs of producers and the demands of consumers. The aim of this study was to develop and select sweet potato genotypes regarding agronomic and physical root parameters. The new genotypes were obtained through the cross-linking of 22 parents with commercial characteristics. Subsequently, 386 experimental genotypes were conducted in the field in an experimental design consisting of augmented blocks with intercalated controls. Aspects related to agronomic, physical root characteristics and resistance to *Euscepes postfasciatus* were explored. Genotypes with higher performance than the controls were identified for all assessed parameters. The genotypes UZBD-K-09, UZBD-K-56 and UZBD-K-78, with purple flesh roots, UZBD-F-15 and UZBD-F-34, with orange flesh, and UZBD-K-70, with a white flesh were selected.

Keywords *Ipomoea batatas* · Orange flesh · Pest resistance · Plant breeding · Purple flesh · White flesh

Introduction

The sweet potato (*Ipomoea batatas* L.) is a vegetable belonging to the *convulvulaceae* family (Gemenet et al. 2020). Originating in Central America, it is cultivated worldwide, displaying rustic characteristics, adaptation to different soils and tolerance to adverse conditions. Its roots contain a high amount of carbohydrates, potassium and minerals, making it an excellent alternative against malnutrition and in favor of a healthy diet (Alvaro et al. 2017; Ju et al. 2017; Vizzotto et al. 2017). Sweet potatoes are also an option for animal feed (Valadares et al. 2019) and exhibit properties that allow it to be used for biofuel production (Silva et al. 2018, 2019).

The world population has increased in the same way as the demand for nutritious and healthy food. Unfortunately, hunger rates have recently increased again, reaching about 820 million people (FAO 2018). Additionally, climate change, especially related to rising temperatures and water stress, threatens plants and food production. In this sense, sweet potatoes, being a rustic, low-cost plant tolerant of adverse conditions, are an excellent alternative to overcome future challenges (Kwak 2019).

The area planted with sweet potatoes in Brazil comprises approximately 53 thousand hectares, with a productivity of 13.9 tons per hectare (FAO 2018). Despite the fact that Brazil exports sweet potatoes, productivity is low when compared to other countries, such as Japan (22.31 t/ha^{-1}), Chine (22.38 t/ha^{-1}), Australia (36.42 t/ha^{-1}) and Senegal (40.41 t/ha^{-1}). The low Brazilian productivity is due to the use of obsolete genotypes that are conserved by producers (Cavalcante et al. 2009). Thus, breeding programs aiming at the development of new and superior genotypes are required.

Sweet potatoes are hexaploid, vegetatively propagated (Yang et al. 2017), self-incompativel (Katayama et al. 2017) and with considerable genetic divergence (Andrade et al. 2017; Vargas et al. 2018). These aspects allow breeding to

✉ André Ricardo Zeist
andrezeist@unoeste.br

[1] University of Western Paulista, Presidente Prudente, São Paulo 19050-920, Brazil

be easily carried out in crosses and a certain speed in obtaining new genotypes. Genetic divergence should be explored in obtaining new and superior genotypes, using cross-breed parents adapted to local conditions and other superior and introduced parents.

Variations in the amount of compounds present in sweet potatoes, such as beta carotene and anthocyanins, influence the color of the flesh (Vizzotto et al. 2017). Orange flesh roots store a significant amount of beta-carotene, making them a good alternative to combat vitamin A deficiency (Islam et al. 2016). Sweet potatoes with purple flesh roots contain anthocyanins and display anticancer, antimutagenic and antihypertensive properties (Zhang et al. 2018). At the same time, white or cream flesh roots are still the most sought after by the South American market.

The expansion of studies that develop and select better genotypes is essential for producers to obtain access to genotypes that meet their needs and consumer requirements (Low et al. 2017). Aiming at a greater competitiveness of new genotypes, the first stages of the selection require exploitation of the maximum agronomic and physical root parameters, aiming at meeting the needs of farmers and high levels of consumer demands. Thus, productivity, a spindle shape of the root and resistance to aspects that affect damage are important parameters. In the case of resistance, the sweet potato root weevil (*Euscepes postfasciatus*) is the most relevant pest in many countries and difficult to control under field conditions (Tsurui-Sato et al. 2018). Thus, resistance to *E. postfasciatus* must be considered in order to develop noteworthy genotypes.

Considering the aforementioned information, the aim herein was to develop and select experimental sweet potato genotypes in terms of agronomic, physical root characteristics and resistance to *E. postfasciatus*.

Materials and methods

Crossings and seed production

Genotypes were obtained in polycross blocks: BRS Rubissol cultivar—elliptical round-shaped roots, with an intense purple color (ruby red) skin and cream flesh tending towards yellow, with more intense yellow spots; BRS Amélia—long elliptical roots, light pink skin with pink pigments and orange flesh; Beauregard—elongated roots, with a light purple skin and orange flesh; Princesa—elongated roots, with a cream-colored peel and flesh; White Brazlândia—elongated roots, with white skin and light cream flesh; Pinkish Brazlândia—elongated roots, with pink skin and cream flesh; Purple Brazlândia—elongated roots, with pink skin and cream flesh; Coquinho—elongated or rounded roots, with pale yellow skin and white flesh; SCS367 Favorita—elongated roots, light yellow skin and orange flesh; SCS368 Ituporanga—rounded roots, white skin and cream flesh; SCS369 Águas Negras—elongated roots with pink skin and cream flesh; SCS370 Luiza—elliptical roots, with a deep purple hue and a deep purple flesh; SCS371 Katiy—long elliptical roots, purple colored skin and white flesh; SC372 Marina—round-elliptical roots, purple skin and yellow flesh; IAPAR 69—fusiform-shaped roots, a pinkish skin and orange flesh; UZBD-08—round-elliptical roots, white skin and white flesh; UZBD-01—elliptical roots, with an intense purple skin and purple flesh; UZBD-02—elongated roots, intense purple skin and flesh; Arapey—ovoid-shaped roots, with a purple colored skin and yellowish flesh; UZBD-06—elongated roots with a purple skin and white flesh and; UZBD-07—elongated roots, with purple colored skin and cream flesh. The policrossing blocks were composed of two lines with 12 plants from each parent. Flowering was stimulated by suspending irrigation for 30 days.

All related genotypes flourished and pollination was carried out at random by insects, knowing only the female parent. However, only genotypes UZBD-01, UZBD-02, UZBD-06, SCS371 Katiy, SCS367 Favorita, SCS368 Ituporanga and SC372 Marina produced seeds, which were collected when their protective capsules were dry.

Chemical scarification and seedling production

For the scarification process, the seeds were dipped in sulfuric acid 98% for 50 min, washed in distilled water and sown in expanded 72-cell polystyrene trays containing substrate based on bio-stabilized pine bark and maintained in a greenhouse. The seedlings were cloned when reaching 5–6 true leaves. In this process, the main sprout was planted in a 10 dm^3 low density polyethylene pots, containing commercial substrate based on bio-stabilized pine bark and adequately identified. This process is required because the sweet potato propagated by seeds produces a single non-commercial root. On the other hand, when multiplied by vegetative propagation, adequate root development is observed. Then, the main branches of each genotype were used to conduct the field experiments.

Design and management of the experimental units

An experimental design comprising augmented blocks with interleaved controls was adopted. Seven families of half sibling clones were evaluated, totaling 386 experimental genotypes, 58 descendants of the female parent UZBD-01 (U1), 48 of UZBD-02 (U2), 73 of UZBD-06 (C), 138 of SCS371 Katy (K), 61 of SCS367 Favorita (F), 02 of SCS368 Ituporanga (I) and 06 of SCS372 Marina (M). 'SCS370 Luiza', 'Beauregard' and 'UZBD-06' were used as interim controls with five augmented blocks. Ten plants were adopted per repetition. Spacing comprised 33 cm between plants and 1.00 m between rows. Planting and cover fertilization were carried out according to chemical soil analyses (Echer et al. 2009). Plants were irrigated according to water requirements using micro-drippers. Weeding was carried out weekly by hand weeding. Cultivation was carried out in a naturally *E. postfasciatus* infested area containing 2.12 ± 0.14 adults per m^2 at 65 days after planting the branches.

Explored parameters

The harvest was carried out at 140 days after sowing. The tuberous roots were grouped according to the color of the root flesh, as purple, orange and white or cream. They were then evaluated regarding the number of commercial roots per plant and production of commercial roots, as g $plant^{-1}$. The appearance of the tuberous roots was determined by means of a scale, where 1—non-standard, with a very irregular shape, the presence of large veins and deep cracks, 2—very uneven, with the presence of large veins and cracks, 3—non-uniform, with large veins and cracks, 4- slightly non-uniform with the presence of veins, and 5—regular fusiform shape, without veins or cracks. Resistance to *E. postfasciatus* was also determined by a scale, where 5—roots free from damage, 4—roots with low damage, 3—few damaged commercial roots, 2—most damaged commercial roots and, 1—unacceptable commercial roots for human and animal consumption. Additionally, their root length and diameter, in cm, were also determined using a graduated ruler and caliper, respectively.

Statistical analyses

An analysis of variance was performed, obtaining the matrices of correlation, variance and genotypic, phenotypic and residual covariance was obtained. The control treatments allowed for error estimations (Barth et al. 2019, 2020). The residual variance and covariance matrix was used to perform Dunett's comparison test ($p \leq 0.05$). The experimental purple flesh genotypes were compared with 'SCS370 Luiza', the orange flesh genotypes, with 'Beauregard' and the white or cream flesh genotypes, with 'UZBD-06'. All statistical analyses were performed using the statistical program genes (Cruz 2013).

Results

Genotype flesh color

Of the 386 experimental sweet potato genotypes, 125 were classified as purple colored flesh, 74 as orange flesh, 73 as white flesh and 52 as cream flesh. Another 62 genotypes only developed secondary roots and did not produce tuberous roots (Fig. 1).

Purple flesh genotype selection

The parameters explored in the experimental purple flesh sweet potato genotypes were significant ($p < 0.05$) when compared to the commercial control 'SCS 370 Luiza'. The experimental genotypes obtained for the characteristics of number of commercial roots, production of commercial roots, root appearance and resistance to *E. postfasciatus* averaged 1.46, 0.72 kg, 2.79 and 2.92, respectively. Concerning the same parameters, 24.59, 24.59, 41.82 and 17.21% of the experimental genotypes presented a greater effect than the control. The standard deviation (SD) and coefficient of variation (CV) were higher for the experimental genotypes compared to the control indicating, genetic variability among the 125 purple flesh genotypes, alongside value ranges (Table 1).

Of the 125 experimental purple flesh genotypes, a total of 28, 32, 28 and 31 were superior to the control commercial cultivar SCS 370 Luiza for number of commercial roots, production of commercial roots, root appearance and resistance to *E. postfasciatus*, respectively. The genotypes UZBD-K-78, UZBD-K-58, UZBD-K-56 and UZBD-U1-45 displayed a number of roots and production of commercial roots over twice as high as 'SCS 370 Luiza' (Fig. 2).

Concerning root appearance and resistance to *E. postfasciatus*, the most noteworthy genotypes in relation to 'SCS 370 Luiza' were UZBD-U2-09 and UZBD-U2-12; and UZBD-K-04, UZBD-K-14 and UZBD-K-72, respectively. In addition to these same parameters, the experimental genotypes UZBD-U2-09, UZBD-C-46, UZBD-K-09, UZBD-K-30, UZBD-K-54, UZBD-K-56 and UZBD-U1-19 were superior than 'SCS 370 Luiza' (Fig. 2).

Of the 125 experimental purple flesh genotypes, eleven were superior to 'SCS 370 Luiza' for at least three of the four explored parameters. The genotypes UZBD-K-58,

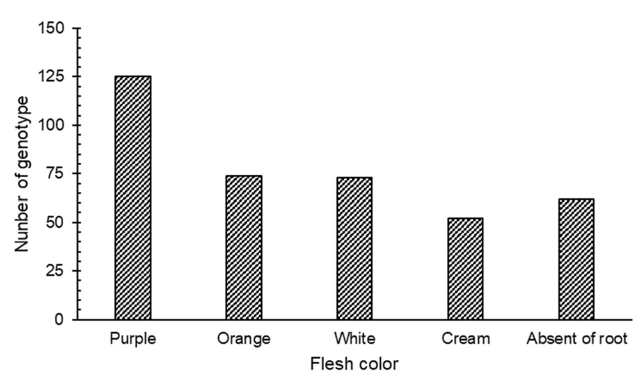


Fig. 1 Flesh color of the experimental sweet potato genotype roots

Table 1 Summary of the analysis of variance and general statistical aspects of the experimental genotypes (GE) of purple flesh sweet potatoes and the control commercial cultivar SCS 370 Luiza for number of commercial roots (NCR, plant^{-1}), production of commercial roots (PCR, g planta^{-1}), root appearance (AP) and resistance to *Euscepes postfasciatus* (R*Ep*)

Variation source	*DF*	Average square			
		NCR	PCR	AP	R*Ep*
Blocks	4	11.95	2.49	18.91	22.64
Treat (adjust)	124	2.05**	0.70**	0.69**	0.69**
Residue	8	0.31	0.03	0.06	0.10
General aspects					
General average		1.49	0.71	2.73	2.95
Control average		2.00	0.66	3.50	3.33
GE average		1.46	0.72	2.79	2.92
Weighted average—μF(Federer)		1.46	0.71	2.66	2.89
General CV (%)		37.16	24.9	9.45	10.71
Control CV (%)		70.88	80.96	20.38	26.35
Experimental type CV (%)		38.06	24.82	9.60	10.81
Control SD		0.35	0.11	0.16	0.21
SD ± of the GE from a same block		0.78	0.25	0.37	0.45
SD ± of the GE from different blocks		0.90	0.29	0.42	0.52
SD ± of the GE and control		0.70	0.23	0.33	0.41
Amplitude		0.00–8.00	0.00–4.48	1.00–4.00	1.00–5.00
GE with effects > than control (%)		24.59	41.82	17.21	25.41

DF degrees of freedom, *CV* coefficient of variation, *SD* standard deviation

**Significant at 1% probability by the F test

UZBD-U1-29, UZBD-K-25, UZBD-U1-44 and UZBD-F-21 were superior only for number and production of commercial roots and the UZBD-K-12 genotypes, UZBD-K-14, UZBD-K-54 and UZBD-K-64 only for root appearance and resistance to *E. postfasciatus*. The genotypes UZBD-K-09, UZBD-K-56 and UZBD-K-78 were superior to 'SCS 370 Luiza' for all explored parameters (Fig. 3).

Orange flesh genotype selection

The parameters explored for experimental orange flesh sweet potato genotypes were significant ($p < 0.05$) when compared to the commercial control 'Beauregard.' Regarding commercial root production, the average of the experimental genotypes was higher than that of the commercial control. Of the 74 experimental orange flesh genotypes, 39.44, 49.29, 7.04 and 64.78% displayed superior effects to 'Beauregard' for number of commercial roots, production of commercial roots, root appearance and resistance to *E. postfasciatus*, respectively. Regarding these same parameters, amplitudes of 0.00–7.00, 0.00–3.48, 0–4.00 and 1.00–4.00 were observed, respectively, although, a standard deviation and coefficient of variation similar to that of the commercial cultivar Beauregard (Table 2) were noted.

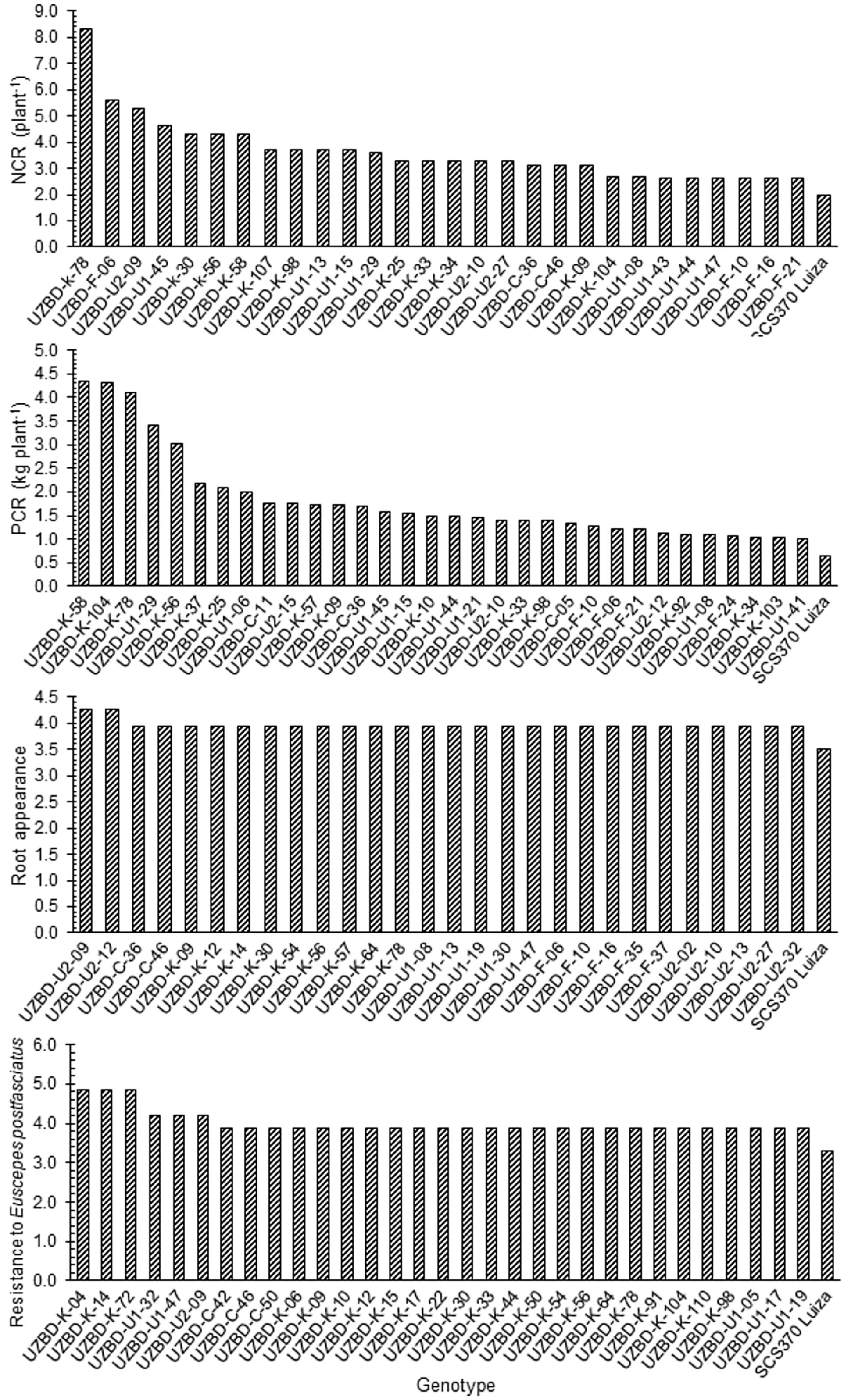
Of the 74 experimental genotypes, 22, 30, 03 and 21 were superior to the commercial 'Beauregard' control for number of commercial roots, production of commercial roots, root appearance and resistance to *E. postfasciatus*, respectively. The experimental genotypes UZBD-F-34, UZBD-C-30, UZBD-U1-25, UZBD-U1-18, UZBD-K-87 and UZBD-K-85 were at least two-fold superior as the commercial control 'Beauregard' for the number and production of roots. Concerning root appearance, only the genotypes UZBD-F-15, UZBD-F-34 and UZBD-U2-05 were superior to 'Beauregard.' Regarding resistance to *E. postfasciatus*, 21 experimental genotypes were superior to 'Beauregard,' with UZBD-C-14, UZBD-C-21, UZBD-C-38 and UZBD-K-32 as the most noteworthy (Fig. 4).

Only UZBD-F-15 and UZBD-F-34 were superior to the commercial cultivar Beauregard control for all parameters. The genotypes UZBD-K-65, UZBD-K-87, UZBD-K-85, UZBD-C-38 and UZBD-K-32 were superior for at least three of the four explored parameters. Eleven experimental genotypes were superior to 'Beauregard' for number and production of commercial roots, and no genotype was superior at the same time for root appearance and resistance to *E. postfasciatus* (Fig. 5).

White and cream flesh genotype selection

The experimental white and cream flesh genotypes presented averages of 0.92, 0.39, 2.29 and 2.81, respectively, for number of commercial roots, production of commercial roots, root appearance and resistance to *E. postfasciatus*. The coefficient of variation (CV) and standard deviation (SD) when compared to the control 'UZBD-06' were much higher and, combining with the amplitudes of 0.00–5.00, 0.00–2.72, 1.00–5.00, 1.00–5.00, demonstrate high genetic

Fig. 2 Experimental genotypes of purple flesh sweet potatoes with superior performance compared to the control commercial cultivar SCS 370 Luiza (Dunnett's test, $p < 0.05$) for number of commercial roots (NCR), production of commercial roots (PCR), root appearance and resistance to *Euscepes postfasciatus*



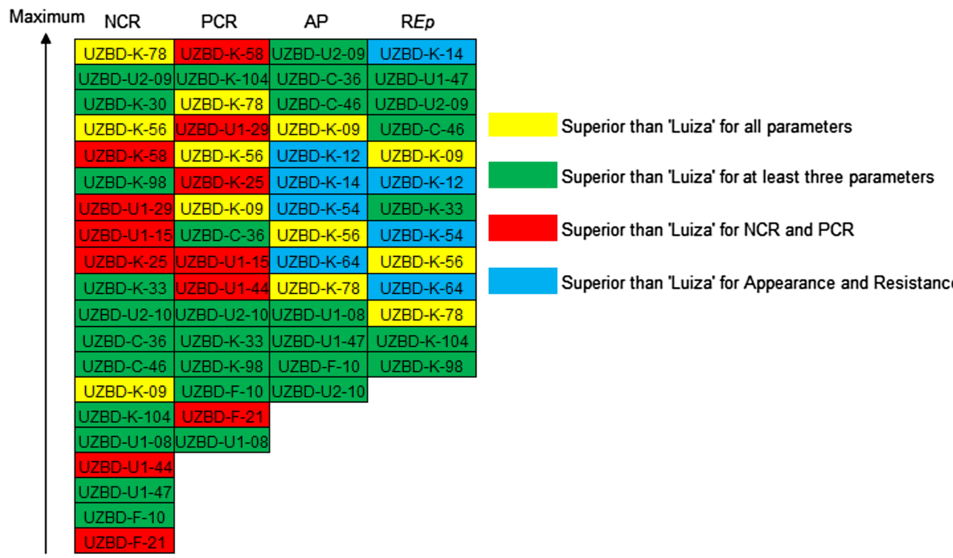


Fig. 3 Scheme illustrating the experimental genotypes of purple flesh sweet potatoes with superior performance compared to the control commercial cultivar SCS 370 Luiza (Dunnett's test, $p<0.05$) for number of commercial roots (NCR, plant^{-1}), production of commercial roots (PCR, g plant^{-1}), root appearance (AP) and resistance to *Euscepes postfasciatus* (R*Ep*)

Table 2 Summary of the analysis of variance and general statistical aspects of the experimental genotypes (GE) of orange flesh sweet potato and control commercial cultivar Beauregard for number of commercial roots (NCR, plant^{-1}), root production (PCR, g plant^{-1}), root appearance (AP) and resistance to *Euscepes postfasciatus* (R*Ep*)

Source of variation		Average square			
	DF	NCR	PCR	AP	R*Ep*
Blocks	4	0.40	0.01	1.33	1.03
Treat (adjust)	73	2.06**	0.58**	1.05**	0.59*
Residue	8	0.01	0.01	0.12	0.13
General aspects					
General average		1.45	0.66	2.72	2.73
Control average		1.52	0.50	4.00	2.80
GE average		1.42	0.69	2.50	2.79
Weighted average—μF(Federer)		1.42	0.68	2.56	2.77
General CV (%)		8.27	7.75	11.62	13.36
Control CV (%)		7.46	9.93	8.47	14.80
Experimental type CV (%)		8.46	7.40	12.61	13.09
Control SD		0.76	0.03	0.20	0.23
SD ± of the GE from a same block		0.17	0.07	0.44	0.52
SD ± of the GE from different blocks		0.19	0.08	0.52	0.60
SD ± of the GE and control		0.19	0.07	0.40	0.46
Amplitude		0.00–7.00	0.00–3.48	0–4.00	1.00–4.00
GE with effects > than the control (%)		39.44	49.29	7.04	64.78

DF degrees of freedom, *CV* coefficient of variation, *SD* standard deviation

**Significant at 1% probability by the *F* test

variability among experimental white or cream flesh genotypes (Table 3).

For number of commercial roots, production of commercial roots, root appearance and resistance to *E. postfasciatus*, only 8.00, 7.20, 2.40 and 2.04% of the experimental genotypes were superior to the 'UZBD-06' control, respectively. For the number of commercial roots, the experimental genotype UZBD-K-53 resulted in twice as many roots as the control 'UZBD-06'. This same was noted for the UZBD-U1-31, UZBD-K-53 and UZBD-K-39 genotypes regarding the production of commercial roots. Concerning root appearance and resistance to *E. postfasciatus*, only the genotypes "UZBD-F-26, UZBD-K-70 and UZBD-K-19" and "UZBD-K-04, UZBD-K-28 and UZBD-C-04" were superior than the control 'UZBD-06' (Fig. 6).

Of the 124 experimental genotypes, UZBD-K-53 and UZBD-K-39 were superior to the control 'UZBD 06' for number and production of commercial roots and the

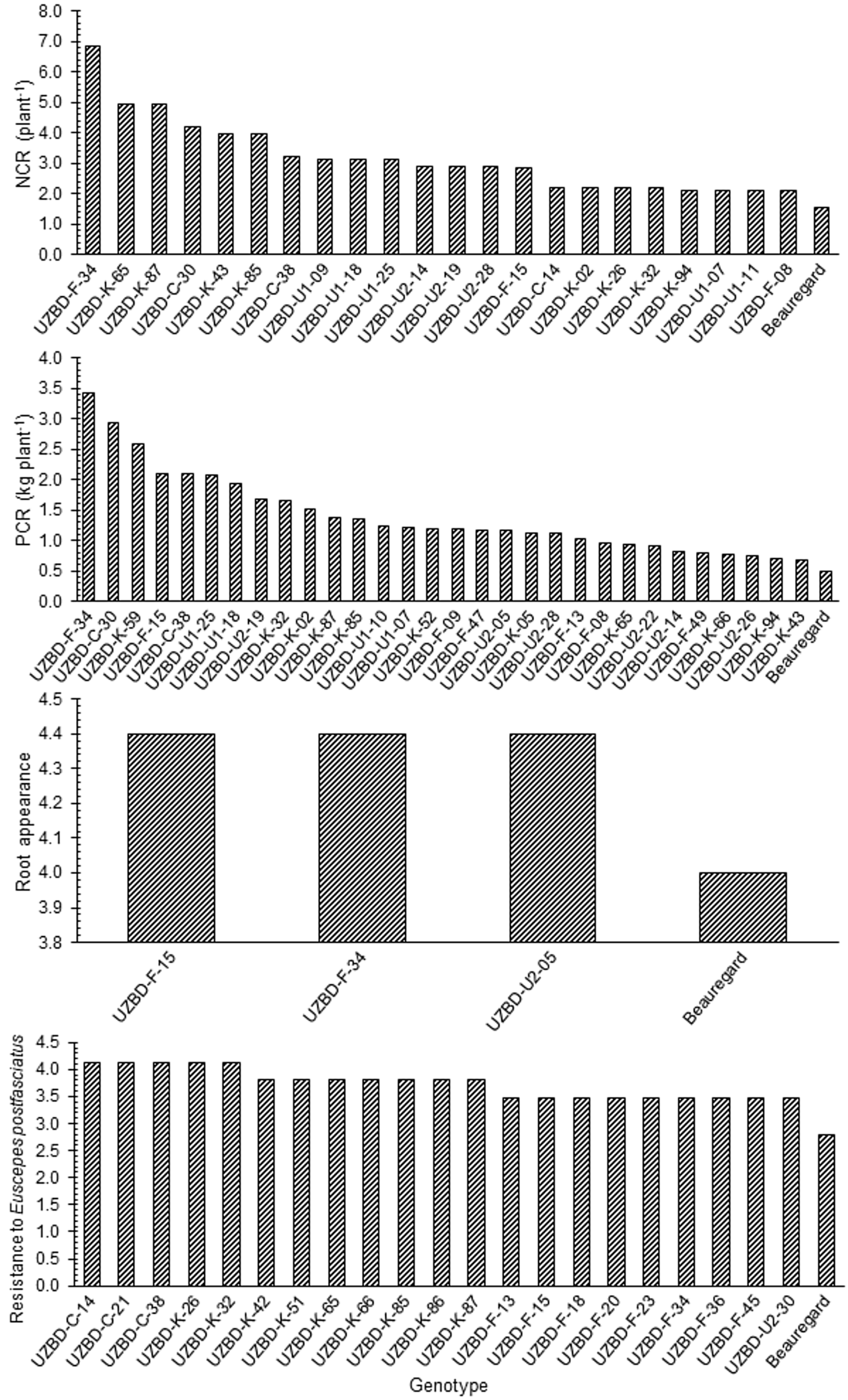


Fig. 4 Experimental genotypes of orange flesh sweet potatoes with superior performance compared to the control commercial cultivar Beauregard (Dunnett's test, $p < 0.05$) for number of commercial roots (NCR), production of commercial roots (PCR), root appearance and resistance to *Euscepes postfasciatus*

genotype UZBD-C-14 was superior for root appearance and resistance to *E. postfasciatus*. UZBD-K-70 was superior to the control concerning three of the four explored parameters (Fig. 7).

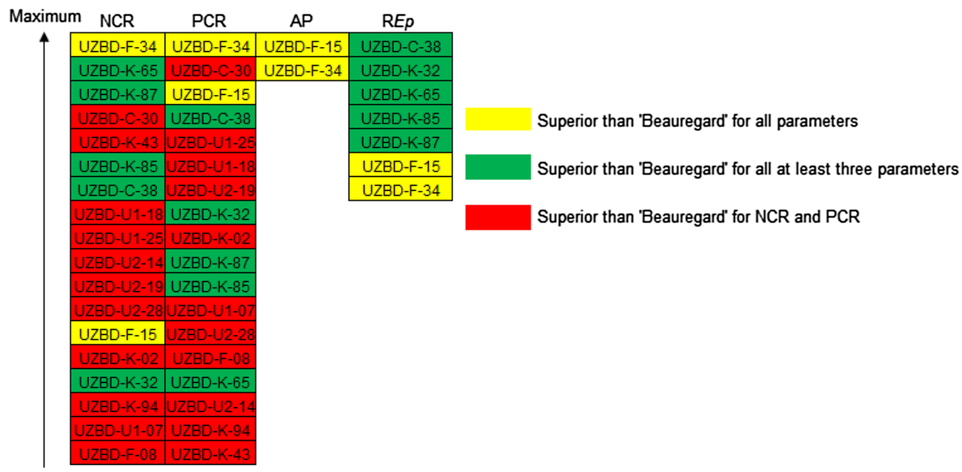


Fig. 5 Scheme illustrating the experimental genotypes of orange flesh sweet potatoes with superior performance compared to the control commercial cultivar Beauregard (Dunnett's test, $p < 0.05$) for number of commercial roots (NCR, plant^{-1}), production of commercial roots (PCR, g plant^{-1}), root appearance (AP) and resistance to *Euscepes postfasciatus* (R*Ep*)

Table 3 Summary of the analysis of variance and general statistical aspects of the experimental genotypes (GE) of white and cream flesh sweet potato and control 'UZBD-06' for number of commercial roots (NCR, plant^{-1}), root production (PCR, g plant^{-1}), root appearance (AP) and resistance to *Euscepes postfasciatus* (R*Ep*)

Sources of variation		Average square			
	DF	NCF	PCR	AP	R*Ep*
Blocks	4	3.01	0.25	0.42	1.46
Treat (adjust)	124	1.33*	0.29**	0.96**	0.85*
Residue	8	1.06	0.02	0.27	0.47
General aspects					
General average		1.03	0.43	2.45	2.89
Control average		2.16	1.06	3.80	4.00
GE average		0.92	0.39	2.29	2.81
Weighted average—μF(Federer)		0.96	0.44	2.18	2.73
General CV (%)		99.54	34.77	21.05	23.57
Control CV (%)		53.57	20.48	14.08	19.33
Experimental type CV (%)		112.34	38.32	22.53	24.27
Control SD		0.65	0.09	0.33	0.43
SD ± of the GE from a same block		1.56	0.21	0.73	0.97
SD ± of the GE from different blocks		1.68	0.24	0.84	1.11
SD ± of the GE and control		1.30	0.19	0.65	0.86
Amplitude		0.00–5.00	0.00–2.72	1.00–5.00	1.00–5.00
GE with effects > than the control (%)		9.73	11.50	6.20	2.65

DF degrees of freedom, *CV* coefficient of variation, *SD* standard deviation

**Significant at 1% probability by the *F* test

Superior genotype characterization

The experimental genotypes selected from purple and orange flesh sweet potatoes displayed longer root length and diameter than their control cultivars SCS370 Luiza and Beauregard, respectively. In contrast, the white flesh genotype UZBD-K-70 exhibited lower root length and diameter than the control 'UZBD-06' (Table 4).

The experimental genotypes UZBD-K-09, UZBD-K-56 and UZBD-K-78, as well as the SCS370 Luiza genotype, displayed dark purple coloring of the skin and flesh. The experimental genotype UZBD-K-70, similarly to the control 'UZBD-06,' presented a purplish red color of the skin and white flesh. The experimental orange flesh genotypes did not show the same coloration as the roots of the commercial cultivar Beauregard, with UZBD-F-15 presenting a white-colored skin and orange flesh and UZBD-F-34, a dark orange skin and light orange flesh (Table 4).

Discussion

In the present study, only sweet potato genotypes superior to the controls were intended for selection. A considerable number of genotypes with commercial root productivity superior to the controls were identified. On the other hand,

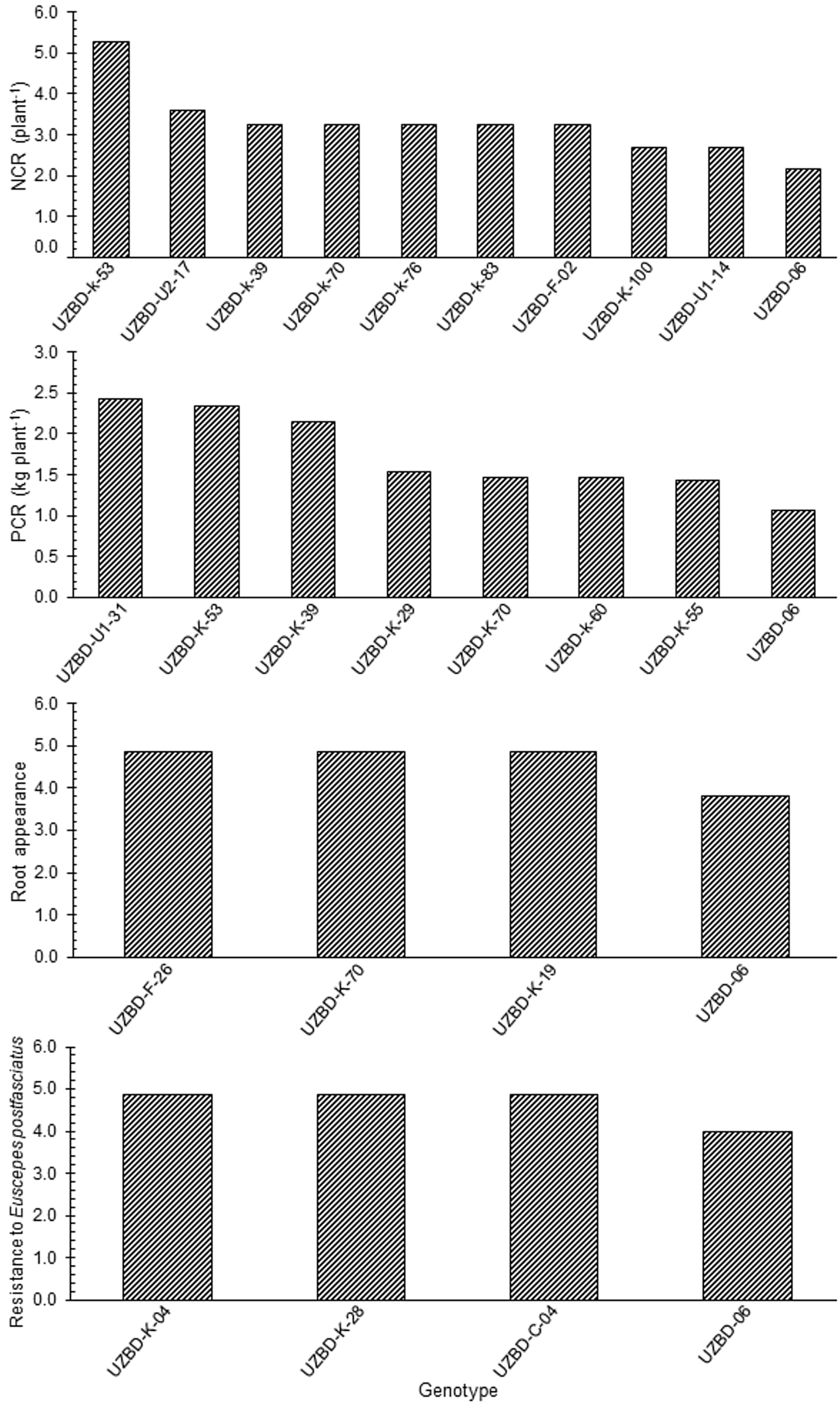


Fig. 6 Experimental genotypes of cream flesh sweet potatoes with superior performance compared to the control 'UZBD-06' (Dunnett's test, $p < 0.05$) for number of commercial roots (NCR), production of commercial roots (PCR), root appearance and resistance to *Euscepes postfasciatus*

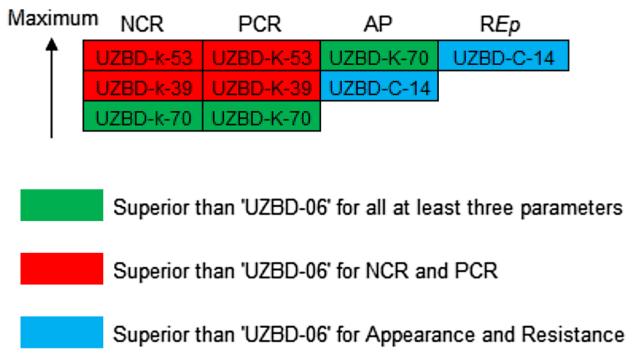


Fig. 7 Scheme illustrating the experimental genotypes of white or cream flesh sweet potatoes with superior performance compared to the control 'UZBD-06' (Dunnett's test, $p < 0.05$) for number of commercial roots (NCR, plant^{-1}), production of commercial roots (PCR, g plant^{-1}), root appearance (AP) and resistance to *Euscepes postfasciatus* (R*Ep*)

Table 4 Length, diameter and skin and flesh color of experimental sweet potato genotypes selected in relation to their controls 'SCS370 Luiza,' 'Beauregard' and 'UZBD-06'

Genotype	Length (cm)	Diameter (cm)	Skin color	Flesh color
SCS370 Luiza	12.35b	5.22b	Dark purple	Dark purple
UZBD-K-09	24.50a	6.50b	Dark purple	Dark purple
UZBD-K-56	27.04a	9.34a	Dark purple	Dark purple
UZBD-K-78	15.56b	6.26b	Dark purple	Dark purple
Beauregard	14.64c	5.97c	Light purple	Orange
UZBD-F-15	19.35a	10.61a	White	Orange
UZBD-F-34	17.56b	7.53b	Orange brown	Light orange
UZBD-06	29.05a	13.42a	Purplish red	White
UZBD-K-70	21.24b	9.80b	Purplish red	White

Means followed by same letters in the columns are not significantly different at $p < 0.05$

new superior sweet potato genotypes were limited concerning root appearance and resistance to *E. postfasciatus*. However, the high phenotypic diversity and heritability of sweet potatoes generally allow for gains through breeding (Dewi et al. 2019). This was evident regarding the purple and orange fleshes root genotypes, selected as superior to the controls for all explored parameters. Additionally, genotypes superior to the control for the white or cream flesh genotypes were also identified for at least 75% of the explored parameters.

Root shape, appearance and strength are relevant parameters in sweet potato breeding programs (Katayama et al. 2017). Commercial cultivars displayed resistance to *E. postfasciatus* below the average of the experimental genotypes obtained herein (Amaro et al. 2017). Using pest resistance parameters to identify superior genotypes allows advances towards the sustainability of sweet potatoes, considering that pests such as *E. postfasciatus* considerably limit the production and quality of commercial roots (Okada et al. 2014). The same aspect applies to the pattern related to root appearance, in order to better meet commercialization requirements (Katayama et al. 2017).

In general, the most widespread and cultivated cultivars by farmers in South America and most countries in Africa are white or cream flesh varieties (Andrade et al. 2017; Low et al. 2017). This is mainly due to the scarcity of genotypes with purple and orange flesh roots. In the present study, due to the good performance of the control UZBD 06, a smaller number of white or cream flesh genotypes was selected.

In Brazil, due to the limitation of sweet potato cultivars with purple and orange fleshes, generally regional, obsolete and without defined origin varieties are used by farmers. Excellent productivity, good appearance and resistance were observed among the experimental purple and orange colored genotypes (Figs. 2, 3, 4, 5), and some genotypes effectively surpassed the commercial control in all parameters. Thus, they may be made available to farmers in the near future in order to better meet their needs and consumer demands.

Due to the fact that sweet potatoes are a hexaploid species (Pipan et al. 2017), a high number of genotypes with high variation in terms of the explored characteristics were obtained herein. The differences in flesh color occur due to the presence of root composition compounds (Alam et al. 2016). White or cream root fleshes generally contain low amounts of compounds such as anthocyanins and carotenoids, or none at all when compared to colored root flesh (Islam et al. 2016; Tanaka et al. 2017).

Purple root flesh are composed of different anthocyanins, mainly cyanidins and peonidines (Li et al. 2019). Generally, the more intense the purple color of the flesh, the higher the anthocyanin content (He et al. 2015). In the present study, three genotypes surpassing all parameters of the commercial control (Fig. 3) were selected, all displaying a dark purple flesh color (Table 4).

Genotypes displaying orange flesh contain carotenoids, natural pigments that confer this color to food items (Alam et al. 2016). β-carotene, present at high concentrations in genotypes with this flesh color is the precursor of the vitamin A (Drapal and Fraser 2019). Despite the nutritional importance of orange flesh sweet potatoes, certain difficulty arise, due to the low yields of their cultivars, especially in times of drought (Andrade et al. 2017). In this study, two noteworthy genotypes were selected, 'UZBD-F-15', with an orange flesh, and 'UZBD-F-34', with a light orange flesh, as they surpassed the control concerning all explored parameters (Fig. 5), being able to supply limitations that prevent the further diffusion of orange flesh sweet potatoes.

E. postfasciatus negatively affects the roots, causing skin deterioration and decreased quality, and the chemical controls mainly adopted for its management are not always efficient (Okada et al. 2014). The selection of resistant genotypes decreases the insect population, maximizes productivity and contributes to a less environmentally harmful agriculture (Nóbrega et al. 2019; Zanin et al. 2018). In this sense, it is important to develop productive genotypes with high root quality and also displaying resistance to *E. postfasciatus*.

Sweet potato crosses were followed by field-level selections for agronomic, physical root characteristics and resistance to *E. postfasciatus* proved promising in enabling new sweet potato genotypes that may contribute to socioeconomic development and better meet consumer demands. A total of 386 sweet potato genotypes were developed UZBD-K-09, UZBD-K-56 and UZBD-K-78, exhibiting purple root flesh, UZBD-F-15 and UZBD-F-34, displaying orange flesh, and UZBD-K-70, with a white flesh, were selected. These genotypes performed better than the controls for all parameters explored.

Acknowledgements The authors thank the Foundation for Research Support of the State of São Paulo (FAPESP) for their support through a scholarship granted to the first author (Process 2019/16730-4).

Author contributions ARZ conceived the research idea; MHSL, NR, ADS, JG and JSP helped to collect the data; JHV contributed to supervision; MHSL, ARZ and ACP analyzed the data and wrote the paper. All authors have read and agreed to the published version of the manuscript.

Compliance with ethical standards

Conflict of interest The authors declare that they have no conflict of interest.

References

Alam MK, Rana ZH, Islam SN (2016) Comparison of the proximate composition, total carotenoids and total polyphenol content of nine orange-fleshed sweet potato varieties grown in Bangladesh. Foods 5:01–10. https://doi.org/10.3390/foods5030064

Alvaro A, Andrade MI, Makunde GS, Dango F, Idowu O, Grüneberg W (2017) Yield, nutritional quality and stability of orange-fleshed sweet potato cultivars successively later harvesting periods in Mozambique. Open Agric 2:464–468. https://doi.org/10.1515/opag-2017-0050

Amaro GB, Fernandes FR, Silva GO, Mello AF, Castro LA (2017) Desempenho de cultivares de batatadocenaregião do Alto Paranaíba-MG. Hortic Bras 35:286–291. https://doi.org/10.1590/s0102-053620170221

Andrade MI, Ricardo J, Naico A, Alvaro A, Makunde GS, Low J, Ortiz R, Grüneberg WJ (2017) Release of orange-fleshed sweetpotato (*Ipomoea batatas* Lam.) cultivars in Mozambique through an accelerated breeding scheme. J AgricSci 155:919–929. https://doi.org/10.1017/S002185961600099X

Andrade EKV, Andrade junior VC, Laia ML, Fernandes JSC, Oliveira AJM, Azevedo AM (2017) Genetic dissimilarity among sweet potato genotypes using morphological and molecular descriptors. ActaSciAgron 39:447–455. https://doi.org/10.4025/actasciagron.v39i4.32847

Barth E, de Resende JTV, Zeist AR, Mariguele KH, Zeist RA, Gabriel A, Camargo CK, Piran F (2019) Yield and quality of strawberry hybrids under subtropical conditions. Genet Mol Res 18:01–10. https://doi.org/10.4238/gmr18156

Barth E, Resende JTV, Moreira AFP, Mariguele KH, Zeist AR, Silva MB, Stulzer GCG, Mafra JGM, Gonçalves LSA, Roberto SR, Youssef K (2020) Selection of experimental hybrids of strawberry using multivariate analysis. Agronomy 10:01–10. https://doi.org/10.3390/agronomy10040598

Cavalcante M, Ferreira PV, Paixão SL, Costa JG, Pereira RG, Madalena JA (2009) Potenciaisprodutivo e genético de clones de batata-doce. ActaSciAgron 31:421–426. https://doi.org/10.4025/actasciagron.v31i3.835

Cruz CD (2013) Genes: a software package for analysis in experimental statistics and quantitative genetics. ActaSciAgron 35:271–276. https://doi.org/10.4025/actasciagron.v35i3.21251

Dewi R, Utomo SD, Kamal M, Timotiwu PB, Nurdjanah S (2019) Genetic and phenotypic diversity, heritability, and correlation between the quantitative characters on 30 sweet potato germplasms in Lampung, Indonesia. Biodiversitas 20:380–386. https://doi.org/10.13057/biodiv/d200211

Drapal M, Fraser PD (2019) Determination of carotenoids in sweet potato (*Ipomoea batatas* L.) tubers: implications for accurate provitamin A determination in staple sturdy tuber crops. Phytochemistry 167:01–06. https://doi.org/10.1016/j.phytochem.2019.112102

Echer FR, Dominato JC, Creste JE (2009) Absorção de nutrientes e distribuição da massafresca e seca entre órgãos de batata-doce. Hortic Bras 27:176–182. https://doi.org/10.1590/S0102-05362009000200010

FAO (2018) Food Agriculture Organization of the United Nations. FAOSTAT database. http://www.fao.org/faostat/en/#home. Accessed 7 Dec 2020

Gemenet DC, Pereira GS, Boeck BD, Wood JC, Mollinari M, Olukolu BA, Diaz F, Mosquera V, Ssali RT, David M, Kitavi MN, Burgos G, Felde TZ, Ghislain M, Carey E, Swanckaert J, Coin LJM, Fei Z, Hamilton JP, Yada B, Yencho GC, Zeng ZB, Mwanga ROM, Khan A, Gruneberg WJ, Buell CR (2020) Quantitative trait loci and differential gene expression analyses reveal the genetic basis for negatively associated β-carotene and starch content in hexaploidsweetpotato [*Ipomoea batatas* (L.) Lam.]. TheorAppl Genet 133:23–36. https://doi.org/10.1007/s00122-019-03437-7

He X, Li X, Lv Y, He Q, He X, Li X, Lv Y, He Q (2015) Composition and color stability of anthocyanin-based extract from purple sweet potato. Food SciTechnol 35:468–473. https://doi.org/10.1590/1678-457X.6687

Islam SN, Nusrat T, Begum P, Ahsan M (2016) Carotenoids and β-carotene in orange fleshed sweet potato: a possible solution to vitamin A deficiency. Food Chem 199:628–631. https://doi.org/10.1016/j.foodchem.2015.12.057

Ju D, Mu T, Sun H (2017) Sweet potato and potato residual flours as potential nutritional and healthy food material. J IntegrAgric 16:2632–2645. https://doi.org/10.1016/S2095-3119(16)61601-5

Katayama K, Kobayashi A, Sakai T, Kuranouchi T, Kai Y (2017) Recent progress in sweetpotato breeding and cultivars for diverse applications in Japan. Breed Sci 67:3–14. https://doi.org/10.1270/jsbbs.16129

Kwak SS (2019) Biotechnology of the sweetpotato: ensuring global food and nutrition security in the face of climate change. Plant Cell Rep 38:1361–1363. https://doi.org/10.1007/s00299-019-02468-0

Li A, Xiao R, He S, An X, He Y, Wang C, Yin S, Wang B, Shi X, He J (2019) Research advances of purple sweet potato anthocyanins: extraction, identification, stability, bioactivity, application, and biotransformation. Molecules 24:01–21. https://doi.org/10.3390/molecules24213816

Low J, Ball A, Magezi S, Njoku J, Mwanga R, Andrade M, Tomlins K, Dove R, Mourik T (2017) Sweet potato development and delivery in sub-Saharan Africa. Afr J Food AgricNutr Dev 17:11955–11972. https://doi.org/10.4314/ajfand.v17i2

Nóbrega DS, Peixoto JR, Vilela MS, Nóbrega AKS, Santos EC, Costa AP, Carmona R (2019) Yield and soil insect resistance in sweet potato clones. Biosci J 35:1773–1779. https://doi.org/10.14393/BJ-v35n6a2019-42452

Okada Y, Yasuda K, Sakai T, Ichinose K (2014) Sweet potato resistance to *Euscepes postfasciatus* (Coleoptera: Curculionidae): larval performance adversely effected by adult's preference to tuber for food and oviposition. J Econ Entomol 107:1662–1673. https://doi.org/10.1603/EC13377

Pipan B, Žnidarčič D, Meglič V (2017) Evaluation of genetic diversity of sweet potato [*Ipomoea batatas* (L.) Lam.] on different ploidy levels applying two capillary platforms. J HorticSci Biotech 92:192–198. https://doi.org/10.1080/14620316.2016.1249963

Silva JOV, Almeida MF, Alvim-Ferraz MC, Dias JM (2018) Integrated production of biodiesel and bioethanol from sweet potato. Renew Energy SI Waste Biomass Biofuel 124:114–120. https://doi.org/10.1016/j.renene.2017.07.052

Silva LFL, Gonçalves WM, Maluf WR, Resende LV, Lasmar A, Carvalho RC, Licursi V, Moretto P (2019) Energy and budget balances for sweet potato-based ethanol production. Pesqagropec bras 54:01–09. https://doi.org/10.1590/s1678-3921.pab2019.v54.26521

Tanaka M, Ishiguro K, Oki T, Okuno S (2017) Functional components in sweetpotato and their genetic improvement. Breed Sci 67:52–61. https://doi.org/10.1270/jsbbs.16125

Tsurui-Sato K, Kumano N, Honma A, Matsuyama T, Haraguchi D, Teruya K, Toyosato T, Tatsuta H (2018) Host plants influence female oviposition and larval performance in west indian sweet potato weevils *Euscepes postfasciatus* (Coleoptera: Curculionidae). ApplEntomolZool 53:107–115. https://doi.org/10.1007/s13355-017-0535-7

Valadares NR, Andrade Junior VCD, Pereira RC, Fialho CMT, Ferreira MAM (2019) Effect of different additives on the silage quality of sweet potato branches. Rev Caatinga 32:506–513. https://doi.org/10.1590/1983-21252019v32n223rc

Vargas PF, Engelking EW, Almeida LCFD, Ferreira EA, Charlo HCDO (2018) Genetic diversity among sweet potato crops cultivated by traditional farmers. Rev Caatinga 31:779–790. https://doi.org/10.1590/1983-21252018v31n329rc

Vizzotto M, Pereira ES, Castro LAS, Raphaelli CO, Krolow AC (2017) Composição mineral em genótipos de batata-doce de polpas coloridas e adequação de consumo para grupos de risco. Braz J Food Technol. 21. https://doi.org/10.1590/1981-6723.17516

Yang J, Moeinzadeh MH, Kuhl H, Helmuth J, Xiao P, Haas S, Liu G, Zheng J, Sun Z, Fan W, Deng G, Wang H, Hu F, Zhao S, Fernie AR, Boerno S, Timmermann B, Zhang P, Vingron M (2017) Haplotype-resolved sweet potato genome traces back its hexaploidization history. Nat Plants 3:696–703. https://doi.org/10.1038/s41477-017-0002-z

Zanin DS, Resende JT, Zeist AR, Oliveira JR, Henschel JM, Lima Filho RB (2018) Selection of processing tomato genotypes resistant to two spotted spider mite. Hortic Bras 36:271–275. https://doi.org/10.1590/s0102-053620180221

Zhang L, Zhao L, Bian X, Guo K, Zhou L, Wei C (2018) Characterization and comparative study of starches from seven purple sweet potatoes. Food Hydrocoll 80:168–176. https://doi.org/10.1016/j.foodhyd.2018.02.006