



**GENETIC DIVERSITY STUDY OF SOME SEED AND MORPHOLOGICAL TRAITS OF
LABLAB PURPUREUS USING CLUSTER, HEIRARCHICAL, AND
PRINCIPAL COMPONENT ANALYSES**

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ABSTRACTS

The study evaluated genetic diversity of some Lablab purpureus accessions using multivariate analyses [Cluster, Hierarchical, and Principal Component Analyses (PCA)]. The plant materials were sourced from farmers' farms in Ogun State, Nigeria, and the International Institute of Tropical Agriculture (IITA), Ibadan, Nigeria. 12 traits (6 seed and 6 morphological traits) were studied. The field plots were established at the Plant Biology Field of the Department of Biological Sciences, Tai Solarin University of Education, Ijagun, Nigeria, using a randomized complete block design (RCBD) with three replicates and a block size of 21m × 50m. Each plot was 1m × 2.5 m. Inter- and intra-row spacing was 1m and 0.25m, respectively, with ten (10) plants per plot. The principal component analysis explains a cumulative variance of 81.014% with four components (PC1 = 35.046%, PC2 = 22.359%, PC3 = 13.060%, and PC4 = 10.549%). The hierarchical analysis, presented with a dendrogram, grouped the 28 accessions into seven linkage groups (clusters) with TSU-2 and TSU-44 being distinct and grouped into cluster 1 and cluster 7, respectively. In conclusion, a significant genetic diversity was observed among the understudied genotypes. Cluster and PCA effectively grouped the genotypes into 7 linkage groups based on the understudied traits, and the selected genotypes show great promise for future breeding of Lablab purpureus. Therefore, the use of genotypes from distinct clusters in this study can be used as parents in the hybridization of this crop. Replication of this study is recommended using molecular markers to complement morphological data.

Keywords: Lablab purpureus, Cluster, PCA, Hierarchical, Hybridization

INTRODUCTION

Lablab purpureus (L.) Sweet, belonging to the family Fabaceae, is a legume native to tropical Africa and widely cultivated in Asia and other parts of the world. It exhibits remarkable adaptability to diverse environments and is recognized for its versatility. All parts of the plant—leaves, pods, seeds, and roots—have economic importance (Islam *et al.*, 2020). Traditionally cultivated in Asia and Africa, it is used for food, fodder, green manure, and soil conservation. In recent years, lablab has gained global attention due to its high protein content, capacity to fix atmospheric nitrogen, and potential to thrive under low-input agricultural systems (Maass *et al.*, 2010). The legume, *Lablab purpureus* (L.) Sweet, commonly known as lablab bean, is an underutilized crop with multifaceted agronomic potential. It is recognized for its drought tolerance, ability to improve soil fertility through nitrogen fixation, and its multipurpose uses—ranging from food and fodder to green manure and cover cropping (Maass *et al.*, 2010). Despite its vast potential, lablab remains genetically underexplored compared to other legumes such as soybean (*Glycine max*) or cowpea (*Vigna unguiculata*), limiting its breeding and improvement. Genetic diversity provides the essential raw material for crop improvement through selection and breeding. It ensures resilience against biotic and abiotic stresses and enhances adaptability to changing climates. Loss of genetic diversity reduces the evolutionary potential of species and poses a significant risk to food security (Dwivedi *et al.*, 2008). In underutilized legumes like lablab, exploring existing genetic variation is crucial for improving traits such as yield, maturity, seed quality, and stress resistance.

Morphological traits are the simplest and most direct tools for assessing genetic variability. Several studies have highlighted the effectiveness of seed and morphological traits in evaluating the diversity of lablab accessions. Traits such as seed size, seed color, pod length, and flowering time



have shown substantial variability among lablab genotypes (Adebisi *et al.*, 2011; Kassa *et al.*, 2021). Although morphological traits may be influenced by the environment, they remain fundamental in initial diversity assessments, especially in resource-limited contexts. For example, Adebisi *et al.*, (2011) reported significant variation in 25 lablab accessions from Nigeria using traits such as days to flowering, plant height, number of pods, and seed weight. Similarly, a study by Kassa *et al.*, (2021) on Ethiopian lablab accessions found considerable diversity in pod length, number of seeds per pod, and hundred seed weight. The morphological and seed traits of *Lablab purpureus*—such as seed size, seed coat color, pod length, plant height, days to flowering, and number of branches—are essential for evaluating genetic variability and selecting promising genotypes for breeding. Phenotypic diversity provides critical insights into the adaptive capacity of a species, particularly when molecular tools are limited or unavailable. Morphological characterization is also the first step in genetic resource management and plays a vital role in developing elite cultivars (Upadhyaya *et al.*, 2011).

Multivariate statistical methods such as cluster analysis, hierarchical cluster analysis (HCA), and principal component analysis (PCA) have emerged as powerful tools for assessing genetic diversity in crop plants. These techniques allow the grouping of accessions with similar traits and help in the identification of the most discriminating traits contributing to diversity (Mohammadi & Prasanna, 2003). PCA reduces dimensionality and highlights the main axes of variation, while cluster and hierarchical analyses visualize relationships among accessions. Collectively, these analyses enhance the efficiency of breeding programs by guiding parental selection and genetic resource management. Cluster analysis groups genotypes based on trait similarity, facilitating identification of distinct clusters that may harbor novel or superior alleles. It provides insights into the genetic structure of populations and aids in germplasm management. Cluster analysis has been successfully applied in legume crops, including lablab (Jaiswal *et al.*, 2022). For instance, Anandan *et al.*, (2018) applied cluster analysis on 40 lablab genotypes and grouped them into distinct clusters based on agronomic and seed characteristics. Hierarchical Cluster Analysis (HCA) is a form of cluster analysis that provides a dendrogram or tree-like structure indicating the relationships among genotypes. The most widely used algorithms in HCA include UPGMA (Unweighted Pair Group Method with Arithmetic Mean) and Ward's method. These methods have been widely applied in crop genetic diversity studies to delineate population structure (Bhandari *et al.*, 2020). In *Lablab purpureus*, hierarchical clustering helps identify distant genotypes suitable for hybridization. Principal Component Analysis (PCA) reduces the dimensionality of trait data and identifies key traits that contribute most to genetic variation. It is particularly useful for simplifying large datasets while retaining most of the original information. In legumes like lablab, PCA has revealed that traits such as seed weight, pod length, and days to flowering are major contributors to genetic divergence (Shivakumar *et al.*, 2022). PCA not only helps in visualizing the distribution of accessions but also guides trait prioritization in breeding.

Recent studies continue to reveal significant diversity among lablab accessions. Kassa *et al.*, (2021) evaluated 100 lablab accessions and found that seed size, flower color, and pod traits were highly variable. PCA revealed that the first three components explained over 70% of the total variance. Similarly, Shivakumar *et al.*, (2022) assessed 50 genotypes using morphological traits and grouped them into five distinct clusters using UPGMA, indicating rich genetic diversity. Furthermore, Jaiswal *et al.*, (2022) studied 60 lablab genotypes and applied PCA, HCA, and cluster analysis, revealing strong differentiation among accessions collected from different eco-geographical regions. Their studies emphasized that genotypes from diverse clusters should be prioritized in hybridization to maximize heterosis. The identification of genetically divergent genotypes provides a foundation for hybrid development and germplasm conservation. When diverse genotypes are crossed, the likelihood of obtaining heterotic F1 hybrids increases, which can lead to improved yield, disease resistance, or climate adaptability (Kumar *et al.*, 2019). Therefore, integrating multivariate analyses into diversity studies enhances the strategic utilization of plant genetic resources. The use of multivariate statistical tools such as cluster analysis, hierarchical clustering, and principal component analysis (PCA) provides a robust approach to classify genotypes based on complex trait information. These methods help in revealing hidden patterns of genetic diversity, grouping genotypes with similar or



complementary traits, identifying key traits contributing to genetic divergence, and reducing data dimensionality for better visualization and interpretation. In the context of *Lablab purpureus*, employing these analyses will offer critical insights into morphological and agronomic trait variability. This is especially valuable for crop improvement strategies aimed at stress resilience, yield enhancement, and adaptation to diverse agro-ecological zones. Furthermore, characterizing genetic diversity ensures the preservation of unique genotypes that may possess valuable genes for disease resistance, early flowering, or seed quality traits. Thus, this study is timely and essential for revitalizing the breeding potential of *Lablab purpureus*, strengthening its genetic base, and enhancing its role in sustainable agriculture and food systems.

This study aimed to determine the genetic divergence of some accessions of *Lablab purpureus* with the following objectives;

- To assess the genetic diversity of selected lablab genotypes.
- To classify genotypes using cluster and hierarchical cluster analysis.
- To identify the major components contributing to phenotypic variability using Principal Component Analysis (PCA).
- To recommend elite genotypes for breeding purposes.

METHODOLOGY

Study Area

The field work was conducted at the research farm of the Department of Biological Science, College of Science and Information Technology, Tai Solarin University of Education, Ogun State, Nigeria. Seeds were sown on March 14th, 2025.

Seed Materials

The seeds were sourced from the Genetic Resources Centre (GRC), International Institute of Tropical Agriculture, Ibadan and some local farmers.

Experimental Design

The field experiments and seed multiplication were laid out in a Randomized Complete Block Design (RCBD) with three replications and a block size of 21m × 50m. Each plot was 1m × 2.5 m. Inter- and intra-row spacing was 1m and 0.25m, respectively, with ten (10) plants per plot.

Data Collection

Data were taken on 6 seed traits and 6 morphological traits as follows;

Traits studied are as follows;

- (1.) Petiole length [Length of petiole from the stem to leaf base using meter rule (mm)].
- (2.) Stem Girth [Measured at the base of the stem with vernier caliper]
- (3.) Number of branches per plant [Counting of the number of branches on each selected plant (Visual assessment)].
- (4.) Plant height [Distance from the ground level to the longest terminal leaf using meter rule (cm)].
- (5.) Terminal leaflet length [Measured as the distance from the leaf tip to the leaf stalk using a meter rule (mm)].
- (6.) Terminal leaflet width [Widest ends across the leaf blade using meter rule (mm)].
- (7.) Seed length [Length of pod in perpendicular position using Digital Vernier Caliper (mm)].
- (8.) Seed width [Length of pod across ends traverse position using Digital Vernier Caliper (mm)].
- (9.) Seed thickness [Measurement of shell thickness using Digital Vernier Caliper (mm)].
- (10.) 100-seed weight [Weight of 100 seeds using weighing balance (g)].
- (11.) Seed coat colour intensity- [scaling of the seed colour visually on a scale of 1 – 8]
- (12.) Seed width/Seed length ratio- [measured as seed width divided by seed length]

Statistical Analyses

- Descriptive statistics: Means and standard deviation.
- Cluster analysis: Euclidean distance method.
- Hierarchical clustering: Using dendrograms to show similarity.
- PCA: Eigenvalues, scree plots, and loading scores interpreted using SPSS (vesion 25)



RESULTS

Table 1: Descriptive Statistics for Linkage Groups (Clusters)

Traits	Cluster 1 N = 1	Cluster 2 N = 3	Cluster 3 N = 8	Cluster 4 N = 8	Cluster 5 N = 2	Cluster 6 N = 3	Cluster 7 N = 1
Plant Height (cm)	212.60 ± 0.00	102.36 ± 5.32	142.63 ± 3.53	118.88 ± 6.99	85.20 ± 1.13	160.60 ± 1.64	134.60 ± 0.00
Stem Girth (mm)	7.04 ± 0.00	7.50 ± 1.55	11.09 ± 1.70	10.23 ± 3.85	6.33 ± 0.71	9.37 ± 2.11	12..58 ± 0.00
Petiole Length	9.20 ± 0.00	7.87 ± 2.13	10.98 ± 8.99	10.73 ± 1.25	8.68 ± 2.74	9.65 ± 3.60	12.04 ± 0.00
Terminal Leaf Width (cm)	8.42 ± 0.00	7.11 ± 1.19	9.11 ± 1.18	8.09 ± 1.05	7.69 ± 1.15	8.87 ± 2.22	10.01 ± 0.00
Number of Branches	8.20 ± 0.00	2.36 ± 0.65	4.20 ± 1.11	3.35 ± 1.30	2.50 ± 0.42	3.00 ± 1.11	4.40 ± 0.00
Terminal Leaf Length (cm)	8.28 ± 0.00	7.45 ± 1.29	9.06 ± 1.18	8.21 ± 0.62	7.50 ± 0.51	8.67 ± 1.58	9.26 ± 0.00
100-seed weight (g)	27.20 ± 0.00	24.29 ± 6.75	24.86 ± 3.79	22.72 ± 1.87	21.97 ± 9.63	26.75 ± 2.26	24.82 ± 0.00
Seed Width (mm)	6.28 ± 0.00	5.44 ± 0.74	5.60 ± 0.21	5.21 ± 0.22	5.53 ± 1.88	5.81 ± 0.59	8.28 ± 0.00
Seed Length (mm)	8.96 ± 0.00	8.29 ± 1.04	8.48 ± 0.62	8.21 ± 0.55	7.65 ± 2.35	8.10 ± 0.14	8.94 ± 0.00
Seed Thickness (mm)	4.14 ± 0.00	1.91 ± 1.14	2.64 ± 0.51	2.45 ± 0.34	2.35 ± 1.06	3.26 ± 0.85	2.86 ± 0.00
Seed Colour Intensity	5.10 ± 0.00	3.54 ± 1.60	4.35 ± 2.47	4.29 ± 2.66	6.85 ± 1.85	5.77 ± 1.85	3.90 ± 0.00
Seed Width/Seed length Ratio (%)	70.00 ± 0.00	65.60 ± 3.78	66.50 ± 4.57	63.63 ± 3.46	59.50 ± 3.54	61.67 ± 6.81	93.00 ± 0.00



In this study, seven clusters were identified using agglomerative hierarchical clustering, with group sizes ranging from one to eight accessions (see table 1). Each cluster is evaluated below based on the average trait values, standard deviations, and their biological implications.

Cluster 1 (N = 1): Elite Vigorous Type

This cluster contains only one genotype, indicating it is phenotypically unique. It has the highest values for plant height (212.60 cm), terminal leaf width (8.42 cm), number of branches (8.20), and 100-seed weight (27.20 g). Its seed traits, including seed width (6.28 mm), seed length (8.96 mm), and seed width-to-length ratio (70%), are above average. It also records a relatively high seed colour intensity (5.10). This accession appears to be a highly vigorous genotype with both superior vegetative growth and seed yield potential. Its isolation into a single cluster reflects a distinct genetic profile. Such an accession would be valuable for breeding programs targeting biomass production and dual-purpose (forage and seed) uses of *Lablab*.

Cluster 2 (N = 3): Low Yield, Low Biomass Group

Cluster 2 has the lowest values for most traits, including plant height (102.36 cm), stem girth (7.50 mm), number of branches (2.36), 100-seed weight (24.29 g), and seed thickness (1.91 mm). This cluster may represent accessions that are less productive, potentially adapted to marginal environments or subject to past selection for early maturity or drought escape traits. The low biomass and reproductive potential of this cluster suggest its limited utility in yield-driven breeding unless specific stress-tolerant genes are being introgressed.

Cluster 3 (N = 8): Intermediate Seed Size, Balanced Growth

Cluster 3, the largest group, shows moderate values across most traits. With plant height (142.63 cm), seed width (5.60 mm), 100-seed weight (24.86 g), and petiole length (10.98 cm), this group appears well-balanced. It combines moderate vigour and seed yield traits, suggesting stability and adaptability.

Cluster 4 (N = 8): Compact Architecture, Modest Yield

This cluster has relatively lower values for seed traits such as seed width (5.21 mm), seed thickness (2.45 mm), and 100-seed weight (22.72 g), while the vegetative traits like plant height (118.88 cm) and terminal leaf width (8.09 cm) are moderate. The seed width-to-length ratio is lower (63.63%), suggesting more elongated seeds.

Cluster 5 (N = 2): Short-Statured, High Colour Intensity

Accessions in Cluster 5 exhibit the lowest values for plant height (85.20 cm) and stem girth (6.33 mm), along with a high seed colour intensity (6.85) and a low seed width-to-length ratio (59.50%). This indicates smaller, narrower seeds with intense pigmentation.

These traits suggest that this group may contain genotypes selected for visual appeal, processing quality, or traditional uses, possibly with bioactive compounds tied to seed pigmentation (e.g., anthocyanins).

Cluster 6 (N = 3): High Biomass and Broad Adaptation

Cluster 6 has above-average values for plant height (160.60 cm), stem girth (9.37 mm), petiole length (9.65 cm), and 100-seed weight (26.75 g). Seed width (5.81 mm) and terminal leaf width (8.87 cm) also suggest strong vegetative development. Moderate seed colour intensity (5.77) and seed shape (61.67%) further indicate broad utility. These genotypes combine good agronomic potential with adaptability, making them strong candidates for inclusion in breeding programs targeting yield, forage value, and adaptation. This agrees with Aliyu *et al.*, (2021) who emphasized selecting high biomass *Lablab* lines for dual-purpose forage and grain production.

Cluster 7 (N = 1): Unique Round-Seeded Type

This cluster is also a singleton (N = 1), and is notable for its very high seed width (8.28 mm) and exceptionally high seed width-to-length ratio (93%), suggesting a very round seed type. The seed thickness (2.86 mm) and other vegetative traits are moderate. This unique profile may represent a distinct morphological variant or a locally selected cultivar. Round seeds are preferred in certain markets for ease of handling and fast cooking. This genotype may serve in quality-focused breeding for culinary traits. According to Chukwu *et al.*, (2023), seed shape is an important consumer

preference trait in local legume markets and can be an indicator of geographic or cultural differentiation.

Table 2: KMO and Bartlett's Test

Kaiser-Meyer-Olkin Measure of Sampling Adequacy	0.547
Approximate Chi-Square	322.613
Bartlett's Test of Sphericity (df)	66
Significance	0.000

Bartlett's test evaluates whether the correlation matrix is an identity matrix (i.e., whether there is or no correlations between variables). A significant result ($p < 0.05$) means that the variables are significantly correlated enough to apply Principal Component Analysis (PCA) or any other factor analysis. Since the significance of the data collected is 0.000 (as shown in the table 2 above), which is highly significant, this means that the data is suitable for dimensional reduction (Principal Component Analysis or any other factor analysis). The dataset passes both tests for PCA.

Table 3: Total Variance Explained

Component	Initial Eigen values			Extraction Sums of Squared Loadings		
	Total	% of Variance	Cummulative %	Total	% of Variance	Cummulative %
1.	4.206	35.046	35.046	4.200	35.046	35.046
2.	2.683	22.359	57.405	2.683	22.357	57.405
3.	1.567	13.060	70.405	1.567	13.060	70.465
4.	1.266	10.549	81.014	1.266	10.549	81.014
5.	0.967	8.059	89.073			
6.	0.449	3.744	92.816			
7.	0.295	2.461	95.278			
8.	0.275	2.296	97.574			
9.	0.126	1.054	98.627			
10.	0.108	0.898	99.525			
11.	0.056	0.468	99.993			
12.	0.001	0.007	100.000			

Extraction Method: Principal Component Analysis

This PCA result in the table 3 shows how much variance (information) each principal component (PC) explains in the dataset.

The table is divided into:

- **Initial Eigenvalues** – the total variance explained by each component before extraction.
- **Extraction Sums of Squared Loadings** – the variance retained after applying the PCA (for components with eigenvalues ≥ 1).

Using Kaiser's Criterion (eigenvalues ≥ 1), only 4 components are retained. These components explain a cumulative variance of 81.014%, which is quite high and indicates strong data reduction with minimal loss of information. Component 1 explains 35.046% of the total variance, the most among all components, indicating it's the most informative dimension. Component 2 explains 22.359%, also significant. Component 3 adds 13.060%. Component 4 adds 10.549%. Each of these contributes meaningfully to explaining variability in the data. The first 2 components explain 57.405% of the total variance. Adding component 3 brings it to 70.465%. Component 4 brings it to 81.014%, which is acceptable for this study. The rest (components 5 to 12) have eigenvalues < 1 and contribute very little individually ($< 8.1\%$ each), and cumulatively add just ~19% more variance. They are considered noise or minor sources of variation and are not retained. Conclusively, the original data with 12 variables was effectively reduced to 4 principal components, retaining over 81% of the information.

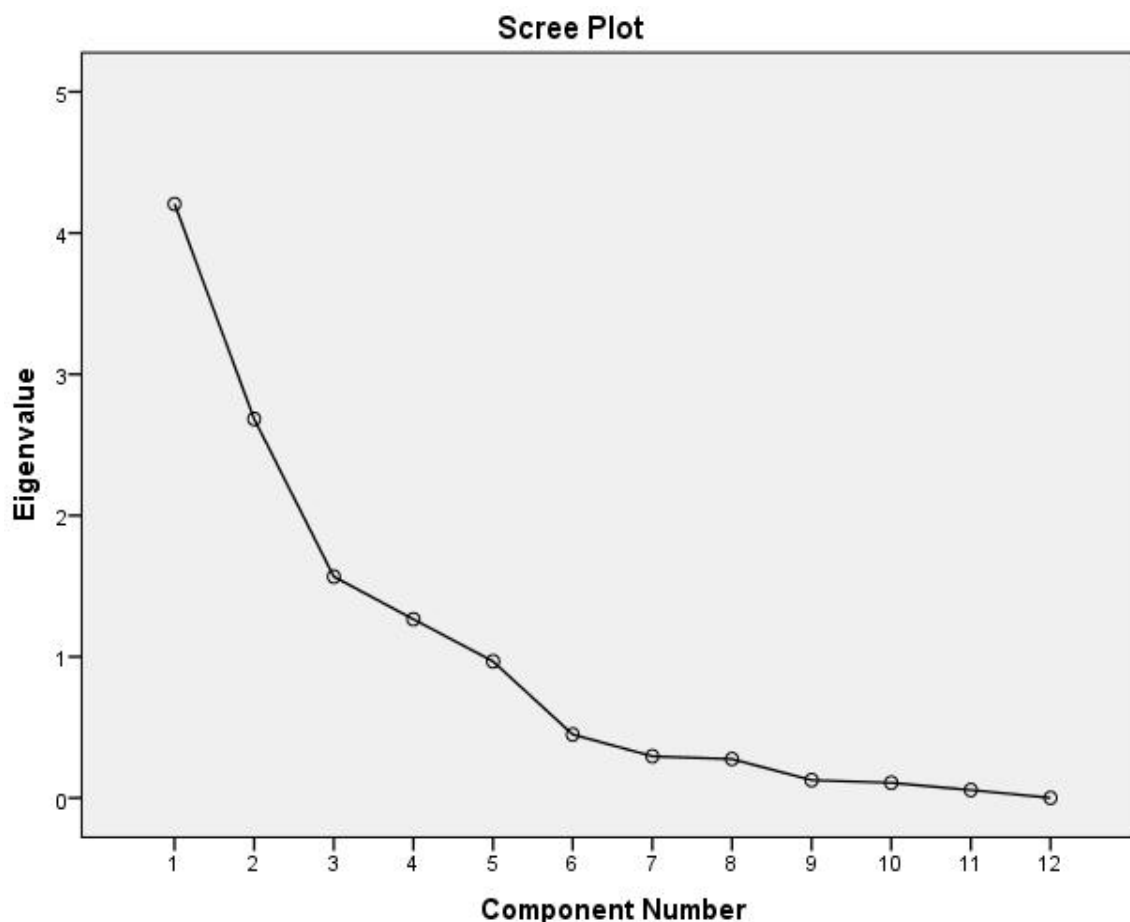


Figure 1: The Scree Plot Showing the Eigen Values and the Component Numbers

Table 4: Principal Component Analysis

	COMPONENT 1	COMPONENT 2	COMPONENT 3	COMPONENT 4
Plant Height	0.623	0.278	-0.190	-0.366
Stem Girth	0.596	-0.492	0.051	-0.338
Petiole Length	0.623	-0.610	-0.084	0.062
Term.Leaf Width	0.858	-0.407	-0.075	0.115
No. of Branches	0.711	-0.090	-0.121	-0.357
Terminal Length	0.806	-0.423	-0.102	0.266
100-Seed Weigth	0.546	0.686	-0.057	0.093
Seed Width	0.551	0.413	0.714	0.060
Seed Length	0.596	0.673	-0.006	0.023
Seed Thickness	0.338	0.728	-0.288	-0.090
Seed Colour	0.287	0.077	-0.197	0.882
Length Ratio (%)	0.182	-0.093	0.925	0.061

Extraction Method: Principal Component Analysis (4 components extracted)

Table 4 above presents the loading coefficients of twelve traits on four principal components. These components cumulatively explain a significant portion of the total variance and reveal the structure of variation among the genotypes.

Component 1: Morphological Vigour and Plant Architecture

The first principal component (PC1) exhibits high positive loadings from terminal leaf width (0.858), terminal length (0.806), number of branches (0.711), petiole length (0.623), and plant height



(0.623). These traits are related to vegetative growth and canopy architecture. The heavy loadings on PC1 suggest that this component primarily represents the general vigour and plant stature of the *Lablab* genotypes.

This agrees with the findings of Ajayi *et al.*, (2023), who noted that plant architectural traits such as plant height and branching pattern are major contributors to genetic variability in legumes under field conditions. Traits like terminal leaf width and petiole length are highly correlated with photosynthetic capacity and biomass production, as supported by Yusuf *et al.*, (2022), who emphasized their role in early seedling vigour and competitive ability.

The prominence of vegetative traits in PC1 indicates their substantial contribution to genetic divergence. This implies that selection for these traits could lead to improved genotypes with enhanced biomass, branching, and potential for better light interception, which are important for both forage and seed productivity.

Component 2: Seed Morphometric Traits

Component 2 (PC2) is dominated by seed thickness (0.728), 100-seed weight (0.686), seed length (0.673), and seed width (0.413). These traits are tightly associated with seed morphology and size. Their strong positive loadings suggest that PC2 represents variation related to seed development and yield potential. Seed traits are key components in domestication and breeding programs due to their direct influence on marketability and seedling establishment. According to Wamalwa *et al.*, (2021), seed weight and size are heritable and stable traits that significantly affect the economic value of legumes. In *Lablab purpureus*, heavier seeds are often associated with higher protein content and better germination rates (Agbo *et al.*, 2020).

Interestingly, stem girth shows a negative loading (-0.492) on PC2, suggesting a trade-off between seed size and stem robustness in some genotypes. This inverse relationship may reflect different adaptive strategies among accessions, possibly indicating genetic divergence due to selective pressures in different agro-ecological zones.

Component 3: Seed Shape and Dimensional Ratios

Component 3 (PC3) exhibits high loading from length ratio (0.925), followed by seed width (0.714). These two traits are related to seed shape, which influences seed handling, packaging, and cooking quality. The length ratio, in particular, is a derived trait representing the ratio of seed length to width, offering a composite index of seed elongation. A study by Ndhlovu *et al.*, (2022) on *Phaseolus vulgaris* emphasized the role of seed shape in market preference and adaptability. Likewise, in *Lablab*, elongated or round seeds may reflect genetic variability tied to domestication or natural selection, especially under traditional farming systems where farmers select based on visual seed traits. The high loading of these derived traits in PC3 underscores their contribution to total variation and their potential as indirect selection criteria for breeding programs aiming at seed uniformity and processing efficiency.

Component 4: Seed Coat Colour and Aesthetic Traits

Component 4 is characterized predominantly by seed colour (0.882), which stands out as a uniquely influential trait in this axis. Seed colour is often associated with consumer preference, market acceptance, and seed coat composition, including tannin and anthocyanin levels, which affect nutritional quality and storability. Recent studies, such as Zhang *et al.*, (2023) on *Vigna unguiculata*, confirm that seed coat pigmentation is controlled by a few major loci and is a critical trait in legume improvement. In *Lablab*, variation in seed colour also reflects underlying genetic differentiation and possible linkage to other biochemical traits such as anti-nutritional factors or seed dormancy (Oladele *et al.*, 2022). Interestingly, this component shows minimal contributions from other variables, emphasizing the uniqueness of seed colour in explaining variability among accessions. It highlights the potential of using seed colour as a marker trait in participatory breeding and conservation efforts, particularly in regions where visual attributes determine adoption.

GENERAL INTERPRETATION OF PCA

The four principal components together explain a substantial proportion of the total phenotypic variance among *Lablab purpureus* genotypes. PC1 and PC2 primarily capture vegetative



and seed yield attributes, while PC3 and PC4 deal with seed dimensional ratios and qualitative traits like colour.

This partitioning of variance aligns with earlier work by Raghuvanshi and Tripathi (2021), who emphasized that PCA is efficient in reducing dimensionality without losing critical information in multivariate trait evaluation. In practical breeding, such reduction allows breeders to focus on key components that explain the most variation, thereby improving selection efficiency.

Moreover, the high loadings on specific PCs suggest that these traits can be used to distinguish accessions in cluster analysis and hierarchical classification. The genetic variability observed among the genotypes indicates significant scope for selection and improvement, a conclusion also reached by Akintayo *et al.*, (2021) in their study of cowpea diversity using similar multivariate tools.

The PCA pattern further reveals that several traits are inter-correlated and should not be treated independently in breeding programs. For instance, the strong correlation of plant height with branching and leaf traits in PC1 suggests that selection for one may simultaneously influence others. Similarly, seed dimensional traits appear to be grouped in PC2 and PC3, indicating shared genetic control or developmental pathways.

This Principal Component Analysis (PCA) result in the table 4 presents the loadings (correlation coefficients) of each trait on the first four principal components (PCs). Each loading indicates how strongly a trait contributes to a particular component. Principal component 1 (PC1) represents the “vegetative growth component”. Traits with high positive loadings are the terminal leaf width (0.806), terminal leaf length (0.806), number of branches (0.711), petiole length (0.623), plant height (0.623), and stem girth (0.596). PC1 represents general vegetative vigour/plant size. Genotypes with high PC1 scores indicate taller plants, thicker stems, more branches, and broader leaves.

Principal component 2 (PC2) represents seed morphology and weight. Traits with high positive loadings are seed thickness (0.728), 100-seed weight (0.686), seed length (0.673), and seed width (0.413), while those with high negative loadings are petiole length (-0.610), stem girth (-0.492) and terminal leaf width (-0.407). PC2 contrasts seed size and weight with some vegetative traits. Accessions scoring high on PC2 indicate larger, heavier seeds but thinner stems and shorter petioles. In Principal component 3 (PC3) seed width/seed length ratio (0.925) and seed width (0.714) have high positive loading, which reflects seed shape, especially the seed width/seed length ratio. High scores indicate seeds that are more elongated or with a higher seed width/seed length ratio. High loading trait in principal component 4 (PC4), for seed colour component, is the seed colour intensity, which captures variation mostly in seed coat colour intensity that is independent of other traits.

In summary of the Principal Component Analysis of this study, the PC1 (vegetative and PC2 (seed size/weight) explain different types of variation-ideal for identifying accessions that balance growth and yield. More so, PC3 (seed shape) and PC4 (seed colour) represent more specific traits useful for breeding or classification.

Table 5: Cluster Membership

Clusters	N	Accessions
Cluster 1	1	TSU-2
Cluster 2	5	TSU-5, TSU-6, TSU-8, TSU-17, TSU-39
Cluster 3	8	TSU-7, TSU-11, TSU-50, TSU-55, TSU-57, TSU-59, TSU-64, TSU-66
Cluster 4	8	TSU-12, TSU-13, TSU-28, TSU-31, TSU-37, TSU-43, TSU-49, TSU-60
Cluster 5	2	TSU-29, TSU-51
Cluster 6	3	TSU-36, TSU-46, TSU-70
Cluster 7	1	TSU-44

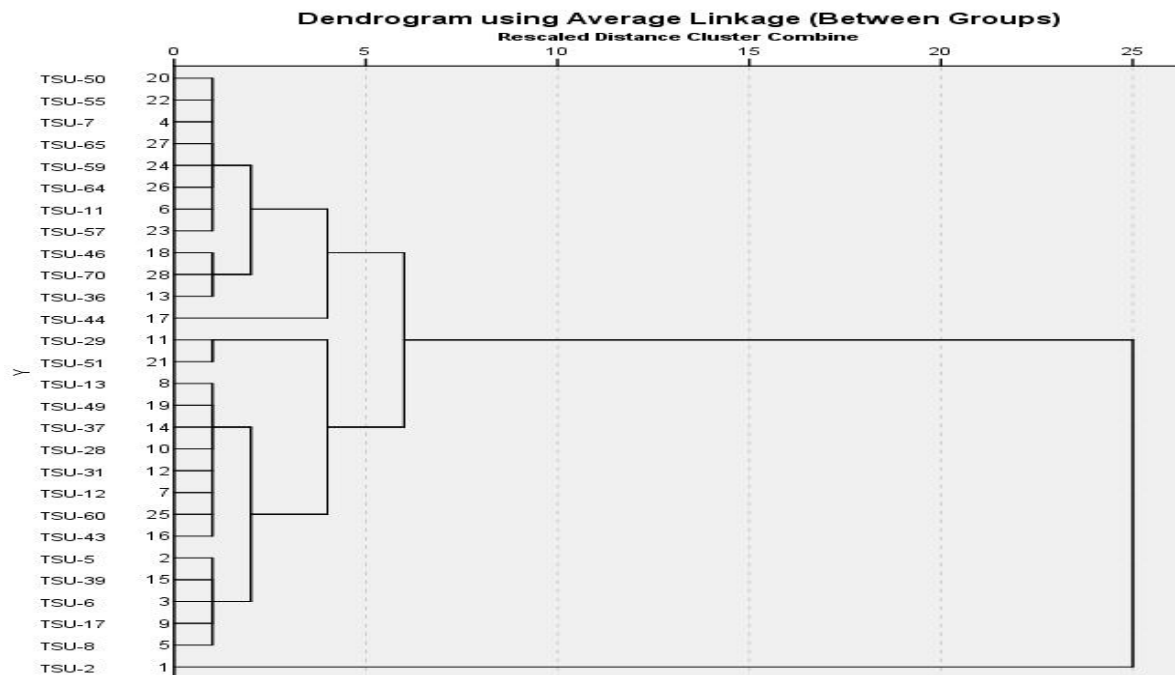


Figure 2: Dendrogram showing the Clusters using Average linkage (between groups)

DISCUSSION

The vigorous traits observed in cluster 1 align with findings by Adebisi *et al.*, (2023), who reported that accessions with high vegetative vigour and seed size often possess superior allelic combinations and stress resilience.

Similar classifications, as found in cluster 2, were reported by Mahama *et al.*, (2021) in *Vigna unguiculata*, where low-performing clusters were identified as potential reservoirs of adaptive traits, though not ideal for direct cultivation.

The role of groups like cluster 3 in conserving genetic diversity and broad adaptability was highlighted by Singh *et al.*, (2022) in cowpea, where mid-range clusters exhibited high ecological flexibility. This group is likely to contain landraces or farmer-preferred types with balanced performance. Their genetic stability across traits makes them suitable as parents in cross-breeding to incorporate adaptability with higher-yielding traits from other clusters.

The combination of compact plant architecture and elongated seeds observed in cluster 4 might reflect selection for certain market traits or niche adaptability. However, the reduced seed thickness and seed weight suggest limited yield performance, making these genotypes less ideal for commercial seed production. The seed traits in this group resemble those identified by Ogundipe *et al.*, (2020) as characteristics of traditional accessions maintained for specific culinary or cultural preferences. Association between seed colour intensity and bioactivity was demonstrated by Kang *et al.*, (2022) in legumes, linking high pigmentation with antioxidant properties. Thus, cluster 5 may be important for breeding nutraceutical varieties.

Aliyu *et al.*, (2021) emphasized selecting high-biomass *Lablab* lines for dual-purpose forage and grain production as found among members of cluster 6. Cluster 7, with moderate vegetative traits, is a unique profile that represents a distinct morphological variant or a locally selected cultivar because round seeds are preferred quality in some markets for ease of handling and fast cooking. This genotype has great value in quality-focused breeding for culinary traits. This finding is in line with Chukwu *et al.*, (2023) who reported that seed shape is an important consumer preference trait in local legume markets and can be an indicator of geographic or cultural differentiation.



The observed diversity among the seven clusters reflects considerable genetic heterogeneity in the *Lablab purpureus* germplasm evaluated. The clustering pattern aligns well with the PCA outcomes, validating the interdependence of both multivariate techniques.

The presence of two singleton clusters (Clusters 1 and 7) suggests that some genotypes are extremely divergent, possibly due to geographic isolation, unique selection pressures, or local adaptation. These outliers can be valuable for hybridization programs aimed at maximizing heterosis (hybrid vigor).

Cluster analysis also facilitates strategic parent selection in breeding programs. Crosses between accessions from distant clusters (e.g., Cluster 1 and Cluster 5 or Cluster 2) are likely to produce transgressive segregants with superior traits. This approach is endorsed by Oyetunde *et al.*, (2021), who recommend using cluster distance as a criterion for selecting parents to maximize variability in progeny.

CONCLUSION AND RECOMMENDATION

The combination of Principal Component Analysis (PCA) and Cluster Analysis has provided deep insights into the structure of phenotypic and genetic variation in *Lablab purpureus*. The PCA identified four principal components that explained most of the total variation, largely driven by plant architectural traits, seed morphometry, shape ratios, and colour intensity.

Cluster and hierarchical analysis further refined this understanding by classifying the genotypes into seven distinct clusters, each with unique trait profiles. The largest clusters (Clusters 3 and 4) exhibit intermediate traits, while singleton clusters (1 and 7) suggest unique genetic resources. The findings emphasize the broad genetic base of the understudied *Lablab accessions* and the opportunity for genetic improvement. Breeders can use the identified clusters to select contrasting parental lines, improve target traits, and enhance adaptation. Furthermore, the identification of clusters with high biomass, superior seed quality, or unique pigmentation can support breeding for multiple uses: food, forage, and functional nutrition. This PCA-based study underscores the significant phenotypic and genetic diversity present among the *Lablab purpureus* accessions. By extracting principal components, the analysis revealed that the most critical traits contributing to variation were plant height, branching, terminal leaf size, seed size (length, width, and thickness), seed weight, and seed colour.

The four extracted components represent distinct agronomic domains:

1. **PC1:** Vegetative vigour and canopy structure,
2. **PC2:** Seed morphometrics and yield potential,
3. **PC3:** Seed shape ratios and dimensions,
4. **PC4:** Aesthetic traits (particularly seed coat colour).

These domains provide a robust framework for germplasm classification, selection, and conservation. The distinct clustering of traits in each principal component suggests that multi-trait selection indices can be developed to guide breeding objectives more efficiently.

The implications of these findings for *Lablab purpureus* improvement are profound. With increasing interest in underutilized legumes for climate-smart agriculture, identifying genotypes with superior agronomic and nutritional traits becomes imperative. The observed diversity provides a genetic reservoir that can be exploited for improving yield, seed quality, and adaptability to varying environmental conditions.

Furthermore, integrating PCA with cluster and hierarchical analyses enables a comprehensive understanding of genotype relationships, facilitating the identification of distinct groups for cross-breeding. This multivariate approach is superior to univariate analyses because it considers trait interdependence and avoids redundancy.

In conclusion, PCA has proven to be a vital tool in this genetic diversity study, unraveling complex relationships among traits and providing insights into selection strategies. The findings provide a scientific basis for the development of ideotypes with optimal combinations of yield, quality,



and stress-resilience traits in *Lablab purpureus*. Future breeding programs should incorporate molecular markers alongside morphological traits to validate and enhance selection accuracy. Future work should use genotypes from distinct clusters as parents in hybridization and incorporate **molecular markers** and **genomic tools** to complement phenotypic diversity, ensuring a more holistic approach to *Lablab* improvement.

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