



**VARIABILITY STUDIES OF YIELD RELATED CHARACTERS IN SWEETPOTATO
(*Ipomoea Batatas* (L.) Lam) GROWN IN OSUN STATE, NIGERIA**

¹Arowolo, A. D., ²Murtadha, M. A., ²Afolabi, M. S., ²Olalekan, K. K., ²Abubakar, A. G.,
²Anifowose, J. A. and ²Akhigbe, O. M.

¹Department of Crop Science, Faculty of Agriculture, University of Ilesa, Osun State, Nigeria

²Department of Agronomy, Faculty of Agricultural Production and Management,
College of Agriculture and Renewable Natural Resources Management,
Osun State University, Ejigbo, Osun State, Nigeria.

Corresponding Author's Email: abiodun_arowolo@unilesa.edu.ng, **GSM:** +2348030413476

ABSTRACT

The study was conducted at the Teaching and Research Farms of Osun State University, Osogbo (Ejigbo campus), and University of Ilesa, Osun State, over two years to assess variation among cultivars of sweet potato. Forty-five accessions were evaluated using a randomized complete block design with three replications, and data were collected on yield and related agronomic traits. Significant effects of genotype, environment, and year were observed for most traits. Genotype $\times$ environment interaction was significant for petiole colour (8.78), internode length (1.12), vine length (3.12), petiole length (0.006), and fresh root yield (1.06), indicating differential cultivar responses across environments. The phenotypic coefficient of variation (PCV) exceeded the genotypic coefficient of variation (GCV) for all traits, suggesting environmental influence on trait expression. PCV ranged from 5.44% for mature leaf length to 148.96% for dry matter, while GCV ranged from 5.44% for mature leaf shape to 86.39% for petiole colour. Heritability was highest (100%) for mature leaf length, leaf shape, and abaxial leaf vein pigmentation, with corresponding genetic advance values of 20.15, 11.21, and 29.59, respectively. Fresh root yield and vine length exhibited moderate heritability coupled with high genetic advance. Significant genotypic and phenotypic correlations were observed among key traits. Path analysis indicated that mature leaf length had the highest direct effect on dry matter, suggesting its importance as a selection criterion for improvement. Overall, the results demonstrate substantial genetic variability and highlight key traits that can be effectively targeted to enhance sweet potato performance and quality in the study environments.

Keywords: Correlation, Genetic, Advance, Variability, Heritability, Coefficient

INTRODUCTION

Sweetpotato (*Ipomoea batatas* (L.) Lam., $2n = 6x = 90$) belongs to the family Convolvulaceae and is one of the most important vegetatively propagated root crops cultivated worldwide (Hejjejar et al., 2023). Global production exceeds 112 million tons, with Malawi (8.051 million tons), Tanzania (4.260 million tons), and Nigeria (4.013 million tons) being leading producers in Africa (FAO, 2024). The crop is widely grown due to its affordability and versatility as a source of food for humans (storage roots and leaves), animal feed, and industrial raw materials (Yan et al, 2022; Katayama et al, 2017). It also provides significant health benefits, including alleviating vitamin A deficiency and reducing the risk of cancer, diabetes, and cardiovascular diseases (Arowolo and Adegbite, 2021). As a hexaploid and highly heterozygous crop, sweetpotato exhibits substantial genetic variability within and between populations, which is essential for crop improvement (Zhang et al., 2004; Tripathi et al., 2016). Genetic variability refers to differences among genotypes or their responses to environmental factors (Badu et al., 2017; Nurul-Afza et al., 2023). Its exploitation has been fundamental to agriculture, providing breeders with diversity necessary for selection and improvement (Govindaraj et al., 2015; Swarup et al., 2021).

The extent of variability is assessed using parameters such as genotypic coefficients of variation (GCV), phenotypic coefficient of variation (PCV), environmental coefficient of variation (ECV), broad sense heritability, genetic advance (GA), and genetic advance a percentage of the mean (GAM) (Demelie and Aragaw, 2016). Higher PCV values than those of GCV indicate environmental influence,



while high GCV suggests exploitable genetic variability (Tripathi *et al.*, 2019; Rahajeng *et al.*, 2020). Broad-sense heritability estimates the proportion of phenotypic variance due to genetic factors and, when combined with GA, provides a reliable basis for selection (Bali *et al.*, 2022). Correlation and path coefficient analyses further clarify relationships among traits and their direct and indirect effects on yield (Schober *et al.*, 2018; Tripathi *et al.*, 2016). This study was therefore conducted across two locations to evaluate the genetic variability among 45 sweet potato accessions in Osun State, Nigeria, with a focus on improving dry matter content.

MATERIALS AND METHODS

Germplasm Collection and Multiplication

A total of 45 sweet potato cultivars were collected in January 2023 from the National Root Crops Research Institute (NRCRI), Umudike, Abia State, as well as farmers in Ibadan (Oyo State), Osunjela (Osun State), and the Federal Capital Territory, Abuja (Table 1). Vine cuttings were multiplied under irrigation at the Teaching and Research Farm, Osun State University, Ejigbo, for two months to obtain sufficient planting materials.

Experimental Sites and Design

Field experiments were conducted during the 2023 cropping season at two locations: the Teaching and Research Farm, Osun State University, Ejigbo (7°54'N, 4°18'E), and the Teaching and Research Farm, University of Ilesa, Ilesa (7°37'N, 4°42'E), Osun State, Nigeria. Land preparation involved clearing and ridge formation using hoes. Soil samples were collected using a zigzag sampling method.

The experiment was laid out in a randomized complete block design (RCBD) with three replications. Each cultivar was planted in three rows with ten cuttings per row. Vine cuttings (30 cm) from mature plants were planted vertically at a spacing of 100 cm × 30 cm, giving a plant population of 33,333 plants ha⁻¹.

Agronomic Practices

NPK (15–15–15) fertilizer was applied at 200 kg ha⁻¹ at five and eight weeks after planting. Weeding was carried out manually at four-week intervals. Pest and disease control involved application of Cyperforce (Cypermethrin 10% EC) at 500 ml ha⁻¹ (20 ml per 15 L sprayer) combined with Mackechnie Gold (60% copper oxide + 12% Metalaxyl).

Data Collection and Analysis

Data were collected from eight randomly selected plants from the inner rows on mature leaf length, petiole length, internode length, vine length, fresh root yield, fresh shoot yield, and dry matter content (DMC), following standard procedures (Boney *et al.*, 2014; Tripathi *et al.*, 2016). Marketable roots were defined as roots weighing more than 150 g (Slosar *et al.*, 2019). Dry matter content was determined by oven-drying 200 g of fresh root samples at 60°C to constant weight, and calculated with the formula used by Mourtala *et al.* (2023).

$$\text{DMC}\% = \frac{\text{dry weight of tubers}}{\text{fresh weight of tubers}} \times 100$$

Combined analysis of variance was performed using R software version 4.5.2. All the parameters, such as genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), environmental coefficient of variation (ECV), broad sense heritability, genetic advance (GA), and genetic advance as a percentage of the mean (GAM) were calculated using the formulas proposed by Boney *et al.* (2014), Singh (2020), and Nurul-Afza *et al.*, (2023).

RESULTS AND DISCUSSIONS

Results of the study revealed a highly significant differences among genotypes, environments, and years for most traits, indicating substantial variability among the sweet potato accessions. Mature leaf length was the only trait not significantly affected. Genotype significantly influenced nearly all traits, as indicated by very low probability values. Year effects were significant for most characters, particularly dry matter (DM), internode length (IL), petiole length (PL), fresh shoot yield (FSY), fresh



root yield (FRY), storage root circumference (SC), and vine length (VL). Environmental effects were also significant for most traits, except mature leaf length (MLL) and FSY. Genotype $\times$ environment interaction was highly significant for internode length, vine length, petiole length, and petiole colour, suggesting differential genotype responses across environments (Mwanga *et al.*, 2021). (Table 1).

Table 1. Analysis of Variance for the Studied Traits

Trait	Mean	Rep	Gen	Year	Env	Gen x Env
SC	7.32	5.68**	5.78**	5.68**	6.26**	0.068
MLL	12.05	0.365	0.478	0.138	0.470	0.459
MLC	2.36	9.48**	2.96**	0.783	2.73**	0.918
PL	15.19	0.206	0.0019*	3.34*	2.24*	0.006*
PC	2.55	2.30**	3.70**	2.37**	1.70**	8.78**
IL	5.22	0.266	6.48**	5.54**	2.35**	1.12**
MLS	4.91	2.23*	1.04*	11.41*	5.51*	1.00
ALVP	2.86	5.76**	5.02**	2.35**	1.26**	1.00
VL	3.86	0.998	5.64**	6.53**	0.0004**	3.12**
FRY	180.70	0.543	1.39*	3.87*	0.083	1.06*
FSY	427.91	0.235	4.35*	9.64*	0.627	0.270
DM	324.24	0.526	2.84**	3.72**	3.52**	0.152

* = Significant at 5% level ** = Significant at 1% level

Rep = Replication; Gen = Genotype; Env = Environment; Gen x Env = Genotype x Environment
 SC = Stand count, MLL = Mature leaf length, MLC = Mature leaf colour, PL = Petiole length, PC = Petiole colour, IL = Internode length, MLS = Mature leaf shape, ALVP = Adaxial leaf vein pigmentation, VL = Vine length, FRY = Fresh root yield, FSY = Fresh shoot yield, DM = Dry matter.

Variability (PCV, GCV, ECV)

The phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for most traits, indicating environmental influence on trait expression. PCV ranged from low values in mature leaf shape (MLS, 5.44%) and mature leaf colour (MLC, 9.78%) to very high values in dry matter (148.96%) and fresh root yield (111.54%). Similarly, GCV ranged from low values in SC (7.49%), MLL (9.07%), MLC (9.78%), and MLS (5.44%) to high values in PC (86.39%), FSY (36.94%), FRY (29.29%), VL (25.04%), and DM (28.97%) (Table 2). Environmental coefficient of variation (ECV) was generally high for most traits, confirming the strong environmental influence, particularly for DM. These results indicate the presence of adequate genetic variability among the genotypes.

Heritability and Genetic Advance

High broad-sense heritability was observed for MLC (100%), MLS (100%), abaxial leaf vein pigmentation (ALVP, 100%), and PC (79%), suggesting strong genetic control of these traits. Conversely, low heritability was recorded for SC (9%), MLL (18%), PL (4%), IL (17%), VL (29%), FRY (7%), FSY (16%), and DM (4%) (Table 2) indicating greater environmental influence and limited effectiveness of direct selection.

Genetic advance (GA) was generally low across traits, except for FSY (129.93%), DM (37.63%), and FRY (28.63%), which showed high values. Genetic advance as a percentage of the mean was low for SC (4.55%), MLL (7.88%), and PL (6.00%); moderate for IL (15.02%), MLS (11.21%), FRY (15.85%), and DM (11.61%); and high for MLC (20.15%), PC (158.60%), ALVP (29.59%), VL (27.84%), and FSY (30.36%) (Table 2). High GA coupled with moderate to high heritability suggests additive gene action, while low GA indicates non-additive effects and environmental influence.



Table 2. Mean, Standard Error (SE), Eeotypic Coefficient of Variance (GCV), Phenotypic Coefficient of Variance (PCV), Environmental Coefficient of Variance (ECV), Broad Sense Heritability (Hb), Genetic Advance (GA) and Genetic Advance as Percent of Mean (GAM) for the Studied Traits

Trait	Mean	SE	GCV(%)	PCV(%)	ECV(%)	Hb(%)	GA	GAM
SC	7.32	0.08	7.49	25.40	24.27	9	0.33	4.55
MLL	12.05	0.11	9.07	21.51	19.50	18	0.95	7.88
MLC	2.36	0.03	9.78	9.78	0.00	100	0.48	20.15
PL	15.19	0.49	14.71	74.27	72.80	4	0.91	6.00
PC	2.55	0.11	86.39	96.93	43.96	79	4.04	158.60
IL	5.22	0.10	17.52	42.09	38.27	17	0.78	15.02
MLS	4.91	0.04	5.44	5.44	0.00	100	0.55	11.21
ALVP	2.86	0.06	14.37	14.37	0.00	100	0.85	29.59
VL	3.86	0.08	25.04	46.38	39.04	29	1.08	27.84
FSY	180.70	8.83	29.29	111.54	107.62	7	28.63	15.85
FRY	427.91	17.21	36.94	92.56	84.87	16	129.93	30.36
DM	324.24	21.01	28.97	148.96	146.12	4	37.63	11.61

SC = Stand count, MLL = Mature leaf length, MLC = Mature leaf colour, PL = Petiole length, PC = Petiole colour, IL = Internode length, MLS = Mature leaf shape, ALVP = Adaxial leaf vein pigmentation, VL = Vine length, FRY = Fresh root yield, FSY = Fresh shoot yield, DM = Dry matter.

Correlation Analysis

Correlation analysis revealed both positive and negative associations among traits. Genotypically, DM showed a significant positive correlation with FRY (0.30) and PL (0.10). Stand count exhibited positive associations with FRY (0.16) and FSY (0.42). MLC was positively correlated with PC (0.38), ALVP (0.20), and FSY (0.36) (Table 3). Internode length showed a strong positive correlation with vine length (0.77) but a negative association with FSY (-0.28). Phenotypically, DM was positively associated with MLL (0.46), IL (0.15), FRY (0.26), and PL (0.18) (Table 3), indicating the importance of these traits in influencing dry matter accumulation.



Table 3. Genotypic (above diagonal) and Phenotypic (below diagonal) Correlation Coefficients among Sweet Potato (*I. batatas*) Traits Studied among the Genotype

	SC	MLL	MLC	PL	PC	IL	MLS	ALVP	VL	FRY	FSY	DM	*
SC	1.00	0.34	0.05	0.23	-0.08*	-0.18*	-0.07	0.06*	0.07*	0.16**	0.42**	0.08	
MLL	-0.08	1.00	0.31	0.57*	-0.12	-0.25	-0.11	0.12	-0.23	0.45	0.41	0.25	
MLC	0.02*	0.15*	1.00	0.23	0.38**	-0.23	0.14	0.20**	-0.17	-0.02	0.36**	0.13	
PL	0.05	0.39**	0.08	1.00	0.07	-0.17	0.03	0.06	-0.17	0.14	0.15	0.10*	
PC	-0.05	-0.06	0.34**	-0.02	1.00	-0.24*	-0.09	0.61**	-0.26	0.02	-0.03	-0.01	
IL	-0.15**	0.14**	-0.11	0.06	-0.12*	1.00	-0.09*	-0.20	0.77**	-0.31**	-0.28**	-0.22	
MLS	-0.03	-0.05	0.14**	0.01	-0.08*	-0.04	1.00	-0.22**	-0.02	-0.20	0.07	0.18	
ALVP	0.02	0.06	0.20**	0.02	0.55**	-0.10	-0.22**	1.00	-0.17	0.24	-0.01	0.04	
VL	-0.04	-0.09	-0.10	-0.06	-0.10	0.33**	-0.01	-0.10	1.00	-0.37	-0.15	-0.16	
FRY	0.22**	-0.10	-0.01	-0.07	0.04	-0.25**	-0.08	0.10	-0.03	1.00	0.27**	0.30**	
FSY	0.15**	0.02	0.17**	0.04	-0.03	-0.16**	0.03	0.00	0.05*	0.21**	1.00	0.51	
DM	-0.10	0.46**	0.05	0.18*	0.01	0.15**	0.06	0.01	0.00	0.26**	-0.03	1.00	

Significant at 5% level **= Significant at 1% level

SC = Stand count, MLL = Mature leaf length, MLC = Mature leaf colour, PL = Petiole length, PC = Petiole colour, IL = Internode length, MLS = Mature leaf shape, ALVP = Adaxial leaf vein pigmentation, VL = Vine length, FRY = Fresh root yield, FSY = Fresh shoot yield.



Path Coefficient Analysis

Path coefficient analysis partitioned correlations into direct and indirect effects. Mature leaf length (0.381) had the highest positive direct effect on dry matter content, followed by fresh shoot yield (0.325) and fresh root yield (0.287), indicating their importance in selection for improved dry matter content. In contrast, internode length (-0.267) and petiole colour (-0.010) exerted negative direct effects on the accumulation of dry matter (Table 4). These results highlight mature leaf length as a key trait for indirect selection to enhance dry matter content in sweetpotato.



Table 4. Direct (diagonal) and Indirect Effect of Different Traits on Dry Matter (DM) at Genotypic Level in Sweet Potato

Parameter	SC	MLL	MLC	PL	PC	IL	MLS	ALVP	VL	FRY	FSY	rg of DM
SC	0.142	0.017	-0.001	0.006	-0.002	0.005	-0.013	0.003	-0.001	0.028	0.227	0.078
MLL	-0.062	0.381	0.016	0.014	-0.003	0.007	-0.022	0.006	0.003	0.008	0.218	0.250
MLC	0.006	0.016	0.089	0.030	0.005	0.051	0.003	0.013	0.042	0.080	0.067	0.134
PL	-0.014	0.029	0.030	0.102	-0.001	0.036	-0.016	-0.008	0.027	0.042	0.080	0.102
PC	0.018	0.141	0.03	-0.001	-0.010	0.036	0.005	0.002	0.027	0.042	0.076	-0.010
IL	-0.014	-0.062	-0.030	-0.017	0.002	-0.267	-0.016	-0.008	-0.123	-0.092	-0.145	-0.217
MLS	-0.005	-0.028	0.018	0.003	0.001	0.019	0.086	-0.008	0.004	-0.061	0.035	0.181
ALVP	0.004	0.029	0.027	0.006	-0.006	0.044	-0.039	0.157	0.027	0.073	-0.003	0.037
VL	-0.006	-0.058	-0.022	-0.017	0.003	-0.166	-0.004	-0.006	0.151	-0.112	-0.079	-0.161
FRY	0.012	0.114	-0.003	0.014	-0.002	0.067	-0.037	0.009	0.060	0.287	0.140	0.301
FSY	0.032	0.101	0.048	0.015	0.003	0.062	0.013	-0.002	0.025	0.082	0.325	0.511

SC = Stand count, MLL = Mature leaf length, MLC = Mature leaf colour, PL = Petiole length, PC = Petiole colour, IL = Internode length, MLS = Mature leaf shape, ALVP = Abaxial leaf vein pigmentation, VL = Vine length, FRY = Fresh root yield, FSY = Fresh shoot yield.



CONCLUSION AND RECOMMENDATION

This study confirms the critical role of genetic variability in sweet potato breeding programmes. The high PCV and GCV values observed across morphological traits demonstrate substantial diversity among the cultivars evaluated. Such variability highlights the inadequacy of simple selection methods in identifying superior accessions. To achieve meaningful genetic improvement, breeding strategies must incorporate deliberate crossing of genotypes with novel and complementary traits. Harnessing this variability through systematic breeding approaches will accelerate the development of improved sweet potato cultivars, thereby enhancing productivity and ensuring the sustainability of breeding efforts. **The integration of molecular characterization** with morphological evaluation should be explored to provide deeper insights into genetic diversity. Similarly, combining conventional selection, crossing, and genomic tools as **long-term breeding strategies** needs to be pursued for durable improvement.

REFERENCES

- Acquaah, G. (2012). **Principles of Plant Genetics and Breeding**. Blackwell, Oxford, pp. 385. <https://doi.org/10.1002/9781118313718>.
- Arowolo, A. D. and Adegbite, B. A. (2021). Nutritional and health benefits of sweet potato that make it consumers' choice. *LAUCER (LAUTECH) Crop and Environmental Reviews*, **2**(1): 52-60. Retrieved from <https://laucers.com/index.php/cer/article/view/23>.
- Ayimbiere, A., Asumboya, G., Atinga, C. A., Akazotiyele, R., & Bodieu, M. (2021). Growth and Yield Characteristics of Five Different Sweet Potato Varieties Grown in the Guinea Savanna Ecological Zone of Ghana. *J Exp Agri Int*, **43**(2): 44-55.
- Asemie, M. M, and Ali, W. M. (2021). Variability and association of traits in sweetpotato [*Ipomoea batatas* (L) Lam.] accessions at Haramaya, eastern Ethiopia. *Journal. Horticulture*. **8**(3): 265-268.
- Badu, M., Asho, P., Patro, T. S. K. and Sasikala, K. (2017). Studies on genetic variability, heritability and genetic advance for growth, yield and quality parameters among orange flesh sweetpotato [*Ipomoea batatas* (L.) Lam.] genotypes. *International Journal of Current Microbiology and Applied Science*, **6**(9): 1894- 1903. <https://doi.org/10.20546/ijcmas.2017.609.233>.
- Bali, B., Thakur, P., Shukla, N., Shankar, D. and Kar, S. (2022). Genetic variability for different quantitative characters in sweet potato *Ipomoea batatas* L. *Electronic Journal of Plant Breeding*, **13**(2): 506-511. Retrieved from <https://www.ejplantbreeding.org/index.php/EJPB/article/view/3922> on 1 May, 2024.
- Begna, T. and Teresa, T. (2024). Genetic Variability and Its Benefits in Crop Improvement: A review. *Middle East Journal of Agriculture Research*, **13**(1): 128-136. <https://doi.org/10.36632/mejar/2024.13.1.7>
- Boney, W., Abner, Y., Akkinapally. R., and Myla, D. (2014). Genotypic variability estimates of agronomic traits for selection in sweetpotato [*Ipomoea batatas* (L.) Lam.] poly crosses population in Papua New Guinea. *Journal of Plant Breeding Genetics*. **2**(03): 131-136. <http://dx.doi.org/10.13140/RG.2.1.4372.3369>.
- Demelie, M. and Aragaw, A. (2016). Genetic variability of sweetpotato on yield and yield related traits at Werer Agricultural Research Center, Ethiopia. *Electronic Journal of Plant Breeding*, **7**(2): 362-367.
- Diaz, F. C., Eyzaguirre, R., David, M. C., Sevillano, R. B., Low, J. W., & Grüneberg, W. J. (2022). Genetic diversity determined by agronomic traits and SSR markers in two South american orange-fleshed sweetpotato breeding populations with potential for population hybrid breeding. *Crop Science*, **62**(1): 83–99. <https://doi.org/10.1002/csc2.20636>.
- Falconer, D. S., & Mackay, T. F. C. (1996). **Introduction to quantitative genetics** (4th ed.). Longman
- FAO (2023). Food and Agriculture Organization crop production statistics (2023), Rome, Italy. FAOSTAT. Agriculture, Agricultural production, Crops Primary, Sweetpotato, Population, Annual Time Series.



- Govindaraj, M., Vetriventhan, M. and Srinivasan, M. (2015). Importance of Genetic Diversity Assessment in Crop Plants and Its Recent Advances: An Overview of Its Analytical Perspectives. *Genetics Research International*. Published online
- Hejjejar, I., Hiremath, S. M., Naik, K. R. and Kolur, S. M. (2023). Genetic Variability, Heritability and Genetic Advance in Sweetpotato [*Ipomoea batatas* (L.) Lam.] Genotypes. *International Journal of Environment and Climate Change*, **13**(9): 2791-2797. <https://doi.org/10.9734/ijecc/2023/v13i92513>
- Jha, G. (2011). Emerging research technology against climate change through selecting ideal genotypes from open pollinated seedling population of sweetpotato (*Ipomoea batatas* (L.) Lam.). *The Ecoscan*. **1**: 179-185.
- Katayama, K., Kobayashi, A., Sakai, T., Kuranouchi, T., and Kai, Y. (2017). Recent progress in sweetpotato breeding and cultivars for diverse applications in Japan. *Breeding Science* **67**: 3–14. <https://doi.org/10.1270/jsbbs.16129> .
- Mahaman Mourtala, I. Z., Maxwell Innocent, N., Habibou, M., & Oselebe, H. (2023). Recent Progress in Breeding for Beta-Carotene, Dry Matter Content and Sugar in Sweet potato [*Ipomoea Batatas* (L.) Lam]-A Review. *European Journal of Agriculture and Food Sciences*, **5**(1): 6–13. <https://doi.org/10.24018/ejfood.2023.5.1.551>.
- Merga, M. A., Zakari, M. M., Abteu, W. G. and Oselebe, H. O. (2025). Genetic diversity and nutritional analysis of sweetpotato [*Ipomoea batatas* (L.) Lam.] genotypes in Abakaliki, Nigeria. *BMC Plant Biology*, **25**: 548 <https://doi.org/10.1186/s12870-025-06558-y>. Retrieved on 7th May, 2025.
- Narasimhamurthy, P. N., Patel, N. B., Patel, A. I. and Koteswara, R. G. (2018). Genetic variability, heritability and genetic advance for growth, yield and quality parameters among sweetpotato [*Ipomoea batatas* (L.) Lam.] genotypes. *International Journal of Chemical Studies*. **6**(4): 2410-3.
- Nurul-Afza, K., Aziz, A., Thiyagu, D., and Shahrilnizam, J. M. S. (2023). Genetic variability, heritability, and genetic gain in sweetpotato (*Ipomoea batatas* L. Lam) for agronomic traits. *SABRAO Journal of Breeding and Genetics* **55**(1): 61-73. <http://doi.org/10.54910/sabao2023.55.1.6>
- Rahajeng, W., Restuono, J., Indriani, F. C. and Purwono, P. (2020). Genetic Parameters of Agronomic Traits in Sweetpotato Accessions. *Biosaintifika: Journal of Biology & Biology Education* (**2**): 240-6. <https://doi.org/10.15294/biosaintifika.v12i2.23780>
- Schober, p., Boer, C., & Schwarte, I. A. (2018). Correlation coefficients: appropriate use and interpretation. *Anesthesia and Analgesia*, **126**(5): 1763–1768. <https://doi.org/10.1213/ane.0000000000002864>.
- Sasmal, M., Mondal, C. K., Garain, P. K. and Acharyya, P. (2015). Evaluation of sweetpotato (*Ipomoea batatas* (L.) Lam.) germplasm suitable for the coastal agroclimatic situation of Sundarbans, West Bengal. *International Journal of Applied and Pure Science and Agriculture*. **6**(5): 49-57.
- Satish, K., Janaki, M., Naidu, L. N. and Krishna, K. U. (2023). Genetic variability analysis for growth, yield and quality attributes in orange fleshed sweet potato [*Ipomoea batatas* (L.) Lam.]. *The Pharma Innovation Journal* **12**(11): 1614-1618.
- Sharavati, M. B., SCinivasa, V., Anusha, R.B., Shubha, A.S. (2018). Genetic variability studies in sweetpotato (*Ipomoea batatas* L. Lam) genotypes under Hill Zone of Karnataka, India. *International. Journal of Current. Microbiology and Applied. Sciences*. **7**(9): 850-858. <https://doi.org/10.20546/ijcmas.2018.709.102>.
- Singh, B. D. (2020). A textbook of plant breeding. *Kalyani Publishers*, New Delhi.
- Slosar, M., Hegedúsová A, Hegedús O, Mezeyová I, Farkaš J, Golian M (2019). The evaluation of selected qualitative parameters of sweet potato (*Ipomoea batatas* L.) in dependence on its cultivar. *Potravinarstvo Slovak Journal of Food Science*. **13**(1): 131-137. <http://dx.doi.org/10.5219/1036>.



- Solankey, S. S. Singh, P. K. and Singh, R. K., (2015). Genetic Diversity and Interrelationship of Qualitative and Quantitative Traits in Sweetpotato. *International Journal of Vegetable Science*, **21**: 236 –248. <https://doi.org/10.1080/19315260.2013.867295>
- Swarup, S., Cargill, E. J., Crossby, K., Flagell, L. Knikern, J. and Glenn, K. C. (2021). Genetic diversity is indispensable for plant breeding to improve crops. *Crop Science*, 61: 839-852.
- Thiyagu, D., Rafii, M. Y., Mahmud, T. M. M., Latif, M. A., Malek, M. A. and Sentoer, G. (2013). Genetic variability of sweetpotato [*Ipomoea batatas* (L.) Lam.]. Genotypes selected for vegetable use. *J. Food, Agri. and Environ.* **11**(2): 340-344.
- Tripathi, V., Chandra, D., Arun, K., Ravi, S. S. (2016). Genetic variability and association studies in sweetpotato [*Ipomoea batatas* (L.) Lam.]. *The Bioscan*, **11**(4): 3203-6.
- Yan, M., Nie, H., Wang, Y., Wang, X., Jarret, R., Zhao, J., Wang, H., and Yang, J. (2022). Exploring and exploiting genetics and genomics for sweetpotato improvement: Status and perspectives. *Plant Comm.* **3**: 100332.
- Zakari, M. M. I., Utobo, E. B., Moussa, Z. S., Abed, J. N., Innocent, I. M. N., & Oselebe, H. O. (2025a). Heterosis and heritability of traits contributing to select high yielding drought stress tolerance sweetpotato breeding lines. *Cogent Food & Agriculture*, **11**(1): 2447899.
- Zakari, M. M., Baina, D. J., Ifeanyi Maxwell, N. I., Habibou, M, Mulugeta, A. M., Ibrahim Bio Yerima, A. R., and Happiness, O. O.(2025b). Agro-Morphological variability among sweetpotato [*Ipomoea batatas* (L) Lam] clones collected from Niger and Nigeria. *Modern Agriculture*; **3**(1): 70013, [https:// doi.org/10.1002/moda.70013](https://doi.org/10.1002/moda.70013). Retrieved on 7th May, 2025.
- Zhang, D., Rossel, G., Kriegner, A., & Hijmans, R. (2004). AFLP assessment of diversity in sweetpotato from Latin America and the Pacific region: Its implications on the dispersal of the crop. *Genetic Resources and Crop Evolution*, **51**(2): 115–120. 0000020853.04508.a0 <https://doi.org/10.1023/B:GRES>.