



Trait Associations and Genetic Parameters in Purple-Fleshed Sweetpotato Genotypes Evaluated at Hawassa, Sidama Regional State, Ethiopia

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Authors' contributions

This work was carried out in collaboration between both authors. Both authors read and approved the final manuscript.

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Abstract

Purple-fleshed sweetpotato (PFSP) is a vital root crop enhancing food and nutrition security, owing to its high anthocyanin content with proven health benefits and industrial potential. This study assessed trait associations and genetic parameters in nine PFSP genotypes during the 2025 main cropping season at Hawassa Agricultural Research Center, using a randomized complete block design with three replications. Nine key traits were evaluated: sweetpotato virus disease (SPVD) severity, vine length, root length and girth, above-ground biomass, number of roots per plant, marketable/unmarketable root yields, and total root yield. Analysis revealed substantial genotypic variability across traits, with genotypic correlations exceeding phenotypic ones, highlighting strong genetic effect. High phenotypic (PCV: 61.6–286.2%) and genotypic (GCV: 59.6–272.9%) coefficients of variation, coupled with genetic advance as a percent of the mean (GAM) up to 536%, indicating robust improvement predictions. Broad-sense heritability (H^2) was very high (93.6–

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99.4%), with higher GAM indicating additive gene action for most traits, which is ideal for selection. Notably, number of roots per plant, root length, and root girth showed positive correlations with yield, serving as reliable selection indices. These findings provide information to develop superior PFSP varieties with enhanced yield, anthocyanin levels, and SPVD resistance, to support food security, nutrition, and agro-industrial applications in Ethiopia.

Keywords: *Correlations; genetic variability; heritability; purple-fleshed; sweetpotato.*

1. Introduction

Sweetpotato (*Ipomoea batatas* (L.) Lam.), with diverse root flesh colors (mainly white, orange, purple, and yellow), is well known for its important role in Sub-Saharan Africa in enhancing food security and improving nutrition, especially amid the challenges of climate change. Its robustness and adaptability to marginal environments including drought tolerance, ease of cultivation, low external input requirements, and short growing period, which make sweetpotato crop vital for climate-affected regions globally (Low et al., 2017; Sapakhova et al., 2023). In regions burdened by rising prices of staple foods, recurrent droughts, conflicts, and rapidly growing populations, adoption of improved sweetpotato varieties and climate-resilient crops through breeding, innovative crop husbandry, and agricultural technologies supports farmer incomes and resilience (Mwanga et al., 2017; Alam et al., 2024). Several studies have highlighted sweetpotato's role during food shortages and its ability to alleviate micronutrient deficiencies such as vitamin A deficiency, with farmers and stakeholders recognizing its reliability as a buffer against food insecurity in vulnerable areas (Low et al., 2017; Sandoval-Ramírez et al., 2021). Sweetpotato provides a rich source of starch, vitamins, antioxidants, and its leaves contribute additional nutritional value, meeting both food and nutrition demands for healthier lives (Steed & Truong, 2008). Specifically, purple-fleshed sweetpotato (PFSP) is rich in anthocyanins, natural pigments with strong antioxidant properties that are linked to health benefits such as lowering the risks of chronic diseases like cardiovascular diseases and certain cancers (Li et al., 2018; Ivane et al., 2024). Moreover, PFSP offers a valuable source of dietary fiber, vitamins, and minerals, contributing to food and nutritional security, especially in regions prone to malnutrition (Low et al., 2017). The evaluation and selection of PFSP varieties are crucial since the crop exhibits wide genetic diversity in traits related to yield, disease resistance, root quality, and nutritional content (Teow et al., 2006; Leal et al., 2024). Varietal selection aims to identify clones with superior agronomic traits such as high yield, drought tolerance, resistance to sweetpotato virus disease (SPVD), and improved anthocyanin content because all of these are essential for enhancing productivity and adoption by farmers (Mwanga et al., 2017). Nowadays, the increasing consumer interest in nutrient-enriched functional foods drives breeding efforts towards cultivars with enhanced health benefits and market potential (Fortune Business Insights, 2025; Pulidindi, 2025). Furthermore, the industrial applications of PFSP, including natural colorants in food and beverage industries, promote economic diversification and value addition (Rodríguez-Mena et al., 2023). In general, evaluating and selecting promising purple-fleshed sweetpotato (PFSP) genotypes offers dual nutritional and economic benefits. Beyond supporting food security and encouraging sustainable agricultural practices, PFSP breeding taps into emerging markets for functional foods and bio-based products (Pulidindi, 2025). Although these benefits are widely recognized, comprehensive information on the variability and trait associations among PFSP varieties in Ethiopia remains scanty (Gurmu et al., 2017). Therefore, the present study was designed to assess trait association and determine selection criteria in purple-fleshed sweetpotato genotypes for further improvements.

2. Materials And Methods

2.1 Experimental Site

“The experiment was conducted during the 2024 main rainy season under rain-fed conditions at the Wondotika site, a sub-station of the Hawassa Agricultural Research Center (HwARC)”. The site's geographic coordinates are 7°06'46"N, 38°23'11"E, at an altitude of 1,708 meters above sea level. The area received an average annual rainfall of 1007 mm, with minimum and maximum air temperatures of 13.3°C and 27.6°C, respectively, and a relative humidity of 62.1%.

2.2 Experimental Materials

Sweetpotato genotypes derived from seven polycross breeding families (n=400) were initially treated with concentrated sulfuric acid (98% H₂SO₄) for 20 to 25 minutes to remove the hard seed coat and enhance germination. The seeds were carefully rinsed with running tap water for 5 minutes and then placed on wet filter paper in Petri dishes, kept in the dark for 48 hours to sprout. After two to three days, germinated seeds were planted on polystyrene seedling trays and later transplanted into 10 L plastic pots containing a mixture of topsoil, sand, and manure in a 3:1:1 ratio, respectively. Cuttings were then taken from each genotype within a family and transplanted to the field. Under field conditions in an observation nursery, the genotypes were characterized for desirable traits following the phenotypic descriptors for sweetpotato (Huamán, 1991). Nine promising genotypes were advanced to the further breeding stage and used in the current study (Table 1).

2.3 Experimental Design and Trial Management

The experiment was conducted from July 28th to December 30th, 2024 using nine advanced PFSP genotypes in a Randomized Complete Block Design with three replications. Each plot with size of 7.2 m² (3m length x 2.4m width), accommodated four rows (ridges for sweetpotato). Rows were spaced 60 cm apart, and plants within each row were spaced 30 cm apart. Replications were separated by 150 cm. Each plot held 40 plants per genotype per replication, with each row (ridge) accommodating 10 cuttings. Standard cultural practices were uniformly applied across all plots, including replanting of dead vines, earthening-up after four weeks, and regular weeding, following recommendations for sweetpotato production in various counties (Grüneberg et al., 2019). No fertilizer was used.

2.4 Data Collected

Data were collected on agronomic traits, including marketable, unmarketable, and total root yield (t/ha); above-ground biomass (t/ha); vine length (cm); root length and girth (cm); and sweetpotato virus disease (SPVD) severity, scored on a 1-9 scale. Measurements followed the standard data recording procedure for sweetpotato at harvest maturity, as described by Grüneberg et al. (2019).

2.5 Data Analysis

2.5.1 Analysis of Genetic Parameters Using Variance Component Estimation

“The phenotypic, genotypic and environmental variances and coefficient of variations were calculated according to the formula suggested by Singh and Chaudhury (1985) based on Randomized Complete Block Design (RCBD)”.

Environmental variance (σ^2_e), =MSe; Genotypic variance (σ^2_g) = $\frac{MS_g - MSe}{r}$

Phenotypic variance (σ^2_p) = $\sigma^2_g + MSe/r$; Phenotypic coefficient of variation (PCV) = $\frac{\sqrt{\sigma^2_p}}{\bar{x}} * 100$

Genotypic coefficient of variation (GCV) = $\frac{\sqrt{\sigma^2_g}}{\bar{x}} * 100$

Where, MS_g is mean square due to genotypes, MS_e is mean square of error (Environmental variance), r is number of replication, σ^2_g is genotypic variance and σ^2_e is environmental variance, σ^2_p = Phenotypic variation, $\bar{x}$ = Grand mean of the characters under study, PCV = phenotypic coefficient of variation, GCV = genotypic coefficient of variation

2.5.2 Estimate of Heritability in Broad Sense

Broad sense heritability (H²) of the traits was estimated according to the formula suggested by Hanson et al. (1956) as follows:

$$H^2 = \sigma^2_g / \sigma^2_p * 100$$

Where, σ^2_g = genotypic variance, σ^2_p = phenotypic variance. “The heritability percentage was categorized as low (<50%), moderate (50-70%) and high (>70%), as suggested by Hanson et al. (1956)”.

2.5.3 Genetic Advance under Selection (GA)

The expected genetic advance expressed under selection in broad sense, assuming selection intensity of 5% of the superior genotypes were estimated in accordance with the procedure described by Allard (1999) as:

$$GA = KH^2 \cdot \sigma_p$$

Where, GA= Expected genetic advance, H^2 = Heritability in broad sense, σ_p = Phenotypic standard deviation, k = the standardized selection differential at 5% selection intensity (K = 2.06)

Table 1. List of PFSP genotypes used for the study

Code	Name of genotype	Pedigree/female parent	Source of seeds	Root yield (t/ha)	Root flesh color intensity
G1	CIP118018-67	PGA12164-21	Ghana	20.33	Intermediate purple
G2	CIP118030-102	PGN16203-18	Ghana	36.16	Deep purple
G3	CIP118030-106	PGN16203-18	Ghana	14.05	Deep purple
G4	CIP118030-100	PGN16203-18	Ghana	16.00	Deep purple
G5	CIP118021-104	PGA14008-9	Ghana	19.13	Deep purple
G6	CIP118034-140	TU-Purple	Ghana	21.00	Deep purple
G7	CIP118034-143	TU-Purple	Ghana	30.97	Deep purple
G8	CIP118005-12	Faara	Ghana	22.78	Deep purple
G9	CIP118005-49	Faara	Ghana	16.05	Deep purple

Note: Deep purple types are richer in acylated anthocyanins, which are more stable and give darker coloration, while intermediate types have less concentrated or different anthocyanin profiles.

2.5.4 Correlation Analysis

“Phenotypic and genotypic correlations were computed following the method described” by Singh and Chaundry (1979) as:

$$r_g = \frac{C_{covx,y}}{\sqrt{\sigma^2_{gx} \cdot \sigma^2_{gy}}} \quad r_p = \frac{P_{covx,y}}{\sqrt{\sigma^2_{px} \cdot \sigma^2_{py}}}$$

Where, r_p and r_g are phenotypic and genotypic correlation coefficients, respectively; $P_{covx,y}$ and $g_{covx,y}$ are phenotypic and genotypic covariance between variables x and y, respectively; σ^2_{px} and σ^2_{gx} are phenotypic and genotypic variances for variable x and y respectively.

$$SE(r_p) = \sqrt{\frac{1-r_p^2}{n-2}}$$

The calculated phenotypic correlation values were tested for its significance using t-test:

$$t = \frac{r_p}{SE(r_p)}$$

Where, n is the number of genotypes tested, r_p^2 is phenotypic correlation coefficient, SE (r_p) = Standard error of phenotypic correlation

The calculated "t" values were compared with the tabulated "t" value at (n-2) degree of freedom at 5% level of significance. Where, n is number of genotypes.

$$SEr_{gxy} = \sqrt{\frac{1-r_{gxy}^2}{h^2x} \cdot h^2y}$$

“The coefficients of correlations at genotypic levels were also tested for their significance by the formula described by Robertson (1959) as indicated below:

$$t = \frac{r_{gxy}}{SEr_{gxy}}$$

Where, h^2x = Heritability of trait x and h^2y = Heritability of trait y, SE r_{gxy} = Standard error of genotypic correlation for character x and y. all the analysis was done using SAS software version 9.3” (SAS Institute, 2011).

3. Results and Discussion

3.1 Analysis of Variance Based on Univariate Test of Statistics

Table 2 presents the variability of genotypes based on measured traits using univariate statistics. In this study, sweetpotato virus disease (SPVD) exhibited a total standard deviation (SD) of 2.06, a pooled SD of 0.92, and a between-genotype SD of 1.96, with an R^2 of 0.81 and an F-value of 54.56 ($p < 0.0001$). The results obtained indicates high variability and a tough proportion of variance explained by genotypic differences in response to disease severity which highlighting significant genetic control over SPVD tolerance/resistance (Mwanga et al., 2021; Tugume et al., 2022). Vine length (VL) presented a total SD of 57.00, a pooled SD of 49.7, a between SD of 32.78, an R^2 of 0.30, and an F-value of 5.22 ($p < 0.0001$). It shows the presence of variability among tested genotypes for this trait, as the moderate R^2 indicates that the genetic variation accounts for about 30% of vine length (RL) variability (Falconer & Mackay, 1996), while the significant F-value supports meaningful genetic effects that are important for selecting vigorous growth traits in sweetpotato. Root length had a total SD of 3.60, a pooled SD of 3.14, a between SD of 2.06, an R^2 of 0.30, and an F-value of 5.20 ($p < 0.0001$). This moderate genetic variance as observed with R^2 (30%) suggests partial heritability and the presence of opportunity for improvement this trait through selection (Falconer & Mackay, 1996). Root girth presented a total SD of 9.04, a pooled SD of 8.23, a between SD of 4.6, an R^2 of 0.23, and an F-value of 3.73 ($p < 0.0007$). The lower R^2 (23%) indicates a stronger environmental influence, yet the significant F-value highlights a genetic component important for root girth improvement (Mwanga et al., 2017). AGFW showed a total SD of 6.70, a pooled SD of 3.00, a between SD of 6.37, an R^2 of 0.81, and an F-value of 54.00 ($p < 0.0001$), suggesting strong genetic control over biomass accumulation, which is closely linked to vigor and biomass yield potential.

The NRPP had a total SD of 1.14, a pooled SD of 0.74, a between SD of 0.94, an R^2 of 0.60, and an F-value of 19.00 ($p < 0.0001$). The moderate to high R^2 indicates significant genetic variability, making this trait a key yield component targeted in breeding (Alam et al., 2024b). MYLD showed a total SD of 11.87, a pooled SD of 5.30, a between SD of 11.26, an R^2 of 0.81, and an F-value of 54.21 ($p < 0.0001$). The high genetic variability, as also explained by univariate statistics, including the high R^2 value explained at 81%, shows its suitability as a primary selection trait in breeding programs (Alam et al., 2024b; Merga et al., 2025). UMYLD had a total SD of 0.12, a pooled SD of 0.09, a between SD of 0.09, an R^2 of 0.47, and an F-value of 11.13 ($p < 0.0001$). The moderate R^2 shows influence by both the genetic potential of each genotype and the environment where they were tested, yet it remains relevant for efforts aiming to reduce losses by selecting suitable genotypes with less wastage, i.e., genotypes with low unmarketable root yield (Alam et al., 2024b; Merga et al., 2025). TYLD displayed a total SD of 11.87, a pooled SD of 5.31, a between SD of 11.32, an R^2 of 0.81, and an F-value of 54.47 ($p < 0.0001$). The strong genetic control is shown by univariate statistics and also by the high R^2 , which indicates TYLD as a key trait for sweet potato improvement (Mwanga et al., 2017).

3.2 Association of Traits among Purple-Fleshed Genotypes

Trait associations between nine selected traits were analyzed at both genotypic and phenotypic levels (Table 3). Some traits showed highly significant ($p < 0.01$) or significant ($p < 0.05$) positive correlations, while others exhibited significant negative correlations. Several trait pairs, however, showed non-significant correlations at both levels. Generally, genotypic correlations were stronger than phenotypic correlations, indicating that genetic factors underlie most trait associations. Specifically, SPVD showed significant negative correlations with VL ($r = -0.50$, $r = -0.28$), RL ($r = -0.43$, $r = -0.27$), RG ($r = -0.70$, $r = -0.30$), AGFW ($r = -0.69$, $r = -0.56$), NRPP ($r = -0.82$, $r = -0.62$), MYLD ($r = -0.83$, $r = -0.73$), and TYLD ($r = -0.83$, $r = -0.73$) at both genotypic and phenotypic levels, respectively (Mukasa et al., 2003). A non-significant negative correlation was observed between SPVD and UMYLD ($r = -0.18$) at the phenotypic level 1. (Lamaro et al., 2023). These negative correlations with yield and agronomic traits, particularly at the genotypic level, indicate that increased disease severity is genetically linked to reduced plant performance and, consequently, lower economic yield like root yield. VL exhibited positive correlations with RL, RG, AGFW, NRPP, MYLD, UMYLD, and TYLD, ranging from $r = 0.37$ to $r = 0.71$ at the genotypic level. Phenotypically, VL had significant positive correlations with RL, AGFW, NRPP, MYLD, and TYLD, “the existence of the positive correlation between storage root yield and other traits suggests that the traits could be used as selection criteria for high storage root yield of sweetpotato” (Gasura et al., 2010; Tumwegamire et al., 2011; Gurmu et al., 2017; Ustari et al., 2023). However, a non-significant negative correlation was observed with RG and a non-significant correlation with UMYLD. The presence of positive correlations suggests that longer vines tend to promote better vegetative growth and root production. RL showed

significant positive correlations with most traits, including MYLD ($r=0.73$, $r=0.47$), except for SPVD ($r=-0.43$, $r=-0.27$) (Gasura et al., 2010; Tumwegamire et al., 2011), which had significant negative correlations at both levels. RL also showed a non-significant positive correlation with RG at the phenotypic level. The positive correlations of RL with root yield and related traits suggest that longer roots contribute to improved marketable and total yield, while the moderate phenotypic correlation with UMYLD ($r=0.30$) hints at potential trade-offs or variability in root quality. RG exhibited non-significant negative correlations with VL ($r=-0.14$), non-significant positive correlations with RL ($r=0.05$) and UMYLD ($r=0.08$), and positive and strong correlations with AGFW ($r=0.85$), NRPP ($r=0.42$), MYLD ($r=0.63$), and TYLD ($r=0.63$) at the genotypic level. At the phenotypic level, RG had a significant negative correlation with AGFW ($r=-0.70$). These associations suggest a direct relationship between RG and yield related traits at the genotypic level, indicating environmental influence on root size-yield associations. AGFW showed a significant negative correlation ($r=-0.56$) with SPVD and a non-significant correlation ($r=0.20$) with UMYLD. Significant positive correlations were observed between AGFW and NRPP, MYLD, and TYLD at both genotypic and phenotypic levels, indicating that vigorous vegetative growth supports yield, although weaker phenotypic correlations suggest environmental effects on trait expression. NRPP showed positive and significant correlations with most traits, including MYLD ($r=0.86$, $r=0.73$), UMYLD ($r=0.70$, $r=0.36$), and TYLD ($r=0.86$, $r=0.73$), except for SPVD ($r=-0.86$, $r=-0.62$) at both levels, indicating that higher numbers of roots per plant drive higher yields and represent a key breeding target (Gurmu et al., 2017). MYLD had positive and significant correlations with all traits except SPVD at both genotypic and phenotypic levels. MYLD was highly correlated with TYLD and NRPP, indicating that marketable roots compose most of the total yield.

Table 2. Univariate test of statistics for nine selected traits of purple-fleshed sweetpotato genotypes evaluated at Wondotika site in 2024

Traits	Total standard deviation	Pooled standard deviation	Between standard deviation	R-square	F value	Pr>F
SPVD	2.06	0.92	1.96	0.81	54.56	<0.0001
VL	57.00	49.7	32.78	0.30	5.22	<0.0001
RL	3.60	3.14	2.06	0.30	5.20	<0.0001
RG	9.04	8.23	4.6	0.23	3.73	<0.0007
AGFW	6.70	3.00	6.37	0.81	54.00	<0.0001
NRPP	1.14	0.74	0.94	0.60	19.00	<0.0001
MYLD	11.87	5.30	11.26	0.81	54.21	<0.0001
UMYLD	0.12	0.09	0.09	0.47	11.13	<0.0001
TYLD	11.87	5.31	11.32	0.81	54.47	<0.0001

Where, SPVD=Sweetpotato virus disease, VL=vine length, RL=root length, RG=root girth, AGFW=Above-ground fresh weight, NRPP=Number of root per plant, MYLD=Marketable root yield, UMYLD=Unmarketable root yield, TYLD=Total root yield

Table 3. Genotypic (above diagonal) and phenotypic (below the diagonal) correlation coefficients among nine traits in 9 PFSP genotypes

Variable	SPVD	VL	RL	RG	AGFW	NRPP	MYLD	UMYLD	TYLD
SPVD		-0.50 **	-0.43 **	-0.70 **	-0.69 **	-0.82 ***	-0.83 ***	-0.37 **	-0.83 **
VL	-0.28 **		0.43 **	0.37 **	0.71 **	0.70 **	0.58 **	0.43 **	0.60 **
RL	-0.27 **	0.40 **		0.61 **	0.62 **	0.52 **	0.73 **	0.68 **	0.74 **
RG	-0.30 **	-0.14 ^{ns}	0.05 ^{ns}		0.85 ***	0.42 **	0.63 **	0.08 ^{ns}	0.63 **
AGFW	-0.56 **	0.44 **	0.40 **	0.27 **		0.51 **	0.66 **	0.20 ^{ns}	0.66 **
NRPP	-0.62 **	0.38 **	0.40 **	0.26 **	0.41 **		0.86 ***	0.70 **	0.86 ***
MYLD	-0.73 **	0.41 **	0.47 **	0.26 **	0.58 **	0.73 ***		0.58 **	0.99 ***
UMYLD	-0.18 ^{ns}	0.18 ^{ns}	0.30 **	0.09 ^{ns}	0.10 ^{ns}	0.36 **	0.40 **		0.59 **
TYLD	-0.73 **	0.41 **	0.47 **	0.23 **	0.58 **	0.73 ***	0.99 ***	0.40 **	

Where, SPVD=Sweetpotato virus disease, VL=vine length, RL=root length, RG=root girth, AGFW=Above-ground fresh weight, NRPP=Number of root per plant, MYLD=Marketable root yield, UMYLD=Unmarketable root yield, TYLD=Total root yield

3.3 Coefficients of Variations

3.3.1 Phenotypic and Genotypic Coefficient of Variation

The genotypic and phenotypic coefficients of variation exhibited a broad range for the quantitative traits assessed (Table 4). In this study, environmental variance was lower than the corresponding genotypic variance, indicating.

Table 4. Estimates of variance components, coefficient of variants, heritability and genetic advances of nine quantitative traits including SPVD reaction for nine promising PFSP genotypes evaluated at Hawassa in 2024

No.	Traits	Variance components			Coefficient of variants			Genetic advances	
		σ^2_g	σ^2_p	σ^2_e	GCV%	PCV%	H ² (%)	GA	GAM %
1	SPVD	46.09	46.38	0.86	161.65	162.15	99.41	13.94	331.96
2	VL	12122.24	12898.61	2329.1	98.23	101.33	93.98	219.88	196.18
3	RL	47.75	51.04	9.86	59.57	61.59	93.56	13.77	118.7
4	RG	230.25	253.27	69.05	272.92	286.23	90.91	29.8	536.05
5	AGFW	484.56	487.61	9.14	238.49	239.24	99.38	45.2	489.76
6	NRPP	10.42	10.6	0.55	114.45	115.45	98.27	6.59	233.72
7	MYLD	1514.27	1523.83	28.68	230.12	230.85	99.37	79.91	472.56
8	UYLD	0.09	0.09	0.01	211.09	214.29	97.04	0.6	428.35
9	TYLD	1528.19	1537.79	28.8	229.28	230	99.38	80.28	470.84

that genetic factors contributed more substantially to the total observed variation. This suggests that the studied traits are primarily genetically controlled, offering potential for improvement through breeding and selection strategies (Allard, 1960; Swanckaert et al., 2020). The phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV), as expected (Falconer & Mackay, 1996). The PCV values ranged from 61.60% for RL to 286.23% for RG, whereas the GCV values ranged from 59.60% for RL to 272.92% for RG. Both PCV and GCV values exceeded 20% for all traits (Table 2), indicating high variability and thus presenting opportunities for effective selection of superior genotypes for targeted traits (Singh & Chaudhury, 1985). “Specifically, a high GCV indicates a low influence of environmental factors on the expression of such traits and a greater possibility for improvements through selection and hybridization” (Falconer & Mackay, 1996; Acquah, 2012; Swanckaert et al., 2020). Additionally, Mwanga et al. (2017) reported high PCV and GCV values for vine length, number of storage roots per plant, individual root weight, and storage root fresh weight in sweetpotato. While, traits with low PCV and GCV values suggest a higher influence of the environment on their expression; hence, selection based on the phenotype alone may not be as effective for the improvement of those traits (Sleper & Poehlman, 2006; Rosero et al., 2020). “However, since the PCV values were only slightly greater than the GCV values, the variability due to the genetic constitution of the genotypes was relatively less influenced by environmental factors” (Singh & Chaudhary, 1979). Accordingly, selection for desirable traits should be reasonably effective for sweetpotato improvement.

3.3.2 Estimates of heritability

In this estimates of heritability, all the traits exhibited a very high level of broad-sense heritability, ranging from 93.56% (RL) to 99.41% (SPVD), shown in Table 4, indicating that the studied traits were strongly influenced by genetic factors (Kang, 2020) and conversely, less influenced by environmental factors (Falconer & Mackay, 1996). “These findings are in agreement with a previous report by Mok et al. (1997), who reported high heritability for the number of storage roots per plant and storage root weight per plant in sweetpotato genotypes”. “However, a study by Mugisa et al., (2022) suggested that in sweetpotato, heritability estimates above 60% are quite adequate for achieving good selection advance”. As suggested by Hanson et al. (1956), “heritability estimates alone are not sufficient for predicting the results of selection unless accompanied by information on genetic advance”.

3.3.3 Expected Genetic Advance as Percent of Mean

In the present study, the expected genetic advance, expressed as a percentage of the mean by selecting the top 5% of the genotypes, varied from 118.7% for RL to 536.05% for RG (Table 4). This indicates that selecting the top 5% of high-performing genotypes from the base population could result in an advance of 118.7% to 536.05% over the population mean. “This indicates that selecting the top 5% of high-performing genotypes from the base population could result in an advance of 118.7% to 536.05% over the population mean”. According to Johnson et al. (1955), “the genetic advance as a percentage of the mean (GAM) is categorized as low (0-10%), moderate (10-20%), and high (>20%). In this study, very high expected GAM values were observed for all traits measured, ranging from 118.7% to 536.05% (Table 4). These high GAM values suggest that these characters are largely governed by additive genes, and selection would be rewarding for the further improvement of such traits” (Falconer & Mackay, 1996). Moreover, high heritability coupled with high genetic advance is a strong indicator of the potential for substantial genetic gain from selection and an important factor for predicting the resultant effect of selecting the best individuals (Johnson et al. 1955; Falconer & Mackay, 1996). In the present study, high heritability, coupled with high GAM values, were observed for all traits measured (Table 4) which highlighting that the selection based on these traits would be rewarding.

4. Conclusion

Estimation of genetic parameters and trait associations is essential, as it provides information that enables breeders to effectively exploit the available genetic variability among purple-fleshed genotypes for traits of interest. This study offers valuable insights into trait associations and genetic variability within nine advanced purple-fleshed sweetpotato genotypes across key agronomic and disease-related traits, highlighting their valuable potential for further breeding. The high phenotypic and genotypic coefficients of variation, coupled with significant genetic advance and broad-sense heritability, indicate opportunities for improvement through breeding and selection. The observed trait associations’ further guide targeted breeding efforts, allowing simultaneous improvement of multiple desirable traits and can be used to develop effective selection criteria for identifying suitable PFSP genotypes for diverse purposes. Overall, improved PFSP can significantly contribute to enhancing food and nutrition security, particularly in regions where sweetpotato serves as a staple crop, and it can play a vital role in industrial applications by supplying raw materials, which in turn can add economic value to the crop.

Disclaimer (Artificial Intelligence)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc.) and text-to-image generators have been used during the writing or editing of this manuscript.

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Competing Interests

Authors have declared that no competing interests exist.

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