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Genetic variability analysis for growth, yield and quality attributes in orange fleshed sweet potato [*Ipomoea batatas* (L.) Lam.]

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Abstract
The current investigation aimed to assess the genetic variability, heritability and genetic advancement as a percentage of the mean for 18 attributes related to the growth, yield and quality of orange-fleshed sweet potato (*Ipomoea batatas*) using 27 different genotypes. This study followed a Randomized Block Design with three replications during the *rabi* season of 2022-23 at the Dr. YSRHU-Horticultural Research station in Peddapuram.
The analysis of variance showed significant differences among the genotypes for all the characteristics examined. Most traits exhibited high levels of Phenotypic Coefficient of Variation (PCV) and Genotypic Coefficient of Variation (GCV), except for leaf lobe length, number of leaves per vine, tuber length, tuber girth, dry matter content and beta carotene content. This suggests a wide range of variability and a broad genetic foundation, with minimal environmental influence. These traits are primarily under the influence of additive genetic effects, indicating potential for improvement through simple selection methods.
Furthermore, a high heritability (greater than 60%) and a substantial genetic advance as a percentage of the mean (over 20%) were observed for all attributes, except for leaf lobe length and tuber girth. This indicates that additive genetic effects predominantly influence these traits, making direct phenotypic selection a useful approach for improvement.

Keywords: Genetic, variability, yield, *Ipomoea batatas* L.

Introduction
The sweet potato, scientifically known as *Ipomoea batatas* (L.) Lam, is a plant with two cotyledons that falls under the Convolvulaceae family. It's a significant starchy tuber crop in tropical and subtropical regions due to its high yield potential and calorie content. Sweet potatoes are a rich source of Pro vitamin A, vitamin B1and vitamin C. Orange-fleshed sweet potatoes, in particular, are gaining importance in tropical tuber crops and are being considered as a regular dietary option to address Vitamin A deficiency, thanks to their high β-carotene content. Consuming orange-fleshed sweet potatoes, either fresh or cooked, can contribute to combating night blindness, a prevalent health issue in rural areas. This crop is cross-pollinated and highly heterozygous due to monoecy, resulting in significant variability, which is essential for crop improvement.
Genetic variability serves as the foundation for breeding programs and is crucial for selecting suitable parents for hybridization. A population with greater variability provides a better chance for selecting desirable traits. Heritability, defined as the ratio of genotypic variance to total phenotypic variance in non-segregating populations, helps assess the heritable portion of variability. Genetic advance measures the progress that can be achieved through selection in a specific trait.
High heritability suggests that a substantial part of phenotypic variation is controlled by additive genetic effects, making it amenable to simple selection techniques. However, heritability alone is insufficient for efficient selection in segregating generations and it needs to be accompanied by information on the magnitude of genetic advance. In this context, a study was conducted to estimate the genetic variability, heritability and genetic advance in 27 orange-fleshed sweet potato genotypes concerning 18 growth, yield and quality traits.

Materials and Methods

The current study aimed to assess the genetic diversity, heritability and genetic advance as a percentage of the mean for 18 characteristics related to growth, yield and quality in 27 different varieties of orange-fleshed sweet potato (*Ipomoea batatas* (L.) Lam.). This investigation was conducted during the *rabi* season of 2022-23 at the Dr. YSRHU-Horticultural Research Station in Peddapuram using a Randomized Block Design with three replications.

In the experimental setup, well-decomposed farmyard manure was applied at a rate of 25 tons per hectare and the entire dose of phosphorus (60 kg P/ha) was incorporated into the soil during land preparation. The field was levelled and divided into plots based on the experiment layout. Sweet potato propagation was carried out using vine cuttings, which were partially treated with Chlorpyriphos (2.5 ml/L) and Carbendazim (2g/L) to protect against pests and diseases, particularly sweet potato weevil infestation. Vines measuring 20-30 cm in length were planted in a slanting position on October 7, 2022, at a depth of 5-7 cm with 2-3 nodes below the soil surface, leaving the rest of the vine above the soil. Plant spacing was set at 60 cm between rows and 20 cm between individual plants, accommodating 83,333 vine cuttings per hectare. Gap filling was carried out with vine cuttings from the maintained nursery to achieve the desired plant density. The recommended fertilizer dosage (120 kg NPK/ha) was applied in the form of Urea, Single Super Phosphate and Muriate of Potash. The entire phosphorus dose was applied at the time of final ploughing, while nitrogen and potassium were applied in three equal split doses at 30, 60and 90 days after planting. The plots were maintained free of weeds, received regular irrigation and required plant protection measures to ensure a healthy crop. The crop was managed following recommended agricultural practices.

During the experiment, five competitive plants were randomly selected and tagged for each genotype in every replication. Data was recorded for various characteristics, including the length of the main vine, vine internodal length, petiole length, number of branches per vine, length and width of leaf lobes, number of leaves per vine, leaf area, number of tubers per vine, tuber length and girth, tuber yield per vine, total tuber yield per hectare, marketable tuber yield per hectare, dry matter content, β-Carotene content, starch content and total sugar content. The collected data was then subjected to statistical analysis.

Statistical analysis included the calculation of variance according to the procedure outlined by Panse and Sukhatme (1985) [20]. Phenotypic and genotypic coefficients of variation (PCV and GCV) were computed using the methods described by Burton and De Vane (1953) [3]. Broad-sense heritability was estimated following the approach of Weber and Moorthy (1952) [19] and genetic advance was determined based on the formula proposed by Johnson *et al.* (1955) [7].

Results and Discussion

The analysis of variance showed that the current experimental material displayed a wide range of variability with significant differences between varieties for all traits (Table 1). This variability can be harnessed through selective breeding. These findings align with previous studies by Engida *et al.* (2007) [5], Shashikanth *et al.* (2008) [14], Sharavati *et al.* (2018) [15] and Murthy *et al.* (2018) [11].

Examining the mean performance (Table 2) of various characters revealed a high degree of variability in the length of the main vine ranging from 111.73 cm to 461.40 cm, leaf lobe width ranging from 2.66 cm to 13.31 cm, leaf area ranging from 5594.83 cm^2 to 27760.28 cm^2, number of tubers per vine ranging from 1.60 to 5.00, tuber yield per vine ranging from 153.60 g to 759.60 g, total tuber yield per hectare ranging from 9.17 t/ha to 42.17 t/ha and marketable tuber yield per hectare ranging from 6.33 t/ha to 34.83 t/ha.

The extent of variability in 27 genotypes across 18 traits, as measured by mean, range, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (h), expected genetic advance and genetic advance as a percentage of the mean (GAM) is presented in Table 2. PCV exceeded GCV for all traits, with a narrow difference between them, indicating minimal environmental influence on trait expression and significant genetic variation. Traits like the length of the main vine, vine internodal length, petiole length, number of branches per vine, width of leaf lobe, leaf area, number of tubers per vine, tuber yield per vine, total tuber yield, marketable tuber yield, starch content and total sugars exhibited substantial PCV and GCV, indicating a wide genetic diversity, limited environmental influence and an additive genetic control, suggesting potential for further improvement through selection. These results are consistent with prior studies by Alam *et al.* (1998) [1], Mohanty *et al.* (2016) [10], Meenakshi *et al.* (2017) [9], Bhadauriya *et al.* (2018) [2], Murthy *et al.* (2018) [11], Sharavati *et al.* (2018) [15], Narayan *et al.* (2022) [12] and Wani *et al.* (2022) [18]. In contrast, moderate variability was observed for traits like the length of leaf lobe, number of leaves per vine, tuber length, tuber girth, dry matter content and beta carotene content suggesting a moderate variation among genotypes. These results are in line with Engida *et al.* (2007) [5], Mohanty *et al.* (2016) [10], Tripathi *et al.* (2016) [16], Meenakshi *et al.* (2017) [9], Murthy *et al.* (2018) [11] and Sharavati *et al.* (2018) [15].

High heritability combined with a high genetic advance as a percentage of the mean was observed for the length of the main vine, vine internodal length, petiole length, number of branches per vine, width of leaf lobe, number of leaves per vine, leaf area, number of tubers per vine, tuber length, tuber yield per vine, dry matter content, total tuber yield, marketable tuber yield, beta carotene content, starch content and total sugars. This suggests that these traits are primarily controlled by additive gene action and selective breeding would be effective. These findings align with earlier research by Emmanuel *et al.* (2016) [21], Meenakshi *et al.* (2017) [9], Murthy *et al.* (2018) [11], Sharavati *et al.* (2018) [15], Wani *et al.* (2022) [18] and Nurul *et al.* (2023) [13] which reported similar observations in sweet potato. Traits like the length of leaf lobe and tuber girth exhibited moderate heritability along with moderate genetic advance indicating the potential for improvement through mass selection and progeny selection. These results are consistent with prior studies by Engida *et al.* (2007) [5], Mohanty *et al.* (2016) [10], Meenakshi *et al.* (2017) [9] and Murthy *et al.* (2018) [11].

Table 1: Analysis of variance for quantitative and qualitative traits in orange fleshed sweet potato [*Ipomoea batatas* (L.) Lam.] genotypes

S. No	Characters	Mean sum of squares		
		Replications (df = 2)	Treatments (df = 26)	Error (df = 52)
1	Vine length(cm)	291.96	16240.78**	211.15
2	Vine internodal length (cm)	0.08	7.01**	0.10
3	Petiole length (cm)	108.12	66.77**	5.69
4	Number of branches per vine	0.18	11.02**	0.23
5	Length of leaf lobe (cm)	2.76	7.04**	2.22
6	Width of leaf lobe (cm)	0.28	20.66**	0.66
7	Number of leaves per vine	131.96	4819.49**	177.43
8	Leaf area (cm^2)	4992995.00	142768072.55**	18054012.63
9	Number of tubers per vine	0.06	3.37**	0.11
10	Tuber length (cm)	0.09	13.65**	1.17
11	Tuber girth (cm)	0.57	7.83**	0.74
12	Tuber yield per vine (g)	296.14	60706.39**	1625.59
13	Dry matter content (%)	3.37	72.07**	11.80
14	Total tuber yield (t/ha)	13.80	181.89**	3.79
15	Marketable tuber yield (t/ha)	12.87	141.00**	3.00
16	Beta carotene content (mg/100g fw)	0.08	3.92**	0.14
17	Starch content (%)	0.84	29.41**	0.71
18	Total sugars (%)	0.06	6.04**	0.08

*, ** indicates significance at 5% and 1% L.O.S

Table 2: Estimates of variability, heritability and genetic advance as percent of mean for different characters of 27 genotypes of orange fleshed sweet potato [*Ipomoea batatas* (L.) Lam.].

s.no	Character	Grand Mean	Range		Phenotypic coefficient of variation (PCV)	Genotypic coefficient of variation (GCV)	Heritability (h2-broad sense)	Genetic advance	Genetic advance as percent mean (%) GAM
			Low	High					
1	Length of main vine (cm)	211.68	111.73	461.40	35.20	34.53	96.19	147.69	69.76
2	Vine internodal length (cm)	5.16	2.99	9.70	30.01	29.36	95.67	3.058	59.15
3	Petiole length (cm)	17.35	11.33	35.54	29.40	26.00	78.19	8.22	47.37
4	Number of branches per vine	7.76	5.14	12.38	25.21	24.44	93.94	3.78	48.80
5	Length of leaf lobe (cm)	11.23	8.65	13.70	17.24	11.27	41.93	1.69	15.04
6	Width of leaf lobe (cm)	5.78	2.66	13.31	46.23	44.65	90.90	5.07	87.71
7	Number of leaves per vine	216.21	147.20	294.20	19.34	18.33	89.85	77.40	35.80
8	Leaf area (cm^2)	14474.92	5594.83	27760.28	49.12	46.90	69.70	11090.37	76.61
9	Number of tubers per vine	3.39	1.60	5.00	32.25	30.72	90.73	2.04	60.27
10	Tuber length (cm)	16.33	12.27	21.20	14.14	12.48	77.91	3.70	22.70
11	Tuber girth (cm)	14.32	12.20	17.24	12.31	10.72	75.93	2.76	19.25
12	Tuber yield per vine (g)	357.00	153.60	759.60	40.89	39.30	92.37	277.84	77.82
13	Dry matter content (%)	28.79	17.87	39.00	19.61	15.56	62.99	7.32	25.45
14	Total tuber yield (t/ha)	19.59	9.17	42.17	40.57	39.34	93.98	15.38	78.56
15	Marketable tuber yield (t/ha)	16.20	6.33	34.83	43.21	41.86	93.85	13.53	83.56
16	Beta carotene content (mg/100g fw)	5.76	4.02	8.42	20.57	19.46	89.54	2.18	37.94
17	Starch content (%)	14.02	6.68	18.54	22.86	22.04	93.01	6.14	43.80
18	Total sugars (%)	4.82	2.47	8.11	29.84	29.21	95.80	2.84	58.91

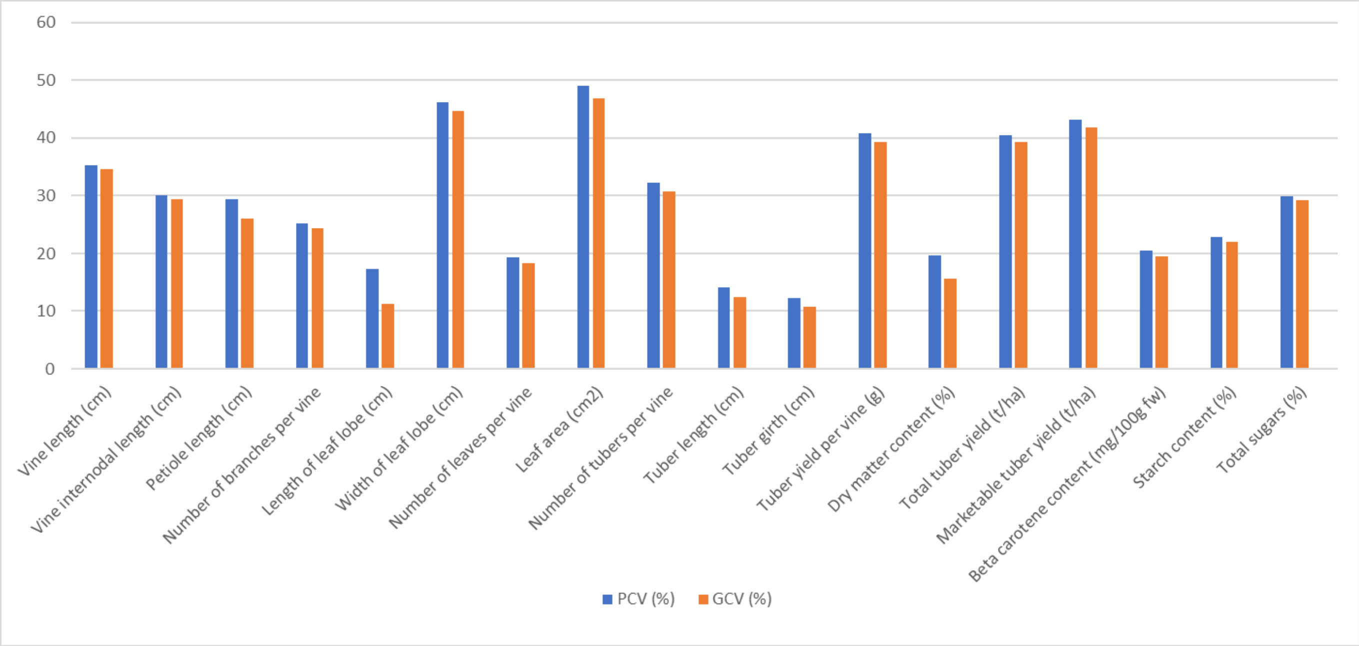

Fig 1: Phenotypic and genotypic coefficient of variation (%) for different characters of orange fleshed sweet potato [*Ipomoea batatas* (L.) Lam.]

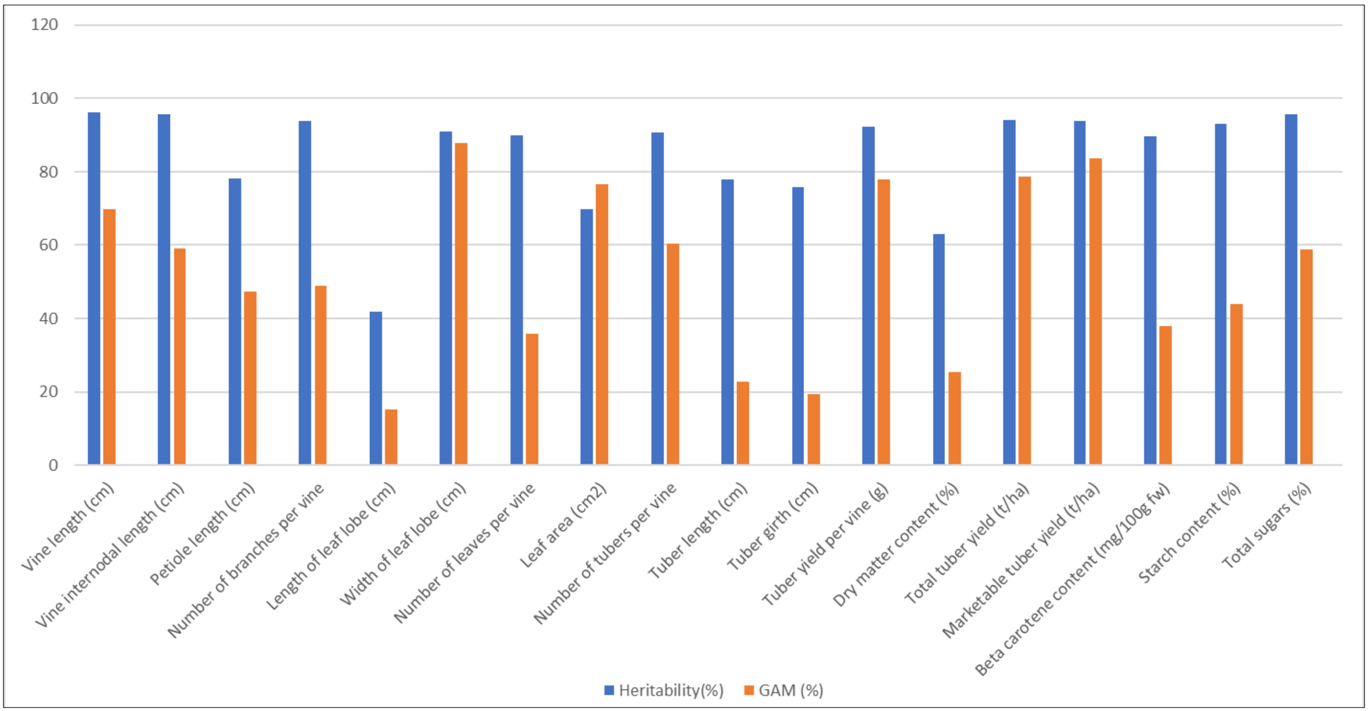

Fig 2: Heritability (%) and genetic advance as percent of mean (%) in different characters of orange fleshed sweet potato [*Ipomoea batatas* (L.) Lam.]

Conclusion

The traits such as the length of the main vine, vine internodal length, petiole length, number of branches per vine, width of leaf lobe, number of leaves per vine, leaf area, number of tubers per vine, tuber yield per vine, total tuber yield, marketable tuber yield, starch and total sugars displayed a high level of phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability and genetic advance as a percentage of the mean. This suggests that these traits are primarily influenced by additive genetic factors with minimal impact from environmental factors on their expression. Consequently, selective breeding holds significant promise for improving sweet potato crop.

References

1. Alam S, Narzary BD, Deka BC. Variability, character association and path analysis in sweet potato (*Ipomoea batatas* (L.) Lam.). Journal of Agriculture Science Society of North East India. 1998;11(1):77-81.
2. Bhadauriya P, Deo C, Ram CN, Verma SK, Sudheer Singh. Studies on Genetic Variability, Heritability, Genetic Advance, Correlation Coefficient and D2 Analysis in Sweet Potato. Indian Journal of Hill Farming. 2018;31(1):207-213.
3. Burton GW, De Vane EH. Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. Agronomy journal. 1953;45(1):578-581.

4. Chaudhary BD, Singh RK. Biometrical Methods in Quantitative Genetic Analysis. Kalyani Publishers, New Delhi; c1982. p. 215-218.
5. Engida T, Dechassa N, Devakara, SEV. Genetic variability for yield and other agronomic traits in sweet potato. Journal of Agronomy. 2007;6(1):94-99.
6. Hanson CH, Robinson HF, Comstock RE. Biometrical studies of yield in segregating population of Korean lespendeza. Agronomy journal. 1956;48(2):267-282.
7. Johnson HW, Robinson HF, Comstock, RE. Estimation pf genetic and environmental variability in soybean. Agronomy journal. 1955;47(3):314-318.
8. Lush JL. Intra-sire correlation and regression of offspring on dam as a method estimating heritability of characters. American Society of Animal science. 1940;33:293-301.
9. Meenakshi B, Ashok P, Kiran Patro, TSKK, Sasikala K. Studies on Genetic Variability, Heritability and Genetic Advance for Growth, Yield and Quality Parameters among Orange Flesh Sweet Potato [*Ipomoea batatas* (L.) Lam.] Genotypes. International Journal of Current Microbiology and Applied Sciences. 2017;6(9):1894-1903.
10. Mohanty P, Ashok P, Rout MK, Sasikala K. Character association and path analysis of sweet potato [*Ipomoea batatas* (L.) Lam.] genotypes. Journal of Crop and Weed. 2016;12(1):76-80.
11. Murthy PN, Patel NB, Patel AI, Koteswararao G. Genetic variability, heritability and genetic advance for growth, yield and quality parameters among sweet potato (*Ipomoea batatas* (L.) Lam.) genotypes. International Journal of Chemical Studies. 2018;6(4):2410-2413.
12. Narayan A, Dileep K, Alam T, Singh RS, Giri GS, Prasad Singh P. Genetic diversity in sweet potato (*Ipomea batatas* (L.) Lam.). The Pharma Innovation Journal. 2022;11(6):2352-2355.
13. Nurul AK, Aziz A, Thiyagu D, Shahrilnizam JM. Genetic variability, heritability and genetic gain in sweet potato (*Ipomoea batatas* (L.) Lam.) for agronomic traits. Journal of Breeding and Genetics. 2023;55(1):61-73.
14. Shashikanth Evoor Patil MP, Madalageri MB. and Mulge R. Genetic variability, heritability and genetic advance in sweet potato (*Ipomoea batatas* (L.) Lam.). Environment and Ecology. 2008;26(1):322-325.
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. International Journal of Current Microbiology and Applied Sciences. 2018;7(1):2319-2326.
16. Tripathi V, Deo C, Kumar A, Ravi S. Genetic variability and association studies in sweet potato (*Ipomoea batatas* (L.) Lam.). An International Quarterly Journal of Life science. 2016;11(4):3203-3206.
17. Vavilov NI. The origin, variation, immunity and breeding of cultivated plants. Soil science. 1951;72(6):482-486.
18. Wani P, Ambresh, Shantappa T, Hanchinmani CN, Bhavidoddi A, Patil S. Genetic variability for yield and yield related traits in orange-fleshed sweet potato (*Ipomoea batatas* L.) Genotypes. International Journal of Horticulture and Food Science. 2022;4(1):183-186.
19. Weber CR, Moorthy. Heritable and Non-heritable Relationship and Variability of oil content and Agronomic characteristics in the F2 generation of soyabean crosses. Journal of Agronomy. 1952;44(3):202-209.
20. Imbo TD, Sukhatme UP. Supersymmetric quantum mechanics and large-N expansions. Physical review letters. 1985;54(20):2184.
21. Emmanuel D, Owusu-Sekyere E, Owusu V, Jordaan H. Impact of agricultural extension service on adoption of chemical fertilizer: Implications for rice productivity and development in Ghana. NJAS: wageningen journal of life sciences. 2016;79(1):41-9.