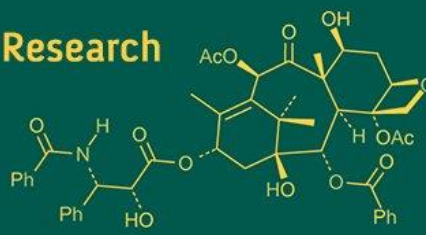
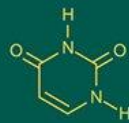


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Phenotypic and genotypic correlation and path coefficient analysis for storage root yield and its contributing traits in sweet potato (*Ipomoea batatas* (L.) Lam.) Genotypes

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Abstract

The primary objective of this study was to investigate the nature and magnitude of phenotypic and genotypic associations among yield and yield-contributing traits in sweet potato genotypes. Understanding these relationships is critical for enhancing storage root yield per plant. Fourteen traits - days to sprouting, leaf area, stem girth, number of vines per plant, storage root length, storage root diameter, average storage root weight, crude fat content, protein content, dry matter content, total soluble solids, iron, zinc, and storage root yield per plant - were evaluated using correlation and path coefficient analysis. The results indicated that genotypic correlation coefficients were consistently higher than phenotypic correlation coefficients, reflecting strong inherent trait associations. Storage root yield per plant showed strong positive phenotypic and genotypic correlations with leaf area, stem girth, number of vines per plant, storage root length, storage root diameter, average storage root weight, and total soluble solids. In contrast, dry matter content exhibited a notable negative association with storage root yield per plant. Path coefficient analysis further revealed that leaf area, stem girth, storage root diameter, and average storage root weight exerted major direct positive effects on storage root yield per plant, with phenotypic and genotypic residual effects of 0.1472 and 0.0202, respectively. Consequently, these traits are recommended as reliable selection indices for the genetic improvement of sweet potato yield.

Keywords: Sweet potato, correlation analysis, path coefficient analysis, yield components, selection indices

Introduction

Sweet potato (*Ipomoea batatas* (L.) Lam.) is a globally significant root crop recognized for its substantial contribution to food security, particularly in developing nations where it supports livelihoods in marginal environments (George *et al.*, 2024) [5]. Its importance is underscored by its favorable nutritional profile-rich in starch, fiber, protein, and essential micronutrients-and its capacity to ensure food security due to its drought tolerance, wide ecological adaptation, and relatively short maturity cycle. Beyond basic sustenance, the integration of orange-fleshed and purple-fleshed cultivars addresses specific nutritional gaps, such as vitamin A deficiency and antioxidant requirements, while simultaneously offering opportunities for commercialization through functional food processing (Mohanraj and Sivasankar, 2014) [12]. However, maximizing the potential of this crop is frequently constrained by its high heterozygosity and hexaploid genome, which complicate the identification of favourable genotypes through traditional breeding practices.

In sweet potato improvement, storage root yield is a complex, polygenic trait influenced by a suite of morphological and quality characteristics (Mohanty *et al.*, 2016; Wani *et al.*, 2025). Breeders often rely on character association studies to identify effective selection indices, as direct selection for yield alone is frequently inefficient (Wani *et al.*, 2025). Earlier investigations into sweet potato have consistently demonstrated significant phenotypic and genotypic correlations between yield and various traits, such as leaf area, stem girth, storage root morphology, and vine architecture (Gurmu *et al.*, 2017 and Wani *et al.*, 2025) [6, 13, 17]. Such associations are essential for understanding the genetic basis of yield variability;

however, simple correlation analysis provides only a measure of the strength and direction of these relationships without revealing the underlying causal mechanisms.

A fundamental limitation of simple correlation is its inability to account for the direct and indirect effects of predictor variables on yield, which can lead to misleading selection strategies if a high correlation is driven by the influence of a third factor rather than a direct relationship (Dewey and Lu, 1959). To circumvent this, path coefficient analysis, as formulated by (Wright, 1934) [4, 18], provides a robust statistical framework by partitioning correlation coefficients into direct and indirect contributions. This technique allows researchers to determine which morphological or quality traits exert the most significant influence on storage root yield, thereby facilitating more precise and efficient selection pressure (Mekonnen *et al.*, 2020). By identifying these key yield-contributing traits through the dissection of these complex interrelationships, breeders can navigate the inherent genetic diversity of the sweet potato genome to achieve reliable improvements in yield (Hullannavar *et al.*, 2025) [8, 11].

The present study aims to evaluate the interrelationships among various morphological, yield, and quality attributes in a diverse set of sweet potato genotypes. By employing both correlation and path coefficient analyses, this study seeks to elucidate the relative importance of traits including days to sprouting, leaf area, stem girth, and storage root quality components in determining storage root yield per plant. The primary objective is to define the direct and indirect pathways influencing yield, thereby identifying reliable selection indices that can streamline future sweet potato breeding programs aimed at developing high-yielding and nutritionally superior varieties.

Materials and Methods

Study Area and Experimental Design

The investigation was carried out during the rabi season (2025-2026) at the regional station, ICAR-CTCRI, Bhubaneswar, Odisha. Thirty-five sweet potato genotypes were assessed by adopting the randomized block design in two replications with in a plot size and spacing of recommended standards prescribed by the CTCRI

Data were recorded for 14 traits: Days to sprouting, Leaf area, Stem girth, Number of vines per plant, Storage root length, Storage root diameter, Average storage root weight, Crude fat content, Protein content, Dry matter content, Total soluble solids, Iron, Zinc, and the dependent variable, Storage root yield per plant.

Procedures for Trait Measurement

Morphological and yield-related traits were recorded using standard field procedures. Leaf area (LA) was estimated using the established formula: where and represent leaf length and breadth, respectively. The number of vines per plant was determined by direct counting. Vine and root dimensions, including Storage root length and Storage root diameter, were measured. The Average storage root weight and Storage root yield per plant were recorded by weighing fresh roots using a digital precision balance at the time of harvest.

Biochemical and quality traits were determined in the laboratory using established protocols. Dry matter content was calculated by drying fresh root slices in an oven at 60-70 °C until a constant weight was achieved (Reddy *et al.*, 2017). Total soluble solids were measured using a digital

refractometer and expressed in °Brix (Ranganna, 2008) [14]. Crude fat content was determined via the Soxhlet extraction method using petroleum ether or hexanes as solvents. Protein content was analyzed using the micro-Kjeldahl digestion and distillation method, applying the standard 6.25 nitrogen-to-protein conversion factor (Jones, 1931) [9]. Mineral concentrations were quantified using an atomic absorption spectrophotometer following wet digestion of samples with a nitric-perchloric acid mixture.

Statistical Analysis

Data were subjected to phenotypic and genotypic correlation and path coefficient analysis. Phenotypic and genotypic correlation coefficients were calculated using variance and covariance components, as described by Al-Jibouri *et al.* (1958). Path coefficient analysis was employed to partition the correlation coefficients into direct and indirect effects, following the methodology originally proposed by (Dewey and Lu, 1959). The path analysis involved solving a set of simultaneous equations where storage root yield per plant (SRYP) was treated as the dependent variable [1, 4].

Results, Discussion, and Conclusion

Results

The correlation analysis revealed that Storage root yield per plant exhibited strong, positive, and statistically significant correlations with Leaf area, Stem girth (SG), Number of Vines per Plant (NVP), Storage Root Length (SRL), Storage Root Diameter (SRD), and Average storage root weight at both genotypic and phenotypic levels ($P < 0.01$). Total soluble solids also showed a significant positive genotypic correlation with SRYP. In contrast, Dry matter content showed notable negative phenotypic ($r = -0.2573$, $P < 0.05$) and genotypic associations with SRYP. Among the independent yield-contributing traits, strong positive associations were observed, particularly among LA, SG, NVP, SRL, and SRD. General observation across the trait pairs was that genotypic correlation coefficients exceeded the corresponding phenotypic correlation coefficients. Other statistically significant associations were recorded for days to sprouting with NVP, and Crude fat content with Zinc and Iron.

The path coefficient analysis partitioned these associations into direct and indirect effects. Leaf area exerted the largest positive direct effect on SRYP (Phenotypic: 0.4669; Genotypic: 0.6960), followed by Stem girth (Phenotypic: 0.2846; Genotypic: 0.1967) and Storage root diameter (Phenotypic: 0.2075). The results are in line with Tirkey *et al.* (2011) [16]. The other traits, including Number of vines per plant, Storage root length, and Average storage root weight, also demonstrated positive direct contributions. Similar results were observed by Harriman *et al.*, 2023 to yield Negative direct or indirect contributions were observed for traits such as Dry matter content, Protein content, and Iron in various combinations. The residual effects for the phenotypic and genotypic path analyses were 0.1472 and 0.0203, respectively, indicating that the measured variables accounted for a substantial proportion of the variation in storage root yield. The results are line with Bhadauriya *et al.*, 2018 [3, 7].

Discussion

The results of this study demonstrate that trait association analysis is an essential tool for sweet potato breeding,

providing a robust framework for selecting high-yielding genotypes. The strong positive genotypic and phenotypic correlations observed between SRYP and primary morphological traits-specifically LA, SG, SRL, SRD, and ASRW-align with findings in other sweet potato germplasm studies Mekonnen *et al.*, 2020; Wani *et al.*, 2025). These traits function as reliable direct selection indices because they possess both significant positive associations and substantial positive direct effects on storage root yield (Bali *et al.*, 2021). The path analysis results further validate that these morphological attributes are not merely indirectly correlated but are major drivers of yield potential (Bhadauriya *et al.*, 2018.)^[2, 3, 11, 17].

A consistent pattern emerged where genotypic correlation coefficients were higher than phenotypic coefficients for the majority of trait pairs. This phenomenon can be attributed to the "masking effect" of the environment on the phenotypic expression of traits, whereas genotypic correlations reflect the inherent genetic relationships, such as pleiotropy and linkage. This divergence suggests that selection based on

genotypic associations is more reliable, as it represents the heritable component of trait variation.

The significant negative association between DMR and SRYP is a critical finding for breeding programs. While high dry matter is often a desired quality trait, its negative correlation with yield indicates a trade-off that complicates simultaneous improvement (Sharavati *et al.* 2018). This negative relationship suggests that allocating photo-assimilates towards high-volume storage root development (as indicated by the positive contribution of LA and SRD) may inherently limit the concentration of dry matter, a pattern previously documented in diverse sweet potato accessions.

The path analysis proved superior to simple correlation in deciphering the complex web of interactions. For example, while some traits showed high phenotypic correlations, the path analysis clarified their direct versus indirect contributions, providing a more precise selection guide (Gurmu *et al.*, 2017). By identifying LA, SG, SRL, SRD, and ASRW as having the largest positive direct effects, this study provides actionable criteria for breeders to increase storage root yield effectively (Mekonnen *et al.*, 2020)^[6, 11, 15].

Table 1: Estimates of phenotypic and Genotypic correlation coefficient for growth, yield and quality parameters in sweet potato genotypes

TRAITS		DSP	LA	SG	NVP	SRL	SRD	ASRW	FAT	PRO	DMR	TSS	IRN	ZNC	SRYP	
DSP	P	1.000 **	0.0821	0.1754	0.1929	-0.0072	0.0921	0.0831	-0.195	-0.0833	0.2045	0.0287	-0.0459	0.0387	0.1646	
	G	1.000 **	0.1267	0.2619	0.3332	-0.0079	0.1483	0.159	-0.2764	-0.064	0.2808	0.075	-0.0491	0.0245	0.2497	
LA	P		1.000**	0.6783 **	0.6422 **	0.5788 **	0.6365 **	0.7285 **	0.2742 *	-0.1719	-0.3255**	0.2597*	-0.0114	-0.0817	0.8579 **	
	G		1.000 **	0.8774**	0.6848**	0.6747**	0.7221**	0.7833**	0.2841	-0.1688	-0.3343*	0.2721	-0.0157	-0.09	0.9554**	
SG	P			1.000 **	0.4946 **	0.4905 **	0.5728 **	0.638 **	0.1925	-0.0476	-0.1996	0.3114**	0.0493	0.0926	0.7837 **	
	G			1.000 **	0.7319**	0.6551**	0.7309**	0.7347**	0.2346	-0.0494	-0.2469	0.3621*	0.061	0.1264	0.9412**	
NVP	P				1.000 **	0.3628 **	0.5366 **	0.5719 **	-0.0286	-0.0292	0.0666	0.3416**	-0.116	0.0324	0.6503 **	
	G				1.000 **	0.4754**	0.6585**	0.6717**	-0.0336	-0.0304	0.0833	0.3923*	-0.1268	0.0254	0.7561**	
SRL	P					1.000 **	0.5541 **	0.6958 **	0.0716	-0.1234	-0.1711	0.0938	-0.0426	-0.0695	0.6025 **	
	G					1.000 **	0.5807**	0.8101**	0.0772	0.1513	-0.169	0.1189	-0.0517	-0.0615	0.6632**	
SRD	P						1.000 **	0.7672 **	0.2347	0.1157	-0.1395	0.1719	-0.007	0.2142	0.722 **	
	G						1.000 **	0.8383**	0.2439	0.1079	-0.1503	0.2022	-0.0006	0.2293	0.7484**	
ASRW	P							1.000 **	0.1746	-0.0331	-0.1857	0.2495*	-0.1739	-0.0104	0.7238 **	
	G							1.000 **	0.1834	-0.0267	-0.1969	0.2793	-0.186	-0.0172	0.7783**	
FAT	P								1.000 **	-0.3293**	-0.2247	0.0735	0.3311**	0.0739	0.2232	
	G								1.000 **	-0.3332	-0.227	0.0738	0.3332	0.0745	0.2318	
PRO	P									1.000**	0.0633	-0.0734	-0.201-0.2046	0.2232	-0.0651	
	G									1.000 **	0.0618	-0.0748		0.2297	-0.0692	
DMR	P										1.000 **	-0.258*	-0.1092	0.0018	-0.2573 *	
	G										1.000 **	-0.2662	-0.1117	-0.0037	-0.2808	
TSS	P											1.000**	0.0424	0.2493*	0.3067 **	
	G											1.000 **	0.0419	0.2615	0.3205	
IRN	P												1.000 **	0.4075**	-0.0069	
	G												1.000 **	0.4109*	0.0013	
ZNC	P													1.000**	0.0673	
	G													1.000 **	0.0717	
SRYP	P														1.000 **	
	G														1.000 **	
DSP	:	Days to sprouting				SRD	:	Storage root diameter				TSS	:	Total soluble solids		
LA	:	Leaf area				ASRW	:	Average storage root weight				IRN	:	Iron		
SG	:	Stem girth				FAT	:	Crude fat content				ZNC	:	Zinc		
NVP	:	Number of vines per plant				PRO	:	protein content				SRYP	:	Storage root yield per plant		
SRL	:	Storage root length				DMR	:	Dry mater content					:			

Table 2: Estimates of Phenotypic and Genotypic path coefficients for growth, yield and quality parameters in sweet potato genotypes

TRAITS		DSP	LA	SG	NVP	SRL	SRD	ASRW	FAT	PRO	DMR	TSS	IRN	ZNC	SRYP
DSP	P	0.0577	0.0383	0.0503	0.0206	-0.0009	0.0191	-0.01085	-0.005	-0.0017	-0.0073	0.0007	0.0019	0.0015	0.1646
	G	0.1194	0.0881	0.0515	0.0544	-0.0008	-0.0096	-0.0147	-0.0202	-0.0048	-0.0166	-0.0025	0.0025	0.0031	0.2497
LA	P	0.0047	0.4669	0.1876	0.0684	0.0737	0.132	-0.0951	0.0071	-0.0035	0.0116	0.007	0.0004	-0.0033	0.8579 **
	G	0.0151	0.6960	0.1726	0.1118	0.0715	-0.0468	-0.0726	0.0208	-0.0129	0.0198	-0.0092	0.0008	-0.0116	0.9554 **
SG	P	0.0105	0.3184	0.2846	0.0535	0.0626	0.1183	-0.08369	0.0052	-0.0011	0.0071	0.0085	-0.0021	0.0038	0.7837 **
	G	0.0312	0.6107	0.1967	0.1196	0.0694	-0.0474	-0.0681	0.0171	-0.0037	0.0146	-0.0122	-0.0032	0.0163	0.9412 **
NVP	P	0.0111	0.2999	0.1380	0.1067	0.0462	0.1113	-0.07465	-0.0007	-0.0005	-0.0023	0.0091	0.0049	0.0013	0.6503 **
	G	0.0397	0.4766	0.1440	0.1633	0.0504	-0.0427	-0.0623	-0.0024	-0.0023	-0.0049	-0.0133	0.0066	0.0032	0.7561 **

SRL	P	-0.0004	0.2702	0.1354	0.0387	0.1273	0.1150	-0.09083	0.0018	-0.0025-0.0115	0.0061	0.0025	0.001	-0.0028	0.6025 **
	G	-0.0009	0.4696	0.1288	0.0776	0.1060	-0.0376	-0.0751	0.0056		0.0100	-0.004	0.0026	-0.0079	0.6632**
SRD	P	0.0053	0.2971	0.1569	0.0572	0.0706	0.2075	-0.10015	0.0061	0.0023	0.0049	0.0046	0.0003	0.0088	0.722 **
	G	0.0177	0.5025	0.1437	0.1075	0.0615	-0.0649	-0.0777	0.0178	0.0082	0.0089	-0.0068	0.00003	0.0296	0.7484**
ASRW	P	0.0048	0.34	0.1764	0.0609	0.0886	0.1591	0.1305	0.0045	-0.0006	0.0066	0.0067	0.0073	-0.0004	0.7238 **
	G	0.0189	0.5452	0.1445	0.1097	0.0859	-0.0544	0.0927	0.0134	-0.0020	0.0116	-0.0094	0.0096	-0.0022	0.7783**
FAT	P	-0.0111	0.1281	0.0557	-0.003	0.0092	0.0487	-0.02279	0.0260	-0.0067	0.008	0.0019	-0.014	0.003	0.2232
	G	-0.033	0.1977	0.0461	-0.0054	0.0081	-0.0158	-0.0170	0.0732	-0.0254	0.0134	-0.0025	-0.0173	0.0096	0.2318
PRO	P	-0.0048	-0.0802	-0.0149	-0.0030	-0.0157	0.024	0.00432	-0.0085	0.0206	-0.0022	-0.0019	0.0085	0.0091	-0.0651
	G	-0.0076	-0.1174	-0.0097	-0.0049	-0.0160	-0.007	0.0024	-0.0244	0.0764	-0.0036	0.0025	0.0106	0.0296	-0.0692
DMR	P	0.0117	-0.152	-0.0551	0.0070	-0.0217	-0.0289	0.02424	-0.0058	0.0013	-0.0357	-0.0069	0.0046	0.00008	-0.2573 *
	G	0.0335	-0.2327	-0.0485	0.0136	-0.0179	0.0097	0.0182	-0.0166	0.0047	-0.0592	0.0089	0.0058	-0.0004	-0.2808
TSS	P	0.0016	0.1213	0.0872	0.0363	0.0119	0.0356	-0.03257	0.0019	-0.0015	0.0092	0.0269	-0.0018	0.0102	0.3067 **
	G	0.0089	0.1893	0.0712	0.0640	0.0126	-0.0131	-0.0259	0.0054	-0.0057	0.0157	-0.0338	-0.0022	0.0337	0.3205
IRN	P	-0.0026	-0.0053	0.0136	-0.0123	-0.0054	-0.0014	0.0227	0.0086	-0.0041	0.0039	0.0011	-0.0423	0.0167	-0.0069
	G	-0.0058	-0.0109	0.012	-0.0207	-0.0054	-0.00004	0.0172	0.0244	-0.0156	0.0066	-0.0014	-0.052	0.0530	0.0013
ZNC	P	0.0022	-0.0381	0.0256	0.0035	-0.0088	0.0444	0.00136	0.0019	0.0046	-0.00007	0.0067	-0.0172	0.0411	0.0673
	G	0.0029	-0.0626	0.0248	0.0041	-0.0065	-0.0148	0.0016	0.0054	0.0175	0.0002	-0.0088	-0.0214	0.1291	0.0717

Phenotypic Residual effect = 0.1472 Genotypic Residual effect = 0.0203 ** Significant at 1% level

Bold and Diagonal values indicate direct effect on yield

DSP	:	Days to sprouting	SRD	:	Storage root diameter	TSS	:	Total soluble solids
LA	:	Leaf area	ASRW	:	Average storage root weight	IRN	:	Iron
SG	:	Stem girth	FAT	:	Crude fat content	ZNC	:	Zinc
NVP	:	Number of vines per plant	PRO	:	protein content	SRYP	:	Storage root yield per plant
SRL	:	Storage root length	DMR	:	Dry mater content		:	

Conclusion

This study confirms that the genetic architecture of sweet potato yield is defined by strong inter-trait associations. Genotypic correlations were generally higher than their phenotypic counterparts, indicating that observed trait relationships are primarily governed by genetic factors rather than environmental fluctuations. The traits Leaf area, Stem girth, Storage root length, Storage root diameter, and Average storage root weight exerted the most significant direct positive effects on Storage root yield per plant. These variables are highly effective as selection criteria for sweet potato breeding programs aimed at improving storage root yield, as they allow for the simultaneous identification of high-performing genotypes while accounting for the trade-offs associated with quality traits like Dry matter content.

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Conflict of interest

The authors declare that there is no conflict of interest regarding the publication of this paper.

References

- Al-Jibouri HA, Miller PA, Robinson HV. Genotypic and environmental variances and covariances in an upland cotton cross of interspecific origin. *Agron J*. 1958;50:533-536. doi:10.2134/agronj1958.00021962005000100020x.
- Bali BI, Thakur P, Singh D, et al. Character association studies in sweet potato (*Ipomoea batatas*). *Int J Curr Microbiol Appl Sci*. 2021;10:1224-1232.
- Bhadauriya PS, Deo C, Ram CN, Verma SK, Singh S. Studies on genetic variability, heritability, genetic advance, correlation coefficient and divergence analysis in sweet potato (*Ipomoea batatas* L.). *Indian J Hill Farming*. 2018;31(1):207-213.
- Dewey DR, Lu KH. A correlation and path analysis of components of crested wheat grass seed production. *Agron J*. 1959;51:515-518.
- George J, Reddy GVP, Wadl PA, Rutter W, Culbreath J, Lau PW, et al. Sustainable sweet potato production in the United States: Current status, challenges, and opportunities. *Agron J*. 2024;116(2):630-660.
- Gurmu F, Shimelis H, Laing M. Correlation and path-coefficient analyses of root yield and related traits among selected sweetpotato genotypes. *S Afr J Plant Soil*. 2017;34:315-321.
- Harriman JC, Okocha PI, Nwofia GE. Analyzing genetic variation for important yield-contributing attributes in genotypes of orange-fleshed sweet potatoes. *J Appl Biotechnol Bioeng*. 2023;10(2):45-49.
- Hullannavar P, Imamsaheb SJ, Peerajade D, et al. Trait interrelationships governing growth, yield, and quality in sweet potato (*Ipomoea batatas* Lam.) genotypes. *Plant Arch*. 2025;26:143.
- Jones DB. Factors for converting percentages of nitrogen in foods and feeds into percentages of proteins. Circular No. 183. Washington (DC): United States Department of Agriculture; 1931.
- Kumar Reddy BP, Begum H, Sunil N, et al. Correlation and path coefficient analysis in muskmelon (*Cucumis melo* L.). *Int J Curr Microbiol Appl Sci*. 2017;6:268.
- Mekonnen B, Gedebo A, Gurmu F. Character association and path coefficient analysis of orange-fleshed sweetpotato (*Ipomoea batatas* Lam.) genotypes evaluated in Hawassa, Ethiopia. *J Plant Breed Crop Sci*. 2020;12:226-234.

12. Mohanraj R, Sivasankar S. Sweet potato (*Ipomoea batatas* [L.] Lam.) A valuable medicinal food: A review. J Med Food. 2014;17(7):733-741. doi:10.1089/jmf.2013.2818.
13. Mohanty P, Ashok P, Sasikala K, et al. Character association and path analyses in sweet potato. Int J Veg Sci. 2016;22:472-478.
14. Ranganna S. Handbook of analysis and quality control for fruit and vegetable products. 2nd ed. New Delhi: Tata McGraw-Hill Education; 2008.
15. Sharavati MB, Srinivasa V, Anusha RB, Shubha AS. Genetic variability studies in sweet potato (*Ipomoea batatas* (L.) Lam.) genotypes under Hill Zone of Karnataka, India. Int J Curr Microbiol Appl Sci. 2018;7(9):850-858. doi:10.20546/ijcmas.2018.709.102.
16. Tirkey PL, Singh J, Chaurasia PC, Sarnaik DA. Character association and path coefficient studies in sweet potato (*Ipomoea batatas* (L.) Lam.) genotypes. J Plant Dev Sci. 2011;3(1):137-143.
17. Wani P, Ambresh, Rani AS, et al. Character association for growth and yield parameters in orange-fleshed sweet potato (*Ipomoea batatas* Lam.) genotypes. J Adv Biol Biotechnol. 2025;28:1-10.
18. Wright S. The method of path coefficients. Ann Math Stat. 1934;5:161-215.