



RESEARCH ARTICLE

Genetic diversity and multilocation field performance of mung bean (*Vigna radiata*) accessions

Mayowa Segun Oladipo^{1a} , Qudrah Olaitan Oloyede-Kamiyo^{1b} , Adedotun Daniel Adewumi^{1c} , Paul Chiedozi Ukachukwu^{1d} , Kehinde Titilope Kareem^{1e} and Modupe Ifejola Joan Timothy^{1f}

¹Institute of Agricultural Research and Training, Obafemi Awolowo University, Moor Plantation, Ibadan, Nigeria

^a: <https://orcid.org/0009-0001-2035-8531>

^b: <https://orcid.org/0000-0002-9409-0259>

^c: <https://orcid.org/0009-0002-3632-5176>

^d: <https://orcid.org/0000-0001-6997-9315>

^e: <https://orcid.org/0000-0003-3176-6861>

^f: <https://orcid.org/0000-0002-7192-7562>

*Correspondence Author:
Qudrah Olaitan Oloyede-Kamiyo
E-mail: qudratkamiyo@gmail.com

Received: January 08, 2026

Revised: May 14, 2026

Accepted: May 30, 2026

ABSTRACT. Genetic diversity provides the necessary accessions needed for breeding programs that aim to develop varieties that are more resilient to biotic and abiotic stress, have higher yields and can adapt to changing climates. Twenty-one selected mung bean accessions were assessed for their field performance, genetic relationships and potential for agricultural improvement. The study was carried out at Ife, Ilora and Ballah in the 2023 cropping season. A randomized complete block design (RCBD) with three replications was used for the experiments at each site. Agronomic, yield, pest and viral disease rating data were collected and analyzed. The location effects were highly significant for all traits. Significant differences were also observed for key agronomic traits including days to 50% flowering and podding, viral severity, insect rating, pod length, and terminal leaf length. Accession TVr-83 had the longest days to 50% flowering and podding. TVr-52 was the most susceptible accession to viral infection and TVr-42 was the most resistant line for pod borer rating. Cluster analysis grouped the accessions into four clusters. Cluster 3, consisting only of TVr-65, exhibited the highest pod weight, while Cluster 4 combined moderate maturity with relatively high yield potential. Principal component analysis revealed that days to 50% senescence, pod weight, and flowering and podding times were major contributors to variation. The findings highlight the presence of useful genetic variability among the accessions, with implications for breeding programs aimed at improving yield, pest resistance, and adaptation.

Keywords: Agronomic traits, cluster analysis, genetic diversity, mung bean (*Vigna radiata*), principal components analysis

INTRODUCTION

The mungbean plant (*Vigna radiata* L.) is a diploid self-pollinating crop. It is also a significant food legume that is usually cultivated and eaten extensively throughout Asia [1]. Mung bean contains zinc (0.02 – 0.04 mg g⁻¹), carbohydrates (63%), protein (25%), iron (0.03 – 0.06 mg g⁻¹) and a low anti-nutritional content in comparison to other beans [2]. It plays a crucial role in sustainable agriculture and food security, particularly in areas with limited resources and challenging climates. Despite its beneficial attributes, mung bean is still regarded as an underutilized legume or orphan crop in Nigeria and other countries in Sub-Saharan Africa [3]. One of the major limiting factors for the production of mung beans is the non-availability of improved seeds of the crop. As global population pressures and climate variability intensify, the importance of enhancing crop productivity and resilience through genetic improvement becomes increasingly paramount.

Therefore, to improve the yield of the crop, it is necessary for plant breeders to research the genetic diversity of existing germplasms to identify accessions with resistance to biotic and abiotic stressors and also possess high yields. Diverse accessions with a broad genetic background are usually selected as parents to produce a strain with a higher frequency of desirable genes and also have a higher potential to produce a wide range of variation in a segregating population. Genetic diversity also provides the necessary accessions needed to develop varieties that are more resilient to biotic and abiotic stress, have higher yields and can adapt to changing climates. Addressing the issues brought on by climate change, which threaten agricultural productivity and food security, also requires an understanding of the field performance and genetic diversity of the current mung bean germplasms. Mung bean, with its capacity to increase soil fertility through its ability to fix atmospheric nitrogen, can be a significant contributor to climate-resilient farming systems [4].

Several studies on disease screening and agronomic performance indicated that mung beans contain a sizable number of resistant accessions and significant variation in yield-related traits used in breeding programs [5, 6, 7]. For instance, [8] evaluated the genetic diversity of 30 mung bean genotypes using morphological traits and revealed significant variation in yield-related traits. Similarly, [9] evaluated different genotypes of mung beans for genetic diversity from different geographic regions and identified accessions with superior agronomic traits suitable for breeding programs. Although these studies highlight the importance of phenotypic data to gain a comprehensive understanding of genetic diversity, however, limited information is available on mung beans that are resistant to insect pests. Therefore, the outcomes of this study have broader implications for enhancing the resilience and sustainability of agricultural systems, particularly in regions prone to climatic variability. The aim of this study is to use morphological traits to assess the genetic diversity among some selected mung bean accessions.

MATERIALS AND METHODS

Sample collection, research location and experimental design

For this study, twenty-one (21) mung bean accessions (TVr-58, TVr-89, TVr-98, TVr-45, TVr-65, TVr-5, TVr-52, TVr-93, TVr-40, TVr-84, TVr-8, TVr-42, TVr-78, TVr-70, TVr-43, TVr-62, TVr-50, TVr-95, TVr-83, TVm-11 and TVm-12) were obtained from the International Institute of Tropical Agriculture (IITA), located in Ibadan, Nigeria. Field trials were conducted at Ile Ife, Ilora and Ballah stations of the Institute of Agricultural Research and Training (IAR&T), Moor Plantation, Nigeria, in the 2023 cropping season (Table 1). Three replications and a randomized complete block design (RCBD) were used to set up the experiment. The size of the plot was 2.4m by 2.4m with a plant spacing of 50 cm by 50 cm between and within the rows. Until the plants reached maturity, every plot was hand-weeded at two-weeks interval. Field pests were managed during both the vegetative and reproductive stages using 300 g L⁻¹ Dimethoate and 15% Lambda-cyhalothrin.

Table 1: Agro-ecological and environmental characteristics of the study locations

Parameter	Ile-Ife	Ilora	Ballah
Agro-ecological zone	Rainforest	Derived Savannah	Southern Guinea savanna
Rainfall	Bimodal (1500 – 1502 mm)	Bimodal (1200 – 1400 mm)	Unimodal (1000 – 1200 mm)
Location	Latitude 8°97'N, Longitude 3°95'E	Latitude 7.77'N, Longitude 3.93'E	Latitude 8.27'N, Longitude 4.25' E
Temperature	25°C - 29°C	22.5°C to 31.4°C	30°C - 35°C
Soil type	Ferric Luvisols or Alfisols.	Alfisol/Lixisol	Luvisols
Reference	[10]	[11]	[11]

Data Collection

The data collected included the number of days to 50% flowering and podding, which was determined by calculating the number of days it takes for 50% of the plants in a plot to flower and develop pods, respectively. Viral severity and insect rating for pod borer infestation were rated on a scale of 1-5, with 1 being excellent and 5 being very poor [12]. The rating was done at the vegetative stage and before the application of insecticides. The number of pods per plant was estimated by getting the average number of pods in 10 selected plants per plot. Pod weight (g), was determined by weighing the total number of pods harvested in each plot. Number of main branches was estimated by calculating the average number of main branches in 10 selected plants per plot. Number of days

to 50% senescence was determined by counting number of days from planting to when 50% of the plants in a plot have started showing signs of senescence. Terminal leaf length in centimeter (cm) was taken by measuring the length of a leaf from each of 10 randomly selected plants within the plot and the average calculated. Peduncle length (cm) was calculated using the average length of ten peduncles, from randomly selected plants within plot. Pod length (cm) was measured from the average of 10 randomly selected pods among the harvested pods/plot.

Statistical analysis

Data were analysed using SAS software version 9.0, and the Duncan Multiple Range Test (DMRT) was used to separate

means. Principal Component Analysis (PCA) was performed to identify the main components contributing to trait variation. Cluster analysis based on agronomic traits was conducted to group accessions with similar performance. Principal Component Analysis (PCA) and Cluster analysis were done using PAST software.

RESULTS AND DISCUSSION

Analysis of variance for location, accession, and interaction effects

The analysis of variance result in table 2 revealed that the location effect was highly significant on all measured traits. This indicates substantial environmental variability across the different test locations, highlighting its strong role in determining crop performance. This pronounced location effect on all traits aligns with previous reports that environmental factors strongly influence mung bean yield and performance [13]. The accession effects were significant for several key traits, including days to 50% flowering and podding, viral severity, days to 50% senescence, insect rating, pod length, and terminal leaf length. This demonstrates the presence of genetic variability among the evaluated accessions for the traits. These traits can also be effectively improved through selection, as similarly reported in earlier studies on mung bean [14].

However, non-significant effects were observed for the number of pods per plant, pod weight, number of main branches, and peduncle length, indicating limited genetic differences among the accessions for these traits in this study. The accession by location interaction effect was highly significant for days to 50% senescence and significant for insect rating, indicating that the performance of the different accessions for these traits varied across the three environments. Significant accession by location interaction effect was also reported for days to 50% senescence in a previous study on cowpea [15]. The non-significant interaction observed for the other remaining traits indicates that their performance was relatively consistent across environments, suggesting that selection for these traits may be conducted across locations without strong location-specific effects. This highlights the importance of evaluating accessions across multiple environments to determine the stable accessions. Similar non-significant accession by location interaction for flowering and other agronomic traits has also been previously reported in mung bean [16].

Mean performance of the accessions

The mean performance of the accessions is presented in Table 3. There was significant variability in the number of

days to 50% flowering among the accessions. TVr-83 had the longest days to 50% flowering (61 days) while TVr-65 had the second-longest (57 days). Longer flowering and podding periods can sometimes be associated with increased yield potential. This is due to extended periods for photosynthesis and growth which might be suitable for environments with longer growing seasons [17]. Early flowering accessions are typically desirable in regions with shorter growing seasons or where early maturing double-cropping seasons are required to escape late-season droughts or pest infestations [18]. Early podding as seen in TVr-5 (50 days) is advantageous for environments where early cropping and reduced plant exposure linked to late season stresses are desirable. However, longer days to podding in genotypes like TVr-83 may allow for an extended period for more nutrient accumulation on the field [19]. The observed variability reflects the adaptability of these genotypes to diverse agroecological conditions, supporting findings reported in previous studies [20].

Disease severity and insect infestation ratings are crucial for understanding plant disease resistance and for reducing crop losses. In terms of resilience to pest and diseases, TVr-52 exhibited the highest severity rating (2.17) followed by TVr-78 (2.00). Most of the other accessions showed an intermediate severity rating (1.20 to 1.83), while several other accessions like TVm-12, TVr-45. Accessions with lower severity like TVr-93 (1.17) could be prioritized for breeding programs focused on disease resistance as they may possess inherent genetic resistance or tolerance to certain diseases [21]. Thus reducing the need for chemical control measures. Rating for insect pest infestation range from 0.83 to 1.83, with TVr-42 showing the least infestation and TVr-83 and TVr-70 showing the highest rating. This result indicated that most of the accessions in this study have inherent traits of resistance to field pests and diseases.

Number of pod per plant is a primary yield trait that is often influenced by both genetic and environmental factors [22]. Accessions TVr-98 and TVm-11 had higher number of pods per plant (41.1 and 40.5) respectively than other accessions indicating their higher yield potential. However, this trait must be considered alongside other yield related traits. Similar variability in pod number has been widely reported in mung bean breeding studies [23]. The number of pods per plant and other yield related traits like pod weight are essential for selecting high-yielding accessions, as they directly contribute to the overall yield of the crop [24]. Pod weight is a crucial determinant of final yield and should be considered in selection programs. It varied significantly among the accessions, with values ranging from 264.06 g in TVm-11 to 705.11 g in TVr-65. Although all entries were statistically similar, numerical differences indicate potential yield advantages in

certain genotypes. Higher pod weight reflects better nutrient assimilation and seed development which is advantageous for breeding high-yielding varieties [24]. These findings are consistent with earlier reports emphasizing the importance of biomass allocation efficiency [25].

Branching increases flowering sites, and potentially enhances yield. In this study TVr-83 had the highest average number of main branches (4.70) which can contribute to higher yield through more pod-bearing points on the plant [26]. However, excessive branching may also lead to intra-plant competition for resources. TVm-12 (2.86) had the fewest number of main branches which might limit its yield potential unless compensated by other factors such as larger pod size or more pods per branch. The days to 50% senescence provide insights into the reproductive development of the plants. In this study, TVr-58 (68.00 days) had shortest days to 50% senescence which may reduce nutrient assimilation during the reproductive stages. TVr-83 and TVr-65 with days to 50% senescence value of 76.40 days and 76.33 days respectively took the longest days to reach senescence, potentially aligning with longer flowering and podding periods. Delayed senescence is often associated with higher yield potential due to extended period on the field for nutrient production [27].

Leaf morphology is an important trait in crop adaptation and productivity and can also be an indicator of photosynthetic ability, overall plant vigor and increased biomass production. TVm-12 had the shortest terminal leaf length (9.13 cm) which might affect its photosynthetic ability. Accessions with longer leaves, such as TVr-89 (13.13 cm), may have an advantage under optimal growing conditions due to increase transpiration and also susceptible to late season drought. Similar trends have been reported in cowpea and other legumes [28]. Peduncle length varied between 9.48 cm in TVr-84 and 14.43 cm in TVr-45. Longer peduncles are desirable as they elevate pods above the canopy, reducing pest damage and facilitating harvesting. Selection for longer peduncles has been emphasized in legume improvement programs [29]. Pod length is a heritable trait and is often used as a selection criterion in breeding programs. There was little variation in the length of the pods among the accessions and the observed variation indicates its potential for genetic improvement. TVm-12 had the shortest pod length (4.94 cm), while TVr-78 (8.67cm) had the longest pod, closely followed by TVr-50 (8.66 cm) and TVr-89 (8.65 cm). Longer pods can accommodate more seeds, and hence, produce higher seed yield [22]. These results are in agreement with previous reports on the relationship between pod traits and yield in mung bean [30].

Table 2: Analysis of Variance for Agronomic and Insect-Related Traits of Accessions across Locations

Source of variation	df	Days to 50% flowering	Days to 50% podding	Viral severity (1-5)	Days to 50% senescence	Insect rating (1-5)	Pods per plant	Pod weight (g)	Pod length (cm)	Number of main branches	Terminal leaf length (cm)	Peduncle length (cm)
Location	2	356.25**	583.77**	19.05**	2288.98**	13.29**	7750.73**	1491903.52**	141.25**	59.75**	26.62**	88.32**
replication	2	67.20	107.78**	0.35	1.00	0.13	1695.89**	1364994.85**	0.46	12.01**	15.26*	57.67**
Accession	20	102.14**	82.61**	0.43*	24.35**	0.43*	303.56	172315.06	17.57**	1.16	8.23**	10.08
Accession x location	40	27.98	20.68	0.36	23.46**	0.44*	387.77	148755.04	5.89	0.73	3.04	5.02
Error	120	23.81	25.93	0.23	6.55	0.26	352.38	154124.80	7.63	0.78	4.10	10.81

***, significant at $p < 0.05$ and $p < 0.01$ respectively

Table 3: Mean result from the 21 mung bean accessions evaluated at three locations in the 2023 cropping season

Variety name	days to flowering	days to 50% podding	Viral severity (1-5)	Insect rating (1-5)	pods per plant	Pod weight (g)	Number of main branches	days to 50% senescence	Terminal leaf length (cm)	Peduncle length (cm)	Pod length (cm)
TVr-83	60.5a	64.88a	1.20c	1.83a	25.48ab	458.01a	4.70a	76.40a	9.74bc	11.94ab	6.56b
TVr-65	57.00ab	59.38b	1.67abc	1.17abc	21.96ab	705.11a	3.41bc	76.33a	11.28ab	13.12ab	8.41a
TVr-84	51.88cd	52.33cd	1.67abc	1.17abc	22.67ab	423.03a	3.65bc	76.00ab	9.70bc	9.48b	6.10b
TVr-93	55.00bc	56.75bc	1.17c	1.17abc	34.39ab	593.68a	3.79abc	74.50abc	12.10a	12.59ab	8.49a
TVm-12	47.13d	51.63cd	1.17c	1.17abc	16.97b	372.52a	2.86c	74.00abc	9.13c	10.07b	4.94c
TVr-95	48.44d	53.56cd	1.83abc	1.67ab	23.45ab	448.60a	3.67bc	72.83abcd	12.50a	11.10ab	8.62a
TVm-11	47.50d	51.25cd	1.40bc	1.20abc	40.54a	264.06a	3.98ab	72.60abcd	12.25a	12.16ab	8.23a
TVr-62	49.11d	53.11cd	1.33bc	1.00bc	26.35ab	539.99a	3.94ab	72.50abcd	11.27ab	10.82ab	7.81a
TVr-78	49.78d	53.44cd	2.00ab	1.33abc	21.14ab	382.17a	3.88ab	72.17abcde	12.27a	12.30ab	8.67a
TVr-89	49.11d	53.78cd	1.67abc	1.17abc	28.37ab	485.89a	3.57bc	72.17abcde	13.13a	14.23a	8.65a
TVr-52	47.56d	52.44cd	2.17a	1.17abc	26.52ab	409.84a	3.46bc	72.17abcde	11.74ab	12.82ab	8.27a
TVr-42	49.33d	52.56cd	1.50abc	0.83c	21.73ab	422.67a	3.89ab	72.00abcde	11.77ab	11.46ab	7.74a
TVr-8	49.56d	53.33cd	1.50abc	1.50abc	24.25ab	472.06a	3.67bc	72.00abcde	11.05abc	12.57ab	8.33a
TVr-70	47.78d	51.33cd	1.50abc	1.83a	28.74ab	265.85a	4.09ab	71.83bcde	11.60ab	13.11ab	8.36a
TVr-5	47.33d	50.33d	1.67abc	1.33abc	28.54ab	556.75a	3.42bc	71.83bcde	11.60ab	13.15ab	8.31a
TVr-43	49.22d	53.33cd	1.50abc	1.33abc	29.38ab	346.46a	3.98ab	71.50cde	11.59ab	12.02ab	8.62a
TVr-40	48.00d	51.89cd	1.83abc	1.33abc	27.04ab	392.97a	3.77abc	70.50cde	12.56a	12.26ab	8.26a
TVr-50	47.67d	52.33cd	1.83abc	1.50abc	18.94b	336.87a	3.40bc	70.33cde	11.42ab	13.29ab	8.66a
TVr-98	49.89d	53.56cd	1.50abc	1.17abc	41.11a	537.20a	3.90ab	70.17cde	10.89abc	11.83ab	8.37a
TVr-45	49.67d	53.33cd	1.17c	1.50abc	31.01ab	612.80a	3.59bc	69.33de	11.78ab	14.43a	8.21a
TVr-58	48.50d	52.13cd	1.40bc	1.80a	34.07ab	606.84a	3.41bc	68.00e	11.11abc	13.00ab	8.40a
Mean	50.00	53.65	1.56	1.34	22.77	458.73	3.71	72.34	11.45	12.07	7.28
CV	9.77	9.50	30.97	37.51	86.60	75.10	23.73	3.54	17.65	12.43	40.26

Clustering of the accessions into distinct groups

The clustering pattern highlights the presence of meaningful genetic divergence among the accessions, which is essential for effective selection and hybridization in breeding programs. The clear separation and grouping of the twenty-one accessions examined in this study into four distinct clusters at a distance of 120 (Figure 1) based on agronomic, yield and other related traits suggests that these characters contributed substantially to the observed variability. These clusters and their respective means (Table 4) represent groups of accessions that share higher genetic similarity within each group than with those in other groups. The presence of multiple clusters indicates significant genetic diversity among the mung bean accessions studied. This diversity is crucial for effective breeding programs aimed at improving traits such as disease resistance, yield and stress tolerance. Identifying accessions with unique genetic backgrounds can help breeders select parent lines that can be used to produce superior hybrids [31].

Cluster 1 which is the largest group consisted of twelve (12) accessions. The members of this cluster generally exhibited moderate values for flowering (49.85 days) and podding (53.79 days) but recorded low pod per plant (19.60) and pod weight (412.59 g). This cluster is characterized by moderate growth related traits but with relatively low yield related traits. This suggests that accessions within this cluster may not be useful for yield improvement purposes but could serve as genetic resource for stability, adaptation, or other stress tolerance studies. Cluster 2 with two (2) accessions that are very closely related suggests that they might have similar genetic traits, share a common parent or possibly contain unique genes. This cluster had the earliest value for flowering and podding among the clusters with values of 47.64 days and 51.29 days respectively. Alongside its early maturity, this cluster also had the highest value for terminal leaf length (11.92 cm) and number of main branches (4.04). Despite this, this cluster had the lowest value for pod weight (264.96 g) which may limit its yield potential. The accessions in this cluster could therefore be valuable as parental lines for environments where early maturity, improved leaf length and branching is desired.

Cluster 3 is highly distinct, with only accession TVr-65 present in it. This cluster with its unique genetic composition highlights the importance of conserving it as a genetic material. Preserving unique genetic materials ensures the availability of a good genetic base for future breeding programmes [32]. This cluster is characterized by late flowering (57.00 days) and podding (59.38) potential, low leaf length (11.28 cm), high pod weight (705.11 g) and pod length (8.41 cm). Its high pod weight clearly separates

this accession from all others, indicating strong genetic potential for yield improvement. However, its late flowering may limit its adaptability to certain agro-ecologies. This observed late flowering time aided its vegetative growth, which further helped to support the high yield present within this cluster. This accession represents an important candidate for hybridization, particularly in crosses aimed at yield improvement. Similar results have been reported in cowpea where high vegetative growth correlates to high yield [33]. Six accessions were present in cluster 4. The mean result from the accessions in the cluster showed that they were intermediate maturing with an average flowering and podding time of 49.92 days and 53.20 days respectively. They also possessed a relatively high yield, with an average pod weight and pods per plant values of 574.54 g and 27.50, respectively thus indicating its high yield potential. This cluster appears to represent a balanced group with favorable yield values coupled with moderate maturity. This combination suggests that accessions in this cluster may already possess desirable agronomic performance and could be considered for direct selection or as elite parents in breeding programs.

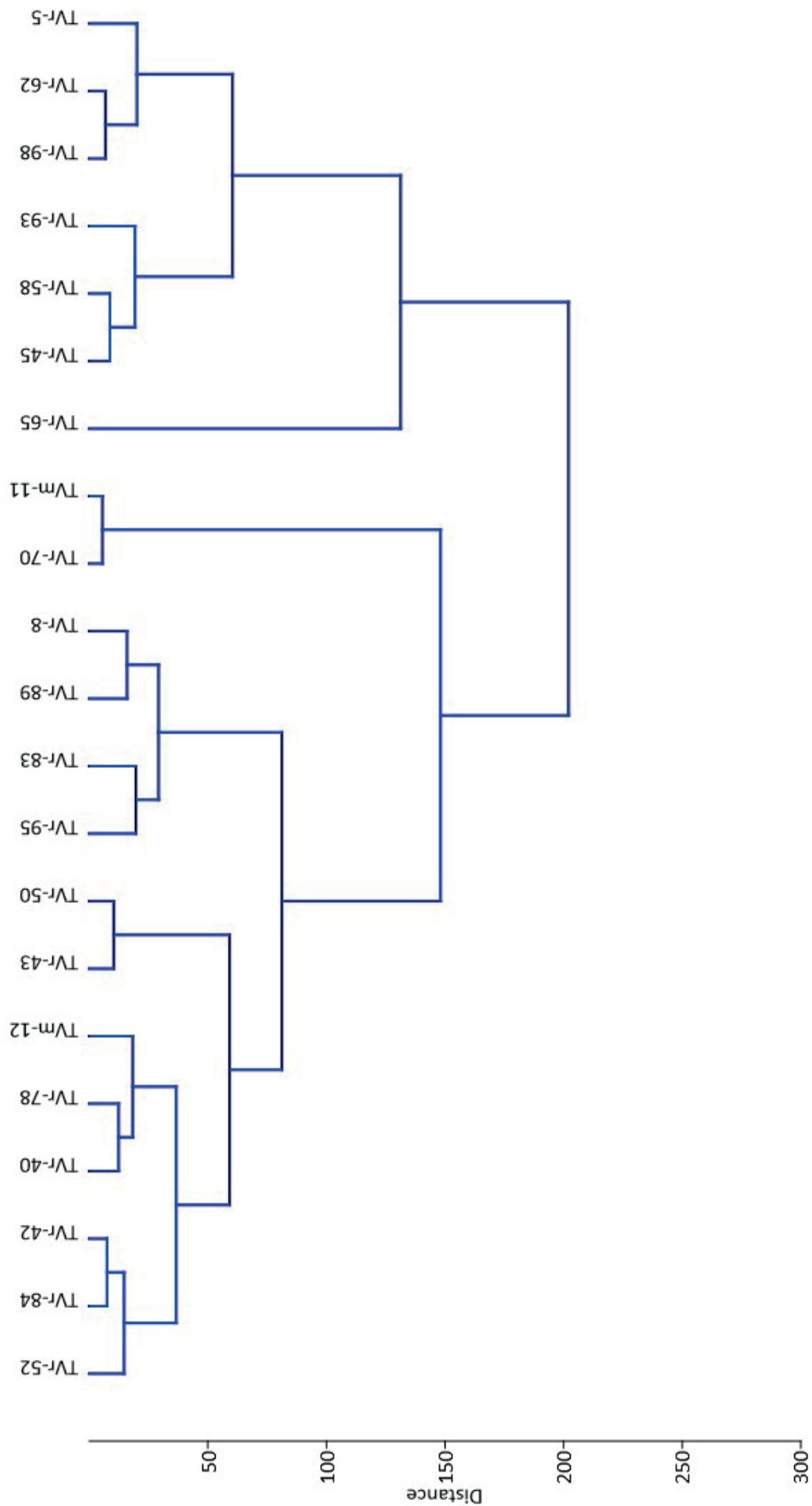


Figure 1: Dendrogram showing the genetic relatedness among the mungbean accessions derived from the cluster analysis

Table 4: Cluster Means and Composition of Accessions Based on Agronomic and Resistance Traits

Cluster	NoA	ACC	D50F	D50P	VSR	ISR	PPP	PW	NMB	D50S	TLL	PEL	PL
Cluster 1	12	TVr-52, TVr-84, TVr-42, TVr-40,											
		TVr-78, TVm-12, TVr-43, TVr-50,	49.85	53.79	1.66	1.33	19.6	412.59	3.71	72.67	11.38	11.6	6.87
		TVr-95, TVr-83, TVr-89, TVr-8											
Cluster 2	2	TVr-70, TVm-11	47.64	51.29	1.45	1.52	27.98	264.96	4.04	72.22	11.92	12.64	6.8
Cluster 3	1	TVr-65	57	59.38	1.67	1.17	21.96	705.11	3.41	76.33	11.28	13.12	8.41
Cluster 4	6	TVr-45, TVr-58, TVr-93, TVr-98, TVr-62, TVr-5	49.92	53.2	1.37	1.33	27.5	574.54	3.68	71.05	11.46	12.64	8.09

NoA: Number of Accessions; ACC: Accessions; D50F: Days to 50% Flowering; D50P: Days to 50% Podding; VSR: Viral Severity Rating; ISR: Insect Severity Rating; PPP: Pods Per Plants; PW: Pod Weight; NMB: Number of Main Branches; D50S: Days to 50% Senescence; TLL: Terminal Leaf Length; PEL: Peduncle Length; PL: Pod Length

Principal Component Analysis (PCA) of the traits studied

The statistical method for reducing the dimensionality of datasets, finding patterns in the datasets, and improving interpretability while also reducing information loss is known as principal component analysis (PCA) [34]. The analysis helps to estimate the breeding values of germplasms and also determine appropriate traits based on the size of loadings on the traits in the Principal Component (PC). The PCA results for the 21 mung bean accessions (Table 5) showed that the first three components had Eigen values greater than 1.0. Principal Component 1 (PC 1) explains 28.39% of the total variance in the dataset, indicating that most of the variation in the mung bean accessions can be attributed to this first component. Principal Component (PC 2) accounts for 22.09% of the total variance. Although its contribution is much smaller than that of PC 1, it still provides valuable information about the underlying variability among the accessions. Principal component (PC3) explains 15.02% of the variance, indicating a further reduction in the importance of the traits that contributes to this component.

Principal component 1 (PC 1) explains the majority of the variance in the dataset, and the trait that loads most heavily on this component is days to 50% senescence with a loading of 0.46. This suggests that days to 50% senescence is the most influential trait in distinguishing among the mung bean accessions along this axis. High loadings indicate a strong influence of the trait on this principal component. Principal component 2 (PC 2), which explains a smaller proportion of the variance compared to PC1, is predominantly influenced by pod weight, with a loading of 0.59. This means that variations in the weight of the harvested pods significantly contributed to the differences among the accessions evaluated. This trait is crucial for yield improvement as it directly affects the total number of pods, and hence, the seed yield of the plant. This result aligns with earlier research demonstrating the importance of pod weight in mung bean yield and productivity [35]. Principal component 3 (PC 3) is primarily influenced by the number of days to 50% flowering and podding, with loadings of 0.55 and 0.51, respectively, indicating that variations in flowering and podding times are important for distinguishing among the accessions. Early flowering and podding are desirable traits for improving adaptation to specific growing seasons and environmental conditions [36].

Table 5: Principal component analysis for the traits assessed among the 21 mung bean accessions evaluated in three locations in 2023

	PC1	PC2	PC3
Days to 50% flowering	0.37	-0.01	0.55
Days to 50% podding	0.41	-0.01	0.51
Viral severity	0.32	-0.02	-0.36
Insect rating	0.32	-0.05	-0.16
Pods per plant	-0.05	0.60	0.05
Pod weight	-0.06	0.59	0.07
No of main branches	-0.13	0.29	0.31
Days to 50 senescence	0.46	-0.07	0.02
Term leaf length	0.21	0.27	-0.24
Ped length	0.36	0.02	-0.22
Pod length	0.28	0.35	-0.27
Eigen value	3.12	2.43	1.65
Variance (%)	28.39	22.09	15.02

CONCLUSION

This study highlights the substantial genetic diversity present in mung bean accessions with respect to field performance and clear implications for breeding. Accessions TVr-65, TVr-45, TVr-93, TVr-98, and TVr-5 showed strong potential for yield improvement due to high pod weight and other favorable yield traits. TVr-42 and TVr-93 exhibited low insect and disease ratings, indicating good resistance. The Principal component Analysis (PCA) results revealed that the first three components had Eigen values greater than 1.0, and PC 1 explained 28.39% of the total variance in the dataset. Days to 50% senescence, pod weight, flowering and podding time were the major contributors to the observed variation. The four clusters identified in this analysis provide a foundation for more detailed genetic studies. The marked difference between TVr-65 in Cluster 3 and accessions in either Clusters 1 or 2 suggests that crosses between them could generate superior segregating populations. Breeders should prioritize the accessions in these clusters for hybridization and selection under multi-environment trials. Future work should integrate molecular marker validation to confirm genetic diversity and assist in marker-assisted selection, thereby improving breeding efficiency and accelerating the development of resilient and high-yielding mungbean varieties.

CONFLICT OF INTEREST

The authors declared that there is no conflict of interest.

AUTHORSHIP CONTRIBUTIONS

Conceptualization: O.M.S., O-K.Q.O., Data curation: O.M.S., O-K.Q.O., T.M.I.J. Funding acquisition: O-K.Q.O., O.M.S., Investigation: A.A.D., U.P.C., T.M.I.J., K.K.T., Methodology: O-K.Q.O., O.M.S., Supervision: O-K.Q.O., K.K.T., Writing – original draft: O.M.S., A.A.D., U.P.C., Writing – review and editing: O-K.Q.O., K.K.T.

FINANCIAL DISCLOSURE

This research was funded by the Institute of Agricultural Research and Training

REFERENCES

- [1] Ha J, Lee SH. Mung bean (*Vigna radiata* (L.) R. Wilczek) breeding. In: *Advances in Plant Breeding Strategies: Legumes* 7. Cham: Springer International Publishing; 2019. p. 371–407.
- [2] Nair RM, Yang RY, Easdown WJ, Thavarajah D, Thavarajah P, Hughes JDA, et al. Biofortification of mungbean (*Vigna radiata*) as a whole food to enhance human health. *J Sci Food Agric*. 2013;93(8):1805–1813.
- [3] Diatta AA, Abaye O, Battaglia ML, Leme JF, Seleiman M, Babur E, et al. Mungbean [*Vigna radiata* (L.) Wilczek] and its potential for crop diversification and sustainable food production in Sub-Saharan Africa: a review. *Technol Agron*. 2024;4(1):e031. doi:10.48130/tia-0024-0030.
- [4] Shahid N. Legumes production under changing climate. In: *Climate Smart Agriculture for Future Food Security*. Singapore: Springer Nature Singapore; 2025. p. 191–221.
- [5] Nair RM, Pandey AK, War AR, Hanumantharao B, Shwe T, Alam AKM, et al. Biotic and abiotic constraints in mungbean production: progress in genetic improvement. *Front Plant Sci*. 2019;10:1340. doi:10.3389/fpls.2019.01340.
- [6] Pratap A, Douglas C, Prajapati U, Kumari G, War AR, Tomar R, et al. Breeding progress and future challenges: biotic stresses. In: Nair RM, Schafleitner R, Lee S-H, editors. *The Mungbean Genome*. Cham: Springer; 2020. p. 55–80. doi:10.1007/978-3-030-20008-4_5.
- [7] Gayacharan, Archak S, Gupta K, Gupta V, Tyagi V, Singh K. Mungbean genetic resources and utilization. In: Nair RM, Schafleitner R, Lee S-H, editors. *The Mungbean Genome*. Cham: Springer; 2020. p. 9–25. doi:10.1007/978-3-030-20008-4_2.
- [8] Gokulakrishnan J, Kumar Sunil B, Prakash M. Studies on genetic diversity in mung bean (*Vigna radiata* L.). *Legume Res*. 2025;35(1):50–52.
- [9] Chen H, Qiao L, Wang L, Wang S, Blair MW, Cheng X. Assessment of genetic diversity and population structure of mung bean (*Vigna radiata*) germplasm using EST-based and genomic SSR markers. *Gene*. 2015;566(2):175–183. doi:10.1016/j.gene.2015.04.043.
- [10] Ande OT, Huising J, Ojo AO, Azeez J, Are KS, Olakojo SA, et al. Status of integrated soil fertility management (ISFM) in southwestern Nigeria. *Int J Sustain Agric Res*. 2017;4(2):28–44. doi:10.18488/journal.70/2017.4.2/70.2.28.44.
- [11] Denton OA, Alemeru MS, Fademi IO, Uthman A, Oyedele A. Assessment of the physical and chemical properties of three contrasting soils under different land use systems. *Curr Res Agric Sci*. 2017;4(4):96–102. doi:10.18488/journal.68.2017.44.96.102.
- [12] Sandhyarani C, Eswari KB, Sudarshanam A. Screening of blackgram PVT entries against thrips and *Maruca vitrata* (Geyer). *Andhra Agric J*. 2009;56(2):201–205.
- [13] Ong PW, Lin YP, Chen HW, Lo CY, Burlayaeva M, Noble T, et al. Environment as a limiting factor of the historical global spread of mungbean. *eLife*. 2023;12:e85725.
- [14] Mogali SC, Hegde GM. Recent advances in mungbean breeding: a perspective. In: Gosal SS, Wani SH, editors. *Accelerated Plant Breeding*, Volume 3. Cham: Springer International Publishing; 2020. doi:10.1007/978-3-030-47306-8_9.
- [15] Muchero W, Roberts PA, Diop NN, Drabo I, Cisse N, Close TJ, et al. Genetic architecture of delayed senescence, biomass, and grain yield under drought stress in cowpea. *PLoS One*. 2013;8(7):e70041.
- [16] Seo H, Kwon H, Satyawat D, Kim MY, Ha J, Lee SH. Identification of novel loci for flowering time in mungbean [*Vigna radiata* (L.) R. Wilczek] using genome-wide association study. *Genes Genom*. 2023;45(7):911–919.
- [17] Wingler A, Soualiou S. Overcoming physiological trade-offs between flowering time and crop yield: strategies for a changing climate. *J Exp Bot*. 2025;76(10):2646–2658.
- [18] Shavrukov Y, Kurishbayev A, Jatayev S, Shvidchenko V, Zotova L, et al. Early flowering as a drought escape mechanism in plants: how can it aid wheat production? *Front Plant Sci*. 2017;8:1950.
- [19] Islam MR, Sarker U, Azam MG, Hossain J, Alam MA, Ullah R, et al. Potassium augments growth, yield, nutrient content, and drought tolerance in mung bean [*Vigna radiata* (L.) Wilczek]. *Sci Rep*. 2024;14(1):9378.
- [20] Ganta TY, Mekbib F, Amsalu B, Tadele Z. Genotype by environment interaction and yield stability of drought tolerant mung bean [*Vigna radiata* (L.) Wilczek] genotypes in Ethiopia. *J Agric Environ Sci*. 2022;7(1):43–62.
- [21] Durojaye HA, Moukoubi YD, Dania VO, Boukar O, Bandyopadhyay R, Ortega-Beltran A. Evaluation of cowpea [*Vigna unguiculata* (L.) Walp.] landraces for bacterial blight caused by *Xanthomonas axonopodis* pv. *vignicola*. *Crop Prot*. 2019;116:77–81. doi:10.1016/j.cropro.2018.10.013.
- [22] Bennett EJ, Roberts JA, Wagstaff C. The role of the pod in seed development: strategies for manipulating yield. *New Phytol*. 2011;190(4):838–853.
- [23] Gayacharan, Tripathi K, Meena SK, Panwar BS, Lal H, Rana JC, et al. Understanding genetic variability in the mungbean (*Vigna radiata* L.) genepool. *Ann Appl Biol*. 2020;177(3):346–357.
- [24] Li M, Liu Y, Wang C, Yang X, Li D, Zhang X, et al. Identification of traits contributing to high and stable yields in different soybean varieties across three Chinese latitudes. *Front Plant Sci*. 2020;10:1642.

- [25] Guanzon IM, Garon CG, Marcelo MF, Miguel CM, Navarro AM, Rivera RC. Shifts in biomass allocation shape yield responses of mung bean [*Vigna radiata* (L.)] to molybdenum and silicon. *J Saudi Soc Agric Sci.* 2026;25(5):69.
- [26] Huang Y, Chen Y, Lin H. Study on optimizing density planting and fertilization strategies to increase bean yield. *Legume Genom Genet.* 2025;16(6):253–269.
- [27] Zhou M, Yang J. Delaying or promoting? Manipulation of leaf senescence to improve crop yield and quality. *Planta.* 2023;258(3):48.
- [28] Chaudhary S, Priya M, Jha UC, Pratap A, Hanumantha Rao B, Singh I, et al. Approaches toward developing heat and drought tolerance in mungbean. In: Jha UC, Nayyar H, Agrawal SK, Siddique KHM, editors. *Developing Climate Resilient Grain and Forage Legumes.* Singapore: Springer Nature Singapore; 2022. p. 205–234. doi:10.1007/978-981-16-9848-4_10.
- [29] Mahla H, Choudhary KB, Sharma R. Unveiling a novel gene inheritance model for peduncle length in moth bean (*Vigna aconitifolia* L.). *Indian J Genet Plant Breed.* 2025;85(4):773–779.
- [30] Tabasum A, Saleem M, Aziz I. Genetic variability, trait association and path analysis of yield and yield components in mungbean [*Vigna radiata* (L.) Wilczek]. *Pak J Bot.* 2010;42(6):3915–3924.
- [31] Allier A, Teyssèdre S, Lehermeier C, Moreau L, Charcosset A. Optimized breeding strategies to harness genetic resources with different performance levels. *BMC Genomics.* 2020;21(1):349.
- [32] Salgotra RK, Chauhan BS. Genetic diversity, conservation, and utilization of plant genetic resources. *Genes.* 2023;14(1):174.
- [33] Aliyu OM, Makinde BO. Phenotypic analysis of seed yield and yield components in cowpea [*Vigna unguiculata* (L.) Walp.]. *Plant Breed Biotech.* 2016;4(2):252–261.
- [34] Hasan BMS, Abdulazeez AM. A review of principal component analysis algorithm for dimensionality reduction. *J Soft Comput Data Min.* 2021;2(1):20–30.
- [35] Jayagond PA, Marawar MW, Lande SS, Ujjainkar VV. Genetic variability and character association studies in mungbean [*Vigna radiata* (L.) Wilczek]. *Int J Adv Biochem Res.* 2025;9(7):1829–1833. doi:10.33545/26174693.2025.v9.i7w.5056.
- [36] Fjellheim S, Boden S, Trevaskis B. The role of seasonal flowering responses in adaptation of grasses to temperate climates. *Front Plant Sci.* 2014;5:431.