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Genetic Diversity of Sweet Potato (*Ipomoea batatas*) Genotypes Using Principal Component Analysis

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ABSTRACT
Sweet potato (Ipomoea batatas) is a nutritionally rich and agronomically versatile crop cultivated across tropical regions. This study evaluated 132 genotypes sourced from NACGRAB and the Ministry of Agriculture, Abeokuta, using Principal Component Analysis (PCA) to assess genetic diversity across 29 morphological and agronomic traits. PCA extracted nine principal components explaining 74.83% of total phenotypic variance. Cluster analysis revealed seven distinct genotype groups, with accessions G97, G56, G92, G26, G101, and G86 exhibiting unique agronomic profiles. These genotypes are recommended for breeding programs targeting yield optimization, pest resistance, and ecological adaptability.

Keywords: Sweet potato, genetic diversity, PCA, morphological traits, breeding.

INTRODUCTION
Sweet potato is the fifth most important food crop globally, contributing significantly to food security in developing countries. Its adaptability to marginal soils, high beta-carotene content, and short maturity cycle make it ideal for nutritional and economic resilience. In Nigeria, sweet potato cultivation is expanding due to its role in combating vitamin A deficiency and supporting smallholder livelihoods. Genetic diversity analysis is essential for crop improvement. Morphological characterization, when combined with multivariate statistical tools such as PCA, enables breeders to identify trait correlations, reduce dimensionality, and classify genotypes based on phenotypic expression. This study applies PCA to a diverse Nigerian sweet potato germplasm to identify elite genotypes for breeding and agronomic deployment.

Materials and Methods
Experimental Site
The experiment was conducted at the Ladoke Akintola University of Technology, Ogbomoso, Nigeria (LAUTECH) Teaching and Research Farm Latitude 8°N, Longitude 4°E), during the 2024 rainy season. The site experiences a tropical climate with an average annual rainfall of 1286 mm.

Planting Materials
A total of 132 sweet potato genotypes were sourced from;

• National Centre for Genetic Resources and Biotechnology (NACGRAB), Ibadan
• Ministry of Agriculture, Abeokuta
Local cultivars from Ikose, Ogbomoso served as checks.
Experimental Design:
The trial was laid out in a single-row unreplicated design. Each plot measured 3 m × 1 m with 1 m inter-row and 0.3 m intra-row spacing. Ten vines per accession were planted per plot.

Data Collection:
Twenty-nine morphological and agronomic traits were recorded, including:
• Vegetative traits: vine pigmentation, internode length, leaf size, petiole pigmentation
• Reproductive traits: flower color, flowering habit, flower stalk length
• Yield traits: number and weight of marketable and non-marketable tubers, tuber shape
• Resistance traits: pest susceptibility

Trait descriptors followed CIP/AVRDC/IBPGR guidelines:
Characterization of sweet potato genotypes was carried out using standardized descriptors developed by the International Potato Center (CIP), the Asian Vegetable Research and Development Center (AVRDC), and the International Board for Plant Genetic Resources (IBPGR). These guidelines provide a comprehensive framework for evaluating morphological, agronomic, and physiological traits to ensure consistency and comparability across studies.

The descriptors applied included plant growth habit (erect, spreading, or trailing), vine length and thickness, internode length, leaf shape, size, and pigmentation, as well as storage root characteristics such as shape, skin color, flesh color, root weight, and number. Floral traits including flowering ability, inflorescence type, peduncle length, and capsule formation were also recorded. In addition, agronomic traits such as pest and disease resistance, drought tolerance, and marketable yield were assessed following the CIP/AVRDC/IBPGR scoring system.

Statistical Analysis:
Data were standardized and subjected to Principal Component Analysis (PCA) using correlation matrices. Components with eigenvalues >1 were retained. Biplot analysis was used to visualize genotype clustering.

RESULTS AND DISCUSSION
Table 1 presents the Eigenvalues and variance percentage of PC components, and Figure 1 presents the visual presentation of Principal Component Analysis showing the genotype dispersion. The PCA analysis revealed substantial genetic diversity among the sweet potato genotypes, with clear clustering that reflects variations in floral, vegetative, and yield-related traits. Genotypes such as G97 and G86 showed higher growth performance, while G20 exhibited strong pest resistance and high tuber yield. Additionally, G92 dense canopy suggests potential for weed suppression, underscoring the utility of PCA in identifying genotypes with traits valuable for agro-ecological intensification. These findings align with the report of Tumwegamire et al. (2017), which

highlights the broad genetic diversity of sweet potato populations in West Africa, which provides resilience and adaptability across diverse agro-ecological contexts.

Table 1: Eigenvalues and Variance

Component	Eigenvalue	% Variation	% Cumulative
PC1	6.59	22.71	22.71
PC2	3.57	12.32	35.03
PC3	2.97	10.26	45.28
PC4	2.00	6.90	52.18
PC5	1.81	6.25	58.43
PC6	1.36	4.68	63.12
PC7	1.24	4.29	67.40
PC8	1.13	3.91	71.31
PC9	1.02	3.51	74.83

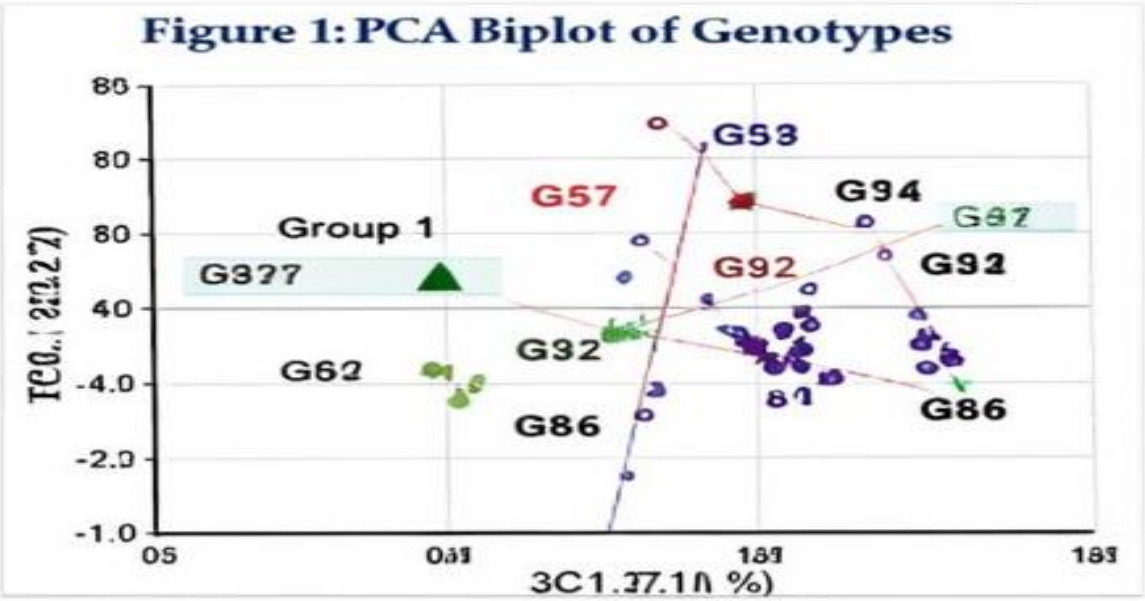

Fig. 1: PCA Biplot showing genotype clustering across PCs.

Table 2 presents the grouping of genotypes based on key agronomic traits, while Figure 2 illustrates the relative contribution of these traits to overall variation. The grouping revealed distinct performance patterns among the accessions. Group 1 (G91) displayed mixed traits with moderate yield, suggesting limited breeding potential compared to other groups. Group 2 (G92) was characterized by long flower stalks and marketable yield, highlighting its suitability for commercial production. Group 3 (G56) stood out with dense canopies, pest resistance, and high tuber yield, making it a strong candidate for agro-ecological intensification. Group 4 (G101) shared similarities with G56 but exhibited moderate vegetative and floral traits, while Group 5 (G86) demonstrated lobed leaves and vigorous vegetative and floral growth, underscoring its potential for breeding programs targeting vigor and reproductive success.

Figure 2 further emphasizes the relative importance of agronomic traits in explaining genetic variation. Sand count contributed the highest proportion (45%), suggesting that soil adaptability and environmental resilience are major differentiators among genotypes. Yield-related traits such as marketable tuber number (35%) and tuber weight (28%) were also significant contributors, confirming their central role in genotype selection. Vegetative traits including vine thickness (25%) and leaf size (19%) accounted for moderate variation, reflecting their importance in canopy development and weed suppression. Floral traits such as flower count (15%) and flower size (8%) contributed less to variation, though they remain relevant for reproductive success and breeding efficiency. Pest susceptibility (8%) had a relatively small contribution. Overall, the results demonstrated that yield-related and vegetative traits were the most influential in differentiating sweet potato genotypes, consistent with previous findings of Rukundo *et al.* (2017) that identified canopy density, pest resistance, and tuber yield as reliable indicators for selecting superior clones and identifying genotypes with desirable agronomic traits for breeding and agro-ecological intensification.

Table 2: Genotype Groups and Agronomic Traits

Group	Accession	Key Traits
1	Majority (126 accessions)	Mixed traits, moderate yield
2	G97	Long flower stalk (17.7 cm), high marketable yield
3	G56	Moderate twining, dark pigmentation, high vegetative growth
4	G92	Dense canopy, weed suppression, vigorous twining
5	G26	Thick vines (18 mm), pest resistance, high tuber yield
6	G101	Similar to G56, moderate vegetative traits
7	G86	Lobed leaves, strong vegetative and floral traits

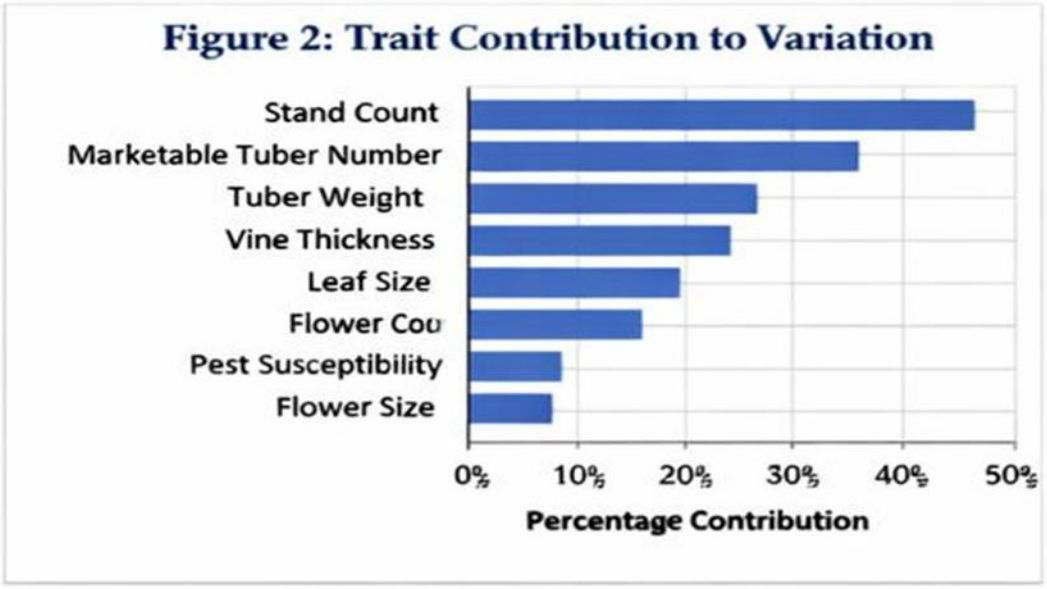

Fig. 2: Trait contribution chart highlighting dominant traits influencing variation

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CONCLUSION

The Nigerian sweet potato genotypes investigated in this study reveal a remarkable breadth of morphological and agronomic diversity, showing their importance as a genetic resource for crop improvement. Within this diversity, genotypes G97, G26, G92, G101, and G86 emerged as particularly promising, exhibiting traits that make them ideal candidates for incorporation into breeding programs aimed at enhancing yield, resilience, and adaptability. Beyond their potential in genetic improvement, several accessions demonstrated strong suitability for cover cropping, weed suppression, and livestock feed, highlighting their value in integrated farming systems. The application of principal component analysis (PCA) proved effective in clustering genotypes and prioritizing traits, offering a robust statistical framework for guiding selection decisions. However, while morphological and agronomic evaluations provided critical insights, future research should integrate molecular markers to complement these approaches, thereby improving the precision and reliability of genotype identification and selection.

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