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TRAIT INTERRELATIONSHIPS GOVERNING GROWTH, YIELD, AND QUALITY IN SWEET POTATO (*IPOMOEA BATATAS* (L.) LAM.) GENOTYPES

Prashanth Hullannavar[1]*, Imamsaheb S. J.[2], Dadapeer Peerajade[3], Gopali J. B.[4] and Arunkumar Bhavidoddi [5]
[1]Department of Vegetable Science, College of Horticulture, U.H.S., Bagalkot, Karnataka, India
[2]AICRP on Tuber Crops, Regional Horticultural Research and Extension Centre,
Kumbapur (Dharwad) - 580005, Karnataka, India.
[3]Department of Genetics and Plant Breeding COH, Bagalkot, Karnataka, India.
[4]ADRE, RHREC, Kumbapur farm, (Dharwad) - 580005, Karnataka, India.
[5]Vegetable science COH, Munirabad, Karnataka, India.
*Corresponding author E-mail: prashanthphullannavar@gmail.com

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ABSTRACT

Twenty-seven elite genotypes of sweet potato (*Ipomoea batatas* (L.) Lam.) were evaluated during the *Rabi* season of 2024–25 at the AICRP on Tuber Crops, Dharwad, Karnataka, to elucidate the genetic variability and interrelationships among growth, yield, and quality attributes. The analysis of variance (ANOVA) indicated highly significant ($p < 0.01$) differences among genotypes for all traits, revealing substantial genetic diversity within the population. The genotypes, comprising 13 purple-fleshed and 14 orange-fleshed types, were characterized for morphological, yield, and biochemical traits including vine length, internodal length, and number of branches vine^{-1}, tuber yield components, and quality constituents such as sugars, starch, β-carotene, anthocyanin, and dry matter content.

Correlation and path coefficient analyses demonstrated that average tuber weight vine^{-1}, number of tubers vine^{-1}, and vine length exerted strong positive direct effects on total tuber yield, identifying them as key selection indices for yield enhancement. The extensive phenotypic variation and significant inter-trait associations observed underscore the presence of a broad genetic base among the evaluated genotypes. These findings provide valuable insights for designing effective breeding strategies aimed at developing high-yielding, nutritionally superior, and pest-tolerant sweet potato cultivars suited to diverse agro-climatic conditions.

***Keywords*:** Analysis of variance, Sweet potato, Growth, Yield, Quality and correlation.

Introduction

Sweet potato (*Ipomoea batatas* (L.) Lam.) is one of the most important starchy root crops cultivated worldwide, valued for its high yield potential, nutritional richness, and capacity to thrive under a broad range of environmental conditions. Belonging to the family *Convolvulaceae*, it is an auto-hexaploid ($2n = 6x = 90$) and a naturally cross-pollinated species that exhibits pronounced heterozygosity and extensive genetic diversity. Its remarkable adaptability to marginal soils, low fertilizer inputs, and erratic rainfall makes it an indispensable component of food and livelihood security, particularly in tropical and subtropical regions. Beyond its agronomic advantages, sweet potato is increasingly recognized as a functional food owing to its rich reserves of carbohydrates, dietary fibre, vitamins, and bioactive compounds. The crop provides a vital source of β-carotene (provitamin A) in orange-fleshed genotypes and anthocyanins in purple-fleshed types, both of which possess strong antioxidant and health-promoting properties.

Globally, sweet potato ranks among the top five food crops, with major production concentrated in Asia, Africa, and South America. In India, it is cultivated across a wide range of agro-climatic zones, particularly in Odisha, Uttar Pradesh, West Bengal, Bihar, Karnataka, and Tamil Nadu (Loebenstein, 2009). Despite its adaptability, the productivity of sweet potato in India remains inconsistent and below the global average. This variation is largely attributable to environmental heterogeneity, suboptimal agronomic practices, and limited region-specific varietal development. The crop's genetic improvement has often been constrained by its complex polyploid nature, which complicates inheritance patterns and hampers the expression of desirable traits. Consequently, a systematic understanding of genetic variability, trait associations, and selection indices is vital for enhancing breeding efficiency and developing genotypes that combine superior yield with nutritional quality.

Yield in sweet potato is a complex, polygenically controlled trait influenced by several interrelated morphological, physiological, and biochemical factors. Traits such as vine length, internodal length, number of branches, and leaf area contribute to canopy architecture and photosynthetic efficiency, while tuber length, diameter, number, and average tuber weight determine sink strength and total yield. Quality attributes such as dry matter, starch, β-carotene, anthocyanin, and sugar content play a crucial role in consumer preference, industrial suitability, and nutritional value. Understanding the nature and magnitude of associations among these traits is therefore essential for identifying key yield determinants and formulating selection criteria for genetic improvement.

Correlation and path coefficient analyses are powerful statistical tools for elucidating the relationships among traits and partitioning total correlation into direct and indirect effects. These methods provide insights into the relative importance of individual characters, enabling breeders to focus on those traits that exert the greatest influence on yield and quality. Previous studies have demonstrated considerable genetic variability among sweet potato genotypes, suggesting ample potential for selection and recombination breeding. However, region-specific investigations integrating yield, quality, and pest-related traits remain limited, particularly under semi-arid conditions such as those prevailing in northern Karnataka.

Against this background, the present study was undertaken to assess the extent of genetic variability and trait interrelationships among 27 elite sweet potato genotypes, comprising both purple- and orange-fleshed types, under the agro-climatic conditions of Dharwad. The investigation aimed to identify key morphological and yield-contributing traits that can serve as reliable selection indices for developing high-yielding, nutritionally enriched, and pest-tolerant cultivars suited to the diverse production environments of southern India.

Materials and Methods

The present investigation was conducted at the All India Coordinated Research Project (AICRP) on Tuber Crops, Regional Horticultural Research and Extension Centre (RHREC), Dharwad, under the University of Horticultural Sciences, Bagalkot, Karnataka, India, during the *Rabi* season of 2024–25. The experimental site falls within the Northern Transition Zone (Agro-Climatic Zone VIII) of Karnataka, forming part of the ecologically significant Western Ghats region. It is situated at an altitude of approximately 768 m above mean sea level and experiences a semi-arid tropical climate characterized by moderate rainfall, warm temperatures, and well-drained lateritic soils of medium fertility. Twenty-seven elite genotypes of sweet potato (*Ipomoea batatas* (L.) Lam.) were evaluated in a Randomized Complete Block Design (RCBD) with three replications. Each plot measured 3.0 × 2.4 m with a spacing of 60 × 20 cm, ensuring uniform plant population and minimizing environmental variability. Recommended agronomic practices for sweet potato cultivation were followed uniformly across all plots, including timely irrigation, weeding, earthing-up, and pest and disease management as per AICRP on Tuber Crops guidelines.

Observations were recorded on five randomly selected plants per replication for growth, yield, and quality traits. Growth parameters such as vine length, internodal length, number of branches per vine, leaf area, and leaf area index were recorded at 120 days after planting. Vine length was measured from the basal node to the vine tip, and internodal length was obtained by dividing total vine length by the number of internodes on the main vine. The number of branches per vine was counted manually, while leaf area was measured using a digital leaf area meter (LICOR LI-3100), and the leaf area index was calculated as the ratio of total leaf area per plant to the ground area occupied. Yield and yield-attributing traits including number of tubers per vine, tuber length, and tuber diameter, average tuber weight per vine, tuber yield per vine, plot yield, and tuber yield per hectare were recorded at harvest. The number of tubers per vine was obtained by counting all harvested tubers, while tuber length and diameter were measured using a measuring scale and Vernier caliper, respectively. Average tuber weight and tuber yield per vine were calculated from total fresh tuber weight, and yield per hectare was extrapolated from plot yield based on the net plot area.

Quality parameters were analyzed from freshly harvested tuber samples. Dry matter content was determined by oven-drying 100 g of sliced tubers at 70 ± 2°C until a constant weight was achieved. Starch content was estimated by the acid hydrolysis method using anthrone reagent (Clegg, 1956) and expressed as a percentage of fresh weight. Reducing sugars were determined by the Nelson–Somogyi method (Somogyi, 1952), and total sugars were estimated by the anthrone method (Hodge and Hofreiter, 1962), while non-reducing sugars were obtained by subtracting reducing sugars from total sugars. The β-carotene content was quantified by the acetone–petroleum ether extraction method (Ranganna, 1986) and expressed in mg 100 g^{-1} fresh weight based on spectrophotometric absorbance at 450 nm. Anthocyanin content was determined by the pH differential method (Giusti and Wrolstad, 2001) and expressed as cyanidin-3-glucoside equivalents.

The data recorded on all quantitative and qualitative parameters were subjected to analysis of variance (ANOVA) following the procedure of Panse and Sukhatme (1957) to test the significance of variability among genotypes. Genotypic and phenotypic correlation coefficients were calculated following Al-Jibouri, Miller, and Robinson (1958) to determine the magnitude and direction of association among growth, yield, and quality traits. Path coefficient analysis was carried out according to the method of Wright (1921), later elaborated by Dewey and Lu (1959), to partition correlation coefficients into direct and indirect effects and identify traits exerting the most substantial influence on tuber yield. All statistical analyses were performed using standard biometrical techniques to ensure accuracy, precision, and reproducibility of results.

Result and Discussion

The analysis of variance revealed highly significant differences ($p < 0.01$) among all twenty-seven sweet potato (*Ipomoea batatas* (L.) Lam.) genotypes for growth, yield, and quality traits (Table 1), indicating the presence of substantial genetic variability within the test population. Pronounced variability was observed across morphological, yield, and biochemical parameters such as vine length, internodal length, number of branches per vine, number of tubers per vine, tuber length, tuber diameter, average tuber weight, and biochemical constituents including starch, sugars, β-carotene, anthocyanin, and dry matter content. The wide genetic divergence among the evaluated entries provides a strong foundation for effective selection and hybridization in sweet potato improvement programmes. Genetic variability in quantitative traits is a prerequisite for identifying potential donors and formulating selection indices for yield and quality improvement. Similar findings of substantial genotypic variation for growth and yield parameters in sweet potato have been reported by Biswas *et al.* (2021), Bali *et al.* (2021), and Choudhary *et al.* (2023), affirming that diverse genotypes harbor considerable scope for selection under contrasting environments. The high magnitude of genotypic variance, coupled with significant differences among entries, confirms the presence of a broad genetic base suitable for selection-driven improvement in yield potential and nutritional composition.

Correlation studies elucidate the degree and direction of association among traits, thereby guiding breeders in the simultaneous improvement of correlated characters. Phenotypic correlation reflects the combined influence of genetic and environmental factors, whereas genotypic correlation provides a more accurate measure of true hereditary association (Falconer and Mackay, 1996; Singh and Chaudhary, 1985). In the present study, the close agreement between genotypic and phenotypic correlations for most traits indicates limited environmental interference, underscoring the stability of inherent genetic relationships (Fig. 1).

Tuber yield per vine exhibited strong and highly significant positive correlations with vine length, number of branches per vine, internodal length, number of tubers per vine, tuber length, tuber diameter, and average tuber weight. This indicates that improvement in any of these characters will likely enhance total tuber yield. These findings are in accordance with Mekonnen *et al.* (2020) and Bali *et al.* (2021), who also reported strong associations of vine length, tuber number, and tuber weight with yield. Recent genomic studies have reinforced these associations through the identification of major QTLs linked to tuber number and weight in sweet potato and related *Ipomoea* species (Yada *et al.*, 2020; Mwanga *et al.*, 2022; Li *et al.*, 2023).

Conversely, leaf area exhibited a significant negative correlation with yield and yield components, suggesting a possible source–sink imbalance where excessive vegetative growth limits assimilate partitioning toward storage roots. This observation aligns with findings by Prarthana *et al.* (2014), Villordon *et al.* (2020), and Khan *et al.* (2022), who emphasized that higher canopy density and delayed senescence may restrict carbohydrate translocation, ultimately reducing tuber bulking efficiency.

While correlation quantifies association, it does not necessarily imply causation. To delineate true cause–effect relationships among yield components, path coefficient analysis was employed following the method of Wright (1921) as refined by Dewey and Lu (1959). The analysis partitioned the total correlation into direct and indirect effects (Table 2), enabling identification of the most influential traits governing yield performance.

Results indicated that vine length, internodal length, leaf area, tuber length, number of tubers per vine, and average tuber weight exerted strong positive direct effects on total tuber yield. Among these, average tuber weight emerged as the most dominant yield-determining trait, suggesting that it can serve as a reliable and stable selection criterion for enhancing productivity. These outcomes corroborate reports by Hajjam *et al.* (2019) and Mekonnen *et al.* (2020), where tuber weight and tuber number were identified as key contributors to total yield under tropical and subtropical conditions.

Internodal length exhibited both direct and indirect contributions to yield, primarily mediated through vine length and tuber weight, as observed by Gurmu *et al.* (2018) and Choudhary *et al.* (2021). Although tuber diameter had a negative direct effect on yield, its positive indirect influence through average tuber weight resulted in an overall positive correlation-suggesting compensatory growth relationships, consistent with Sharavati *et al.* (2018). Leaf area, on the other hand, demonstrated a negative direct effect but positive indirect effects through vine length and tuber weight, reaffirming the source–sink trade-off noted in earlier studies (Villordon *et al.*, 2020; Khan *et al.*, 2022).

Recent integrative analyses further support these findings: Das *et al.* (2021) and Mwanga *et al.* (2022) highlighted that the yield compensation mechanism in sweet potato involves a dynamic balance between tuber number and individual tuber weight, shaped by both genetic regulation and environmental adaptation. Thus, genotypes with optimal source–sink coordination and higher average tuber weight tend to achieve superior yield stability and energy-use efficiency under diverse agro-ecological conditions.

Conclusion

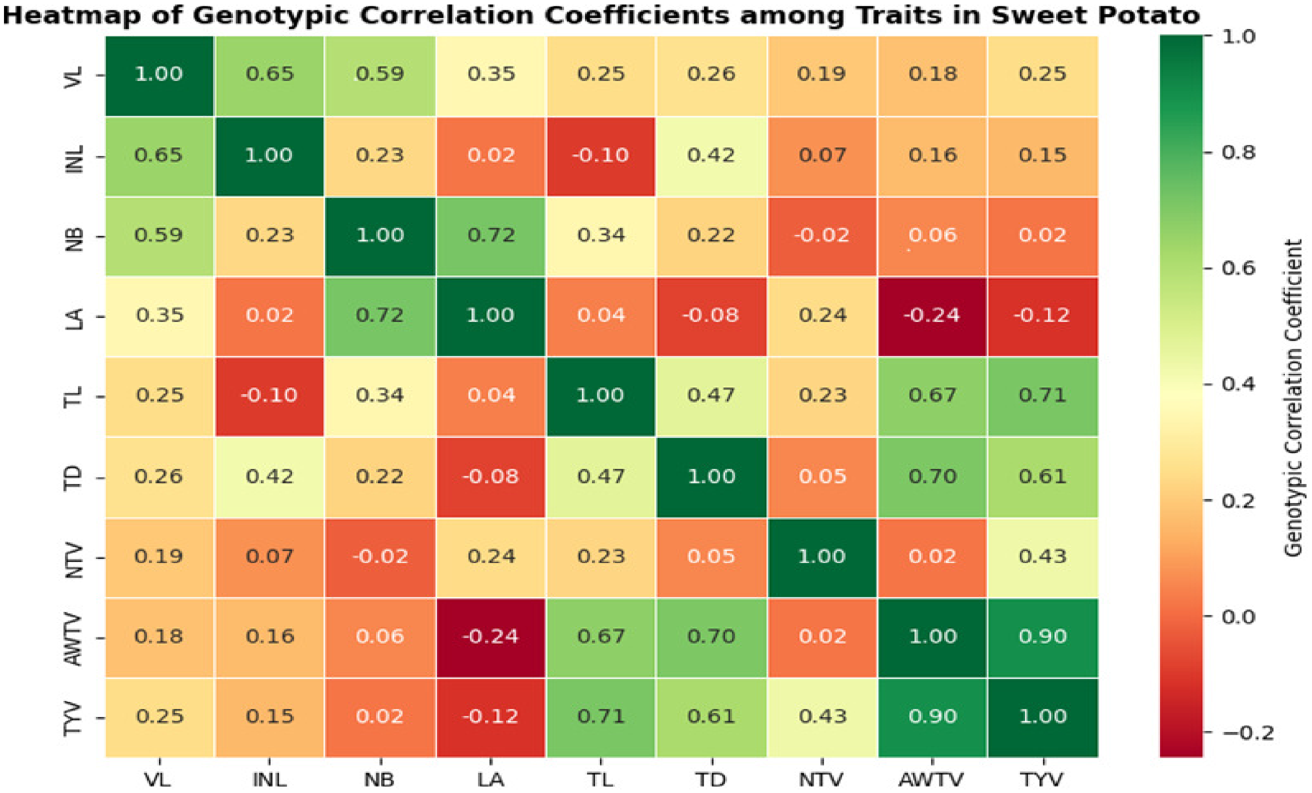
The present investigation demonstrated pronounced genetic variability among twenty-seven elite sweet potato (*Ipomoea batatas* (L.) Lam.) genotypes evaluated under the semi-arid conditions of Dharwad. The highly significant differences observed across all growth, yield, and quality traits confirm the existence of a broad genetic base, providing ample scope for effective selection and varietal improvement. Correlation and path coefficient analyses provided deeper insights into the interrelationships among traits influencing yield performance. Vine length, internodal length, number of tubers per vine, and particularly average tuber weight exhibited strong positive direct effects on tuber yield, indicating their pivotal role in yield determination. The consistency between genotypic and phenotypic correlations suggested that these relationships were largely governed by genetic factors and were relatively stable across environments. Conversely, excessive leaf area demonstrated a negative direct association with yield, highlighting the importance of maintaining an optimal source–sink balance for efficient assimilate partitioning and storage root development.

Overall, average tuber weight emerged as the most reliable and efficient selection index for yield enhancement in sweet potato breeding programmes. The identification of these key yield-contributing traits provides a practical framework for developing high-yielding, nutritionally rich, and climate-resilient cultivars. Integrating these findings into selection and hybridization strategies will significantly strengthen ongoing efforts toward the genetic improvement and sustainable intensification of sweet potato production in diverse agro-ecological regions.

Table 1 : Analysis of variability for growth, yield and quality traits among sweet potato genotypes

S. No	Source of variance/ characters	Treatment	Replication	Error	SEm±	CD (5%)	CD (1%)
	Degree of freedom	26	2	52			
1	Vine length (cm)	20536.61	136.54	265.43	9.41	26.69	35.57
2	internodal length (cm)	5.84	0.30	0.15	0.22	0.64	0.85
3	Number of branches vine^{-1}	15.01	2.01	0.80	0.40	1.13	1.51
4	Leaf area (cm^2)	5729911.21	213748.60	121592.30	201.32	571.32	761.25
5	Leaf area index	3.98	0.15	0.08	0.17	0.48	0.63
6	Tuber length (cm)	27.24	6.03	3.45	1.07	3.05	4.06
7	Tuber diameter (cm)	2.31	0.48	0.20	0.26	0.73	0.97
8	Number of tubers vine^{-1}	1.27	0.42	0.14	0.22	0.62	0.82
9	Average weight of tuber vine^{-1}	914.38	312.88	124.60	6.44	18.29	24.37
10	Tuber yield vine^{-1}	19456.12	3777.96	1364.82	21.33	60.53	80.65

11	Tuber yield plot^{-1} (kg/plot)	50.61	9.83	3.55	1.09	3.09	4.11
12	Tuber yield (t/ha)	97.64	18.96	6.85	1.51	4.29	5.71
13	Harvest index (%)	238.92	14.99	17.42	2.41	6.84	9.11
14	Pest incidence (%)	0.28	0.19	0.08	0.16	0.45	0.6
15	Reducing sugar (%)	2.62	0.03	0.07	0.15	0.43	0.57
16	Non-reducing sugar (%)	14.79	0.84	0.80	0.52	1.46	1.95
17	Starch comtent(%)	22.86	0.96	1.59	0.73	2.07	2.75
18	Total sugar (%)	5.98	0.01	0.02	0.08	0.23	0.31
19	β-carotene content (mg 100g $^{-1}$FW)	40.95	0.14	0.16	0.23	0.65	0.87
20	Anthocyanin content (mg 100g $^{-1}$ FW)	2804.17	2.20	0.97	0.57	1.61	2.15
21	Dry matter content (%)	36.50	5.87	2.24	0.86	2.45	3.27



	VL	INL	NB	LA	TL	TD	NTV	AWTV	TYV
VL	1.00	0.65	0.59	0.35	0.25	0.26	0.19	0.18	0.25
INL	0.65	1.00	0.23	0.02	-0.10	0.42	0.07	0.16	0.15
NB	0.59	0.23	1.00	0.72	0.34	0.22	-0.02	0.06	0.02
LA	0.35	0.02	0.72	1.00	0.04	-0.08	0.24	-0.24	-0.12
TL	0.25	-0.10	0.34	0.04	1.00	0.47	0.23	0.67	0.71
TD	0.26	0.42	0.22	-0.08	0.47	1.00	0.05	0.70	0.61
NTV	0.19	0.07	-0.02	0.24	0.23	0.05	1.00	0.02	0.43
AWTV	0.18	0.16	0.06	-0.24	0.67	0.70	0.02	1.00	0.90
TYV	0.25	0.15	0.02	-0.12	0.71	0.61	0.43	0.90	1.00

Fig 1. Shows critical value

*** = significant at 0.05 %,**

**** = significant at 0.01 %**

G = Genotype correlation coefficient

P = Phenotypical correlation coefficient

VL - Vine length (cm)
INL - Internodal length (cm)
NB - Number of branches vine $^{-1}$
LA - Leaf area (cm²)
TL - Tuber length (cm)
TD - Tuber diameter (cm)
NTV - Number of tubers vine $^{-1}$
AWTV - Average weight of tuber vine $^{-1}$ (g)
TYV - Tuber yield vine^{-1} (g)

Fig. 1 : Estimation of genotypic correlation coefficient and phenotypic correlation coefficient

Table 2 : Estimation of path correlation coefficient analysis of yield and yield components

Traits	VL	INL	NB	LA (cm²)	TL	TD	NTV	AWTV	TYV
VL	**0.052**	0.003	-0.061	0.019	0.018	-0.015	0.073	0.158	0.247
INL	0.034	**0.005**	-0.024	0.001	-0.007	-0.024	0.028	0.142	0.154
NB	0.031	0.001	**-0.103**	0.040	0.024	-0.012	-0.009	0.049	0.021
LA (cm²)	0.018	0.001	-0.074	**0.056**	0.003	0.005	0.092	-0.218	-0.118
TL	0.013	0.001	-0.035	0.002	**0.071**	-0.026	0.087	0.599	0.710
TD	0.014	0.002	-0.023	-0.005	0.033	**-0.056**	0.020	0.627	0.612
NTV	0.001	0.001	0.002	0.014	0.016	-0.003	**0.375**	0.017	0.432
AWTV	0.009	0.001	-0.006	-0.014	0.048	-0.039	0.007	**0.890**	0.896

Residual effect square = 0.0199

VL - Vine length (cm)
INL - Internodal length (cm)
NB - Number of branches vine $^{-1}$
LA - Leaf area (cm²)
TL - Tuber length (cm)
TD - Tuber diameter (cm)
NTV - Number of tubers vine $^{-1}$
AWTV - Average weight of tuber vine $^{-1}$ (g)
TYV - Tuber yield vine^{-1} (g)

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