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PLANT BREEDING

Influence of growing seasons on sweet potato genotype selection for animal feeding

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ABSTRACT. Environmental conditions significantly impact the performance of sweet potato genotypes, necessitating the study of genotype x environment (GE) interactions to select genotypes adaptable to varying cultivation conditions. This study aimed to assess GE interactions in sweet potatoes for animal feed and identify high-performance genotypes suitable for different seasons. We conducted two tests during the Brazilian winter of 2019 and summer of 2020. Employing a partially balanced triple lattice experimental design with 100 treatments (92 sweet potato genotypes and eight controls) and three replications, we measured vine green matter yield (VGMY), percentage vine dry matter (PVDM), vine dry matter yield (VDMY), percentage of root dry matter (PRDM), and roots dry matter yield (RDMY). We ranked genotypes, highlighting the best performers for individual and combined seasons. Significant differences in VGMY, PRDM, and RDMY were observed for GE interaction. VGMY, VDMY, and PRDM favored the summer season, while PVDM and RDMY performed better in the winter season. Genotypes 2018-31-713, 2018-72-1438, 2018-31-666, 2018-12-252, 2018-19-461, 2018-19-389, 2018-38-946, 2018-31-689, and 2018-37-864 proved most suitable for VGMY and VDMY across growing seasons. Genotypes 2018-28-514, 2018-15-268, and 2018-19-443 demonstrated potential in percentage vine dry matter. Genotypes 2018-31-666, 2018-72-1438, and 2018-15-277 are recommended for PRDM in both seasons. Genotypes 2018-19-464, 2018-28-556, 2018-55-1154, 2018-28-543, 2018-53-1038, 2018-72-1432, and 2018-19-443 exhibited greater potential for RDMY, making them ideal for animal feed in both growing seasons.

Keywords: *Ipomoea batatas* L.; genotype x environment interaction; BLUP; genetics; forage; environmental conditions.

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Introduction

Sweet potato (*Ipomoea batatas* L.) is a versatile crop with low production costs, making it suitable for year-round cultivation in regions with tropical and subtropical climates (Vital, Benício, Lins, Viana, & Messias, 2023). Its applications range from animal feed and human consumption to ethanol production (Costa et al., 2022; Donato et al., 2020; Silva et al., 2022). Although primarily used for human consumption, non-standard or unfit-for-consumption tuberous roots are often discarded, presenting an opportunity for animal feed utilization (Donato et al., 2020).

Sweet potato vines, too, hold potential in both human and animal feed but remain underutilized. Often, when not used for replanting, the branches are wasted (Andrade Júnior et al., 2014), despite their nutritional value (Baba, Nasiru, Karkarna, Muhammad, & Rano, 2018), especially for animal diets (Klinger, Silva, Toledo, Falcone, & Goulart, 2018; Galla et al., 2020; Melesse, Chalew, & Nurfeta, 2020; Oladeji, Akinbola, Faniyi, Tirado-Estrada, & Molina, 2022; Zhang et al., 2022).

Vines can be supplied in various forms, including natura (Gonçalves Neto et al., 2011; Silva et al., 2022), silage (Andrade Júnior et al., 2014; Sun et al., 2023), or hay (Andrade Júnior et al., 2020; Donato et al., 2020). Supplementing animal feed with sweet potato vines enhances growth, intestinal health, and immunity in animals (Zhang et al., 2022). Therefore, sweet potatoes can serve as an alternative animal feed source during periods of forage scarcity (Donato et al., 2020). However, the lack of specific cultivars designed for this purpose limits its widespread adoption.

Breeding programs for sweet potatoes intended for animal feed prioritize traits such as high fresh and dry matter yield of vines, favorable bromatological contents, pathogen resistance, and more (Andrade Júnior et al., 2014; Kagimbo, Shimelis, & Sibiya, 2019; Silva et al., 2022). The hexaploid nature (2n = 6x = 90) and self-incompatibility of sweet potato species (King & Bamford, 1937) result in significant genetic variability, allowing for the development of genotypes tailored to different locations and seasons (Ebem, Afuape, Chukwu, & Ubi, 2021; Senff, Milcheski, Konkol, & Fioreze, 2021; Silva et al., 2022). Sweet potato genotypes exhibit substantial environmental interaction, leading to variations dependent on geographical locations and seasons (Senff et al., 2021; Nigussie, Gebeyehu, Mulugeta, & Guadie, 2022). Identifying and quantifying this interaction is essential for developing cultivars adapted to diverse environments (Ngailo, Shimelis, Sibiya, Mtunda, & Mashilo, 2019).

GE interaction refers to how cultivars perform across different environments (Mustamu, Tjintokohadi, Gruneberg, Karuniawan, & Ruswandi, 2018). Environmental conditions can significantly impact sweet potato quality and yield (Karan & Sanli, 2021). Studies have shown that sweet potato clones' interaction with planting times influences traits such as root diameter, marketable roots, total roots, average root weight, and root yield (Senff et al., 2021; Gasura et al., 2021). Additionally, Mahmud et al. (2021) found that growing environments had a significant influence on root production.

Despite these observations, no scientific studies have evaluated the effects of growing seasons and GE interaction on the selection of sweet potato genotypes for animal feeding. Therefore, this study aimed to evaluate GE interactions in sweet potatoes for animal feed and select high-performance genotypes suitable for cultivation in different seasons throughout the year.

Material and methods

The experiments were conducted at the Technology Development and Transfer Center of the Federal University of Lavras (UFLA), situated in Ijaci, Minas Gerais State, Brazil (altitude: 918 m; latitude: 21°14'16" S; longitude: 45°08'00" W). The first experiment took place from April 2nd to October 4th, 2019 (winter season), while the second experiment occurred from October 15th, 2019, to April 26th, 2020 (summer season).

During these cultivation periods, the environmental conditions were as follows: winter season: average temperature of 21.28°C, an average minimum of 14.44°C, average maximum of 26.89°C, precipitation of 195.1 mm, average relative humidity of 65.38%, and average wind speed of 1.63 m s^{-1} (Figure 1); and summer season: average temperature of 24.28°C, an average minimum of 18.59°C, average maximum of 28.80°C, precipitation of 1,346.9 mm, average relative humidity of 71.73%, and average wind speed of 1.29 m s^{-1} (INMET, 2022).

Both experiments employed a partially balanced triple lattice experimental design with 100 treatments and three replications. To minimize genotype-related bias, randomization of rows and columns between adjacent plots followed the recommendations of Bueno Filho and Gilmour (2003). The treatments consisted of 92 experimental sweet potato genotypes, derived from polycrossing among 55 genotypes from the UFLA germplasm bank, and eight pre-evaluated controls. The controls included the commercial cultivars Brazlândia Roxa, Princesa, Uruguaiana, BRS Amélia, and Beauregard, as well as the genotypes UFVJM-57, UFVJM-58, and UFVJM-61. All genotypes were assessed in both growing seasons.

The experimental process involved soil preparation through plowing and harrowing, followed by creating windrows with a height of 0.35 m. Each windrow was subdivided into plots, each containing 10 plants spaced at 1.00 m between rows and 0.30 m between plants. The first experiment used segments of sweet potato vines collected from the UFLA germplasm bank, while the second experiment utilized branches obtained during the harvest of the first experiment after measuring the canopy weight. Nutritional recommendations followed the guidelines outlined in Silva et al. (2022). Drip irrigation was employed, and other cultural practices were performed manually according to crop requirements.

Both experiments were harvested 180 days after planting (DAP). Agronomic data were collected from the central eight plants in each plot. These included vine green matter yield (VGMY), expressed in ton ha^{-1}, calculated by weighing the cut vines at ground level; vine dry matter yield (VDMY), in ton ha^{-1}, calculated by multiplying vine yield by the percentage of vine dry matter; percentage of vine dry matter (PVDM), at which 200 g vines were collected, cut, and died in an oven at 65°C until constant weight (Gonçalves Neto et al., 2011), calculated as follows: $PVDM(\%) = \frac{sample\ dry\ weight\ (g)}{sample\ green\ weight\ (g)} x100$; percentage of roots dry matter (PRDM) at which 200 g roots were collected, cut, and died in an oven at 65°C until constant weight (Gonçalves Neto et al., 2011), calculated as follows: $PRDM(\%) = \frac{sample\ dry\ weight\ (g)}{sample\ green\ weight\ (g)} x100$; and root dry matter yield (RDMY) by multiplying total root yield by the percentage of root dry matter, expressed as ton ha^{-1}.

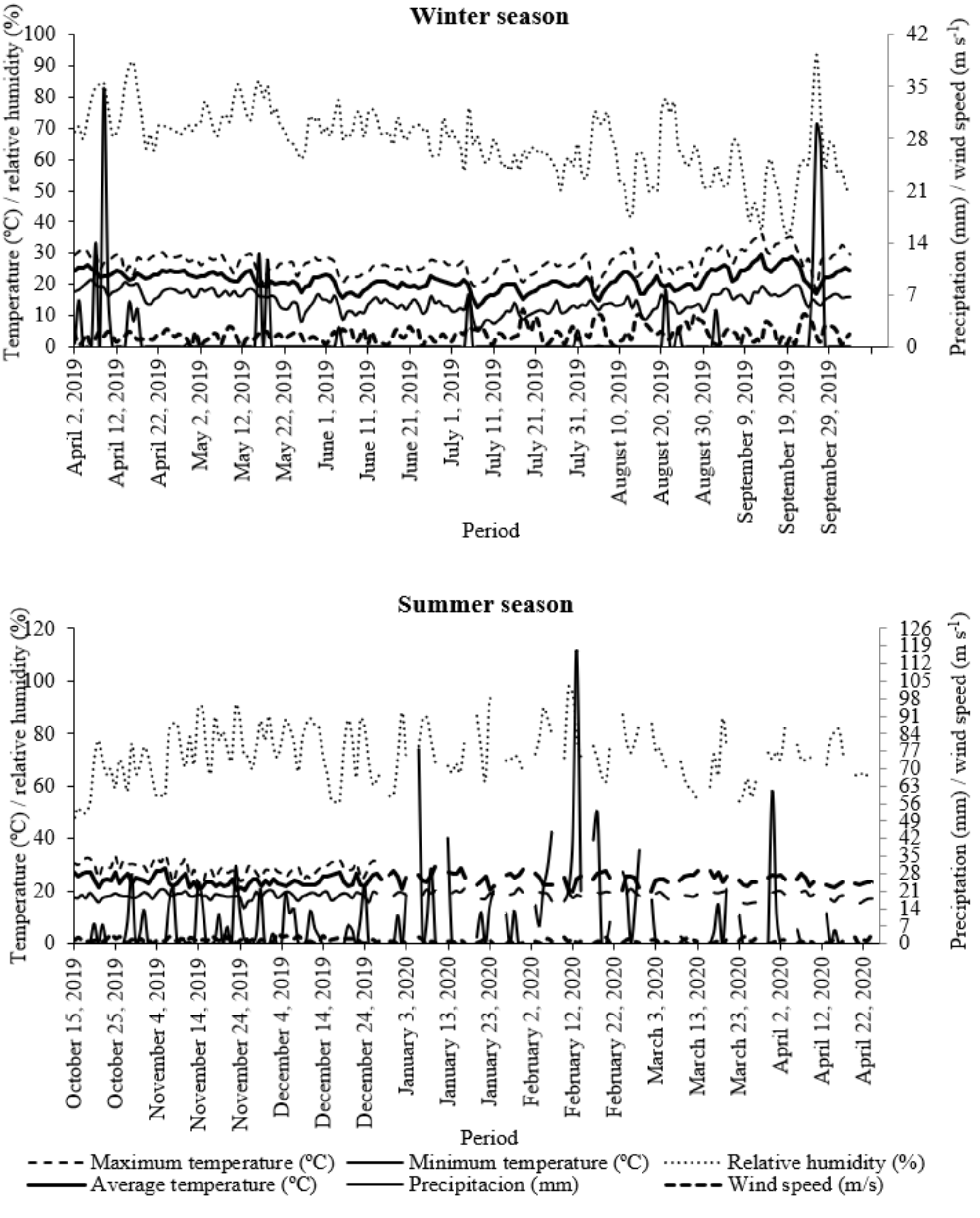

Figure 1. Meteorological data of precipitation (mm), maximum temperature (°C), minimum temperature (°C), average temperature (°C), relative humidity (%), and wind speed (m s^{-1}) corresponding to the periods of winter cultivation (April 2nd to October 4th, 2019) and summer (October 15th, 2019, to April 26th, 2020) (INMET, 2022).

Box and Cox's (1964) methodology was employed to determine the most suitable transformation for normal approximation. The transformation constants (λ) for each characteristic were as follows: VGMY ($\lambda = 0.229$), PRDM ($\lambda = -0.552$), RDMY ($\lambda = 0.406$), VDMY ($\lambda = 0.487$), and PVDM ($\lambda = 0.342$). The "boxcox" function from the "MASS" package in the R statistical software (R Core Team, 2022; Ripley et al., 2022) was used to evaluate confidence limits for λ in the Box-Cox transformation. In addition to the original scales, we also provided averages on the transformed scale to facilitate model fitting. The back-transformed scale for these averages was obtained using the "bxcx()" function from the "sae" package in R (Molina & Marhuenda, 2015).

Genotypic values were estimated using Best Linear Unbiased Prediction (BLUP) from the mixed model: $\frac{y_{ijk}^{\lambda}-1}{\lambda} = \mu + g_i + s_k + b_{j(k)} + gs_{ik} + e_{ijk}$, where λ is the transformation constant previously estimated via maximum likelihood; y_{ijk} represents observations for genotype i-th, block j-th, and season k-th; μ is the average for the observations; g_i is the random effect of genotype i; s_k is the fixed effect of season k; $b_{j(k)}$ is the fixed effect of block, rows and columns j within season k; gs_{ik} is the random effect of the interaction between genotype i and season k; e_{ijk} is the effect of random experimental error. The vectors g, gs, and e follow a multivariate normal distribution with a mean of zero and covariances given by $G = I \: x \: \hat{\sigma}_G^2$, $GS = I \: x \: \hat{\sigma}_{GS}^2$, and $R = I \: x \: \hat{\sigma}_E^2$, with these parameters to be estimated. Linear mixed models were fitted using the "lmer" function from the "lme4" package (Bates, Mächler, Bolker, & Walker, 2015) in the R statistical software (R Core Team, 2022).

To assess the effectiveness of local control, an analysis of variance was conducted. Mixed models were applied to estimate the variance of genotype-environment interaction ($\hat{\sigma}_{GS}^2$), genetic variance ($\hat{\sigma}_G^2$), and experimental error variance ($\hat{\sigma}_E^2$). The significance of the variance components for the random effects of genotypes and genotype-environment interaction was verified through the Likelihood Ratio Test (LRT).

Broad-sense heritability was calculated for selection between plot means (h^2_P) using the formula:

$$h_P^2(\%) = \frac{\hat{\sigma}_G^2}{\hat{\sigma}_G^2 + \hat{\sigma}_{GS}^2 + \hat{\sigma}_E^2} x100$$

Additionally, broad-sense heritability for selection between genotype means (h^2_G) was calculated with the formula:

$$h_G^2(\%) = \frac{\hat{\sigma}_G^2}{\hat{\sigma}_G^2 + \frac{\hat{\sigma}_{GS}^2}{3} + \frac{\hat{\sigma}_E^2}{6}} x100$$

where: h^2 represents heritability in the broad sense; $\hat{\sigma}_G^2$ is the genotypic variance; $\hat{\sigma}_{GS}^2$ is the variance of genotype-by-environment interaction; and $\hat{\sigma}_E^2$ is the variance of experimental error.

Heritability values below 20% indicate low heritability, between 20 and 50% suggest moderate heritability and values exceeding 50% represent high heritability (Santos, Spehar, Capone, & Pereira, 2018).

Finally, BLUP values were ranked, highlighting the top 10 highest and the three lowest genotype performances for each season. Likewise, the genotypes were ranked according to their performance for the two combined seasons. Additionally, genotypic correlations between the evaluated traits were estimated using Pearson's method at a significance level of 5% via t-test approximation.

Results and discussion

The sweet potato genotypes were significantly influenced by the fixed effect of growing season on VGMY ($p \leqslant 0.001$), VDMY ($p \leqslant 0.001$), PVDM ($p \leqslant 0.05$), and RDMY ($p \leqslant 0.001$) traits (Table 1). This indicates that varying environmental conditions during different growing seasons affected vine and root production.

Table 1. F test for the effects of the season (S) and genetic parameters of variance of genotype-environment interaction ($\hat{\sigma}_{GS}^2$), genetic variance ($\hat{\sigma}_G^2$), the variance of the experimental error ($\hat{\sigma}_E^2$), heritability in the broad sense for selection between plot averages (h^2_P) and heritability in the broad sense for selection between genotype averages (h^2_G) for agronomic traits of the vine green matter yield (VGMY), vine dry matter yield (VDMY), percentage of vine dry matter (PVDM), percentage of roots dry matter (PRDM) and root dry matter yield (RDMY). UFLA, Lavras, Minas Gerais State, Brazil.

Agronomic trait	Fixed effect	Random effect						
		Genetic parameters						
	S	$\hat{\sigma}_{GS}^2$		$\hat{\sigma}_G^2$		$\hat{\sigma}_E^2$	$h^2_P(\%)$	$h^2_G(\%)$
	p-value	$\hat{\sigma}_{GS}^2$	*p*-value	$\hat{\sigma}_G^2$	*p*-value			
VGMY	0.0002^{***}	0.38	$<0.001^{***}$	0.30	$<0.001^{***}$	0.77	20.76	54.18
VDMY	0.0008^{***}	0.27	0.095^{ns}	0.20	$<0.001^{***}$	1.16	12.43	41.69
PVDM	0.0246^{*}	0.11	62.701^{ns}	0.12	$<0.001^{***}$	3.90	2.80	14.41
PRDM	0.3522^{ns}	<0.00	$<0.001^{***}$	<0.00	$<0.001^{***}$	<0.00	51.31	82.97
RDMY	0.0001^{***}	0.46	$<0.001^{***}$	0.72	$<0.001^{***}$	0.85	35.45	70.89

p-value: value p of the F test at 5% significance. ***Significant for $p \leqslant 0.001$; **significant for $p \leqslant 0.01$; *significant for $p \leqslant 0.05$; ^{ns}not significant.

The random effect of genotype showed significant differences ($p \leqslant 0.001$) for all traits: VGMY, VDMY, PVDM, PRDM, and RDMY (Table 1). Regarding the genotype by environment interaction effect, VGMY, PRDM, and RDMY characteristics exhibited significant differences ($p \leqslant 0.001$). These results align with Nigussie et al. (2022), who also found that the performance of sweet potato clones is influenced by genotype, environmental conditions, and genotype-environment interaction. This influence is primarily attributed to the thermal variations observed between seasons, in addition to differences in rainfall and air humidity (Figure 1). Although the variance components of the genotype-by-environment interaction are significant, it is possible to select stable genotypes for both growing seasons by considering the variation among genotypes. It is also important to assess the performance of genotypes in terms of VDMY and PVDM characteristics, which did not exhibit a significant effect on the genotype-environment interaction.

Furthermore, PRDM exhibited the highest heritabilities for selection between plot averages (h^2_P = 51.31%) and genotypes (h^2_G = 82.97%) (Table 1). This suggests a substantial genetic variability for PRDM, coupled with minimal environmental influence. The heritabilities of the traits for selection between plot averages (h^2_P) indicate the contribution of the plot average to the next generation. VGMY (h^2_P = 20.76%) and RDMY (h^2_P = 35.45%) displayed moderate heritability, whereas PVDM (h^2_P = 2.80%) and VDMY (h^2_P = 12.43%) showed low heritability. This suggests that the genetic variance for these traits was lower than the environmental variance.

Regarding heritabilities based on genotype (h^2_G), high values were found for VGMY (h^2_G = 54.18%), RDMY (h^2_G = 70.89%), and PRDM (h^2_G = 82.97%) (Table 1). Rukundo, Shimelis, Laing, and Gahakwa (2017) also reported high heritability values for VGMY (h^2_G = 50%) and PRDM (h^2_G = 75%), similar to the values found in this study. Kagimbo et al. (2019) reported a high heritability for the PRDM trait (h^2_G = 84%). The high h^2_G values observed in this study suggest that the selection of superior genotypes can lead to significant genetic gains in subsequent generations (Kagimbo et al., 2019).

VDMY (h^2_G = 41.69%) and PVDM (h^2_G = 14.41%) displayed moderate and low heritability, respectively (Table 1). Therefore, selecting genotypes for these traits may be challenging due to the environmental influences between growing seasons.

It is worth noting that in species propagated asexually, such as sweet potatoes, broad-sense heritability is important because additive and non-additive genetic actions are fixed and transferred to clones (Rukundo et al., 2017). In this case, estimated genetic values consist of an additive portion of the total phenotypic variance (Tessema, Mohammed, & Abebe, 2022). Nevertheless, these superior genotypes also have the potential for selection in the current stage of the genetic improvement program.

Back-transformed averages were used to select genotypes for the characteristics of individual and joint seasons (Table 2). These back-transformed averages closely approximate the averages on the original scale, making them a more suitable basis for plant selection.

Table 2. Ranking of the BLUPs estimates of the genotypic values of the 10 best genotypes and the three with the lowest performance and the standard error of these estimates for the agronomic characteristics vine green matter yield, vine dry matter yield, percentage of vine dry matter, percentage of roots dry matter and root dry matter yield in the summer and winter planting seasons separately and jointly. UFLA, Lavras, Minas Gerais State, Brazil, 2023.

Rank	Vine green matter yield								
	Summer			Winter			Summer and Winter		
	Genotype	Estimate[1]	Standard error	Genotype	Estimate[1]	Standard error	Genotype	Estimate[1]	Standard error
1	2018-31-666	15.73	8.22	2018-31-713	25.83	7.91	2018-31-713	10.40	5.15
2	2018-72-1438	12.62	7.91	2018-12-252	20.90	8.00	2018-72-1438	9.71	5.15
3	2018-72-1429	10.97	8.22	2018-72-1438	19.19	7.91	2018-31-666	9.60	5.26
4	2018-19-389	10.44	7.91	2018-19-461	18.14	8.00	2018-12-252	8.97	5.26
5	2018-74-1512	9.54	7.91	2018-31-666	15.73	8.00	2018-19-461	7.89	5.26
6	2018-1-89	9.41	7.91	2018-28-556	13.99	7.91	2018-19-389	6.95	5.15
7	2018-8-198	9.27	7.91	2018-38-946	13.64	7.91	2018-38-946	5.84	5.15
8	2018-74-1507	8.80	7.91	2018-5-133	13.29	7.91	2018-31-689	5.28	5.15
9	2018-12-252	8.50	8.22	2018-65-1252	13.07	7.91	2018-74-1507	5.28	5.15
10	2018-31-713	8.26	7.91	2018-8-181	12.81	7.91	2018-37-864	5.26	5.15
...	...	...	...	...	...	...	...	...	...
98	2018-72-1380	-16.49	7.91	2018-67-1323	-20.31	7.91	2018-72-1381	-8.68	5.15
99	UFVJM-57	-17.76	7.91	Uruguaiana	-25.82	8.00	Uruguaiana	-9.60	5.26
100	Beauregard	-47.27	8.76	Beauregard	-36.01	8.17	Beauregard	-25.41	5.45
Transformed average		6.69	0.18		4.55	0.18		5.62	1.07
Average on back-transformed scale		57.72	1.19		22.55	1.19		37.01	2.61
Average on original scale		62.10	22.82		25.86	22.86		43.26	26.56

Rank	Vine dry matter yield								
	Summer			Winter			Summer and Winter		
	Genotype	Estimate[1]	Standard	Genotype	Estimate[1]	Standard	Genotype	Estimate[1]	Standard

			error			error			error
1	2018-28-514	4.47	2.04	2018-31-713	5.69	2.04	2018-31-713	2.42	1.30
2	2018-72-1438	3.61	2.04	2018-12-252	4.87	2.06	2018-72-1438	2.33	1.30
3	2018-72-1429	3.28	2.11	2018-19-461	4.50	2.06	2018-12-252	2.05	1.33
4	2018-31-666	3.23	2.11	2018-72-1438	4.22	2.04	2018-19-461	1.87	1.33
5	2018-1-89	2.56	2.04	2018-38-946	3.30	2.04	2018-31-666	1.85	1.33
6	2018-31-713	2.43	2.04	2018-65-1252	3.01	2.04	2018-28-514	1.76	1.30
7	2018-19-389	2.40	2.04	2018-31-666	2.97	2.06	2018-38-946	1.43	1.30
8	2018-74-1512	2.07	2.04	2018-28-556	2.83	2.04	2018-19-389	1.40	1.30
9	2018-8-198	2.03	2.04	2018-37-864	2.77	2.04	2018-37-864	1.26	1.30
10	2018-12-252	2.03	2.11	2018-5-133	2.70	2.04	2018-31-689	1.17	1.30
...	...	...	...	...	...	...	...	...	...
98	2018-72-1476	-3.48	2.11	Uruguaiana	-3.58	2.06	Beauregard	-2.07	1.44
99	2018-29-598	-3.78	2.04	BRS-Amélia	-3.59	2.04	BRS-Amélia	-2.10	1.30
100	2018-72-1409	-4.03	2.04	Beauregard	-4.87	2.14	2018-29-598	-2.11	1.30
Transformed average		3.82	0.18		1.94	0.18		2.88	0.95
Average on back-transformed scale		8.67	1.19		3.91	1.19		6.05	2.18
Average on original scale		9.21	4.34		4.26	4.34		6.64	4.30

Rank	Percentage of vine dry matter								
	Summer			Winter			Summer and Winter		
	Genotype	Estimate[1]	Standard error	Genotype	Estimate[1]	Standard error	Genotype	Estimate[1]	Standard error
1	2018-28-514	1.68	0.65	Uruguaiana	1.06	0.65	2018-28-514	0.82	0.45
2	Uruguaiana	0.59	0.66	2018-15-268	0.83	0.65	Uruguaiana	0.55	0.46
3	2018-19-443	0.37	0.65	2018-28-514	0.78	0.65	2018-15-268	0.39	0.45
4	2018-65-1249	0.34	0.65	2018-19-443	0.48	0.65	2018-19-443	0.28	0.45
5	2018-15-268	0.33	0.65	2018-38-941	0.28	0.65	2018-65-1249	0.17	0.45
6	2018-54-1082	0.32	0.65	2018-19-461	0.26	0.65	2018-38-941	0.17	0.46
7	2018-46-995	0.27	0.66	2018-38-946	0.25	0.65	2018-54-1082	0.16	0.45
8	2018-72-1380	0.24	0.65	2018-36-840	0.24	0.65	2018-36-840	0.15	0.45
9	2018-55-1156	0.24	0.65	2018-72-1428	0.23	0.65	2018-72-1432	0.15	0.45
10	2018-72-1432	0.23	0.65	2018-74-1481	0.21	0.65	2018-72-1428	0.14	0.46
...	...	...	...	...	...	...	...	...	...
98	2018-53-1038	-0.97	0.65	2018-72-1409	-0.55	0.65	2018-29-598	-0.51	0.45
99	2018-29-598	-1.06	0.65	2018-53-1038	-0.71	0.65	2018-53-1038	-0.56	0.45
100	2018-72-1476	-1.15	0.66	2018-72-1476	-0.78	0.65	2018-72-1476	-0.64	0.46
Transformed average		10.91	0.28		12.27	0.28		11.59	0.68
Average on back-transformed scale		14.74	1.29		16.66	1.28		15.69	1.71
Average on original scale		14.80	3.42		16.67	3.50		15.78	3.04

Rank	Percentage of roots dry matter								
	Summer			Winter			Summer and Winter		
	Genotype	Estimate[1]	Standard error	Genotype	Estimate[1]	Standard error	Genotype	Estimate[1]	Standard error
1	2018-31-666	5.84	2.37	2018-36-840	7.53	2.37	2018-31-666	4.67	1.73
2	2018-72-1407	5.68	2.37	2018-72-1438	5.39	2.37	2018-72-1438	4.32	1.73
3	2018-36-807	5.30	2.37	Brazlândia Roxa	4.91	2.37	Brazlândia Roxa	4.23	1.73
4	2018-19-387	5.04	2.46	2018-31-666	4.74	2.37	2018-74-1481	3.90	1.73
5	UFVJM-57	4.86	2.37	2018-74-1481	4.57	2.37	UFVJM-57	3.77	1.73
6	2018-19-464	4.78	2.37	2018-53-1038	4.42	2.37	2018-15-277	3.69	1.73
7	2018-72-1432	4.75	2.37	2018-74-1479	4.28	2.44	2018-36-840	3.66	1.73
8	Brazlândia Roxa	4.66	2.37	2018-15-277	3.99	2.37	2018-19-464	3.62	1.73
9	2018-72-1438	4.40	2.37	2018-31-689	3.90	2.37	2018-37-869	3.25	1.73
10	2018-15-277	4.38	2.37	2018-19-461	3.86	2.37	2018-31-672	3.24	1.73
...	...	...	...	...	...	...	...	...	...
98	2018-12-252	-8.31	2.37	2018-68-1361	-7.86	2.37	2018-12-252	-6.33	1.73
99	Beauregard	-18.80	2.46	Uruguaiana	-18.69	2.56	Uruguaiana	-17.32	1.93
100	Uruguaiana	-20.55	2.61	Beauregard	-21.33	2.44	Beauregard	-17.71	1.80
Transformed average		1.54	0.003		1.54	0.003		1.54	0.003
Average on back-transformed scale		31.83	1.00		30.92	1.00		31.33	1.003
Average on original scale		32.46	4.24		31.37	4.56		31.90	4.31

Rank	Root dry matter yield								
	Summer			Winter			Summer and Winter		
	Genotype	Estimate[1]	Standard error	Genotype	Estimate[1]	Standard error	Genotype	Estimate[1]	Standard error
1	UFVJM-58	8.82	2.36	2018-19-464	5.95	2.36	2018-19-464	5.12	1.63
2	2018-28-556	8.37	2.36	2018-28-556	4.85	2.36	2018-28-556	5.01	1.63
3	2018-19-464	7.56	2.36	2018-72-1432	4.23	2.36	UFVJM-58	4.40	1.63
4	2018-72-1432	6.95	2.36	2018-65-1249	3.89	2.36	2018-72-1432	4.24	1.63
5	2018-53-1038	6.30	2.36	UFVJM-61	3.65	2.36	2018-19-443	3.41	1.63
6	2018-19-443	5.62	2.36	2018-55-1154	3.49	2.36	UFVJM-61	3.18	1.63
7	2018-19-391	5.44	2.36	2018-19-443	3.38	2.36	2018-55-1154	3.15	1.63
8	2018-55-1154	4.84	2.36	2018-28-543	3.32	2.36	2018-28-543	3.07	1.63
9	2018-28-543	4.79	2.36	2018-15-299	3.25	2.36	2018-53-1038	2.96	1.63
10	2018-72-1418	4.78	2.36	2018-31-666	3.18	2.36	Brazlândia Roxa	2.78	1.63
...	...	...	...	...	...	...	...	...	...
98	2018-36-840	-7.05	2.36	2018-15-268	-5.27	2.40	2018-36-840	-4.35	1.63
99	2018-74-1479	-7.88	2.44	2018-19-387	-5.51	2.40	2018-15-268	-5.06	1.67
100	2018-15-268	-8.09	2.44	2018-74-1479	-7.06	2.40	2018-74-1479	-5.66	1.67
Transformed average		2.14	0.14		3.11	0.14		2.62	0.49
Average on back-transformed scale		4.66	1.14		7.47	1.14		5.97	1.57
Average on original scale		6.00	5.02		7.92	5.00		6.98	4.35

[1] The estimate indicates the selection gain relative to the average on back-transformed scale.

Regarding the performance of genotypes in different growing seasons, the back-transformed scale average for VGMY was 57.72 ton ha^{-1} in the summer and 22.55 ton ha^{-1} in the winter (Table 2). The yield difference between the seasons was 35.17 ton ha^{-1}, with VGMY being 155.96% higher in the summer season. This difference can be attributed to the environmental conditions in the southern hemisphere, as the summer season typically has more precipitation and higher temperatures than the winter season, promoting vegetative growth (Senff et al., 2021). In this experiment, the summer season had a higher average temperature, precipitation, and relative humidity (4.54°C, 1,151.80 mm, 4.53%, respectively) compared to the winter season (Figure 1). The abundant availability of water and nutrients in the summer season contributes to a higher leaf area index, surpassing the optimal percentage (Peixoto, 2020).

Temperature has a significant influence on biochemical reactions, including photosynthesis, chloroplast membrane integrity, and plant respiration (Taiz, Zeiger, Møller, & Murphy, 2017). Low temperatures, such as those experienced during the winter, lead to a rapid reduction in carbohydrate synthesis (Taiz et al., 2017). Under these conditions, photosynthesis is limited due to reduced phosphate levels in the chloroplast, resulting in decreased demand for phosphate trioses and the inhibition of phosphate entry into the cytosol (Taiz et al., 2017). Villavicencio, Blankenship, Yencho, Thomas, and Raper (2007) also reported that low temperatures are unfavorable for shoot development, given that sweet potatoes thrive in tropical climates. According to Peixoto (2020), this reduced growth of the canopy leads to a lower leaf area index, causing decreased radiation absorption, which, in turn, results in reduced photosynthesis and decreased vine productivity.

Despite VGMY being lower in winter, its value remains relevant, making it a viable option for animal feed during periods of food scarcity. Sweet potato vines have a suitable bromatological composition for animal feed (Viana et al., 2011; Pedrosa et al., 2015). Therefore, selecting genotypes with good aerial part bromatological quality is essential for maximizing the plant's utility (Andrade Júnior et al., 2020). Pedrosa et al. (2015), in their evaluation of 15 sweet potato genotypes, found that the average crude protein content (CP) in the vines was 12% of dry matter, the average acid detergent fiber (ADF) content was 34.7% of dry matter, and the average neutral detergent fiber (NDF) content was 46.6% of dry matter. When compared to other common animal feed crops, such as maize [PB = 9.5%; FDA = 4.63%; NDF = 16.31% of dry matter], soybean bran [PB = 4.84%; FDA = 1.15%; NDF = 18.72% of dry matter], sugar cane silage [PB = 3.41%; ADF = 44.32%; NDF = 74.45% of dry matter], wet corn grain silage [PB = 7.60%; FDA = 3.13%; NDF = 13.72% of dry matter], grass hay [PB = 9.98%; FDA = 43.04%; NDF = 76.72% of dry matter] (Persichetti Júnior et al., 2014), sweet potato shows superiority in CP content. Considering that values below 40% ADF and below 60% NDF do not affect feed intake by animals (Pedrosa et al., 2015), it suggests that sweet potato has superior bromatological quality compared to grass hay and sugar cane silage, making it a promising choice for animal feed.

The ranking of genotypes for VGMY varied with the seasons (Table 2). Only five genotypes, namely 2018-12-252, 2018-31-666, 2018-31-713, and 2018-72-1438, were consistently ranked among the top ten in both individual seasons. Furthermore, they exhibited estimated gains of 8.97, 9.60, 10.40, and 9.71 ton ha^{-1} above the average on the back-transformed scale (37.01 ton ha^{-1}) and estimated VGMY values ranging between 45.96 and 47.41 ton ha^{-1}. It is worth noting that, on average, Beauregard and Uruguaiana (genotype controls) exhibited low VGMY performance, with combined season productivities of 11.60 and 27.41 ton ha^{-1}, respectively. This underscores the potential of the studied genotypes when compared to the controls.

The average VGMY values obtained in this study, whether considered separately or combined for seasons, are consistent with findings in other works (Table 2). For instance, Silva et al. (2022) also evaluated the control UFVJM-57, which yielded an average VGMY of 47.08 ton ha^{-1} in the summer, while in this study, it produced 39.96 ton ha^{-1}. This discrepancy highlights the influence of location and soil type on these varying performances.

Genotypes demonstrated the highest VDMY performance in the summer, with an average on the back-transformed scale of 8.67 ton ha^{-1}, whereas during the winter, the average was 3.91 ton ha^{-1} (Table 2). This corroborates the high VGMY observed in the summer, which results from the close relationship between these traits.

Among the top ten genotypes in individual seasons, four also ranked as the best genotypes in the combined analysis, specifically 2018-31-713, 2018-72-1438, 2018-12-252, and 2018-31-666. These genotypes exhibited an average of 2.16 ton ha^{-1} higher than the back-transformed scale average (6.05 ton ha^{-1}) across the combined seasons.

Andrade Júnior, Elsayed, Azevedo, Santos, and Ferreira, (2018) evaluated the VDMY of UFVJM-58 in Diamantina-MG and obtained an average of 5.85 ton ha^{-1} during the summer season (November to May), which is lower than the 10.01 ton ha^{-1} observed in this study during the same season (Table 2). Pedrosa et al. (2015), when assessing 15 sweet potato genotypes in Couto de Magalhães de Minas-MG, found an average VDMY of 5.5 ton ha^{-1}, even over 230 days. These results underscore the significant influence of edaphoclimatic factors on genotype performance, which can vary under different cultivation conditions. The findings from these studies suggest the importance of conducting at least two genotype evaluation tests in breeding programs to identify clones with greater adaptability, stability, and reduced sensitivity to genotype-environmental influences (Mustamu et al., 2018).

Although there was a low variation between growing seasons for PVDM, it remained significant (Tables 1 and 2). The summer season yielded an average on the back-transformed scale of 14.74% of canopy dry matter, while the winter produced 16.66% of vine dry matter. This minimal variation indicates that PVDM had a limited influence on VDMY. Consequently, VDMY was primarily influenced by VGMY, as evidenced by their similar rankings (90%) irrespective of the evaluation period. In contrast, PVDM performed better in winter.

These results align with the correlations established between the variables (Table 3). VGMY exhibited a high positive and significant correlation with VDMY (R = 0.88***), which is expected as VGMY is a production component of VDMY. Andrade Júnior et al. (2018) also reported a highly significant correlation between these traits (R = 0.98), indicating that the easier-to-measure trait can be effectively evaluated. Additionally, although it was low, a significant correlation was observed between VDMY and PVDM (R = 0.29**), as well as between VGMY and PRDM (R = 0.38***). These findings are important for understanding trait associations in plant breeding programs and selecting the most efficient methods for evaluating key variables (Dewi, Utomo, Kamal, Timotiwu, & Nurdjanah, 2019; Tessema et al., 2022).

The genotypes 2018-28-514, 2018-15-268, 2018-19-443, and Uruguaiana stood out in both individual seasons for the PVDM trait and are ranked in the top four in the joint analysis (Table 2). Despite differences in rankings, the variations observed between genotypes were minimal (< 1.5%). Donato et al. (2020), in their evaluation of 10 sweet potato genotypes for hay production during summer cultivation, found an average dry matter content of vines at 17.98%. These values closely align with the averages observed across different seasons in this study. According to Santos et al. (2019), genotypes with high PVDM indicate elevated levels of essential nutrients for animals, contributing to their feed efficiency. Thus, selecting genotypes with good PVDM and VDMY is crucial to meeting animals' dietary needs throughout the year.

Table 3. Genotypic correlation between the agronomic traits of vine green matter yield (VGMY), vine dry matter yield (VDMY), percentage of vine dry matter (PVDM), percentage of roots dry matter (PRDM), and root dry matter yield (RDMY) through the BLUP estimate. UFLA, Lavras, Minas Gerais State, Brazil, 2023.

Characteristics	VGMY	VDMY	PVDM	PRDM	RDMY
VGMY	1.00	0.88^{***}	-0.05^{ns}	0.38^{***}	-0.02^{ns}
VDMY	-	1.00	0.29^{**}	0.17^{ns}	-0.12^{ns}
PVDM	-	-	1.00	-0.19^{ns}	-0.15^{ns}
PRDM	-	-	-	1.00	0.19^{ns}
RDMY	-	-	-	-	1.00

p-*value*: value *p* of the t test at 5% probability. ***Significant for $p \leq 0.001$; **significant for $p \leq 0.01$; *significant for $p \leq 0.05$; ^{ns}not significant.

The average on the back-transformed scale for PRDM in the summer was 31.83%, while in the winter it was 30.92% (Table 2). The difference between seasons was not significant (Table 1), but the variation between genotypes contributed to a significant genotype-by-environment interaction. Oliveira et al. (2022), when assessing the agronomic performance of genotypes across four locations during the summer and winter seasons, found that PRDM was influenced by genotypes but did not exhibit differences in the genotype-by-environment interaction. Karan and Şanli (2021), evaluating four genotypes over two years and two locations, also found significant differences between genotypes. However, they reported that PRDM has a limited environmental effect.

Genotypes 2018-31-666, 2018-72-1438, 2018-15-277, and the cultivar Brazlândia Roxa excelled among the top 10 genotypes for PRDM in both individual seasons (Table 2). These genotypes also distinguished themselves in the combined analysis, with gains of 4.67%, 4.32%, 3.69%, and 4.23% higher than the average on the back-transformed scale (31.33%). As a result, their PRDM estimates ranged between 35.02% and 36.00%. In contrast, the Beauregard and Uruguaiana cultivars consistently displayed lower percentages, regardless of the season, at 13.62% and 14.01%, respectively, in the combined seasons.

Commonly, sweet potato roots contain 30% dry matter, with 70% corresponding to starch, 10% to sugars, and 5% to proteins (Karan, Şanli, 2021). The average PRDM values found in this study are similar to those reported by other authors, such as 30.07% by Oliveira et al. (2022) and 30.42% by Karan and Şanli (2021). This performance is satisfactory as it ensures a higher protein content for animal consumption.

The average RDMY in winter was 7.47 ton ha^{-1} on the back-transformed scale, which is 60.30% higher than that observed in the summer season (4.66 ton ha^{-1}) (Table 2). In addition to high temperatures, the summer season was characterized by heavy rainfall (Figure 1). The accumulated precipitation during the experiment in the summer season (1346.9 mm) exceeded the recommended levels for sweet potato production, typically ranging from 500 to 600 mm during cultivation (Montes, 2013). These environmental factors promote excessive vegetative growth (Senff et al., 2021), which can delay the development of tuberous roots (Villavicencio et al., 2007) and reduce the accumulation of reserves in the roots due to competition for photoassimilates (Njiti et al., 2013). Consequently, the plants vegetated excessively in the summer, leading to a reduction in total root production and RDMY.

During the summer season, there is increased solar radiation, contributing to higher photosynthetic activity and an increased demand for CO_2, resulting in the expansion of stomatal openings (Peixoto, 2020; Taiz et al., 2017). In this condition, the plant loses water to the environment in its quest for more photosynthesis products (Peixoto, 2020). In the winter season, when precipitation is less abundant and there is limited soil moisture, even with irrigation, plants regulate stomatal openings to minimize water loss through transpiration while optimizing CO_2 intake (Peixoto, 2020). This reduction in water availability prompts the plant to prioritize root elongation over stem and leaf growth (Taiz et al., 2017). Thus, there is greater root development compared to leaves, which can be seen as an adaptation to drought (Taiz et al., 2017).

When considering RDMY collectively, six genotypes (2018-19-464, 2018-28-556, 2018-72-1432, 2018-19-443, 2018-55-1154, and 2018-28-543) consistently ranked as the best in both summer and winter seasons (Table 2). These genotypes exhibited an average estimate of four ton ha^{-1} higher (approximately 67%) than the average on the back-transformed scale in the combined analysis (5.97 ton ha^{-1}). Three controls (UFVJM-58, UFVJM-61, and Brazlândia Roxa) were among the top ten best genotypes in the combined analysis, with estimates of 4.40, 3.18, and 2.78 ton ha^{-1} higher than the average on the back-transformed scale, respectively. However, when considering the seasons individually, UFVJM-58 stood out only in the summer, and UFVJM-61 only in the winter.

Andrade Júnior et al. (2018) evaluated 40 sweet potato genotypes and found an average RDMY of 8.93 ton ha^{-1}. This value was higher than the one we found, regardless of the period analyzed (Table 2). These authors also evaluated the control UFVJM-58 and observed an RDMY of 7.10 ton ha^{-1}, while ours was 10.37 ton ha^{-1}. Quantitative traits, including branch and root yield, and genotypes are highly influenced by environmental factors (Silva, Ponijaleki, & Suinaga, 2012). Thus, such differences found between the studies are related to the effects of IGE.

It is common for sweet potato crops to have harvest cycles ranging from 120 to 180 days (Andrade Júnior et al., 2018; Azevedo et al., 2014; Silva et al., 2022; Senff et al., 2021), allowing for up to three cultivation cycles per year. Achieving this requires genotypes adapted for year-round cultivation. Additionally, many producers grow their seedlings, typically in separate areas. Therefore, selecting genotypes adapted and stable for both growing seasons (summer and winter) simplifies the process of obtaining propagative material with broad adaptability. This is because there is the possibility of reusing vines from the current harvest for later planting. This approach reduces the need for additional land to produce seedlings for subsequent cultivation.

Conclusion

The vine green matter yield, percentage of root dry matter, and root dry matter yield of sweet potato are significantly influenced by genotype-environment interactions. Vine green matter yield, vine dry matter yield, and the percentage of root dry matter were favored in the summer season, while the percentage of vine dry matter and root dry matter yield were favored in the winter season. The following genotypes excel in specific traits, regardless of the growing season: Vine Green Matter Yield and Vine Dry Matter Yield: 2018-31-713, 2018-72-1438, 2018-31-666, 2018-12-252, 2018-19-461, 2018-19-389, 2018-38-946, 2018-31-689, and 2018-37-864. Percentage of Vine Dry Matter: 2018-28-514, 2018-15-268, and 2018-19-443. Percentage of Root Dry Matter: 2018-31-666, 2018-72-1438, and 2018-15-277. Root Dry Matter Yield: 2018-19-464, 2018-28-556, 2018-55-1154, 2018-28-543, 2018-53-1038, 2018-72-1432, and 2018-19-443.

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