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Selecting orange-fleshed sweet potato genotypes using selection indices

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ABSTRACT

Vitamin A deficiency is common in developing countries. Sweet potato can be an ally in reversing this situation since it has a low acquisition cost and high market availability. In addition, some genotypes have orange-flesh roots, rich in beta-carotene, which is the precursor of vitamin A. Thus, the objective of this research was to select orange-fleshed sweet potato genotypes using two selection indices (Smith and Hazel and Mulamba & Mock). For this purpose, seven half-sibling families with orange flesh roots (141 experimental genotypes and the commercial cultivar Beauregard) were evaluated, assessing yield-related traits, external appearance of roots, pulp color intensity, and susceptibility to *Euscepes postfasciatus*. The genotypes UZBD-C-14, UZBD-U1-25, UZBD-F-15, UZBD-C-30, UZBD-K-32, UZBD-U1-10, UZBD-L2-14, and UZBD-L5-67 were the most promising, showing greater balance for the evaluated characters. Furthermore, these genotypes are suitable for new studies to confirm their productive performance and root quality and evaluate the biochemical parameters that prove the inheritance of the character regulating biofortification mediated by carotenes.

Keywords: *Ipomea batatas*, *Euscepes postfasciatus*, betacarotene, orange flesh, polyploid, selection index.

RESUMO

Seleção de genótipos de batata-doce de polpa laranja utilizando índices de seleção

A deficiência de vitamina A é frequente nos países em desenvolvimento. Neste contexto, a batata-doce pode ser uma aliada na reversão desse quadro, uma vez que apresenta baixo custo de aquisição e elevada disponibilidade de mercado. Além disso, alguns genótipos apresentam polpa de coloração laranja, rica em betacaroteno, que é o precursor da vitamina A. Assim, objetivou-se com a presente pesquisa selecionar genótipos de batata-doce de polpa laranja por meio do emprego de dois índices de seleção (Smith e Hazel e Mulamba & Mock). Para tanto, foram avaliadas sete famílias de meio irmãos com raízes de polpa laranja (141 genótipos experimentais e a cultivar comercial Beauregard), verificando-se os parâmetros produtivos, aparência externa das raízes, a intensidade de cor da polpa e suscetibilidade à *Euscepes postfasciatus*. Dessa forma, os genótipos UZBD-C-14, UZBD-U1-25, UZBD-F-15, UZBD-C-30, UZBD-K-32, UZBD-U1-10, UZBD-L2-14 e UZBD-L5-67 apresentaram-se mais promissores, demonstrando maior equilíbrio para os caracteres avaliados. Ademais, esses genótipos estão aptos a novos estudos, com propósito de confirmar o desempenho produtivo e de qualidade de raízes, além dos parâmetros bioquímicos que comprovem a herança do caráter que regula a biofortificação mediada pelos carotenos.

Palavras-chave: *Ipomea batatas*, *Euscepes postfasciatus*, betacaroteno, índice de seleção, poliploide, polpa laranja.

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Vitamin A deficiency (VAD) is one of the most serious health problems in developing countries (Begum *et al.*, 2021) and can cause anemia, infections, xerophthalmia, cancer, and death (McTiernan, 2021). The World Health Organization (WHO) recognizes that VAD affects approximately 19 million pregnant women and 190 million children of preschool age worldwide. The majority of them are located in the regions of Africa and Southeast Asia (Shikuku *et al.*, 2019; Begum *et al.*, 2021). In Brazil, VAD has been considered a public health problem in recent decades, especially in the Northeast region and in some places in the Southeast and North regions. VAD is a deficiency disease that appears mainly among groups of low socioeconomic status who eat poorly and live in unsatisfactory sanitary conditions (Machado Júnior *et al.*, 2017).

Vitamin A is an essential component of the human diet. This substance can be ingested in two ways: with provitamin

A, which consists of ingesting the substance's precursor, the so-called carotenes, from vegetables and fruits; and preformed vitamin A, which comes from animal sources, called retinol (Begum *et al.*, 2021). It is estimated that carotenes from vegetables contribute to approximately 68% of vitamin A in people's diets globally and 82% in developed countries (Machado Júnior *et al.*, 2017). Usually, orange or yellow foods have a high content of beta-carotene, an important precursor of vitamin A (Low *et al.*, 2017; Bento, 2021).

In this sense, the orange-fleshed sweet potato (*Ipomoea batatas*) has the potential to combat vitamin A deficiency due to its high content of beta-carotene (Low *et al.*, 2017) and provitamin A (Bento, 2021). In addition, this crop has a high yield and low production costs, which favors a high supply on the market and a low acquisition price, making it suitable for the dietary needs of vitamin A in communities lacking these resources (Bento, 2021). However, in Brazil, sweet potato roots with white or cream pulp and purplish-red skin (from the Canadian standard) are the most cultivated and consumed. Much of this aspect is due to the scarcity and low diffusion of colored pulp sweet potatoes, which are nutritionally more relevant and even the most valued by the export market. Thus, there is a need to develop and select orange-fleshed sweet potato genotypes (Leal *et al.*, 2021), which are generally biofortified (Low *et al.*, 2017; Bento, 2021).

Thus, food fortification is presented as an alternative to reduce vitamin A deficiency (Machado Júnior *et al.*, 2017; Bento, 2021). Currently, plant genetic improvement has contributed to the development and introduction of biofortified products, which have a higher content of nutrients and vitamins, improving the human diet. Genetic improvement of vegetables for nutritional biofortification is a promising strategy for increasing the concentration of carotenoids in agricultural products and preventing vitamin A deficiency (Machado Júnior *et al.*, 2017; Prasad & Shivay, 2020; Bento, 2021).

In recent years, sweet potato genetic improvement has mainly focused on yield. In contrast, studies on nutritional composition have not followed this evolution, requiring research aimed at the biofortification process (Nkhata *et al.*, 2020). Additionally, providing roots of commercial standards that are minimally acceptable to consumers is also crucial, considering traits such as root appearance and shape (Tsurui-Sato *et al.*, 2018). These root-related traits are closely related to susceptibility to soil pests, such as the West Indian sweet potato weevil (*Euscepes postfasciatus*) (Katayama *et al.*, 2017). The weevil is one of the most damaging soil pests for sweet potato and is very difficult to control (Tsurui-Sato *et al.*, 2018; Leal *et al.*, 2021); therefore, genetic resistance becomes extremely important (Leal *et al.*, 2021).

Selection based on a single trait is inappropriate because, despite leading to a superior final product concerning this trait, it can lead to unsatisfactory performance for other characters (Barth *et al.*, 2020). One way to increase selection success is to use simultaneous selection for various characteristics using selection indices. The use of selection indices for multiple characters makes it possible to obtain more productive and adapted genotypes by bringing together several favorable characters in a single individual or population (Vieira *et al.*, 2017). In general, a selection index should allow the ranking of genotypes when considering several characters simultaneously (Barth *et al.*, 2020). Due to the great genetic variability of sweet potato, selection for numerous purposes is possible, and selection for just one trait can lead to agronomic unsuitability for other characteristics (Otoboni *et al.*, 2020; Leal *et al.*, 2021). Thus, using selection indices based on a set of variables that bring together several attributes of economic interest becomes necessary.

Thus, the objective of this work was to select orange-fleshed sweet potato genotypes using two selection indices [Smith and Hazel (parametric) and Mulamba & Mock (non-parametric)]. For this, seven half-sibling families with orange pulp roots (141 experimental genotypes and the commercial cultivar Beauregard) were evaluated regarding yield-related traits, external appearance of the roots, intensity of pulp color, and susceptibility to *Euscepes postfasciatus*.

MATERIAL AND METHODS

Experiment location

The experiment was conducted in the spring/autumn cycle of 2019/2020 in Presidente Prudente (22°07"S, 51°27"W). According to the Köppen classification, the climate is Aw, with an average annual temperature and precipitation of 25°C and 1,400 to 1,500 mm, respectively, characterized by hot and humid summers and mild dry winters. The soil is classified as medium-textured dystrophic Red Argisol (Santos *et al.*, 2018).

Plant material and experimental design

The experiment was conducted in an augmented block design with intercalated controls. Seven families of half-sibling clones with orange pulp roots from a segregating population of 2,000 plants were evaluated. Based on agronomic traits and visual physical characteristics of roots, 141 experimental genotypes were pre-selected. The commercial cultivar Beauregard (long-shaped roots with light purple skin and orange pulp) was used as the intercalated control. The vines used as propagation structures came from a nursery for maintaining adult plants free of viruses and arthropod pests, from which only the apical part was used. Branches with 15 buds were used, keeping eight below and seven above the ground. The useful area of each plot consisted of 1 m², containing three branches of each treatment, spaced 0.33 m between plants and 1.0 m between rows that were 0.4-0.5 m high.

Experimental conduction

For soil preparation, heavy plowing was performed twice, and light harrowing was carried out three times. Cultivation practices, liming, and base and top dressing were carried out as recommended for the crop, according

to soil chemical analysis (Echer *et al.*, 2015). Fertilization was carried out in the planting furrow, applying 20 kg ha^{-1} of N, 80 kg ha^{-1} of P_2O_5, and 60 kg ha^{-1} of K_2O. The topdressing fertilization was divided into two applications of 30 kg ha^{-1} of N and K_2O at 30 and 60 days after planting. Irrigation was performed with a micro dripper installed on each plant and supplied daily for the first 10 days after planting the branches and every four days thereafter. Each irrigation lasted approximately 40 min with a flow rate of 1.5 L/h H_2O per micro dripper. Weed control was manually performed.

Ridging was performed at 45 and 90 days after planting as recommended for the crop in the West Paulista region (Echer *et al.*, 2015). The cultivation was carried out in an area naturally infested with *E. postfasciatus*, containing 2.09 adults per m^2 at 65 days after planting the branches.

Parameters assessed

The harvest was carried out 140 days after planting the branches. Then, tuberous roots were evaluated for the number of total roots (NTR) and commercial roots (NCR) and the production of total roots (PTR) and commercial roots (PCR) in kg $plant^{-1}$. Commercial roots weighed more than 80 g and were uniform in shape, without mechanical damage or damage from pests or cracks (Perrud *et al.*, 2021). The average mass of commercial roots (AMCR) was determined by the relationship between PCR and NCR. The percentage of commercial roots (%CR) was determined considering the PCR in relation to the PTR. The appearance of commercial roots (AR) was determined using a scale of notes: 1= non-standard, with a very irregular shape, presence of large veins and deep cracks; 2= very uneven, with large veins and cracks; 3= non-uniform, with large veins and cracks; 4= slightly uneven with veins; 5= regular fusiform shape, without veins or cracks.

Resistance to *E. postfasciatus* (REp) was determined using a rating scale (Leal *et al.*, 2021): 5= roots free from damage; 4= roots with rare damages; 3= few commercial roots damaged; 2= majority of commercial roots damaged; 1= commercial roots unacceptable for human and animal consumption. Pulp color (PC) was evaluated using a visual rating scale, in which 1= light orange; 2= intermediate orange; and 3= intense/dark orange.

Statistical analysis

Analysis of variance was performed to obtain the matrices of correlation, variance, and genotypic, phenotypic, and residual covariance. The control treatment allowed error estimation (Barth *et al.*, 2020). A classic parametric selection index suggested by Smith (1936) and Hazel (1943) was used, as well as the non-parametric index based on the sum of ranks of Mulamba & Mock (1978). In both selection indices, for the parameters NTR, NCR, PTR, AMCR, AR, REp, PC, and %CR, the weights of 2, 5, 2, 5, 4, 5, 5, 5, and 4 were assigned, respectively. Twenty-one experimental genotypes were selected with each index. Genes software (Cruz, 2013) was used for the statistical analyses.

RESULTS AND DISCUSSION

The experimental genotypes had average values of 5.89 for NTR, 2.28 for NCR, 1.20 kg for PTR, 0.66 kg for PCR, 266.47 g for AMCR, 2.26 for AR, 2.21 for REp, 1.24 for PC, and 55.56% for CR. Of the 141 experimental genotypes developed, genotypes were superior in relation to the Beauregard control in four of the nine parameters, namely, NTR, NCR, PTR, and PCR (Table 1).

Based on the estimated coefficients of variation, it is possible to infer the presence of genetic variability for

Table 1. General statistical aspects of the experimental genotypes (GE) of sweet potato and the control commercial cultivar Beauregard for number of total roots (NTR), number of commercial roots (NCR), production of total roots (PTR), production of commercial roots (PCR), average mass of commercial roots (AMCR), appearance of commercial roots (AR), resistance to *E. postfasciatus* (REp), pulp color (PC), and percentage of commercial roots (%CR). Presidente Prudente, UNOESTE, 2020.

Parameter	NTR	NCR	PTR	PCR	AMRC	AR*	REp^{+}	PC$^{\circ}$	%CR
General average	5.80	2.28	1.17	0.65	270.32	2.35	2.27	1.33	56.83
Control average	4.59	2.23	0.70	0.52	324.70	3.70	3.10	2.50	74.68
GE average	5.89	2.28	1.20	0.66	266.47	2.26	2.21	1.24	55.56
Weighted average - µF(Federer)	5.86	2.26	1.20	0.66	268.41	2.28	2.22	1.26	55.70
General CV(%)	14.82	17.36	14.35	20.71	74.55	32.85	40.46	23.75	12.95
Control CV(%)	18.76	17.72	24.08	26.22	62.06	20.93	29.74	12.64	9.86
Experimental genotype CV(%)	14.61	17.34	13.95	20.41	75.63	34.23	41.53	25.33	13.25
Control SD	0.54	0.24	0.10	0.08	127.46	0.48	0.58	0.20	4.65
SD ± of the GE from the same block	1.21	0.55	0.23	0.19	285.01	1.09	1.30	0.44	10.41
SD ± of the GE from different blocks	1.49	0.68	0.29	0.23	349.07	1.34	1.59	0.54	12.75
SD ± of the GE and control	1.15	0.53	0.22	0.18	270.39	1.03	1.23	0.42	9.87

*AR, in which 1= non-standard, with a very irregular shape, presence of large veins and deep cracks, 2= very uneven, with large veins and cracks, 3= non-uniform, with large veins and cracks, 4= slightly uneven with veins, and 5= regular fusiform shape, without veins or cracks.$^{+}$REp, in which 5= roots free from damage, 4= roots with rare damage, 3= few commercial roots damaged, 2= majority of commercial roots damaged, and 1= commercial roots unacceptable for human and animal consumption. $^{\circ}$PC, in which 1= light orange, 2= intermediate orange, and 3= intense/dark orange.

the experimental genotypes relative to AMCR, AR, REp, and %PC, with values of 75.63, 34.23, 41.53, and 25.33%, respectively (Table 1). Genetic variability is normally expressed in greater proportion in species that have not undergone effective domestication as have sweet potato. In addition, allogamous polyploid species are more likely to express variability through targeted crosses or polycrosses. With greater variability expressed in a population, the chances of obtaining genotypes with transgressive segregation are higher (Katayama *et al.*, 2017; Otoboni *et al.*, 2020). Therefore, the genetic variability among experimental genotypes is extremely relevant, considering that they can contribute to the selection of traits favorable to agronomic performance and root quality (Leal *et al.*, 2021).

Heritability was estimated for NTR, NCR, PTR, PCR, AMCR, AR, REp, PC, and %CR, with values of 97.77, 97.81, 97.65, 96.43, 63.63, 37.19, 51.68, 81.77, and 96.24%, respectively (Table 2). The values indicate that for most traits, the expressed phenotype was mainly due to heritable genetic effects, with little influence from the environment. These results also prove that the environmental effects were not prominent for characters of quantitative polygenic inheritance. However, for traits with greater evaluation subjectivity (AR and REp), the heritability values were moderate, indicating the influence of the environment on their phenotypic expression, allowing us to infer that these characters have lower probabilities of being inherited in the descendants. In contrast, the high heritability values indicate that these characters can be more easily heritable, allowing greater safety for breeders during selection (Sarker, 2020). High heritability results indicate a good possibility of genetic gain with selection.

Higher heritability magnitudes indicate higher genetic gains in the present work (Table 2). Recurrent intrapopulation selection gradually increases the frequency of favorable alleles for quantitative traits through repeated cycles of selection and recombination. The estimates of the phenotypic and genotypic correlation coefficients were positive and presented a high magnitude. Thus, when applying selection to increase one of the traits evaluated, a response correlated to the other traits is obtained, which is a great advantage since the direction of selection is the same for these characters (Barth *et al.*, 2020; Leal *et al.*, 2021). For uncorrelated characters, the selection can be made independently. The phenotypic correlation coefficients surpassed the genotypic correlation coefficients for AR and REp, which shows that genetic factors were less important than environmental factors in expressing these characters, hindering selection.

In the rank index, the selected genotypes had means of 10.46, 5.49, 2.22, 1.75, 399.15, 3.62, 3.71, 1.57, and 88.02% for NTR, NCR, PTR, PCR, AMCR, AR, REp, PC, and %CR, respectively. For these traits, this index obtained 76.65, 139.30, 83.30, 157.86, 31, 21.99, 34.54, 20.03, and 55.83% in the selection gain, respectively. For PC, the rank index provided a selection gain of 20.03% compared to only 0.2% for the classic index (Table 3). PC is directly correlated with the carotenoid content present in the root pulp, which is a precursor of vitamin A (Low *et al.*, 2017; Bento, 2021), an important component in the complex synthesis of retinol (Begum *et al.*, 2021). The Mulamba & Mock index detected selection gains of 20% for pulp color, which allows us to infer the existence of variability in the populations of half-siblings evaluated and that it is possible to promote sweet potato biofortification with vitamin A

Table 2. Mean of all experimental genotypes (Xo) of sweet potato, heritability estimates (h^2), mean of selected individuals (Xs), selection gain (SG), and selection gain percentage (SGP) for number of total roots (NTR), number of commercial roots (NCR), production of total roots (PTR), production of commercial roots (PCR), average mass of commercial roots (AMCR), appearance of commercial roots (AR), resistance to *E. postfasciatus* (REp), pulp color (PC) and percentage of commercial roots (%CR) using indices of selection. Presidente Prudente, UNOESTE, 2020.

Traits	Xo	h^2 (%)	Mulamba & Mock (1978)			Smith (1936) and Hazel (1943)		
			Xs	SG	SGP (%)	Xs	SG	SGP (%)
NTR	5.86	97.77	10.46	4.49	76.65	5.14	-0.70	-11.98
NCR	2.26	97.81	5.49	3.16	139.30	2.90	0.62	27.40
PTR	1.20	97.65	2.22	1.00	83.30	2.31	1.08	90.46
PCR	0.66	96.43	1.75	1.05	157.86	1.71	1.01	152.00
AMCR	268.41	63.63	399.15	83.19	31.00	745.01	303.29	112.99
AR*	2.28	37.19	3.62	0.50	21.99	3.12	0.31	13.83
REp^{+}	2.22	51.68	3.71	0.76	34.54	2.83	0.31	14.11
PC$^{\circ}$	1.26	81.77	1.57	0.25	20.03	1.26	-0.00027	-0.02
%CR	55.70	96.24	88.02	31.09	55.83	84.97	28.16	50.56

*AR, in which 1= non-standard, with a very irregular shape, presence of large veins and deep cracks, 2= very uneven, with large veins and cracks, 3= non-uniform, with large veins and cracks, 4= slightly uneven with veins, and 5= regular fusiform shape, without veins or cracks.$^{+}$REp, in which 5= roots free from damage, 4= roots with rare damage, 3= few commercial roots damaged, 2= majority of commercial roots damaged, and 1= commercial roots unacceptable for human and animal consumption. $^{\circ}$PC, in which 1= light orange, 2= intermediate orange, and 3= intense/dark orange.

through genetic improvement.

In the classical index, the means of the selected experimental genotypes were 5.14, 2.90, 2.31, 1.71, 745.01, 3.12, 2.83, 1.26, and 84.97 for NTR, NCR, PTR, PCR, AMCR, AR, REp, FC, and %CR, respectively. Among these traits, AMCR and PCR stand out, providing more than 100% selection gain according to this index (Table 3).

The highest selection gains were obtained in the selection of ranks for almost all traits, except for PTR and AMCR. The averages of the genotypes selected in the rank index for NTR and PTR were significantly higher, while in the classic index, the averages for AMCR were significantly higher (Table

Table 3. Orange-fleshed sweet potato genotypes selected using the classic selection indices of Smith (1936) and Hazel (1943) – (SH) and ranks of Mulamba & Mock (1978) – (MM) based on the number of total roots (NTR), number of commercial roots (NCR), production of total roots (PTR), production of commercial roots (PCR), average mass of commercial roots (AMCR), appearance of commercial roots (AR), resistance to *E. postfasciatus* (REp), pulp color (PC), and percentage of commercial roots (%CR). Presidente Prudente, UNOESTE, 2020.

Genotype	Rank order		NTR	NCR	PTR	PCR	AMRC	AR*	Rep^{+}	PC^{0}	%CR
	MM	SH									
UZBD-C-14	1^{0}	4^{0}	3.0	3.0	2.0	2.0	658.3	4.0	4.0	2.0	100.0
UZBD-U1-25	2^{0}	6^{0}	3.0	3.0	2.2	2.2	725.0	4.0	3.0	1.0	100.0
UZBD-F-15	3^{0}	5^{0}	11.0	3.0	2.8	2.2	718.3	4.0	3.0	1.0	77.8
UZBD-C-30	7^{0}	2^{0}	12.0	4.0	4.2	2.8	702.5	4.0	2.0	1.0	66.5
UZBD-K-32	8^{0}	11^{0}	3.0	2.0	1.6	1.5	765.0	3.0	4.0	1.0	95.3
UZBD-U1-10	13^{0}	10^{0}	3.0	1.0	3.4	1.3	1340.0	3.0	3.0	1.0	39.6
UZBD-L2-14	16^{0}	7^{0}	6.0	6.0	2.4	2.4	392.5	4.0	3.0	1.0	100.0
UZBD-L5-67	10^{0}	17^{0}	6.0	4.0	1.4	1.4	337.5	4.0	5.0	2.0	99.0
UZBD-L3-17	-	1^{0}	3.0	3.0	3.2	3.2	1073.3	2.0	2.0	1.0	100.0
UZBD-F-34	5^{0}	20^{0}	11.0	7.0	5.6	5.6	496.4	4.0	3.0	2.0	61.7
UZBD-K-59	-	3^{0}	8.0	2.0	4.9	4.9	1295.0	2.0	2.0	1.0	53.1
UZBD-K87	4^{0}	-	10.0	5.0	1.7	1.7	274.0	4.0	4.0	1.0	79.2
UZBD-K-02	12^{0}	14^{0}	7.0	2.0	1.8	1.8	705.0	3.0	3.0	1.0	79.7
UZBD-K-85	6^{0}	-	13.0	4.0	1.9	1.9	337.5	3.0	4.0	1.0	71.6
UZBD-K-66	-	8^{0}	1.0	1.0	0.8	0.8	760.0	4.0	4.0	1.0	100.0
UZBD-L1-30	9^{0}	-	17.0	17.0	3.0	3.0	177.1	4.0	4.0	1.0	100.0
UZBD-F-49	-	9^{0}	2.0	1.0	0.8	0.8	750.0	3.0	3.0	1.0	88.8
UZBD-K-65	11^{0}	-	36.0	5.0	2.9	0.9	187.0	4.0	4.0	1.0	32.6
UZBD-U2-05	-	12^{0}	3.0	2.0	2.3	1.1	555.0	4.0	2.0	1.0	48.8
UZBD-F-47	-	13^{0}	10.0	2.0	1.8	1.1	565.0	3.0	2.0	1.0	63.0
UZBD-U1-07	14^{0}	-	2.0	2.0	1.3	1.3	660.0	2.0	3.0	2.0	100.0
UZBD-F-08	15^{0}	-	2.0	2.0	1.1	1.1	530.0	3.0	3.0	2.0	100.0
UZBD-K-05	-	15^{0}	1.0	1.0	1.0	1.0	1015.0	2.0	2.0	1.0	100.0
UZBD-L2-38	-	16^{0}	1.0	1.0	0.7	0.7	710.0	2.0	2.0	1.0	100.0
UZBD-K-43	17^{0}	-	6.0	4.0	0.8	0.7	168.8	4.0	3.0	1.0	85.4
UZBD-U1-18	18^{0}	-	6.0	3.0	2.2	2.0	676.7	1.0	2.0	1.0	91.0
UZBD-U2-19	-	18^{0}	5.0	3.0	2.7	1.6	545.0	3.0	2.0	1.0	60.4
UZBD-L5-34	19^{0}	-	47.0	21.0	3.2	2.3	109.0	5.0	4.0	1.0	72.4
UZBD-K-52	-	19^{0}	3.0	1.0	1.7	1.2	1190.0	2.0	3.0	1.0	68.4
UZBD-F-09	20^{0}	-	3.0	2.0	1.6	1.2	617.5	3.0	2.0	2.0	76.7
UZBD-K-26	21^{0}	-	4.0	2.0	0.6	0.5	242.5	4.0	4.0	1.0	87.4
UZBD-L4-12	-	21^{0}	4.0	2.0	1.5	1.3	670.0	2.0	1.0	1.0	89.3

AR, in which 1= non-standard, with a very irregular shape, presence of large veins and deep cracks, 2= very uneven, with large veins and cracks, 3= non-uniform, with large veins and cracks, 4= slightly uneven with veins, and 5= regular fusiform shape, without veins or cracks.$^{+}$REp, in which 5= roots free from damage, 4= roots with rare damage, 3= few commercial roots damaged, 2= majority of commercial roots damaged, and 1= commercial roots unacceptable for human and animal consumption. $^{\circ}$PC, in which 1= light orange, 2= intermediate orange, and 3= intense/dark orange.

3). The Mulamba & Mock index has been shown to be satisfactory compared with other indices in terms of selection gain (Berilli *et al.*, 2013).

In yellow passion fruit breeding, studies recommend the selection index of Mulamba & Mock for providing greater selection gains (Gonçalves *et al.*, 2007; Silva *et al.*, 2009). However, when applying a selection index in strawberry breeding, Vieira *et al.* (2017) observed that the Smith and Hazel indices provided greater selection gain than Mulamba & Mock and Genotype Ideotype. Additionally, several authors have evaluated the use of selection indices in different cultures, with the best one varying according to each situation (Barth *et al.*, 2020; Rezende *et al.*, 2014).

Of the 141 experimental sweet potato genotypes tested, 32 were selected using the classical and rank-based indices. Of the 32 genotypes selected, only eight were selected simultaneously by both indices, namely, UZBD-C-14, UZBD-U1-25, UZBD-F-15, UZBD-C-30, UZBD-K-32, UZBD-U1-10, UZBD-L2-14, and UZBD-L5-67. Despite using the same weights for all traits, 24 genotypes were selected by only one selection index. The UZBD-C-14 genotype stands out, which was selected for its best classification in the rank index and ranked second in the classic index. However, from the genotypes selected in both indices, only six have an intermediate orange flesh color, and the others are light orange-fleshed (Table 3).

Regarding sweet potato for table use, in addition to yield, it is important that the genotypes have good appearance, pest resistance, and good food quality (Katayama *et al.*, 2017). Using selection indices, the gain in an isolated trait can be neutral or reduced; however, it will be compensated by the distribution of genetic gains in the set of traits (Gonçalves *et al.*, 2007; Vieira *et al.*, 2017; Barth *et al.*, 2020). Thus, the selection applied in the present study is relevant, where multiple traits were considered to identify superior experimental genotypes.

In developed countries, sweet potato has been valued as a food that promotes good health due to its nutrient content and secondary nutritional compounds (Katayama *et al.*, 2017). Additionally, this aspect should be considered even more relevantly in underdeveloped countries, where basic food is still a challenge. Therefore, selecting experimental sweet potato genotypes with high levels of bioactive compounds simultaneously with agronomic traits is vital to developing cultivars that can better meet human nutritional requirements and growers' needs (Otoboni *et al.*, 2020).

The genotypes UZBD-C-14, UZBD-U1-25, UZBD-F-15, UZBD-C-30, UZBD-K-32, UZBD-U1-10, UZBD-L2-14, and UZBD-L5-67 selected through both selection indices used in this work are promising to move forward in the breeding program of orange-fleshed sweet potato. Furthermore, these genotypes are also suitable for further studies to confirm their yield performance and quality of roots and dissect the biochemical parameters that prove the nutritional characteristics related to biofortification.

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