

Phenotypic diversity of mung bean [*Vigna radiata* (L.) Wilczek] genotypes based on qualitative traits, in South Ethiopia

Tekle Yoseph^{1*}, Firew Mekbib², Berhanu Amsalu³, and Zerihun Tadele⁴

¹*Southern Agricultural Research Institute, Jinka Agricultural Research Centre, P.O. Box 96, Jinka, Ethiopia;*

²*Haramaya University, School of Plant Sciences, P.O. Box 138, Dire Dawa, Ethiopia;*

³*Ethiopian Institute of Agricultural Research, Melkassa Agricultural Research Center Adama, Ethiopia;*

⁴*University of Bern, Institute of Plant Sciences, Altenbergrain 21, 3013 Bern, Switzerland.*

Abstract

Understanding genetic diversity is vital for the conservation and utilization of genetic resources of crops. To date, the available information on genetic resource collection, phenotypic characterization, and conservation of mung bean genotypes in Ethiopia is limited. To fill these knowledge gaps, the present study was conducted at Jinka Agricultural Research Center during the 2018 cropping season. The objective of the study was to determine the extent of genetic diversity among mung bean genotypes using qualitative morphological traits. A total of 60 mung bean genotypes were evaluated using a 6×10 alpha lattice design replicated twice. Data on 30 qualitative traits were collected and subjected to the Shannon-Weaver diversity index (H') and multivariate analyses. The estimate of H' ranged from 0.00 for germination type to 0.96 for seed shape. The first seven principal components explained 94.0% of the total variation. In general, leaf pubescence, attachment of primary leaves, pod attachment to the peduncle, and seed shape were prominent genetic variations among mung bean genotypes, and were the most effective traits for distinguishing among mung bean genotypes and could be used as selection criteria for improvement. Cluster analysis based on qualitative traits revealed four distinct groups. The highest inter-cluster distance was found between Cluster I and IV (44.67). This investigation revealed the existence of enormous genetic diversity of mung bean genotypes which should be exploited by comprehensive mung bean variety development programs.

Keywords: Divergence, Diversity index, Genetic resources, Qualitative traits

Original submission: March 28, 2022; **Revised submission:** December 23, 2023; **Published online:** December 30, 2023

***Corresponding author's address:** Tekle Yoseph, Email: tekeyoseph486@gmail.com

Authors: Firew Mekbib: Firew.mekbib@gmail.com; Berhanu Amsalu: berhanua.fenta@gmail.com; Zerihun Tadele: zerihun.tadele@ips.unibe.ch

INTRODUCTION

Mung bean [*Vigna radiata* (L.) Wilczek] is an important legume crop (Rahim et al., 2010). It is a short-duration legume and belongs to the third largest family of flowering plants, with approximately 650 genera and nearly 20,000

species (Doyle, 2003). Cytological studies have indicated that mung bean has a diploid chromosome number of $2n = 2x = 22$ (Kang et al., 2017).

The study of genetic diversity is important for the development of crop varieties. The study of plant genetic resources as a part of biodiversity conservation realizes cultivated varieties in current use and obsolete cultivars as well as wild and weedy species as useful biological resources for food security (Ulukan, 2011; Ogwu et al., 2014). As suggested by Mohan et al. (2014), the characterization of germplasm helps to form the groups with specific traits and also provides the idea about those traits that help for distinguishing the genotypes from each other. An emphasis has been placed on the morphological characterization to assess the variability among genotypes and some of the agro-morphological traits which could be used as a morphological marker in crop improvement (Tantasawat et al., 2010).

The grouping of genotypes based on agro-morphological traits can easily be detected by the naked eyes and can be used in the mung bean breeding program for improving the physical quality of seed. Morphological traits can be used to assess phenotypic variation in growing environments and are also used as tools for the indirect analysis of genetic variability and diversity. Tabasum et al. (2010) reported the genetic variability in ten green gram genotypes and the extent to which the traits associated with yield could be useful for establishing selection criteria for high seed yield in mug bean breeding.

Genetic diversity is an important factor and a prerequisite in any breeding program. Quantifying genetic diversity is indispensable for designing and accelerating breeding programs. Therefore, the collection, conservation, characterization, and evaluation of available germplasm is important to determine the magnitude of genetic diversity for further breeding programs. Information on the nature and degree of genetic diversity can assist plant breeders in choosing the best genotypes as parents for hybridization (Denton and Nwangburuka, 2011; Nwosu et al., 2013).

Characterization of germplasm is important to classify genotypes based on morphological traits that might be used to assess the variability among

germplasm (Tantasawat et al., 2010). Some of the agro-morphological traits may be used as morphological markers in crop improvement. It also helps in the assessment of genetic variability and diversity present in available germplasm. Therefore, morphological characterization helps in the effective utilization of germplasm in crop improvement programs. This trait can also be used as a morphological marker for screening breeding material at the seedling stage. Similarly, stem color, petiole color, and pod color can also be used for the identification of material at the post seedling stage.

Information on qualitative traits based on genetic diversity and characterization of mung bean genotypes in Ethiopia is absent. Therefore, the present study was undertaken with the specific objectives of determining the extent of genetic diversity and identifying the phenotypic patterns using qualitative traits.

MATERIALS AND METHODS

Study Area and Design

The field experiment was conducted from March to June 2018 at Jinka Agricultural Research Center (JARC) during the main cropping season. Jinka Agricultural Research Center is located 729 km southwest of Addis Ababa at 360 33' 02.7" E, 050 46' 52.0" N, and at an altitude of 1420 m above sea level. The maximum, minimum, and average temperatures of the center are 27.680C, 16.610C, and 22.14oC, respectively while the mean annual rainfall is 1381 mm. The soil type of the center is Cambisols (Mesfin et al., 2017).

Experimental Materials

A total of sixty mung bean genotypes were used in this study. Out of these, forty-four genotypes were obtained from Melkassa Agricultural Research Center (MARC), and sixteen genotypes were collected from the Southern Nations, Nationalities, and Peoples (SNNP) region of Ethiopia.

Table 1. List of genotypes used for this diversity study.

Genotype	Code	Genotype	Code	Genotype	Code	Genotype	Code
VC6489-9-1	G38	N-26	G43	NLLP-MGC-04	G4	Acc003	G47
NLLP-MGC-10	G10	NLLP-MGC-16	G16	NVL-1	G44	Acc004	G48
NLLP-MGC-06	G6	VC2778A(KPS2)	G29	NLLP-MGC-15	G15	Acc005	G49
NLLP-MGC-20	G20	VC6469-12-34A	G37	HARSHA	G39	Acc006	G50
NLLP-MGC-14	G14	NLLP-MGC-09	G9	NLLP-MGC-08	G8	Acc007	G51
NLLP-MGC-19	G19	VC6368(46-40-4)	G34	NLLP-MGC-05	G5	Acc008	G52
NLLP-MGC-21	G21	NLLP-MGC-01	G1	NM92(VC6370-92)	G31	Acc009	G53
NLLP-MGC-11	G11	NLLP-MGC-24	G24	NLLP-MGC-23	G23	Acc0010	G54
NLLP-MGC-12	G12	VC6492-59A	G35	V2709 BG	G42	Acc0011	G55
VC1973A	G28	VC6370(30-65)	G33	NLLP-MGC-27	G27	Acc0012	G56
VC6510-151-1	G36	NLLP-MGC-07	G7	VC3890A	G30	Acc0013	G57
CN9-5	G41	NLLP-MGC-26	G26	NLLP-MGC-25	G25	Acc0014	G58
NLLP-MGC-02	G2	NLLP-MGC-17	G17	NLLP-MGC-22	G22	Acc0015	G59
NM94(VC6371-94)	G32	NLLP-MGC-18	G18	Acc001	G45	Acc0016	G60
BARI-MUNG 2	G40	NLLP-MGC-03	G3	Acc002	G46	NLLP-MGC-13	G13

Genotypes with initial “Acc”, that is accession, are from Southern Nations, Nationalities, and Peoples Region (SNNPR) and other genotypes are obtained from Melkassa Agricultural Research Center (MARC).

Experimental Design and Procedures

The experiment was laid out using a 6×10 alpha lattice design. The plot size was 4.5 m² with 3 m length and 0.3 m width, and the distance was 0.5 m between rows, and 0.05 m between plants, respectively. The distances between plots, intra - blocks, and replications were 1, 1.5, and 2 m, respectively. Two seeds per hill were planted and one seed per hill was left after thinning, and one row accommodated 12 plants. For this experiment, 100 kg ha⁻¹ NPS and 50 kg ha⁻¹ urea fertilizer were applied, and weeding was carried out twice.

Data Collection

The descriptor of mung bean developed by the International Board for Plant Genetic Resources (IBPGR, 1980) was followed for data collection. A total of 30 qualitative traits were collected on a plot basis. The qualitative traits used and their phenotypic classes were: seed germination habit (epigeal, hypogeal), growth pattern (determinate,

indeterminate), attachment of primary leaves at two leaf stage (sessile, sub-sessile, petiolate), growth habit (erect, semi-erect, spreading, semi-prostrate, prostrate, climbing at pod maturity), stem color (light green, dark green, light purple, dark purple, others), leafiness at 50% flowering (sparse, intermediate, abundant) leaf pubescence (glabrous, very sparsely, sparsely pubescent, moderately pubescent, densely pubescent), petiole pubescence (glabrous, pubescent, moderately pubescent, densely pubescent), lobbing of terminal leaflet (unlobbed, shallow, intermediate, deep, very deep at first pod maturity), terminal leaflet lobe shape (lanceolate, broadly ovate, ovate, rhombic, others), stipule size (small, medium, large), stipule shape (ovate, lanceolate, others), stem pubescence (glabrous, sparsely, moderately pubescent, highly pubescent), raceme position at first pod mostly above, in upper canopy, throughout canopy), calyx colour (green, purplish green, greenish purple, others), corolla color (yellow, greenish yellow, yellowish green, green-purplish yellow,

others), bracteole size (small, intermediate, large), bracteole shape (linear, lanceolate, others), flowering period (asynchronous, intermediate, synchronous), pod attachment to peduncle (erect, horizontal, horizontal-pendent, pendent, others), pod pubescence (glabrous, sparsely, moderately pubescent, densely pubescent), pod curvature (straight, slightly curved, curved), pod beak shape, (pointed, blunt, others), constriction of pod between (absent, slight, pronounced), pod cross section (semi flat, round, others), seed shape (globose, ovoid, narrowly ellipsoid, cubical to oblong, kidney shaped, drum shaped, others), seed colour (white, cream, light brown, intermediate brown, dark brown, grey, mottled grey, mottled brown, mottled cream, light cream, green brown, chocolate, black), lusture on seed surface (absent, present), mottling on seed surface (absent, slight, intermediate, heavy), hilum shape (concave, plain, convex, others).

Data Analyses

Phenotypic frequency distribution for the traits was computed for all genotypes. The Shannon-Weaver diversity index (H') was computed using the phenotypic frequencies of each qualitative trait as described by Hennink and Zeven (1990) by using the following formula

$$H' = - \frac{\sum_{i=1}^n P_i \ln P_i}{\ln(n)}$$

Where P_i = the proportion of individuals (genotypes) in the i th class and n -class trait and n is the number of phenotypic classes for a given trait, $\ln(n)$ is the natural logarithm $\ln(n)$. H' was estimated for each trait and standardized by dividing it by \log_{10} and normalized to keep the H' values between 0.00 and 1.00. The diversity index was classified as high ($H' \geq 0.60$), intermediate ($0.40 \leq H' \leq 0.60$), or low ($0.10 \leq H' \leq 0.40$), as described by Firdissa et al. (2005). All diversity index analyses were conducted using the Microsoft Excel computer program. The non-normalized ' H' ' values were used for the analysis of variance. Hierarchical (Ward, 1963) clustering was performed using frequency distribution of phenotypic classes. The standard genetic distances from the portion of phenotypic classes were used to construct a dendrogram by ward method subjected to Minitab Statistical Software

version 17. The average intra and inter-cluster distances were calculated using the generalized Mahalanobis's D^2 statistics (Mahalanobis, 1936). The pseudo-F statistics (PSF), and pseudo-T2 statistics were considered for defining optimum cluster numbers (Milligan and Cooper, 1988). The contribution of each trait to divergence as described by Sharma (1998) with the formula [$CTIC = \frac{SD}{\bar{x}} \chi 100$] where SD and \bar{x} are the standard deviation and mean performance of each trait, respectively. Principal components analysis is expected to reduce the observed variables into a small number of components and was computed using Minitab Software Version 17. In a principal component analysis, the values were standardized to have unit variance and a mean of zero. .

RESULTS

Morphological Diversity Analysis based on Qualitative Traits

Frequency Distribution

Morphological characterization of genotypes based on qualitative traits indicated a high level of variation among the genotypes (Table 2), and that the studied morphological traits were polymorphic with different levels of variability. This result is supported by the earlier report of Hapsari *et al.* (2018) among one hundred and twelve mung bean genotypes. On the contrary, Kaur *et al.* (2017) reported that no significant differences were observed among the studied morphological traits (plant habit, stem color, stem pubescence, petiole color, premature pod color, pod pubescence, pod curvature, seed color, and seed shape) on mung bean genotypes.

In this study, all the genotypes showed an epigeal germination habit (Table 2), which is in agreement with the previous results reported by Bisht *et al.* (2005) on mung bean. Similarly, Harouna *et al.* (2020) reported that among the 160 accessions of wild *Vigna* legumes, cowpea and the landrace of *Vigna vexillata* had, an epigeal germination habit, which is also shared by most accessions of *Vigna reticulata* and *Vigna racemosa*.

The growth pattern showed that 96% of the phenotypic classes were determinate type followed by 4% indeterminate type (Table 2).

This finding contradicts the earlier reports by Sowmya *et al.* (2019) who observed that out of 76 mung bean accessions, 66 accessions (86.84%) showed indeterminate growth patterns while 10 accessions (13.16%) showed determinate growth pattern. Similarly, Popoola *et al.* (2017) reported that all the 26 *Vigna vexillata* (L.) accessions, showed an indeterminate growth pattern. For growth habit, semi-erect was the most frequently observed phenotypic class at 85%, followed by erect at 4%, spreading at 4%, semi-prostrate at 4% and prostrate at 2% (Table 2). Contrastingly, the climbing type was the least observed phenotypic class, with a mean frequency of 1% (Table 2). The present study showed that the semi-erect type was the most predominant phenotypic class. Singh *et al.* (2014) similarly observed that among the 104 mung bean genotypes, 90.38% had semi-erect growth habits, while 5.77% had a spreading type of growth habit, and 3.85% had shown an erect growth habit. Likewise, Patel *et al.* (2019) reported that out of the 44 mung bean genotypes, 47.73% had semi-erect growth habits, 15.91% had erect, and 13.64% showed the spreading type of growth habit. Correspondingly, Gonné *et al.* (2013) reported that semi-erect was the most frequently observed phenotypic class on cowpea genotypes. Sessile type of primary leaf attachment (55%) was the most frequent phenotypic class followed by sub-sessile 33% while the least frequently observed phenotypic class was petiolate with a mean frequency of 12% (Table 2). Bisht *et al.* (2005) also recorded that sessile 100% types in all the species of mung bean, which coincides with the work of Harouna *et al.* (2020) who reported that among the 160 accessions of wild *Vigna* legumes, the *Vigna vexillata* landrace 100% showed sessile, *Vigna racemosa* accessions 83.33% showed the sub-sessile type of primary leaf attachment, the landrace of *Vigna vexillata* also exhibited 81.67% was sub-sessile type of primary leaf attachment, while the *Vigna reticulata* accessions shared 46.15%, sub-sessile phenotypic class.

Light green stem color 88% was the most frequent phenotypic class followed by dark green

9% and light purple 3%, respectively (Table 2). Dark purple stem color was the least observed phenotypic class with the mean frequency of 0%. Singh *et al.* (2014) similarly reported that out of the 104 mung bean genotypes, about 95.19% were found to be green stem color. Patel *et al.* (2019) also reported that among the 44 mung bean genotypes, 38.64% showed green stem color, whereas 61.36% had green with purple stem color. This finding is also supported by the previous works on different pulse crops based on stem color (Jain *et al.*, 2002; Katiyar *et al.*, 2008; Singh *et al.*, 2014; Kaur *et al.*, 2017) in mung bean, Chakrabarthy and Agarwal (1989) in black gram; Yadav and Srivastava (2015), Gnyandev (2009), Joshi and Yasin (2014) in chickpea; Durga *et al.* (2015) in horse gram; and Kumar and Shrikant (2016) in cowpea. Kaur *et al.* (2017) reported that anthocyanin coloration recorded at the seedling stage was present in all the varieties and hence indicated no variation.

Leafiness at 50% flowering was intermediate 76% followed by sparse 13% and abundant 11% (Table 2). The intermediate type of leafiness was the most frequently observed phenotypic class in this study in line with Harouna *et al.* (2020) on *Vigna racemosa*, *Vigna reticulata* accession, and cowpea, while it contradicts the observations on rice bean and the landrace of *Vigna vexillata* that showed an abundant leafiness (Harouna *et al.*, 2020).

About 75% of the studied mung bean genotypes showed sparsely pubescent type of leaf while the glabrous type was the least frequently observed phenotypic class with the mean frequency of 2% (Table 2). This finding contradicts with the results of Harouna *et al.* (2020) who reported that among 160 accessions of wild *Vigna* legumes, *Vigna vexillata* land race showed 100% very sparsely pubescent type of phenotypic class, and rice bean showed 100% moderately pubescent type of phenotypic class, cowpea showed 100% glabrous type of phenotypic class, *Vigna racemosa* accessions showed 33.33% glabrous, 33.33% moderately pubescent and 33.33% sparsely pubescent type of phenotypic class. *Vigna reticulata* accessions showed 28.85% very sparsely pubescent, 17.3% sparsely pubescent, 25% moderately pubescent and 28.85% densely

pubescent type of phenotypic class, *Vigna vexillata* 26.67% very sparsely pubescent, 22.06% sparsely pubescent, 31.67% moderately pubescent and 20% densely pubescent type of phenotypic class, *Vigna ambacensis* showed 30.95% very sparsely pubescent, 4.77% sparsely pubescent, 59.52% moderately pubescent and 4.76% densely pubescent type of phenotypic class were observed.

Around 74% of the studied mung bean genotypes had moderately pubescent petiole; while the glabrous type of petiole was the least frequently observed on the studied mung bean genotypes (Table 2). Similarly, Harouna *et al.* (2020) reported that among the 160 accessions of wild *Vigna* legumes studied for the trait petiole pubescence, rice bean showed 100% moderately pubescent type of phenotypic class. Contrastingly, Harouna *et al.* (2020) reported that *Vigna vexillata* landrace and cowpea showed 100% glabrous type of phenotypic class, *Vigna racemosa* accessions showed 33.33% glabrous, 33.33% pubescent and 16.67% moderately pubescent, and 16.67% densely pubescent type of phenotypic class, *Vigna reticulata* accessions showed 7.69% glabrous, 13.46% pubescent, 36.54% moderately pubescent and 42.3% densely pubescent type of phenotypic class, *Vigna vexillata* 5% glabrous, 50% pubescent, 43.33% moderately pubescent and 1.67% densely pubescent type of phenotypic class, *Vigna ambacensis* showed 30.95% very sparsely pubescent, 1.9% glabrous, 14.29% pubescent and 23.81% densely pubescent type of phenotypic class were observed. A similar result was reported by Singh *et al.* (2014), who found that out of the 104 mung bean genotypes, the glabrous type was not observed. Lobbing of the terminal leaflet was intermediate with the mean frequency of 80% while very deeply lobbed 1% was the least observed phenotypic class on the studied mung bean genotypes (Table 2). This result is in agreement with the report of Harouna *et al.* (2020) among the 160 accessions of wild *Vigna* legumes, rice bean showed 100% an intermediate type of phenotypic class, while it contrasts with that of *Vigna vexillata* landrace, cowpea and *Vigna racemosa* accessions showed 100% unlobed type of phenotypic class, *Vigna*

reticulata accessions showed 96.15% unlobed and 3.85% intermediate type of phenotypic class, *Vigna vexillata* 95% unlobed, 1.67% intermediate and 3.33% was deep. For the trait lobing of the terminal leaflet *Vigna ambacensis* showed 97.62% unlobed and 2.83% intermediate types of phenotypic class were observed.

Terminal leaflet lobe shape was ovate with the mean frequency of 83% while lanceolate 2% was the least observed phenotypic class on the studied mung bean genotypes (Table 2). This finding contradicted the report of Popoola *et al.* (2017) who observed that among the 26 *Vigna vexillata* (L.) accessions, lanceolate leaflet shape was dominant at 50% in thirteen accessions, ovate leaflet shape 34.61% in nine accessions, and ovate-elliptic shape 11.53% in three accessions while only one accession had heterophytic shape (ovate-lanceolate leaflet) with the mean frequency of 3.84%. This result is supported by the report of Harouna *et al.* (2020) among the 160 accessions of wild *Vigna* legumes, cowpea showed 100% ovate phenotypic class, *Vigna ambacensis* showed 83.33% ovate and 16.67% lanceolate, *Vigna racemosa* accessions showed 66.67% ovate and 33.33% lanceolate, *Vigna reticulata* accessions showed 53.85% ovate, 38.46% lanceolate and 7.69% other types of phenotypic class. On the contrary, rice bean showed 100% other types of phenotypic class. Medium stipule size with the frequency 80% followed by small 12% and large 8%, respectively were observed on mung bean genotypes under study (Table 2). This finding conforms to the report of Harouna *et al.* (2020) among the 160 accessions of wild *Vigna* legumes, 67% of *Vigna racemosa* had the medium stipule size variant, as well as 56% of the *Vigna reticulata* accessions. Contrastingly, *Vigna vexillata* landrace, cowpea rice bean had 100% large variant of the stipule size trait, while the small size variant was observed in 45% and 52% of *Vigna ambacensis* and *Vigna vexillata*, respectively.

The glabrous pubescent type had a mean frequency of 82% while highly pubescent type (1%) was the least observed phenotypic class (Table 2). This result is in agreement with

Harouna *et al.* (2020) who reported that among the 160 accessions of wild *Vigna* legumes, *Vigna vexillata* landrace and cowpea showed (100%) glabrous type of phenotypic class; on the other hand; rice bean showed 100% highly pubescent type of phenotypic class, *Vigna racemosa* accessions showed 50% sparsely pubescent, 33.33% glabrous and 16.67% moderately pubescent, *Vigna reticulata* accessions showed 55.77% medium, 25% small, 19.23% sparsely pubescent and 17.31% glabrous, *Vigna vexillata* showed 33.33% moderately pubescent, 33.33% sparsely pubescent and 18.33% highly pubescent, *Vigna ambacensis* showed 35.71% sparsely pubescent, 33.33% highly pubescent and 30.95% moderately pubescent was the observed phenotypic class.

Phenotypic observations of raceme position showed 76% of the mung bean genotypes had their raceme positions on the upper canopy (Table 2). Green calyx and yellow corolla colors were the most frequently observed phenotypic classes with the frequency of 90% and 89%, respectively for mung bean genotypes under study. Similar findings were reported by several researchers on different pulse crops based on flower morphological characters (Singh *et al.*, 2014; Kaur *et al.*, 2017; Patel *et al.*, 2019) in mung bean; Chandrashekhara (2008) and Das *et al.* (2014) in French bean; Yadav and Srivastava (2002), Gnyandev (2009) and Joshi and Yasin (2014) in chickpea, also on cowpea by (Basavaraj *et al.*, 2013; Kumar and Shrikant, 2016), Kumar *et al.* (2013) in Guar; and Durga *et al.* (2015) in horse gram.

Intermediate bracteole size was the most frequently observed phenotypic class with the frequency 85%; whereas, among the three bracteole shape phenotypic classes, linear bracteole shape was the most frequently observed with the frequency 90% in the studied mung bean genotypes (Table 2). Among the three flowering periods, asynchronous (flowering greater than 30 days) was the most frequent with a frequency of 85% for the mung bean genotypes under study.

The pendent type was the most frequently observed phenotypic class with a frequency of

66% and the erect type was the second most frequent phenotypic class with the frequency 28% among the listed phenotypic classes observed for pod attachment to peduncle for the mung bean genotypes under study (Table 2). This finding is in agreement with the result of Hapsari *et al.* (2018), who reported that among 122 mung bean genotypes, 86 genotypes 70.49% showed the pendent type of phenotypic class, and 36 genotypes 29.51% showed an erect type of phenotypic class.

Glabrous pod pubescent was the most frequent phenotypic class with the frequency of 84%, while dense pod pubescent was the least observed phenotypic class with the frequency 3% for mung bean genotypes under study (Table 2). This finding is in agreement with Harouna *et al.* (2020) who reported that among the 160 accessions of wild *Vigna* legumes, *Vigna vexillata* landrace, cowpea, and rice bean showed 100% glabrous type of phenotypic class, on the other hand; *Vigna racemosa* accessions showed 50% glabrous, 33.33% sparsely pubescent and 16.67% moderately pubescent, *Vigna reticulata* accessions showed 42.3% densely pubescent, 28.85% sparsely pubescent, 26.92% moderately pubescent and 9.61% erect, *Vigna vexillata* showed 48.33% horizontal, 33.33% others and 1.92% glabrous, *Vigna ambacensis* showed 85.71% sparsely pubescent, 9.52% densely pubescent and 4.76% moderately pubescent type of phenotypic class observed.

Approximately 86% of the genotypes had slight pod curvature while 6% genotypes had curved (sickle-shaped). This result is in agreement with Harouna *et al.* (2020) who showed that among the 160 accessions of wild *Vigna* legumes, more than 50% of the studied wild accessions showed the “slightly curved” form of the pod curvature trait, which was similar to cowpea 100% slight pod curvature. While; contradicting results were observed for rice bean and the *Vigna vexillata* landrace commonly shared the 100% straight form of the trait with 14% of *Vigna ambacensis* 10% of *Vigna vexillata* and (48%) of *Vigna reticulata* accessions showed straight pod curvature, *Vigna vexillata* 38% and *Vigna*

racemosa 33% accessions showed the curved form of the pod curvature trait.

Among the evaluated genotypes, about 97% of them had a slight constriction of pod between seeds (Table 2). Similarly, Harouna *et al.* (2020) reported that among the 160 accessions of wild *Vigna* legumes, a slight constriction of the pod between seeds was the form found in cowpea 100% and 24% of *Vigna ambacensis*, 23% of *Vigna reticulate*, and 33% of *Vigna racemosa* accessions. While most of the studied wild *Vigna* accessions (more than 50%) had no constriction of the pod between seeds (variant: “absent”), as found in the *Vigna vexillata* landrace. The pronounced form of the trait was observed only in rice bean and 15% of *Vigna ambacensis*, as well as 12% of *Vigna reticulate* accessions.

For seed shape, ovoid seed shape was the most frequently observed phenotypic class with frequency 75% for the mung bean genotypes under study. Sowmya *et al.* (2019) reported that out of 76 mung bean accessions, 43 accessions 56.58% showed oval seed shape while 33 accessions 43.42% showed drum seed shape. For seed color, the green-brown phenotypic class was the most phenotypic class with a frequency of 87% while white cream, light brown, intermediate brown, dark brown, mottled brown, mottled cream, light cream, chocolate, and black were the least observed phenotypic class on mung bean genotypes under study (Table 2). It indicates that green-brown seed color was the most frequent occurring in 87% among 60 mung bean genotypes (Table 2). In contrast, Singh *et al.* (2014) reported that the proportion of genotypes with greenish-purple was found to be 94.23% among the 108 mung bean genotypes. Wang *et al.* (2018) reported that among 184 mung bean accessions, green seeds accounted for 78%. Similarly, Hapsari *et al.* (2018) reported that among 122 mung bean genotypes, 61 genotypes 50% showed green seed color, 57 genotypes 46.72% showed mixed seed color, and 4 genotypes 3.28% showed brown seed color.

The phenotypic class mottling on seed surface was not observed on 85% of mung bean genotypes while slight and intermediate

phenotypic classes were observed on around 8 and 7% of mung bean genotypes under study (Table 2). In this study, it was possible to classify genotypes based on seed physical features. Singh *et al.* (2014) also suggested that seed physical characters may also serve as morphological markers to characterize mung bean genotypes. Plain, concave, and convex hilum shapes were the most frequently observed phenotypic classes (Table 2).

Shannon-Weaver Diversity Indices

Assessment of genetic diversity is vital in any crop improvement program to identify high yielding genotypes (Rhman and Munur, 2009). Shannon-Weaver diversity indices (H') are used to compare phenotypic diversity among qualitative characters. In the present study, the Shannon-Weaver diversity index (H') was adopted to compute the diversity of mung bean genotypes based on the diversity frequency of 30 qualitative morphological traits. The estimates of the Shannon-Weaver diversity index (H') depicted the observed phenotypic characters, the (H') values ranged from 0.15 for constriction of pod between seeds to 0.96 for seed shape (Table 2). Traits such as growth habit, attachment of primary leaves, leafiness at 50% flowering, leaf pubescence, lobbing of the terminal leaflet, terminal leaflet lobe shape, stipule size, stem pubescence, raceme position (at first pod), pod attachment to the peduncle, and seed shape showed Shannon diversity values of 0.65, 0.95, 0.72, 0.88, 0.73, 0.67, 0.64, 0.63, 0.70, 0.84 and 0.96, respectively exhibited high percentages contribution to the total variation compared to others. The overall mean value for ($H' = 0.54$) confirmed the existence of certain level of diversity among the mung bean genotypes. All phenotypic classes showed a high diversity index except germination type ($H' = 0.00$), indicating that there was a balanced frequency distribution of phenotypic classes and high genetic diversity for the studied traits. Similarly, Borines *et al.* (2019) reported that 13 out of 29 traits or 44.83% have $H' > 0.50$, hence considered as moderately to highly diverse. A low H' indicates unbalanced frequency classes for an individual trait and lack of diversity for the

trait. A high level of phenotypic diversity among the 60 mung bean genotypes was recorded which gives a key to look for variety development through direct selection.

Overall mean diversity index (H') was fairly high for all the studied traits except in some of the traits (Table 2). The highest overall mean diversity index (H') was recorded for seed shape ($H'=0.96$, followed by attachment of primary leaves ($H'=0.95$) and leaf pubescence ($H'=0.88$), respectively. The high level of diversity index (H') indicated the availability of high genetic potential of mung bean genotypes and also the presence of many important desirable genes for mung bean improvement for the intended traits and further genetic studies. The low level of

diversity for some of the phenotypic classes such as germination type, growth pattern, stem color, calyx color, petiole pubescence, bracteole shape, flowering period, constriction of pod between seeds, seed color, lusture on the seed surface, and hilum shape had a low level of diversity might indicate the existence of a narrow genetic base and a small sample size highly contributed to a low level of diversity index. This finding is in line with the previous results by Wuletaw and Endeshaw (2003) on grass pea, who reported that the low level of a diversity index noted was associated with poor sampling during collection and other natural and artificial selection.

Table 2. Frequency distribution and Shannon-Weaver Diversity Indices ('H') of 30 qualitative traits of Mung bean genotypes at Jinka, in 2018.

Character & description	Frequency (%)	H'	Character & description	Frequency (%)	H'
1. Germination		0	9. Lobbing of the terminal leaflet		0.73
Epigeal	100		Unlobbed	9	
Hypogeal	0		Shallow	7	
2. Growth pattern		0.17	Intermediate	80	
Determinate	96		Deep	3	
Indeterminate	4		Very deep (at first pod maturity)	1	
3. Growth habit		0.65	10. Terminal leaflet lobe shape		0.67
Erect	4		Lanceolate	2	
Semi-erect	85		Broadly ovate	4	
Spreading	4		Ovate	83	
Semi-prostrate	4		Rhombic	8	
Prostrate	2		Others	3	
Climbing	1		11. Stipule size		0.64
4. Attachment of primary leaves		0.95	Small	12	
Sessile	33		Medium	80	
Sub-sessile	55		Large	8	
Petiolate (at the two-leaf stage)	12		12. Stipule shape		0.5
5. Stem color		0.43	Ovate	80	
Light green	88		Lanceolate	20	
Dark green	9		Others	0	
Light purple	3		13. Stem pubescence		0.63
Dark purple	0		Glabrous	82	
6. Leafiness (at 50% flowering)		0.72	Sparsely	9	
Sparse	13		Moderately pubescent	8	
Intermediate	76		Highly pubescent	1	
Abundant	11		14. Raceme position (at first pod)		0.7
7. Leaf pubescence		0.88	Mostly above	17	
Glabrous	2		In upper canopy	76	
Very sparsely	8		Throughout canopy	7	
Sparsely pubescent	75		15. Calyx color		0.39
Moderately pubescent	9		Green	90	
Densely pubescent	6		Purplish green	5	
8. Petiole pubescence		0.16	Greenish purple	5	
Glabrous	2		Others	0	
Pubescent	20				
Moderately pubescent	74				
densely pubescent	4				

Table 2. Continued.

Character & description	Frequency (%)	H'	Character & description	Frequency (%)	H'
16. Corolla color		0.45	24. Constriction of pod between seeds		0.15
Yellow	1		Absent	2	
Greenish-yellow	5		Slight	97	
Yellowish green	5		Pronounced	1	
17. Bracteole size		0.52	25. Pod cross-section		0.58
Small	6		Semi-flat	27	
Intermediate	85		Round	73	
Large	9		Others	0	
18. Bracteole shape		0.39	26. Seed shape		0.96
Linear	90		Globose	4	
Lanceolate	5		Ovoid	75	
Others	5		Narrowly ellipsoid	5	
19. Flowering period		0.42	Cubical to oblong	6	
Asynchronous	85		Kidney shaped	5	
Intermediate	15		Drum shaped	5	
Synchronous	0		Others	0	
20. Pod attachment to the peduncle		0.84	27. Seed color		0.47
Erect	28		White	0	
Horizontal	2		Cream	0	
Horizontal-pendent	4		Light brown	0	
Pendent	66		Intermediate brown	0	
Others	0		Dark brown	0	
21. Pod pubescence		0.59	Grey	5	0.5
Glabrous	84		Mottled grey	8	
Sparsely	9		Mottled brown	0	
Moderately pubescent	4		Mottled cream	0	
Densely pubescent	3		Light cream	0	
22. Pod curvature		0.5	Green brown	87	
Straight	8		Chocolate	0	
Slightly curved	86		28. Lusture on the seed surface		0.42
Curved (sickle-shaped)	6		Absent	15	
23. Pod beak shape		0.54	Present	85	
Pointed	23				
Blunt	77				
Others	0				

Table 2. Continued.

Character & description	Frequency (%)	H'
29. Mottling on the seed surface		0.53
Absent	85	
Slight	8	
Intermediate	7	
30. Hilum shape		0.36
Concave	44	
Plain	52	
Convex	4	
Others	0	
Densely pubescent	6	
Overall mean		0.53

Principal Component Analysis

The principal component analysis is a multivariate technique used to observe relationships among several variables. It involves a mathematical procedure that transforms some possibly correlated variables into a smaller number of uncorrelated variables and studies the patterns of variation and the relative importance of each trait in explaining the observed variability. In the present study, the principal component analysis based on the 30 qualitative traits was computed. Hair *et al.* (1998) suggested that the principal component (PCs) with eigenvalues greater than unity, and component loadings greater than ± 0.3 were considered to be meaningful and valuable. Therefore, the first four principal components with eigenvalues greater than unity explained 90.0% of the total variations (Table 3). Principal component 1 (PC1) alone accounted for 75% of the total variation. Attachment of primary leaves, terminal leaflet lobe shape, stipule size, stipule shape, stem pubescence, bracteole shape, pod attachment to the peduncle, pod curvature, pod beak shape, mottling on seed surface, and hilum shape had the highest loadings on PC1. Accordingly, the attachment of primary leaves, stipule size, stipule shape, stem pubescence, raceme position (at first pod), bracteole shape, pod attachment to the

peduncle, pod curvature, pod beak shape, mottling on seed surface, and hilum shape had a relatively better value for variation coefficient on PC1 axis. These were the most distinctive traits that had significantly brought the variations among the genotypes. The second principal component (PC2), explained 8% of the total variations and was highly positively correlated with corolla color, bracteole size, flowering period, lusture on the seed surface, and it was also highly negatively correlated with seed color, constriction of pod between seeds and leaf pubescence. Growth pattern, leafiness (at 50% flowering) lusture on the seed surface, flowering period, bracteole size, and corolla color were the most distinctive characteristics on the PC2 axis, while PC3 explained 4% of the total variations and correlated highly positively with growth habit, petiole pubescence, lobbing of the terminal leaflet, corolla color, bracteole size, flowering period and pod pubescence, pod cross-section and lusture on seed surface while it correlated highly negatively with growth pattern.

Consequently, on the PC3 axis, the most distinctive characteristics causing the variation among the genotypes were growth habit (0.446), petiole pubescence (0.302) and pod pubescence (0.302). . Meza *et al.* (2013) indicated that the first three principal components explained 34.18% of the total variation and reported that the

first flowering time, ripened pod color, and pod harvest time of common beans were considered as the most distinctive characteristics.

Based on the first three PCs, growth habit, leafiness (at 50% flowering), corolla color, bracteole size, flowering period, pod cross-section and lusture on a seed surface were prominent characteristics in the screening of mung bean genotypes. Similarly, Ekbiç and Hasancaoğlu (2019) suggested that seed main

color, seed secondary color, pod color, pod cross-section, and stringiness were prominent characteristics in the screening of common bean genotypes. The remaining PCs explained 7% of the total variation that was mainly associated with growth habits. Therefore, from all the characters, growth habit was found as the most discriminative trait differentiating genotypes collected from southern Ethiopia.

Table 3. Principal Component Analysis (PCA) in Qualitative Traits of 60 Mung Bean Genotypes.

Traits	PC1	PC2	PC3	PC4
Growth pattern	-0.163	0.215	-0.268	-0.033
Growth habit	0.043	0.074	0.446	0.747
Attachment of primary leaves	0.201	0.16	-0.119	0.065
Stem color	0.18	-0.077	0.291	0.029
Leafiness (at 50% flowering)	0.185	0.25	0.124	-0.067
Leaf pubescence	0.191	-0.249	-0.014	-0.043
Petiole pubescence	0.178	-0.205	0.302	-0.073
Lobbing of terminal leaflet	0.192	-0.212	0.082	-0.081
Terminal leaflet lobe shape	0.202	-0.077	-0.153	0.026
Stipule size	0.203	0.082	-0.152	0.067
Stipule shape	0.202	-0.08	-0.155	0.041
Stem pubescence	0.2	-0.092	-0.169	0.046
Raceme position (at first pod)	0.202	-0.012	-0.18	0.055
Calyx color	0.198	-0.184	-0.037	-0.029
Corolla color	0.175	0.279	0.209	-0.088
Bracteole size	0.185	0.248	0.117	-0.043
Bracteole shape	0.2	0.154	-0.135	0.079
Flowering period	0.175	0.279	0.209	-0.088
Pod attachment to peduncle	0.2	0.158	-0.125	0.074
Pod pubescence	0.178	-0.205	0.302	-0.073
Pod curvature	0.203	0.083	-0.151	0.074
Pod beak shape	0.201	-0.022	-0.193	0.072
Constriction of pods b/n seeds	0.19	-0.259	-0.017	-0.043
Pod cross section	0.104	0.182	0.243	-0.586
Seed shape	0.194	-0.216	-0.069	-0.017
Seed color	0.189	-0.263	-0.018	-0.042
Lusture on seed surface	0.167	0.249	0.046	-0.038
Mottling on seed surface	0.2	0.158	-0.125	0.074
Hilum shape	0.2	0.157	-0.128	0.076
Eigen value	21.8	2.36	1.27	1.02
Proportion	0.75	0.08	0.04	0.03
Cumulative	0.75	0.83	0.87	0.90

PC= Principal component

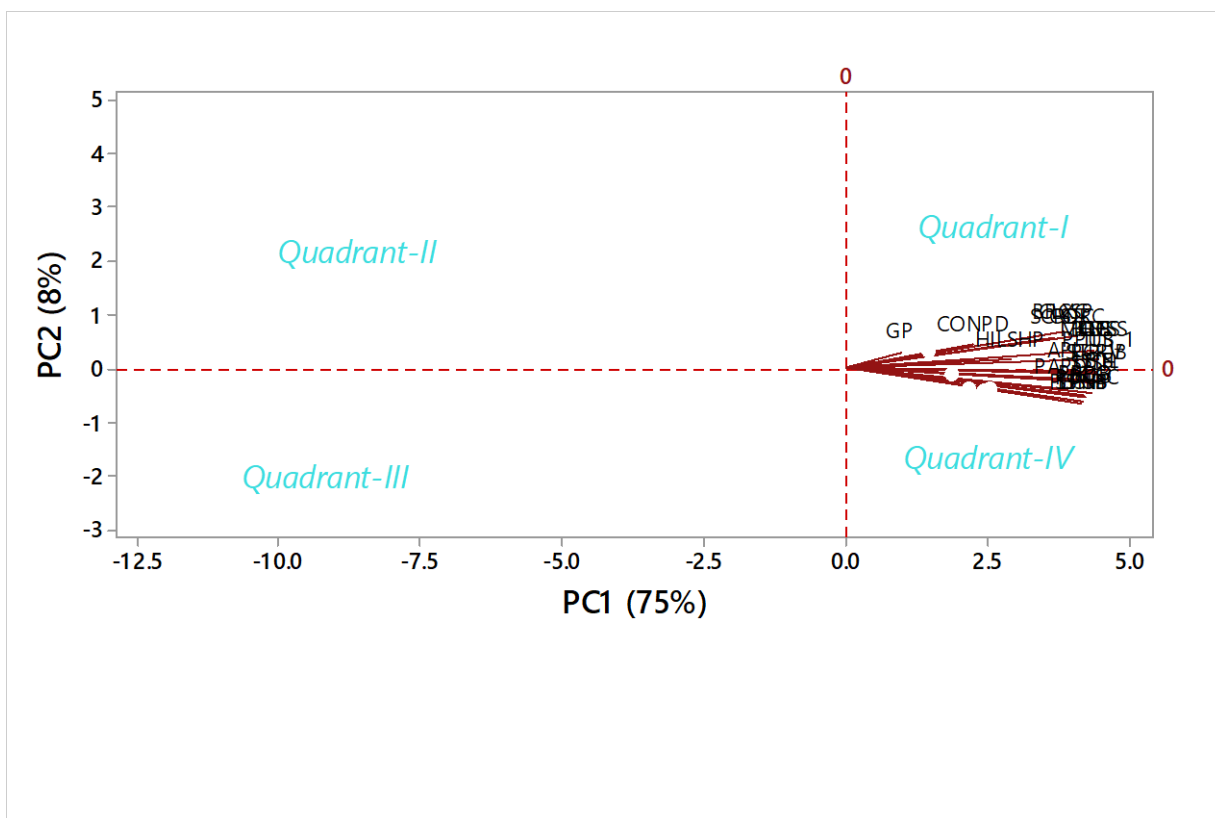


Figure 1. Biplot showing an Association of 30 Qualitative Traits of Genotypes.

Cluster Analysis

Cluster analysis was done based on similarity among the genotypes which gave the relative position of genotypes in the group. A study was conducted to determine the morphological genetic diversity among the 60 mung bean genotypes based on the qualitative traits (Table 4, 5, 6, and; Figure 2). The genotypes were grouped into four different clusters based on the studied 30 qualitative traits (Table 4), indicating the existence of the genetic divergence among the genotypes which might give a better chance to select the genotypes with different weights for mung bean improvement. Based on the **cluster** data, several researchers emphasized the importance of involving diverse parents in crossing programs to achieve high heterotic responses and transgressive segregants in early generations for improved seed yield and other targeted traits. . The result showed that there were significant variations observed among the mung bean genotypes for the studied qualitative traits. Singh *et al.* (2010) suggested that emphasis must be given to the genetic diversity of mung bean genotypes. Therefore, genotypes may be selected from a dendrogram based on genetic diversity, and assembling the genotypes based on their similarity is of paramount importance. Basnet *et al.* (2014) reported that the multivariate analysis involving the qualitative traits clearly showed the alignment of the different genotypes into different clusters according to the similarity indices. The use of diverse parents to increase the chance of getting superior varieties has been reported by (Katiyar *et al.*, 2009; Tantasawat *et al.*, 2010; Narasimhulu *et al.*, 2013).

A dendrogram condenses genetic similarity among mung bean genotypes based on the 30 qualitative traits (Figure 2). The number of genotypes varied from three in (Cluster III) to forty-five in Cluster I (Table 4). The first cluster was the largest, consisting of forty-five genotypes, and accounts for 75% of the total genotypes. The second and fourth clusters consisted of six genotypes each and accounted for 20%, while the third cluster consisted of three genotypes and accounts for 5%. In this study, cluster I and cluster IV have the largest inter-cluster distance of 44.67 units (Table 5), indicating that more emphasis should be given to cluster I for selecting genotypes as parents for crossing with the genotypes of Cluster IV for the studied traits.

As per the contribution of traits for inter-cluster analysis, the traits were classified as high contributors ($CTIC \geq 74\%$), intermediate contributors ($70\% \leq CTIC \leq 74\%$), and low contributors ($CTIC < 70\%$). Accordingly, traits such as leafiness at 50% flowering, leaf pubescence, petiole pubescence, pod attachment to the peduncle, pod beak shape, constriction of pod between seeds, and seed shape were the major contributors of genetic divergence in the entire genotypes, while growth pattern, attachment of primary leaves and hilum shape were low contributors to the divergence on mung bean genotypes (Table 6). Likewise, Toscana *et al.* (2017) reported growth habits, plant pigmentation, terminal leaflet shape, twinning tendency, pod attachment to the peduncle, and seed shape were the major traits with major contributors for inter-cluster of 30 cowpea genotypes.

Table 4. Distribution of the 60 Mung bean Genotypes in Four Cluster Groups.

Cluster	Number of genotypes	Genotypes Included Under Clusters 1-4
Cluster I	45	G1, G2, G3, G4, G5, G6, G7, G8, G9, G10, G11, G12, G13, G14, G15, G16, G17, G18, G20, G21, G22, G23, G24, G25, G26, G27, G28, G29, G30, G31, G32, G33, G34, G35, G36, G37, G38, G39, G40, G41, G42, G43, G44, G45
Cluster II	6	G46, G47, G48, G49, G50, G51
Cluster III	3	G52, G53, G54
Cluster IV	6	G57, G58, G55, G56, G59, G60

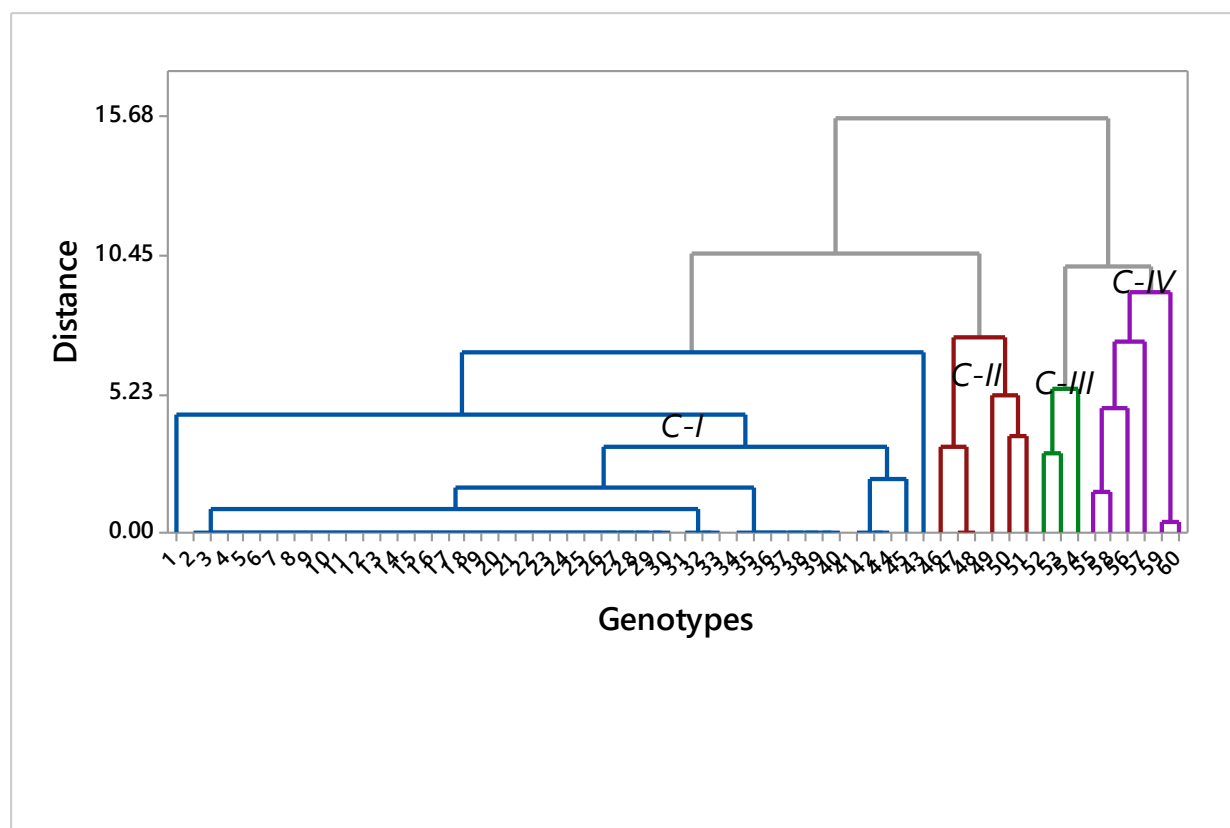


Figure 2. Hierarchical Clustering of the pattern of 60 mung bean genotypes (UPGMA) based on 30 qualitative characters.

Table 5. Average intra-cluster (bolded diagonal) and inter-cluster (off-diagonal) generalized squared distance (D^2) values for qualitative traits.

Clusters	I	II	III	IV
I	4.81	17.00 ns	30.56 ns	44.67*
II		3.76	13.63 ns	28.40ns
III			3.67	16.15 ns
IV				7.15

**, * indicates significant at 1% and 5% level of significant; $\chi^2_{28} = 41.34$ and 48.28 at 5% and 1%, probability level, respectively.

Table 6. Levels of trait contribution for inter-cluster analysis of 60 mung bean genotypes.

Traits	CI	CII	CIII	CIV	Mean	Std	CTIC (%)
GP	0.18	0.18	0.28	0.21	0.21	0.05	22.20
GH	0.42	0.42	0.42	1.37	0.66	0.48	72.24
APL	0.74	0.82	0.64	1.33	0.88	0.31	34.82
STC	0.36	0.36	0.36	1.18	0.57	0.41	72.57
LFNS	0.57	0.57	0.38	1.72	0.81	0.61	75.71
LPUB	0.57	0.57	0.38	1.72	0.81	0.61	75.71
PPUB	0.48	0.59	0.42	1.65	0.79	0.58	74.01
LBTL	0.50	0.50	0.50	1.63	0.78	0.57	72.20
TLLS	0.44	0.44	0.44	1.46	0.70	0.51	73.38
STS	0.50	0.50	0.50	1.63	0.78	0.57	72.20
STSH	0.50	0.50	0.50	1.63	0.78	0.57	72.20
STPUB	0.47	0.47	0.47	1.54	0.74	0.54	72.54
RPO	0.55	0.55	0.55	1.79	0.86	0.62	72.09
CLXC	0.33	0.33	0.33	1.09	0.52	0.38	73.08
CORC	0.36	0.36	0.36	1.18	0.57	0.41	72.57
BRCS	0.42	0.42	0.42	1.37	0.66	0.48	72.24
BRCS	0.33	0.33	0.33	1.09	0.52	0.38	73.08
FLP	0.42	0.42	0.42	1.37	0.66	0.48	72.24
PAPD	0.58	0.68	0.09	1.44	0.70	0.56	80.02
PPUB	0.44	0.44	0.44	1.46	0.70	0.51	73.38
PCR	0.47	0.47	0.47	1.54	0.74	0.54	72.54
PBSHP	0.57	0.57	0.38	1.72	0.81	0.61	75.71
CONPS	0.18	0.18	0.18	0.61	0.29	0.22	74.78
PDCSC	0.55	0.55	0.55	1.80	0.86	0.63	72.46
SSHP	0.57	0.57	0.38	1.71	0.81	0.61	75.33
SCRL	0.23	0.39	0.39	1.06	0.52	0.37	71.39
LSS	0.42	0.42	0.42	1.37	0.66	0.48	72.24
MOTSS	0.42	0.42	0.42	1.37	0.66	0.48	72.24
HSP	0.55	0.42	0.30	0.94	0.55	0.28	50.28

CTIC = Contribution Inter Cluster Divergence, GP= growth pattern, APL= attachment of primary leaves, STC= stem color, LFNS= leafiness at 50% flowering, LPUB= leaf pubescence, PPUB= petiole pubescence, LBTL= lobbing of the terminal leaflet, TLLS= terminal leaflet lobe shape, STS= stipule size, STSH= stipule shape, STPUB= stem pubescence, RPO= raceme position (at first pod), CLXC= calyx color, CORC= corolla color, BRCS= bracteole size, BRCS= bracteole shape, FLP= flowering period, PAPD= pod attachment to peduncle, PPUB= pod pubescence, PCR= pod curvature, PBSHP= pod beak shape, CONPS= constriction of pod between seeds, PDCSC= pod cross-section, SSHP= seed shape, SCRL= seed color, LSS= lusture on the seed surface, MOTSS= mottling on the seed surface, HSP= hilum shape

CONCLUSIONS

Morphological characterization of mung bean genotypes based on qualitative traits significantly contributes for better assessment of the genotypes and identification of the best genotypes with desirable traits for the further breeding program. In the present study, a wide range of phenotypic

diversity was recorded among tested mung bean genotypes for genetic enhancement through direct selection for desirable traits. The highest diversity index (H') was obtained for seed shape, while the lowest value was recorded for constriction of pod between seeds from the entire genotypes. The first seven principal components explained 94% of the total variation. In general, the presence of maximum

genetic diversity among mung bean genotypes based on qualitative traits leads to a high chance for hybridization for future variety improvement. Cluster analysis identified four distinct groups based on qualitative traits. Hence, future studies should consider the distribution of genetic diversity, serving as a benchmark for the collection, characterization, and conservation of genotypes. .

Moreover, the conventional approaches of characterization as adopted in this study have certain limitations in identifying duplicates; therefore, adoption of advanced diversity analysis tools like biochemical and molecular approaches which could accurately contribute to estimating the level of genetic diversity should be used.

ACKNOWLEDGEMENT

The authors extend their gratitude to the Southern Agricultural Research Institute (SARI) for the financial support towards this research. Also, the authors' deep gratitude and acknowledgement goes to Melkassa Agricultural Research Center (MARC) for providing the mung bean genotypes for this study. The authors also recognize Jinka Agricultural Research Center (JARC) for its administrative facilitation during implementation of this research.

CONFLICTS of INTEREST

The authors declare that there is no conflict of interest.

REFERENCES

- Basavaraj, M., V.K., Deshpande, and, B.S. Vyakaranahal. 2013. Characterization of Cowpea Genotypes Based on Quantitative Descriptors. *The Bioscan*, 8(4): 1183-1188. [[Scholar Google](#)]
- Basnet, K.M., N.R., Adhikari, and M.P., Pandey. 2014. Multivariate Analysis Among the Nepalese and Exotic Mungbean [*Vigna radiata* (L.) Wilczek] Genotypes Based on the Qualitative Parameters. Department of Plant Breeding and Genetics, Institute of Agriculture and Animal Science, Nepal. [[Scholar Google](#)]
- Bisht, I., K., S., Lakhanpaul, M., Latha, P., Jayan, and B., Biswas. 2005. Diversity and Genetic Resources of Wild *Vigna* Species in India. *Genetic Resources and Crop Evolution*, 52: 53-68. [[Scholar Google](#)]
- Borines, N. O. M., Borromeo, T. H., dR De Chavez, H., and Capistrano, M. P. 2019.. Ex situ conservation of agro-biodiversity of major food legumes in the Philippines. In IOP Conference Series: Earth and Environmental Science, 230(1):p. 012113. [[Scholar Google](#)]
- Das, R., U. Thapa, S. Debnath, Y. A. Lyngdoh, and D. Mallick. 2014. Evaluation of French bean (*Phaseolus vulgaris* L.) genotypes for seed production. *Journal of Applied and Natural Science*, 6(2): 594-598. [[Scholar Google](#)]
- Denton, O.A., and C.C., Nwangburuka. 2011. Heritability, Genetic Advance and Character Association in Six Yield Related Characters of *Solanum anguivi*. *Asian Journal of Agricultural Research*, 5(3): 201-207. [[Scholar Google](#)]
- Doyle, J.J. 1994. Phylogeny of the Legume Family: An Approach to Understanding the Origins of Nodulation. *Annual Review of Ecology and Systematics*, 25(1): 325-349. [[Scholar Google](#)]
- Durga, K.K., R., Ankaiah, R., M., Ganesh. 2015. Characterization of Horse Gram Cultivars Using Plant Morphological Characters. *Indian J. Agril. Res.*, 49(2): 215-221. [[Scholar Google](#)]
- Ekbiç, E. and E.M., Hasancaoğlu. 2019. Morphological and Molecular Characterization of Local Common Bean [*Phaseolus Vulgaris* (L.)] Genotypes. *Applied Ecology and Environmental Research*, 17(1): 841-853. [[Scholar Google](#)]
- Firdissa E., B., Endeshaw, B., Getachew, and A., Börner 2005. Phenotypic Diversity in Durum Wheat Collected from Bale and Wello regions of Ethiopia, *Plant Genetic Resource*, 3 (1): 35–43. [[Scholar Google](#)]
- Gnyandev, B. 2009. Seed Technological Studies in Chickpea Varieties [*Cicer arietinum* (L.)]. Ph. D. Thesis (Unpublished) Submitted to University of Agricultural Sciences, Dharwad, Karnataka (India).
- Gonné, S., W.L., Venasius, and A., Laminou. 2013. Characterization of Some Traditional Cowpea Varieties Grown by Farmers in the Soudano-Sahelian zone of Cameroon. *International Journal of Agriculture and Forestry*, 3(4): 170-177. [[Scholar Google](#)]
- Hair, J.F., J.R., Andrsn, R.E., Tatham, and W.C., Black. 1998. *Multivariate Data Analysis*, 5th (eds.), Prentice-Hall International, Inc, London.
- Hapsari, R.T., T., Trustinah, and R., Iswanto. 2018. Diversity of Local Indonesian Mungbean Germplasm Based on Morphological Quantitative and Qualitative Traits. The 2nd International Conference on Biosciences (ICoBio). IOP Conf. Series: Earth and Environmental Science, 197(1): 1-8. DOI: 10.1088/1755-1315/197/1/012036. [[Scholar](#)]

- [Google\]](#)
- Harouna, D.V., P.B., Venkataramana, A.O., Matemu, and P.A., Ndakidemi, 2020. Agro-Morphological Exploration of Some Unexplored Wild Vigna Legumes for Domestication. *Agronomy*, 10(111): 1-26. DOI:10.3390/agronomy10010111. [[Scholar Google\]](#)
- Hennink, S. and Zeven, A.C. 1990. The Interpretation of Shannon-Weaver Within-Population Variation Indices, *Euphytica*, 51: 235-240. [[Scholar Google\]](#)
- IBPGR (International Board for Plant Genetic Resources). 1980. Descriptors for Mungbean. Rome, Italy.
- Jain, S.K., D., Khare, M.S., Bhale, and N.D., Raut. 2002. Characterization of Mung Bean Varieties for Verification Of Genetic Purity. *Seed Tech News*, 32(1): 200-201.
- Joshi, P. and M., Yasin. 2014. Characterization of Diverse Angular, Owl's Head and Pea Seed Shapes Germplasm of Chickpea (*Cicer arietinum* L.). *J. Medi. Pharma. Allied Sci.*, 3(6): 1-9.
- Kang, Y.J., S.S., Ahra Bae, L., Taeyoung, L., Jayern, S., Dani, Y.K., Moon, and L., Suk-Ha. 2017. Genome-wide DNA Methylation Profile in Mungbean. *Sci. Rep.* 7: 40503. DOI: 10.1038/srep40503. [[Scholar Google\]](#)
- Katiyar, P.K., G.P., B.B., Dixit and Singh. 2008. Morphological Characterization of Green Gram [*Vigna radiata* (L.) Wilczek] Varieties And Their Application for Distinctness, Uniformity and Stability Testing. *Indian J. Agri. Sci.*, 78(5): 439-444. [[Scholar Google\]](#)
- Katiyar, P.K., G.P., Dixit, B.B., Singh, H., Ali, and M.K., Dubey, 2009. Non-hierarchical Euclidean Cluster Analysis for Genetic Divergence in Mungbean Cultivars. *J. Food Legumes*, 22: 34-36. [[Scholar Google\]](#)
- Kaur, R., A.K., Toor, G., Bassi, and T.S., Bains, 2017. Characterization of Mungbean [*Vigna radiata* (L.) Wilczek] Varieties Using Morphological and Molecular Descriptors. *International Journal of Current Microbiology and Applied Sciences*, 6(6): 1609-1618. [[Scholar Google\]](#)
- Kumar, S. and Shrikant. 2016. Evaluation of Cowpea [*Vigna unguiculata* (L.) Walp] Cultivars Using Morphological Indices. *Asian J. Multidisciplinary Studies*, 4(6): 158-164.
- Kumar, S., U.N., Joshi, V., Singh, J.V., Singh, and M.L., Saini, 2013. Characterization of Released and Elite Genotypes of Guar [*Cyamopsis tetragonoloba* (L.) Taub.] from India Proves Unrelated to Geographical Origin. *Genet. Resour. Crop Evol.*, 60(7): 2017-2032. [[Scholar Google\]](#)
- Mahalanobis, P.C. 1936. On the Generalized Distance in Statistics. *Proc Nat Inst Sci India*, 2: 49-55.
- Mesfin, K., Tesfaye, S., Girma, K., and G., Tsegaye. 2017. Description, Characterization, and Classification Of The Major Soils in Jinka. *Journal of Soil Science and Environmental Management*, 8(3): 61- 69. [[Scholar Google\]](#)
- Meza, N., J.C., Rosas, J.P., Martín, and Ortiz, J.M. 2013. Biodiversity of Common Bean [*Phaseolus vulgaris* (L.)] in Honduras. Evidenced by Morphological Characterization. *Genetic Resources and Crop Evolution*, 60(4): 1329-1336. [[Scholar Google\]](#)
- Milligan, G.W and Cooper, M.C. 1985. An Examination of Procedures for Determining the Number of Cluster in Data Set. *Psychometrika*, 50(2): 159-179. [[Scholar Google\]](#)
- Mohan, S.C., S.B., Mishra, P., Anil, and A., Madhuri, 2014. Morphological Characterization and Discriminant Function Analysis in Mungbean [*Vigna radiata* (L.) Wilczek] germplasm. *Electronic Journal of plant breeding*, 5(1): 87-96. [[Scholar Google\]](#)
- Narasimhulu, R., N.V., Naidu, P.M., Shanthi, V., Rajarajeswari, and K.H.P. Reddy, 2013. Genetic Variability and Association Studies for Yield Attributes in Mungbean. *Indian J. Plant Sci.*, 2(3): 82-86. [[Scholar Google\]](#)
- Nwosu, D.J., S., Aladele, J.O., C., Adeosun, Nwadike, and E.N., Awa, 2013. Cross-compatibility and F1 Reproductive Potential of Cultivated Cowpea Varieties and a Wild Relative (Subsp. *unguiculata* var. *spontanea*). *Greener Journal of Agricultural Sciences*, 3(5): 391-395.
- Ogwu, M.C, M.E, Osawaru, and C.M. Ahana, 2014. Challenges in Conserving and Utilizing Plant Genetic Resources. *International Journal of Genetics and Molecular Biology*, 6(2): 16-22. [[Scholar Google\]](#)
- Patel, J.D., J.B. Patel, and C.P., Chetariya. 2019. Characterization of Mung bean [*Vigna radiata* (L.) Wilczek] Genotypes Based on Plant Morphology, *Ind. J. Pure App. Biosci.*, 7(5): 433-443. [[Scholar Google\]](#)
- Popoola, J.O., A., Adebambo, S., Ejoh, P., Agre, A.E., Adegbite, and C.A. Omonhinmin. 2017. Morphological Diversity and Cytological Studies

- in Some Accessions of *Vigna vexillata* (L.) A. Richard. Annual Research and Review in Biology, 9(5): 1-12. [[Scholar Google](#)]
- Rahim, M.A., A.A., Mia, F., Mahmud, N., Zeba, and K.S., Afrin. 2010. Genetic Variability, Character Association and Genetic Divergence in Mungbean [*Vigna radiata* (L.) Wilczek]. Plant Omics Journal, 3(1): 1-6. [[Scholar Google](#)]
- Rhman, M.M. and A.Z.A., Munur. 2009. Genetic Divergence Analysis of Lemon. Journal of Bangladesh Agricultural University, 7(1): 33-37.
- Singh, A.K., A. Mishra, and A., Shukla. 2010. Genetic Evaluation and Identification of Genetic Donors in Black Gram [*Vigna mungo* (L.)] revealed by Agro-Morphological Traits and Seed Storage Protein Analysis. World Applied Science Journal, 10(4): 477-488. [[Scholar Google](#)]
- Singh, C.M., S.B., Mishra, A., Pandey, and M. , Arya, 2014. Morphological Characterization and Discriminant Function Analysis in Mungbean [*Vigna radiata* (L.) Wilczek] Germplasm. Electronic Journal of Plant Breeding, 5(1): 87-96. [[Scholar Google](#)]
- Sowmya, T., K K., Durga, K., Venkateshwaran, K., Keshavulu, and A., Vidyasagar. 2019. Characterization of Green Gram Genotypes for Qualitative Traits. Agricultural Science Digest, 39: 81-89. [[Scholar Google](#)]
- Tabasum, A., M., Saleem, and I., Aziz. 2010. Genetic Variability, Trait Association and Path Analysis of Yield and Yield Components in Mungbean [*Vigna radiata* (L.) Wilczek]. Pak J. Bot., 42: 3915–3924. [[Scholar Google](#)]
- Tantasawat, P., J., Trongchuen, T., Prajongjai, P., Chutamas, S., Worapa, and M., Thitiporn. 2010. Variety Identification and Genetic Relationships of Mung Bean and Black Gram in Thailand Based on Morphological Characters and ISSR Analysis. African Journal of Biotechnology, 9 (27): 4452-4464. [[Scholar Google](#)]
- Toscana, N.D., K., Bertrand, B.D., Honoré, A., Mariette. 2017. Evaluation of the Genetic Variation of Cowpea Landraces (*Vigna unguiculata*) from Western Cameroon Using Qualitative Traits. Notulae Scientia Biologicae, 9(4): 508-514. [[Scholar Google](#)]
- Ulukan, H. 2011. 'The Use of Plant Genetic Resources and Biodiversity in Classical Plant Breeding', Acta Agriculturae Scandinavica, Section B - Plant Soil Science, 61(2): 97-104. [[Scholar Google](#)]
- Wang, L., P., Bai, X., Yuan, H., Chen, S., Wang, X., Chen, and X., Cheng, 2018. Genetic diversity assessment of a set of introduced mung bean accessions (*Vigna radiata* L.). The crop journal, 6(2): 207-213. [[Scholar Google](#)]
- Ward, J.R.1963. Hierarchical Grouping to Optimize and Function. Journal of The American Statistical Association, 58(301): 236-244. [[Scholar Google](#)]
- Wuletaw, T. and B., Endashaw. 2003. Phenotypic Diversity of Ethiopian Grass Pea (*Lathyrus sativus* L.) in Relation to Geographical Regions and Altitudinal Range. Genetic Resources and Crop Evolution, 50(5): 497-505. [[Scholar Google](#)]
- Yadav, R.D.S. and J.P., Srivastava. 2002. DUS Characteristics of Chickpea Varieties. Seed Tech. News, 32: 29-30.