Journal of Genetics, Genomics & Plant Breeding 9(4)162-172(October, 2025)
ISSN (Online): 2581-3293 DOI: 10.63551

RESEARCH ARTICLE

Heritability, variability and character association of thirty mung bean genotypes assessed in Owerri Southeastern Nigeria

C.S. Ejiogu[1], J.U. Agbim[2], N.C. Onwubiko[1], A.A. Ngwuta[1], K.J. Nnadi[1], I.F. Umar[1], C.B. Kanu[1]

1 Department of Crop Science and Technology, School of Agriculture and Agricultural Technology, Federal University of Technology, Owerri, 460114 Imo State, Nigeria

2 Department of Crop Science, Faculty of Agriculture, Imo State University, Owerri, 460222 Imo State, Nigeria.

Corresponding authors email: chigoziestephenejiogu@gmail.com

Manuscript received: September12, 2025; Decision on manuscript, October 12,2025; Manuscript accepted: October15, 2025

Abstract

This study was conducted as an introductory genotype trial to evaluate the potential for introducing mung bean (*Vigna radiata L.* Wilczek) into the cropping systems of southeastern Nigeria, where it is not traditionally cultivated. Thirty genotypes were collected from IITA and evaluated at the Center for Agricultural Research and Extension of the Federal University of Technology, Owerri. As an introductory trial, the performance of the genotypes was benchmarked against global yield standards for the crop. Analysis of variance revealed significant differences among genotypes for all morphological and yield traits, indicating a substantial genetic base for selection. Narrow differences between phenotypic and genotypic coefficients of variation for most traits revealed minimal environmental influence on their expression. There was a significant positive correlation among the morphological and yield traits assessed. Furthermore, high heritability estimates as well as high expected genetic advance were observed for key yield components such as pod weight and number of pods per plant, indicating that these traits are governed by additive gene action and will respond effectively to selection. Cluster analysis grouped the 30 genotypes into five distinct clusters. The most divergent accession was identified as Tvr-2, which formed a solitary cluster, highlighting its unique genetic background. Furthermore, genotypes Tvr-3 and Tvr-109 (Cluster III) were identified as the best-performing accessions for the majority of agronomic and yield traits and achieved yields up to 1300.74 kg/ha a level competitive with global productivity averages-demonstrating the crop's high potential for the region. The clear separation of Tvr-2 into a unique cluster, based on its distinct phenotypic profile, presents an optimal opportunity for hybridization with the elite performers from Cluster III. We therefore recommend the use of the highly divergent Tvr-2 for crossing with the high-yielding genotypes (Tvr-3 and Tvr-109) to create broad genetic variability and combine favorable traits for the development of superior mung bean cultivars in future breeding programs.

Keywords: Variation, genotype, heritability, selection, improvement

Introduction

The mung bean (*Vigna radiata* (L.) R. Wilczek) is a legume cultivated for its edible seeds and sprouts. Mung bean grows in a wide range of climatic conditions and has shown to be a fast-growing legume. It grows greatly under most adverse arid and semi-arid conditions (Mogotsi, 2006). It is a highly nutritious crop and contains sufficient amounts of protein, dietary fiber, minerals, vitamins and significant amounts of bioactive compounds capable of meeting basic human nutritive requirements. It offers a vast array of health benefits such as its hypoglycemic, hypolipidemic and antihypertensive effects, in addition to its anticancer and immune boosting abilities. (Liyanage *et al.*, 2018, Ali *et al.*, 2014, Guptar *et al.*, 2018, Chai *et al.*, 2019). Mung bean production is mainly (90 %) situated in Asia: India is the largest producer with more than 50 % of world production but consumes almost its entire production. Mung bean is a highly nutritious crop, yet its global productivity is low, averaging only 400 kg ha^{-1} (Nair *et al.*, 2013). This is exemplified in newer regions like Ethiopia, where a significant yield gap persists between potential yields reported from research (exceeding 1,650 kg ha^{-1}) and the approximately 1,235 kg ha^{-1} achieved by farmers, primarily due to a lack of locally adapted varieties and optimal agronomic practices (Asrate *et al.*, 2012; CSA, 2018). Germplasm evaluation plays a vital role in identification of superior genotypes for different qualitative and quantitative characters in crop breeding programmes which may be further used to create variability by hybridization. The information and assessment of genetic variability in the existing germplasm of a particular crop is sought as prerequisite (Appalaswamy and Reddy, 2004). Plant genetic resources are the most valuable and essential basic raw materials to meet the current and future needs of crop improvement programmes (Paroda *et al.*, 1991). The analysis of genetic variability provides the fundamental data on the genetic properties of a population, which is essential for formulating effective breeding strategies for crop improvement (Gudmewad *et al.*, 2018). In addition, heritability of a plant trait is very important in determining the response to selection because it implies the extent of transmissibility of traits into next generations (Surek and Beser, 2003).

Increased seed yield an important goal of breeders. But seed yield itself is a product of interaction of many component traits which influence yield directly or indirectly. So, it is important to see the contribution of each of the traits in order to give more attention to those having the highest influence on yield (Malek *et al.*, 2014). Also, having a clear understanding of the relationship between yield and its component traits is of great importance to a breeder for making adequate use of these relationships in selecting desirable genotypes for yield improvement programs (Ismail *et al.*, 2001, Kumar and Shukla, 2002). For an effective breeding program for crop variety development through hybridization, the analysis of genetic diversity is one of the useful tools and plays a fundamental role in identification of parents (Kwon *et al.*, 2002, Mazid *et al.*, 2013). Moreover, better knowledge on genetic diversity could help to achieve long-term selection gain (Chowdhury, 2002). As a traditional method, morphological traits are utilized in assessing genetic divergence and classify existing germplasm materials. However, this technique, a low level but powerful taxonomic tool, has been utilized for the preliminary grouping of germplasm prior to their characterization using more precise marker technologies. Despite its nutritional and agronomic benefits, mung bean is not a traditionally cultivated crop in southeastern Nigeria. Hence, this study was conducted as an introductory genotype trial to evaluate the potential for introducing mung bean into the cropping systems of southeastern Nigeria.

The specific objectives were to assess the amount of genetic variability among thirty adapted genotypes, determine the heritability of key agronomic traits, and identify divergent and high-yielding accessions suitable for future breeding programs in the region.

Materials and methods

Owerri lies at latitude 05° 27°N and longitude 07° 02°E at an elevation of 55 meters above sea level and is in the tropical rainforest region of southeastern Nigeria. The area has a bimodal pattern of rainfall with peaks in July and September. It has a minimum and maximum annual temperature of 20°C and 32 °C respectively and mean annual rainfall of 2500 mm and relative humidity of 85-89 % (Nwosu and Adeniyi, 1980). The experiment was laid out in a Randomized Complete Block Design (RCBD) with thirty mung bean varieties which was replicated three times. As this was an introductory genotype trial for a crop not yet cultivated in the region, no local check variety was available. Instead, the performance of all genotypes was evaluated on their own merit with the ultimate benchmark being their potential to achieve yields competitive with global standards for the crop, thereby assessing their suitability for introduction into the cropping systems of southeastern Nigeria. An experimental field measuring 12.8 m x 5.6 m (71.68 m2) was mapped out. The field was then subdivided into three blocks 1 m apart. Each block measured 12.8 m×1.2 m and contained 30 mung bean genotypes arranged in single row plots with 8 plants per genotype. The plants had an inter row and intra row spacing of 0.4m and 0.15m respectively. The genotypes were completely randomized within each block. The mung bean genotypes assessed include Tvr-1, Tvr-2, Tvr-3, Tvr-4, Tvr-6, Tvr-7, Tvr-9, Tvr-10, Tvr-11, Tvr-12, Tvr-13, Tvr-17, Tvr-54, Tvr-55, Tvr-56, Tvr-61a, Tvr-63, Tvr-64, Tvr-65, Tvr-67, Tvr-68, Tvr-69, Tvr-61b, Tvr-72, Tvr-109, Tvr-110, Tvr-111, Tvr-117, Tvr-123 and Tvr-124. Data collected include plant girth, height, number of leaves, number of pods per plant, pod length, pod girth, pod weight, number of seeds per pod, 100-seed weight and yield/ha. All the data were subjected to Analysis of Variance (ANOVA) test using Genstat software while the mean separation was done using Least Significant Difference at 5% level of probability using the procedure described by Obi (2002). Pearson's correlation and cluster analysis were done using SPSS. Genetic parameters were estimated by the formula given by Werf, (2009) and Malek *et al.,* (2014).

Results and discussion

Information regarding the mean performances of 30 mung bean genotypes based on morphological and yield attributes is shown in Table 1. The tallest plants were observed in Tvr-109 with mean height value of 29.27 cm while Tvr-61a was the shortest with a mean height value of 7.87 cm. The highest mean number of leaves of 6.83 was obtained in Tvr-3, while the lowest mean number of leaves was obtained in Tvr-61a with a value of 2.33. Tvr-109 were observed to have the largest leaf area possessing a mean leaf area of 1805.66 cm2 and closely followed by Tvr-3 with a mean leaf area of 1560.15 cm2. The smallest mean leaf area was observed in Tvr-54 with a mean leaf area of 57.75 cm2. Tvr-61a produced the fewest number of pods per plant with an average of 1.67 pods per plant. On the other hand, Tvr-124 produced the highest number of pods, with an average of 18.33 pods per plant. This was closely followed by Tvr-3 which produced an average of 16.00 pods per plant. For pod length, Tvr-109 on average produced the longest pods with a mean pod length of 9.15 cm, followed by Tvr-72 with a mean pod length of 8.21 cm. Tvr-54 produced the shortest pods on average with a mean pod length of 3.24 cm. Tvr-109 produced the highest number of seeds per pod with a mean number of 11 seeds. This was closely followed by Tvr-124 and Tvr-55 with mean values of 10.67 and 10 seeds per pod respectively.

Table 1: Mean performances of mungbean genotypes based on morphological and yield attributes

Genotypes	Height	Number of leaves	Leaf area (cm^2)	Number of pod	Pod length	Number seed	100 Seed weight (g)	Yield/ha (kg)
Tvr-1	12.1	4.0	224.0	2.3	6.2	7.3	17.1	183.7
Tvr-2	26.2	6.3	1270.2	13.3	8.1	8.7	53.0	697.8
Tvr-3	26.1	6.8	1560.2	16.0	7.1	9.0	97.4	1201.0
Tvr-4	16.1	4.3	369.1	6.3	5.5	6.7	46.9	484.0
Tvr-6	11.3	5.7	193.7	0.0	0.0	0.0	0.0	0.0
Tvr-7	13.0	3.3	111.7	0.0	0.0	0.0	0.0	0.0
Tvr-9	11.4	4.0	131.1	5.3	7.2	9.0	26.5	353.6
Tvr-10	18.8	6.2	674.2	11.0	8.0	5.0	87.2	645.9
Tvr-11	20.2	6.0	714.2	9.0	8.0	8.3	34.5	430.6
Tvr-12	12.2	4.2	155.1	5.3	7.4	8.0	15.5	183.7
Tvr-13	13.0	4.3	188.8	2.0	6.1	6.3	13.6	134.3
Tvr-17	13.1	3.8	139.4	2.0	5.3	5.7	5.1	43.0
Tvr-54	10.1	3.0	57.8	2.0	3.2	3.3	8.0	38.5
Tvr-55	14.1	3.7	121.2	2.0	6.6	10.0	6.7	112.6
Tvr-56	14.4	3.8	158.7	3.0	6.4	7.0	13.7	153.6
Tvr-61a	7.9	2.3	63.0	1.7	4.9	5.0	6.8	50.4
Tvr-63	10.9	3.8	202.0	3.0	5.9	4.3	22.9	150.1
Tvr-64	12.0	3.8	127.2	4.3	5.9	6.3	15.6	145.2
Tvr-65	12.9	3.8	121.0	0.0	0.0	0.0	0.0	0.0
Tvr-67	14.8	4.0	147.1	2.0	6.2	7.0	6.4	63.7
Tvr-68	16.2	4.7	265.5	4.7	7.7	9.0	19.6	255.3
Tvr-69	11.7	3.8	236.8	0.0	0.0	0.0	0.0	0.0
Tvr-61b	25.2	6.5	955.6	7.3	7.7	8.7	47.8	627.2
Tvr-72	27.2	5.7	1133.1	10.0	8.2	9.7	68.2	959.0
Tvr-109	29.3	6.3	1805.7	13.0	9.2	11.0	79.8	1300.7
Tvr-110	15.6	6.3	543.4	13.7	3.9	6.0	104.2	925.9
Tvr-111	11.9	4.2	139.4	5.7	7.6	9.7	28.4	414.3
Tvr-117	14.7	4.2	257.4	5.7	6.5	5.3	51.1	454.3
Tvr-123	22.5	5.2	581.7	10.0	7.1	5.7	69.0	604.0
Tvr-124	25.8	6.3	1004.3	18.3	8.1	10.7	62.4	998.0
LSD(0.05)	5.0	1.3	408.8	5.2	1.0	2.0	45.6	521.3

Tvr-6, Tvr-7, Tvr-65 and Tvr-69 produced no pod and as such there were no seeds. The 100 seed weight ranged from 5.08g to 104.17g with the highest value obtained from Tvr-110 and the lowest from Tvr-17. Tvr-109 had the highest mean yield with 1300.74 kg/ha which was closely followed by Tvr-3 with 1200.99kg/ha. The lowest mean yield was 38.52kg/ha obtained from Tvr-54. The result from correlation analysis of the various mung bean characters evaluated is presented in Table 2. From the table, it can be observed that 100 seed weight and yield per hectare were positively correlated to the growth parameters recorded which includes girth, height, number of leaves and leaf area. 100 seed weight and yield per hectare were also positively correlated to pod length, pod girth, pod weight as well as number of seeds per pod.

Narrow sense heritability, phenotypic variance, genotypic variance, phenotypic and genotypic coefficient of variation (PCV and GCV) as well as genetic advance were calculated and the results are presented in Table 3. The results showed narrow differences between phenotypic variance and genotypic variance for most of the traits. All the characters exhibited high heritability which ranged from 74.00 % in 100-seed weight to 99.50 % in pod girth. The highest PCV and GCV were observed for pod weight (94.56% and 88.78% respectively) and the lowest PCV and GCV were recorded for leaf area (6.77% and 6.51% respectively). Narrow differences between PCV and GCV were also observed for most of the traits. The genetic advance as percent of the mean (GA%) ranged from 44.81% in plant girth to 97.44% in plant height. The narrow differences between PCV and GCV observed for all traits assessed gives an indication of minimal influence of environmental factors on the expression of the traits and a chance of high selection gain. High heritability values for all the traits indicate a high degree of gene influence on the traits which also indicates less influence of environmental factors on the expression of these traits and the chance of high gain from phenotypic selection. The heritability estimates help the breeders in selection on the basis of phenotypic performance. Heritability and GA with GCV values can provide a very good image of the amount of advancement to be expected through phenotypic selection (Malek *et al.,* 2014). Therefore, high values of heritability and GA in conjunction with high GCV for characters like pod weight, number of pods per plant, 100-seed weight and yield can be considered as favorable morphological traits for mung bean improvement through effective phenotypic selection of these traits and considerable expected genetic gain from selection for these characters can be achieved. This also indicates that these characters are under the control of additive gene action and would respond very well to continuous selection and is in line with reports by Malek *et al.,* (2014). Current results also suggest that mung bean yield could be increased through the selection of higher number of pods per plant with higher number of seeds per pod. Therefore, in mung bean, number of pods per plant and number of seeds per pod can be considered as the major and effective characters influencing the seed yield in mung bean. Malek *et al.,* 2014 reported that correlation analyses indicate that pod number per plant and seeds per pod appeared to be the first order yield components and priority should be given in the course of selection due to having strong associations as well as high direct effects on seed yield. Significant positive correlations of plant height, number of leaves, leaf area and pods per plant, seeds per pod, and 100- seed weight with seed yield indicate that in selecting high yielding genotypes these characters are very important selection criteria. These results also are in agreement with the results reported by others in soybean (Faisal *et al.,* 2007, Machikowa and Laosuwan, 2011). Highly significant and positive correlation between seed yield per plant and yield per ha indicates that in mung bean individual plant yield contributed significantly towards yield per unit area. This is also in agreement with results reported by Malek *et al.,* (2014) in soybean and Kadams and Sajo (1998) in Bambara groundnut. The cluster analysis based on agro-morphological traits resulted in the grouping of the 30 mung bean genotypes into five distinct clusters (Figure 1), with the composition detailed in Table 4. The analysis revealed a clear hierarchy of performance among the clusters, with mean trait values provided in Table 5. The most significant finding was the identification of Cluster III, comprising only Tvr-3 and Tvr-109, as the unequivocally elite group. This cluster achieved the highest mean values for nearly all traits, including yield per hectare (1250.87 kg), establishing these genotypes as prime candidates for direct selection and cultivation.

Table 2: Pearson correlation matrix for mungbean plant characteristics in Owerri West Southeast Nigeria

Traits	Girth	Height	Number of leaves	Leaf area	Days to 50% anthesis	Number of pods	Pod length	Pod girth	Pod weight	Pod weight	Number of seeds
Girth	-										
Height	0.9^{**}	-									
Number of leaves	0.8^{**}	0.8^{**}	-								
Leaf area	0.9^{**}	0.9^{**}	0.8^{**}	-							
Days to 50% anthesis	0.3	0.3	0.2	0.2	-						
Number of pods	0.7^{**}	0.8^{**}	0.8^{**}	0.8^{**}	0.4^{*}	-					
Pod length	0.6^{**}	0.6^{**}	0.4^{*}	0.5^{**}	0.9^{**}	0.6^{**}	-				
Pod girth	0.4^{*}	0.4^{*}	0.2	0.4^{*}	0.8^{**}	0.5^{**}	0.9^{**}	-			
Pod weight	0.8^{**}	0.9^{**}	0.8^{**}	0.9^{**}	0.4^{*}	1.0^{**}	0.6^{**}	0.5^{**}	-		
Number of seeds	0.5^{**}	0.6^{**}	0.4^{*}	0.5^{**}	0.8^{**}	0.6^{**}	0.9^{**}	0.8^{**}	0.6^{**}	-	
100 Seed weight (g)	0.7^{**}	0.7^{**}	0.8^{**}	0.8^{**}	0.3	0.9^{**}	0.5^{**}	0.5^{**}	0.9^{**}	0.5^{*}	-
Yield/ ha(kg)	0.7^{**}	0.9^{**}	0.8^{**}	0.9^{**}	0.3	0.9^{**}	0.6^{**}	0.5^{**}	1.0^{**}	0.6^{**}	0.9^{**}

Significant at the 0.05 level (2-tailed) and at the 0.01 level (2-tailed)

In contrast, Cluster I, the largest group with 21 genotypes, consistently demonstrated the lowest performance across measured traits, representing a pool of poorly adapted genotypes under these trial conditions. The stark phenotypic divergence within the germplasm was further highlighted by two unique clusters. Cluster II, a solitary group containing only Tvr-2, was defined by its extremely late flowering (58 days to anthesis), making it a unique genetic resource despite its intermediate yield. Conversely, Cluster V (Tvr-72 and Tvr-124) was characterized by the earliest flowering (39 days) but the poorest overall yield, indicating a combination of early maturity with low productivity. Cluster IV genotypes (Tvr-10, Tvr-11, Tvr-61b, Tvr-123) displayed intermediate performance, situated between the elite and low-performing groups. The grouping of the thirty (30) mung bean genotypes into five clusters based on their agronomic performance indicate that the genotypes evaluated exhibited notable genetic variation in terms of morphological traits. Ngwuta (2008) reported that clustering helps to reduce the size of the data generated from evaluations into manageable groups based on certain variables which will permit the selection of the best entities within any desired group. Ojo *et al.*, (2012); Cui *et al.*, (2001) and Iqbal *et al.*, (2008) also reported formation of different number of clusters using morphological characters in diverse legume genotypes.

The dendrogram tends to group some of the genotypes possessing similar morphological traits into the same cluster. Similar results were also reported in soybean and other crops by Cui *et al.*, (2001) Iqbal *et al.*, (2008) and Rafii *et al.*, (2012). The solitary clustering of Tvr-2 identifies it as the most genetically distinct genotype in this trial. Its most striking characteristic is its significantly later flowering (58 days to 50% anthesis) compared to the elite, high-yielding genotypes in Cluster III (43 days). This major phonological difference is a primary driver of its divergence. In a breeding context, such a genotype is not just a statistical outlier but a valuable reservoir of unique alleles. Crosses between Tvr-2 and early-flowering, high-yielding lines from Cluster III are likely to produce populations with a wide range of flowering times and maturities, allowing breeders to select for ideotypes most suited to specific growing windows or changing climatic conditions in Southeastern Nigeria. The superior performance of Cluster III (Tvr-3 and Tvr-109) across nearly all traits is not coincidental but likely results from a favorable combination of genes governing plant architecture and sink strength. Their tall stature, large leaf area (indicating high photosynthetic capacity), and high pod number create an ideal 'source-to-sink' relationship for high yield. The strong positive correlations observed between these traits further support that selection for this synergistic trait complex is feasible. The high heritability and genetic advance for these components indicate that this superior phenotype is highly heritable and can be fixed in subsequent generations. When these findings are viewed holistically, a clear breeding strategy emerges. The high heritability and strong correlation of yield components confirm that phenotypic selection will be effective. The cluster analysis then provides the essential parental lines to execute this strategy: use the high-yielding, well-adapted genotypes from Cluster III as recurrent parents to uphold performance, and strategically introgress novel diversity from the highly divergent Tvr-2 to break yield ceilings and introduce resilience. This strategy effectively leverages the significant genetic variability and high heritability present in this germplasm, providing a clear and actionable pathway for the development of superior, locally-adapted mung bean cultivars for southeastern Nigeria.

Table 3: Estimation of genetic parameters of eleven different morphological characters and yield attributes among 30 Mung bean genotypes

Trait	Genotypic	Phenotypic	Heritability	GCV	PCV	GA
Plant girth	0.1	0.1	92.3	22.6	23.6	44.8
Height	65.7	72.2	91.0	49.6	52.0	97.4
Number of leaves	2.5	3.0	85.1	34.1	37.0	64.9
Leaf area	877.0	948.4	92.5	6.5	6.8	12.9
Pod weight	4.5	5.2	88.2	88.8	94.6	85.9
Pod girth	0.3	0.3	99.5	41.6	41.6	85.3
Pod Length	6.9	7.0	98.2	45.2	45.7	92.3
Number of pods per plant	22.9	26.3	87.3	80.2	85.8	77.2
Number of seeds per pod	9.7	10.2	95.0	48.5	49.8	97.4
100-seed weight	728.8	988.7	73.7	80.4	93.7	71.1
Yield	112273.0	146189.3	76.8	64.3	73.3	58.0

Figure 1: Dendrogram illustrating the clustering of mung bean genotypes into five groups based on agro-morphological traits. See Table 3 for cluster members and their performance summary

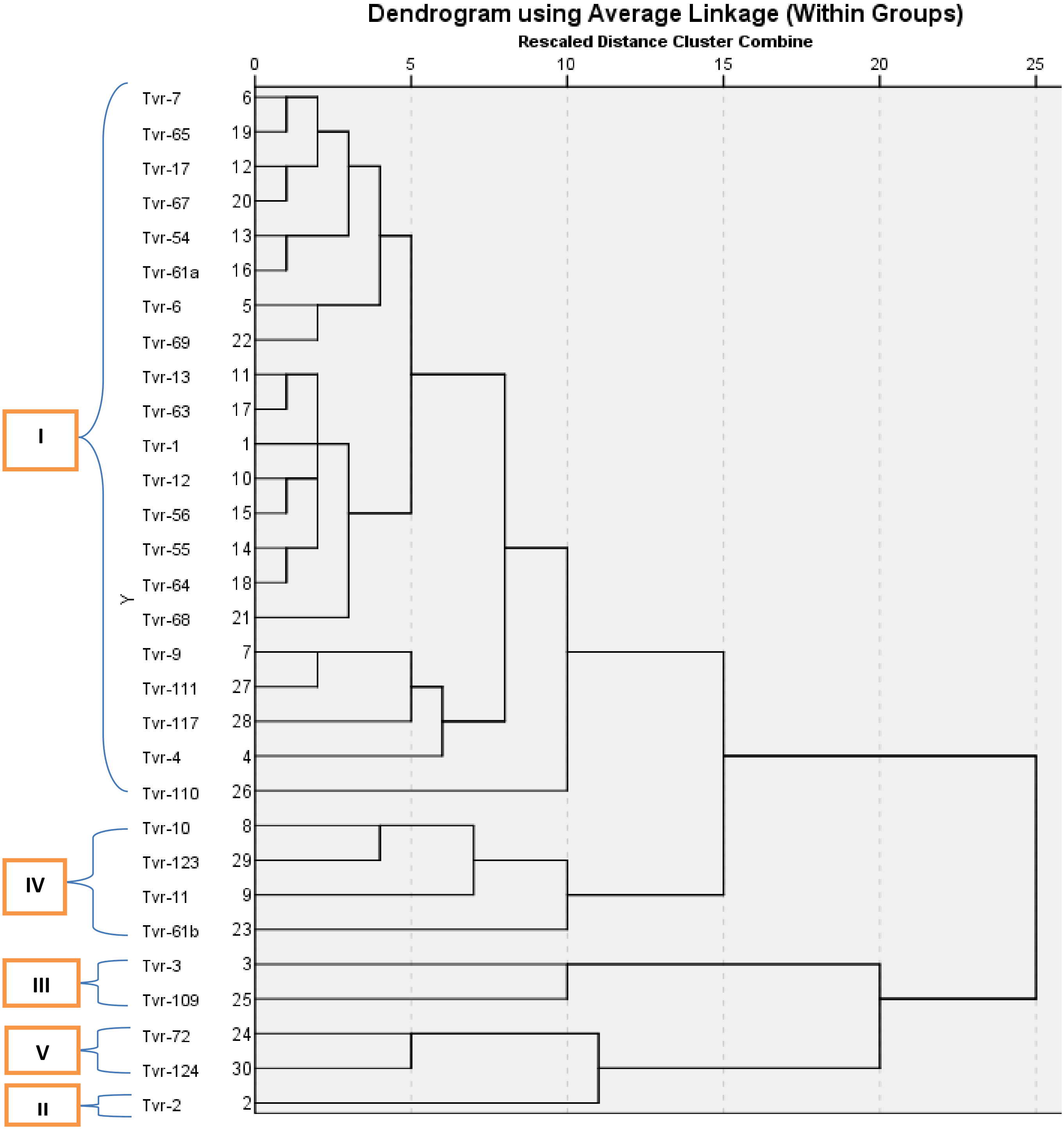

Table 4: Cluster composition and agronomic performance profile of mungbean genotypes evaluated in Owerri, Southeastern Nigeria

Cluster	No of genotypes	Genotypes	Performance summary
I	21	Tvr-1, Tvr-4, Tvr-6, Tvr-7, Tvr-9, Tvr-12, Tvr-13, Tvr-17, Tvr-54, Tvr-55, Tvr-56, Tvr-61a, Tvr-63, Tvr-64, Tvr-65, Tvr-67, Tvr-68, Tvr-69, Tvr-110, Tvr-111, Tvr-117	Lowest performing group for vegetative growth and yield
II	1	Tvr-2	Divergent, late-flowering genotype with intermediate yield
III	2	Tvr-3, Tvr-109	Elite, high-yielding group with superior performance across all traits
IV	4	Tvr-10, Tvr-11, Tvr-61b, Tvr-123	Intermediate performers for all traits
V	2	Tvr-72, Tvr-124	Early flowering but very low-yielding group.

Table 5: Cluster means for different traits of mungbean genotypes evaluated in Owerri

Trait			Cluster		
	I	II	III	IV	V
Girth	1.5	1.8	2.1	1.7	1.4
Height	14.1	26.1	27.7	19.3	12.2
No of leaves	4.3	6.2	6.6	5.9	3.8
Leaf Area	232.5	1090.8	1682.9	628.3	149.8
Days to 50% anthesis	54.0	58.0	43.0	54.0	39.0
Number of pods	5.5	12.3	14.5	10.9	2.0
Pod length	6.9	8.0	8.1	6.8	4.3
Pod girth	1.5	1.6	1.9	1.5	1.1
Pod weight	2.1	4.9	7.6	4.2	0.7
Number of seeds	7.9	9.4	10.0	6.3	4.7
100 seed weight (g)	34.5	57.9	88.6	73.7	8.8
Yield/ha (kg)	392.3	820.5	1250.9	651.6	83.9

Hence in conclusion this study establishes a compelling foundation for the introduction of mung bean to southeastern Nigeria by revealing significant genetic variability and high heritability for key yield traits among the thirty evaluated genotypes. The identification of elite, high-yielding accessions Tvr-3 and Tvr-109 which achieved yields competitive with global standards—provides immediate candidates for cultivar selection. Furthermore, the discovery of Tvr-2 as the most divergent genotype offers a unique genetic resource to broaden the breeding base.

We therefore propose a targeted breeding strategy: capitalizing on the high heritability of pod number and weight by crossing the divergent Tvr-2 with the elite performers Tvr-3 and Tvr-109. This approach is designed to maximize heterosis and genetic gain, enabling the development of adapted, high-yielding mung bean cultivars for the region. Based on the findings of this study, the following specific actions are recommended for the successful introduction and improvement of mung bean in southeastern Nigeria. Immediate Cultivar Promotion: Genotypes Tvr-3 and Tvr-109 should be advanced to multi-location yield trials across the region for rapid release and dissemination to farmers as promising new cultivars. Parental Selection for Hybridization: A structured breeding program should be initiated, using Tvr-2 as a divergent parent in crosses with Tvr-3 and Tvr-109 to create segregating populations for the selection of superior recombinant lines. Selection Criteria: Future selection in these populations should prioritize the number of pods per plant and pod weight, as these traits exhibited high heritability and strong positive correlation with yield.

References

1. Appalaswamy, A and Reddy, G.L.K 2004. Genetic divergence and heterosis studies of mungbean (*Vigna radiata* (L.) Wilczek), Legume Res., 21:115-118.
2. Asrate, A, Gurum, F, Alemayehu, F and Rezene, Y 2012. Analysis of multi-environment grain yield trials in mung bean (*Vigna radiata* L.) based on GGE bipot in southern Ethiopia. J. Agril. Sci. Techno., 14(2):389-398.
3. Chai, W.M, Wei, Q.M, Deng, W.L, Zheng, Y.L, Chen, X.Y, Huang, Q, Ou-Yang, C and Peng, Y.Y 2019. Anti-melanogenesis properties of condensed tannins from *Vigna angularis* seeds with potent antioxidant and DNA damage protection activities. Food Funct., 10:99-111.
4. Chowdhury, M.A, Vandenberg, B and Warkentin, T 2002. Cultivar identification and genetic relationship among selected breeding lines and cultivars in chickpea (*Cicer arietinum* L.). Euphytica, 127(3):317-325
5. Central Statics Authority 2018. Bulletin No 584. Central statics authority agricultural sample survey of area and production of major crops, Ethiopia.
6. Faisal, M.A.M, Ashraf, M, Qureshi, A.S and Ghafoor, A 2007. Assessment of genetic variability, correlation and path analyses for yield and its components in soybean. Pakistan J. Bot., 39(2):405-413.
7. Gudmewad, R.B, Misal, A.M, Ghodke, M.K and Dhuppe, M.V. 2018. Genetic and association studies in linseed (*Linum utitatissimum* L.). J. Genet., Genom. Plant Breed., 2(2):7-14.
8. Gupta, N., Srivastava, N. and Bhagyawant, S.S. 2018. Vicilin- a major storage protein of mungbean exhibits antioxidative potential, antiproliferative effects and ace inhibitory activity, PloS ONE, 13:e0191265
9. Hanson, G.H., Robinson, H.F. and Comstock, R.F. 1956. Biometrical studies of yield in segregating population of Korean Lespedeza, Agron. J., 48:268-272
10. International Institute of Tropical Agriculture 2009. Yam (*Dioscorea species*). Available at: http://www.iita.org/yam. Ibadan, Nigeria.
11. Ismail, A.A., Khalifa, M.A. and Hamam, A.K.. 2001. Genetic studies on some yield traits of durum wheat. Asian J. Agri. Sci., 32:103-129
12. Kadams, A.M. and Sajo, A.A. 1998. Variability and correlation studies in yield and yield components in Bambara groundnut. J. Applied Sci. Manageme., 2:66-70.

13. Kumar, P and Shukla, R.S. 2002. Genetic analysis for yield and its attributed traits in bread wheat under various situations, Jawaharlal Nehru Krishi Vishwa Vidyalaya Res. J., 36:95-97.
14. Kwon, S.J., Ha, W.G. and Hwang, H.G. 2002. Relationship between heterosis and genetic divergence in “Tongil”-type rice. Plant Breed., 121(6):487-492.
15. Liyanage, R., Kiramage, C., Visvanathan, R., Jayathilake, C., Weththasinghe, P., Bangamuwage, R., Jayawardana, B.C. and Vidanarachchi, J. 2018. Hypolipidemic and hypoglycemic potential of raw, boiled and sprouted mung beans (*Vigna radiata* L. Wilczek) in rats., J. Food Biochem., 42:e12457.
16. Machikowa, T. and Laosuwan, P. 2011. Path coefficient analysis for yield of early maturing soybean, Songklanakarin. J. Sci. Techno., 33(4):365-368.
17. Malek, M.A., Mohd, Y.R., Shahida, M.S.A., Ujjal, K.N. and Monjurul, M.A.M. 2014. Morphological characterization and assessment of genetic variability, character association and divergence in soybean mutants. The Scienti. World J., 2014:12.
18. Mazid, M.S., Rafii, M.Y., Hanafi, M.M, Rahim, H.A., Shabanimofrad, M. and Latif, M.A. 2013. Agro-morphological characterization and assessment of variability, heritability, genetic advance and divergence in bacterial blight resistant rice genotypes. South African J. Bot., 86:15-22.
19. Mogotsi, K.K. 2006. *Vigna radiata* (L) R.Wilczek, In: Brink, M and Belay, G (editor). Prota I: Cereals and Pulses/Cereals et legumes sees (CD.Rom). PROTA, Wageningen Netherlands.
20. Nair, R.M., Yang, R.Y, Easdown, W.J., Thavarajah, D., Thavarajah, P. and Hughes, J.A. 2013. Biofortification of mungbean (*Vigna radiata*) as a whole food to enhance human health. J. Sci. Food Agricul., 93:1805-1813.
21. Nwosu, A.C. and Adeniyi, E.O. 1980. Imo State: A Survey of resources for development. Nigeria Institute for Social and Economic Research (Niser) Ibadan, Nigeria. pp 310.
22. Obi, I.U. 2002. Statistical Methods of Detecting Differences between Treatment means and research methodology issues in laboratory and field experiments. AP Express Publishers, limited, 3 Obollo Road, Nsukka - Nigeria. pp 117.
23. Paroda, R.S. and Arora, R.K. 1991. Plant genetic resources: general perspective, In Plant genetic resources; conservation and management. New Delhi, Malhotra publishing house pp 1-23
24. Surek, H. and Beser, N. 2003. Selection for grain yield and yield components in early generations for temperate rice. Philippine J. Crop Sci., 28(3):3-15.
25. Werf, J. 2009. Estimation of genetic parameters. Genetic evaluat. Breed., pp 7-22.

.