Abstract

Mung bean is an important pulse crop grown by poor farmers in marginal and drought-prone areas of Ethiopia. Information on the extent of genetic divergence in mung bean is vital to identify diverse genotypes for crop improvement and the efficient utilization of the existing genetic resources. Therefore, the objectives of the study were to assess the extent and pattern of morphological diversity among the mung bean genotypes and to identify the traits contributing to the genetic diversity using multivariate analyses. The experiment was conducted using 60 mung bean genotypes at Jinka Agricultural Research Center during the 2018 cropping season. The first seven principal components explained 80.1% of the total variation. Almost all the studied traits were important contributors to the divergence. The cluster analysis based on quantitative traits revealed four distinct groups. The highest inter-cluster distance was recorded between cluster I and cluster IV ($D^2=43.16$ units). The minimum inter-cluster distance was noted between cluster III and cluster IV ($D^2=12.16$ units). The maximum and minimum intra-cluster distances $D^2$ were recorded within cluster I ($D^2=6.49$ units) and cluster III ($D^2=3.53$ units), respectively. The range of intra and inter-cluster distance was 3.53 to 6.49 units and 12.16 to 43.16 units, respectively. Hence, the high genetic distance exhibited within and among clusters has to be exploited through the crossing and selection of the most divergent parents for future mung bean breeding programs.

Keywords: Clustering, Genetic Distance, Mung Bean, PCA

Introduction

Mung bean [Vigna radiata (L.) Wilczek] is an important short-season grain legume, well suited to smallholder production under adverse climatic conditions [1]. It is a cheap source of dietary protein with high levels of iron compared to many other legumes [2].

Morphological traits are routinely used for estimating genetic diversity and to analyze genetic relationships among the genotypes [3]. Reported that evaluation of germplasm is useful not only in the selection of core collection but also important for breeding programs. Suggested that future progress in mung bean breeding requires imperative action to identify mung bean genotypes with favorable agronomic traits for further improvement programs [4].

Therefore, broad genetic diversity is needed to achieve mung bean breeding goals. Indicated that mung bean genotypes exhibited a wide range of variation for most of the studied traits. Reported that the collection of diverse local cultivars and their subsequent genotyping would enhance germplasm diversity and provide information, both of which are beneficial for developing collection strategies and breeding purposes with desirable agro-morphological characteristics. Indicated that the multivariate techniques may be an efficient tool in the quantitative estimation of genetic variation to select germplasm more systemically and effectively and to develop strategies to incorporate useful diversity in their breeding programs [5-7].
Quantification of the magnitude of the genetic diversity and classifying it into homogeneous groups to facilitate identification of genetic variability enable breeders to select traits of interest for the mung bean improvement program. The analysis of genetic diversity in germplasm collections can also facilitate the classification and identification of groups of accessions with superior characteristics to be used for breeding purposes [8-10].

Hence, characterization of genetic diversity needs comprehensive statistical procedures, such as D^2 statistics and multivariate analysis, namely principal component analysis and cluster analysis that have been considered as the best tools for choosing promising genotypes for a future breeding program in mung bean. Therefore; these techniques are used for clustering a large number of genotypes into homogeneous groups, the genetic distance among and within clusters, and principal component analysis for identifying the most important contributing traits for the genetic diversity and identifying superior cowpea genotypes. Furthermore, limited studies have been reported on mung bean globally in Ethiopia. However, most of these studies were conducted using a very limited number of genotypes on fewer quantitative traits. Moreover, there is no sufficient information on the genetic diversity of mung bean genotypes by using multivariate analyses. Therefore, the objectives of the present study were to assess the extent of genetic diversity among 60 mung bean genotypes using phenotypic traits, to cluster the genotypes into homogenous groups, estimate the genetic distance and relationships between genotypes, and identify the major traits contributing to the diversity using multivariate techniques [11-21].

**Materials and Methods**

**Descriptions of the Study Area**

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 36°33’02.7”E, 05°46’52.0”N, and at an altitude of 1420 m above sea level. The maximum, minimum, and average temperatures of the center for ten years (2009-2019) are 27.68°C, 16.61°C, and 22.14°C, respectively; while the mean annual rainfall is 1381 mm. The soil type of the center is Cambisols [22].

**Experimental Materials**

A total of 60 mung bean genotypes were used for this study. Of these, 44 were obtained from Melkassa Agricultural Research Center (MARC), and 16 genotypes were collected from Southern Nations, Nationalities, and People’s (SNNP) region.

**Experimental Design and Procedures**

The experiment was laid out using a 6 x 10 alpha lattice design. The plot size was 3 m long, 0.3 m between rows, and 0.05 m between plants. It consists of five rows accommodating 60 plants per row. The distance between plots, intra blocks, and replications was 1, 1.5, and 2 m, respectively.

**Data Collection**

The descriptor of mung bean developed by the International Board for Plant Genetic Resources was followed for data collection. The data collected on a plot basis include days to flowering (days), days to maturity (days) [23]. The data collected on the plant basis from ten plants were: plant height (cm), number of primary branches per plant, number of pods per plant, number of seeds per pod, pod length (cm), peduncle length (cm), number of pods per cluster, terminal leaflet length (cm) and terminal leaflet width (cm). The data were collected from the central three rows for the determination of seed yield, hundred seed weight (g), seed yield per plot (g), biomass (g), and harvest index (%).

**Data Analyses**

The means of seventeen traits were used and standardized to a mean of zero and a unit variance to avoid biases due to differences in the scales of measurements. A series of multivariate analyses such as Minitab Statistical Software were used. The principal component analysis was performed using the correlation matrix to determine principal components, proportions of eigenvalues, and the scores of the principal components. Hierarchical cluster analysis was performed to group genotypes and construct a dendrogram by using Minitab software. The Euclidean distance was measured for the dissimilarity of the genotypes. The average intra and inter-cluster distances were calculated using the generalized Mahalanobis’s D2 statistics. The pseudo-F statistics (PSF), and pseudo-T2 statistics were considered for defining optimum cluster numbers. The contribution of each trait to divergence as described by with the formula [CTIC =SD/X χ100] where x and SD are the mean performance and standard deviation of each trait, respectively [24-30].
tion in variation if a proportion of variation higher than 75% of the total variation is considered for characterization and evaluation of genetic collections for all legumes [34]. Correspondingly, reported that 78% variation was explained by the first five PCs for eleven quantitative traits on eighty-one mung bean genotypes. Also, indicated that 63.79% variation was justified by the first three principal components for 18 quantitative characters of six hundred and forty-six mung bean accessions. Likewise, took the first four principal components with eigenvalues >1, contributed 78.7% of the total variance amongst forty mung bean genotypes. Similarly, used the first three principal components with eigenvalues greater than 1 contributed 78% of the total variance amongst eighty-one mung bean genotypes [35-37].

The relative contributions of the PCs are explained by individual PCs, but the highest share was explained by the first principal component PC1 (22.4%), which contributed a high proportion of total variation and the rest six PCs had the proportion of 57.7% of the total variance, respectively. The first principal component (PC1) with eigenvalue 4.246 accounted high proportion of the total variance (22.4%) and the remaining three principal components viz., PC2, PC3, and PC4 with eigenvalue 2.861, 2.468, and 1.926 recorded 15.1, 13.0, and 10.10% of the total variance, respectively, while the other PCs (PC 5 to PC 7) had weak or no discriminatory power (Table 1). These results are in agreement with who reported that the first PC with the eigenvalue of 2.6 accounted for 32.60% of the total variation and the remaining three PCs with the eigenvalue of 1.7, 1.1, and 1.0 recorded 20.4, 11.3 and 10.2 %, respectively and accounted for 53.3% of the total variance and had the most discriminatory power while the rest four PCs had weak discriminatory power on seventy-four mung bean genotypes, similarly reported by on 74 mung bean genotypes [38, 39].

The present study depicted that all the studied traits have contributed significantly to the variations towards the PCs through their loading effects. Thus, the most important descriptors were those associated with the first seven principal components. The criterion of was chosen to determine the cut-off limit for the coefficients of the proper vectors [40]. According to this criterion, traits with coefficient values greater than 0.3 were considered as those traits having a large effect and to be considered important while traits having a coefficient value lesser than 0.3 were considered not to have important effects on the overall variation observed in the present study. As suggested by who observed that the loading effect of any traits greater than 0.3 was regarded as meaningful [41].

In this investigation, seed yield per hectare (0.451) and harvest index (0.464) in PC1 had high loading effects (Table 1). Therefore; the first principal component was much influenced by yield and yield-related traits. This result disagrees with the report of on the 26 accessions of the Vigna vexillata, who observed that the reproductive characters were effectively discriminated against the accessions [42]. But the second component was contrastingly much influenced by the vegetative characters namely; days to flowering (0.358), to physiological maturity (0.363) and it had also affected significantly by a hundred seed weight (0.338). The third principal component was largely influenced by days to flowering (0.412), days to maturity (0.404), petiole length (0.451), and peduncle length (0.451). This result is in line with the previous report of on 61 mung bean genotypes. This implies that the yield-related characteristics are close together when the second principal component is related to days to flowering and days to maturity. The third principal component exhibited positive effects on days to flowering, days to maturity, petiole length, and peduncle length [43].

The fourth component was strongly influenced by pods per cluster (0.454) and seeds per pod (0.308) while this component was manipulated negatively by terminal leaf width (-0.469) (Table 1). The fifth component was given the prominence of pod length (0.392) and the number of seeds per pod (0.440) while it was negatively manipulated by the number of primary branches per plant (-0.446). The sixth component was strongly influenced by terminal leaf length (0.670) while it was negatively affected by seed yield per plant (-0.419). The seventh component was greatly influenced by the number of primary branches per plant (0.316), the number of pods per plant (0.373), and pod length (0.611). Therefore, the above traits are the important productivity factors and hence these traits could be effectively used for selection among the tested genotypes for yield improvement programs in mung bean. In general, the first seven principal components with an eigenvalue of more than 1.0 accounted for 80.1% of the total variation. Similarly, noted 93.57% genetic variability comprised of the first seven PCAs [44]. Likewise, reported that about 84.52% of the variability from the first three PCs on 25 black gram genotypes [37]. Also, Singh et al. (2010) reported the first eight PCA together explained 98.79% of variance present on advanced black gram lines [45].
Table 1: Principal Component Analysis (PCA) on Quantitative Traits of Mung Bean Genotypes

<table>
<thead>
<tr>
<th>Traits</th>
<th>PC1</th>
<th>PC2</th>
<th>PC3</th>
<th>PC4</th>
<th>PC5</th>
<th>PC6</th>
<th>PC7</th>
</tr>
</thead>
<tbody>
<tr>
<td>Days to 90% flowering</td>
<td>-0.103</td>
<td>0.358</td>
<td>0.412</td>
<td>0.146</td>
<td>0.133</td>
<td>0.073</td>
<td>-0.250</td>
</tr>
<tr>
<td>Days to 90% maturity</td>
<td>-0.105</td>
<td>0.363</td>
<td>0.404</td>
<td>0.142</td>
<td>0.134</td>
<td>0.070</td>
<td>-0.251</td>
</tr>
<tr>
<td>Number of branches</td>
<td>-0.023</td>
<td>0.148</td>
<td>0.036</td>
<td>-0.119</td>
<td>-0.446</td>
<td>0.211</td>
<td>0.316</td>
</tr>
<tr>
<td>Pods per cluster</td>
<td>0.156</td>
<td>0.090</td>
<td>0.284</td>
<td>0.454</td>
<td>-0.228</td>
<td>-0.147</td>
<td>0.097</td>
</tr>
<tr>
<td>Petiole length</td>
<td>0.161</td>
<td>-0.260</td>
<td>0.451</td>
<td>-0.227</td>
<td>0.135</td>
<td>0.082</td>
<td>0.053</td>
</tr>
<tr>
<td>Pods per plant</td>
<td>0.111</td>
<td>0.155</td>
<td>0.221</td>
<td>0.239</td>
<td>-0.393</td>
<td>-0.208</td>
<td>0.373</td>
</tr>
<tr>
<td>Plant height</td>
<td>0.198</td>
<td>0.059</td>
<td>-0.082</td>
<td>0.046</td>
<td>-0.106</td>
<td>0.149</td>
<td>-0.064</td>
</tr>
<tr>
<td>Pod length</td>
<td>0.068</td>
<td>0.197</td>
<td>0.024</td>
<td>0.114</td>
<td>0.392</td>
<td>0.159</td>
<td>0.611</td>
</tr>
<tr>
<td>Peduncle length</td>
<td>0.161</td>
<td>-0.260</td>
<td>0.451</td>
<td>-0.227</td>
<td>0.135</td>
<td>0.082</td>
<td>0.053</td>
</tr>
<tr>
<td>Seeds per pod</td>
<td>-0.020</td>
<td>-0.277</td>
<td>0.020</td>
<td>0.308</td>
<td>0.440</td>
<td>-0.094</td>
<td>0.218</td>
</tr>
<tr>
<td>Terminal leaf length</td>
<td>0.076</td>
<td>-0.192</td>
<td>0.071</td>
<td>0.181</td>
<td>-0.059</td>
<td>0.670</td>
<td>-0.188</td>
</tr>
<tr>
<td>Terminal leaf width</td>
<td>0.198</td>
<td>-0.017</td>
<td>0.179</td>
<td>-0.469</td>
<td>0.025</td>
<td>-0.208</td>
<td>0.193</td>
</tr>
<tr>
<td>Seed yield per plant</td>
<td>0.287</td>
<td>0.076</td>
<td>-0.084</td>
<td>0.179</td>
<td>0.222</td>
<td>-0.419</td>
<td>-0.178</td>
</tr>
<tr>
<td>Hundred seed weight</td>
<td>0.241</td>
<td>0.338</td>
<td>-0.046</td>
<td>-0.259</td>
<td>-0.016</td>
<td>0.170</td>
<td>0.056</td>
</tr>
<tr>
<td>Biomass yield</td>
<td>-0.190</td>
<td>0.218</td>
<td>-0.179</td>
<td>0.061</td>
<td>0.260</td>
<td>0.287</td>
<td>0.252</td>
</tr>
<tr>
<td>Seed yield per hectare</td>
<td>0.451</td>
<td>0.062</td>
<td>-0.135</td>
<td>0.087</td>
<td>0.069</td>
<td>0.106</td>
<td>-0.038</td>
</tr>
<tr>
<td>Harvest index</td>
<td>0.464</td>
<td>-0.019</td>
<td>-0.064</td>
<td>0.046</td>
<td>-0.044</td>
<td>0.059</td>
<td>-0.097</td>
</tr>
<tr>
<td>Eigen value</td>
<td>4.246</td>
<td>2.861</td>
<td>2.468</td>
<td>1.926</td>
<td>1.475</td>
<td>1.200</td>
<td>1.033</td>
</tr>
<tr>
<td>Proportion</td>
<td>0.224</td>
<td>0.151</td>
<td>0.130</td>
<td>0.101</td>
<td>0.078</td>
<td>0.063</td>
<td>0.054</td>
</tr>
<tr>
<td>Cumulative</td>
<td>0.224</td>
<td>0.375</td>
<td>0.505</td>
<td>0.606</td>
<td>0.684</td>
<td>0.747</td>
<td>0.801</td>
</tr>
</tbody>
</table>

PC= Principal component

The extent of variance and relationship among different traits as explained by the loading plot (Figure 1) displayed the magnitude of the relationship between the quantitative traits. The genotypes allotted in quadrant-I were similar by their terminal leaf length, terminal leaf width, peduncle length, pods per plant, and harvest index. These traits had a relatively strong association and have a positive contribution to the discrimination of genotypes. In the second quadrant, genotypes were strongly associated with a single trait namely, the number of seeds per pod. Genotypes assigned in the third quadrant were strongly associated with the number of primary branches per plant, biomass yield, and days to maturity. Genotypes found in the fourth quadrant were similar for seed yield per hectare, plant height, seed yield per plant, pod length, pods per cluster, and hundred seed weight (Figure 1). Moreover, the scattered plot showed that the genotypes were distributed more or less equally in all quadrants. The scatter plot consisting of four quadrants illustrated the distribution of mung bean genotypes according to the diversity of their morphological characteristics. These could be used by breeders to identify the presence of genetic variability within the tested genotypes and select the donor parents for specific traits. Genotypes overlapped in the two principal axes have a similar phenotypic expression of the traits.

The loading plot indicates the similarity and differences among the studied traits. In the biplot, the traits found near to the origin such as the number of primary branches per plant, pods per cluster, and terminal leaf length have smaller loading effects and also had little influence. Traits like pods per plant, peduncle length, days to maturity, pods per plant, hundred seed weight, and harvest index are far from the origin and had higher loading and great influence in this classification. Among the studied traits, days to maturity, seed yield per plot, and harvest index have higher loading effects, indicating that these traits had great influence. Therefore, the loading plot reflecting the contributions of the characters to PC1 and PC2. Furthermore, genotypes classified using quantitative traits were explained by the first two dimensions PC1 and PC2 (Figure 2). Genotypes closer to each other and overlapping on the loading plot had similar characteristics whereas; those genotypes far apart from each other and those found distantly far from the origin are genetically diverse.

Most of the genotypes were concentrated in the second, third, and fourth quadrant and few genotypes in the first quadrant. The genotypes G7, G9, G60, and G36 were realized to have diverged greatly from the other genotypes.
Genetic Divergence Analysis
The genetic distances among the genotypes based on the studied 17 quantitative traits were estimated using $D^2$. The result revealed that the $D^2$ between the clusters was highly significant ($P\leq0.01$), suggesting high diversity among genotypes. Therefore, based on the $D^2$ results, the studied 60 genotypes were grouped into four clusters with a variable number of genotypes, revealing the presence of a considerable amount of genetic diversity.

Clustering of genotypes
The analysis of variance was highly significant among the divergent genotypes for all the 17 traits under study, which revealed the presence of considerable variability among the genotypes. This finding is in agreement with the report of who observed highly significant differences among the mung bean genotypes for all the studied 13 traits and thus indicated the presence of substantial amounts of diversity among the genotypes [46]. This suggested that adequate opportunity is available for the selection of superior genotypes aimed at enhancing the genetic yield potential of mung bean. Based on this, 60 mung bean genotypes were grouped into four groups based on the similarity of the studied traits (Figure 4.3). Similarly, Popoola et al. (2017) reported that the 26 acces-
sions of the Vigna vexillata were segregated into three clusters, cluster 1 consists of 15 accessions subdivided into two groups, cluster 2 is comprised of 10 accessions while cluster 3 has one accession [38]. Classified 75 mung bean genotypes into 11 major groups. Similarly, classified 344 mung bean accessions into 5 major and 1 minor cluster. Similarly, reported that the 30 mung bean genotypes were grouped into six clusters. While grouped fifty cowpeas genotypes into twelve clusters [47-50].

Understanding the level of genetic diversity in germplasm is helpful to plant breeders as it supports their decision on the selection of parental genotypes and is important in widening the genetic base of cowpea breeding [51]. The pattern of distribution of genotypes among various clusters reflected the presence of considerable genetic variability among the genotypes under study. The genotypes belonging to the same cluster are designated to be more closely related than those belonging to different clusters. Monogenotypic clusters indicated that such genotypes might have completely different genetic makeup from the remaining genotypes and each other, thus leading to the formation of the separate cluster. A maximum number of genotypes were comprised of cluster I (20), followed by cluster II (17) and cluster IV (14). The minimum genotypes (9) comprised Cluster III (Figure 3). A dendrogram summarizing the homogeneities between mung bean genotypes based on 18 traits is depicted in Figure 3. The tested genotypes were grouped into different clusters with various numbers of genotypes. The number of genotypes per cluster varied from 9 to 20 genotypes into each cluster. Cluster I was the largest cluster comprising 20 genotypes, followed by Cluster II and Cluster IV contained 17 and 14 genotypes, respectively, while the rest cluster III contained 9 genotypes.

Cluster Mean Performance

As improvement in seed yield and other related characters is a basic objective in any breeding program, thus cluster means need to be considered for the selection of genotypes. The mean values of 17 quantitative traits per cluster are presented in Table 2. In this study, the mean values varied among clusters for all traits. Genotypes that took shorter days to flower and to attain maturity were found in Cluster-I, while those genotypes took extended time for flowering and maturity found in Cluster-II, Cluster-III, and Cluster-IV. The maximum petiole lengths were exhibited on Cluster I and Cluster II while the minimum was noted on Cluster IV. The maximum mean values for terminal leaf length and terminal leaf width were observed on Cluster I and Cluster II while the minimum was noted on Cluster IV. The highest mean values for peduncle length were noted on Cluster I and Cluster II whereas; the minimum was noted on Cluster III and Cluster IV. The highest plant height was exhibited on Cluster I and Clusters IV while the minimum was noted on Cluster II and Cluster III. The mean values for the number of primary branches per plant were maximum on Cluster I, Cluster II and Cluster III while the minimum was noted on Cluster IV. The highest mean values of pod length were recorded in Cluster III and Cluster IV while the minimum was recorded on Cluster I and Cluster II. The highest mean values of pods per cluster and pods per plant were recorded in Cluster I and Cluster IV while the minimum was recorded on Cluster II and Cluster III. The maximum mean values for seeds per pod were recorded for Cluster I, Cluster II and Cluster III while the minimum was recorded on Cluster IV. The maximum seed yield per plant was recorded.
on Cluster IV while the minimum was recorded on Cluster I, Cluster II and Cluster III. The maximum mean values for a hundred seed weight and seed yield per hectare were recorded on Cluster I and Cluster IV while the minimum was recorded on Cluster II and Cluster III. The highest biomass yields were exhibited on Cluster III and Cluster IV while the minimum was noted on Cluster I and Cluster II.

Generally, Cluster IV showed the best performance for most of the traits in general and showed the highest mean performance for pod length, plant height, pods per cluster, pods per plant, hundred seed weight, seed yield per hectare, and harvest index. Therefore, cluster IV would be preferable for the selection of parents with high mean values and more effective for the improvements of genotypes. On the contrary, Cluster II and Cluster III had minimum values for yield and yield-related traits; this showed the poorest performance of traits.

In general, there was a highly significant variation in mean performance among clusters in most traits. Therefore, this is a good opportunity to select potential parents across the cluster for specific traits for future mung bean improvement. In general, the variation observed among 60 mung bean genotypes for the quantitative traits suggests that the presence of inherent genetic diversity among mung bean genotypes. Similar results have also been reported by various authors.

In this study, the levels of trait contribution for inter-cluster divergence studies for mung bean genotypes showed that CTIC (%) of ≥ 25% as a high contributor, ≥ 10% < 25% as a medium contributor, and < 10% as a little contributor for inter-cluster divergence. On the contrary, reported that the levels of trait contribution for inter-cluster divergence for cowpea ≥ 15% as a high contributor, ≥ 8% < 15% as a medium contributor, and < 8% as a little contributor for inter-cluster divergence in Ethiopia. In this study, as presented in Table 2, the CTIC (%) for seed yield per hectare (38.50%), seeds per pod (31.25%), pods per plant (30.15%), and harvest index (29.07%), indicating that these traits were the major contributors for a genetic divergence to the entire genotypes. The CTIC (%) for days to flowering (1.87%), days to maturity (1.19%), and terminal leaf width (7.9%), signifying that these traits were slight contributions to the genetic divergence. Generally, the variation observed among the 60 mung bean genotypes indicated that the studied agronomic traits might reveal diversity among mung bean genotypes. This finding is supported by the previous reports of on cowpea genotypes.

<table>
<thead>
<tr>
<th>Traits</th>
<th>Clusters</th>
<th>Mean</th>
<th>Std</th>
<th>CTIC (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Clusters CI</td>
<td>Clusters CII</td>
<td>Clusters CIII</td>
<td>Clusters CIV</td>
<td></td>
</tr>
<tr>
<td>DTF</td>
<td>40.44</td>
<td>42.00</td>
<td>42.00</td>
<td>42.00</td>
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<tr>
<td>DTM</td>
<td>89.83</td>
<td>92.00</td>
<td>92.00</td>
<td>92.00</td>
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<td>PTL</td>
<td>8.70</td>
<td>8.24</td>
<td>7.26</td>
<td>6.36</td>
</tr>
<tr>
<td>TLL</td>
<td>5.87</td>
<td>4.80</td>
<td>5.71</td>
<td>4.60</td>
</tr>
<tr>
<td>TLW</td>
<td>10.56</td>
<td>9.56</td>
<td>8.91</td>
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<td>PDCL</td>
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<td>32.11</td>
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<td>9.59</td>
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<td>PPC</td>
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</tr>
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</tbody>
</table>

DTF=days to flowering, DM=days to maturity, PTL=petiole length (cm), TLL=terminal leaf length (cm), TLW=terminal leaf width (cm), PDL=peduncle length (cm), PHT=plant height (cm), BRN=number of primary branches per plant, PODL=pod length (cm), PPC=number of pods per cluster, PPP=number of pods per plant, SPP=number of seeds per pod, SYPP=seed yield per plant (g), HSW=hundred seed weight (g), SYLD=seed yield (kg ha⁻¹), BM=biomass yield (kg ha⁻¹), HI=harvest index, CTIC=Contribution Inter Cluster Divergence.
Intra and Inter-Cluster Distance

The values for squared distances ($D^2$) indicated that there were significant differences observed between clusters I with Clusters III and IV ($P \leq 0.01$), while no significant variations were observed among Cluster I and Cluster II, Cluster II with Cluster III, Cluster II with Cluster IV, Cluster III with Cluster IV. The range of intra and inter-cluster distance was 3.53 to 6.49 units and 12.16 to 43.16 units, respectively (Table 3). The highest average inter-cluster $D^2$ was recorded between cluster I and Cluster IV ($D^2 = 43.16$ units) followed by Cluster I and Cluster III ($D^2 = 31.63$ units), suggesting the highest genetic divergence existing between the genotypes of these clusters and expected to give a higher frequency of better transgressive segregants or desirable combinations for development of useful genetic stocks or varieties. Therefore, these two clusters were more genetically divergent from each other. As per inter-cluster distance (from Cluster I, III, and IV), selection of parents for hybridization program among genotypes from diverse Clusters would achieve novel recombinants that increase efficiency for improvement of seed yield in mung bean. The nearest inter-cluster distance was found between clusters III and IV (12.16 units) followed by Clusters II and III (13.24 units). Those genotypes that showed non-significant variations among the clusters did not have a diverse gene pool and they have a narrow genetic base. Thus, crossing parents from these clusters might not give higher heterotic value in the future hybrid breeding program in the subsequent generations and will not get a wide range of variability in the segregating population.

The maximum intra-cluster distance ($D^2$) was recorded in Cluster II (6.49 units) followed by cluster III (5.70 units) and cluster IV (4.63 units), respectively. The present study indicates that the genotypes in clusters II and III were more divergent than any other clusters. Thus, the genotypes belonging to the distant clusters could be used for the mung bean breeding program to get a wider range of variability. Also, genotypes from these two distinct Clusters II and III could be utilized as a parent for a hybrid breeding program or recombinant breeding program owing to their wider within-group distance. While the lowest $D^2$ was recorded in Cluster IV (3.53 units), which showed the presence of less genetic variability or diversity within these clusters. In general, the intra-cluster distance was much less than the inter-cluster one. This result is in line with the reports of on cowpea genotypes. marked that such intra- and inter-cluster distances might arise due to the differential genetic makeup of the genotypes. The intra-cluster distance values indicate the closeness of the genotypes falling in the same cluster. The clusters exhibiting an intra-cluster distance of 0.00 reveal to be monogenotypic and consequently less heterogeneous; on the other hand, high intra-cluster $D^2$ values indicate a more genetic divergence between genotypes belonging to the same cluster and therefore more heterogeneous. According to success of the hybridization followed by selection depends largely on the choice of parents showing high genetic diversity for traits of interest. Therefore, such intra-cluster heterogeneity among the genotypes constituents’ obtained in the present experiment might serve as a guideline to choose parents for the recombination breeding program. It indicated that these cluster pairs were most divergent or in other words, the genotypic constituent of these cluster pairs comprised the genes from most distantly related parents in respect of the characters studied. The genotypes belonging to different clusters separated by high estimated statistical distance may be used in the hybridization program for crop improvement as well as for studying the inheritance pattern of different characters in mung bean. The above results further revealed that considering individual characters the genotypes were more divergent than those considering a constellation of characters.

Table 3: Average Intracluster (Bolded Diagonal) and Inter-Cluster (Off-Diagonal) Generalized Squared Distance ($D^2$) Values for Quantitative Traits

<table>
<thead>
<tr>
<th>Clusters</th>
<th>I</th>
<th>II</th>
<th>III</th>
<th>IV</th>
</tr>
</thead>
<tbody>
<tr>
<td>I</td>
<td>6.49</td>
<td>18.96ns</td>
<td>31.63**</td>
<td>43.16**</td>
</tr>
<tr>
<td>II</td>
<td>5.70</td>
<td>13.24ns</td>
<td>25.02*</td>
<td></td>
</tr>
<tr>
<td>III</td>
<td></td>
<td>3.53</td>
<td>12.16ns</td>
<td></td>
</tr>
<tr>
<td>IV</td>
<td></td>
<td></td>
<td>4.63</td>
<td></td>
</tr>
</tbody>
</table>

**,** indicates significant at 1% and 5% level of significant; $\chi^2_{15} = 25.00$ and 30.58 at 5% and 1%, probability level, respectively.

Conclusions

Morphological characterization of mung bean genotypes based on quantitative traits showed that the existence of polymorphism on mung bean genotypes. Plant height, the number of primary branches, the number of clusters per plant, the number of pods per cluster, and the number of pods per plant are the major yield contributing characters and hence during selection, attention should be given to these characters for the development of high yielding mung bean genotypes. Pod length was the most important trait that positively contributed to principal component analysis to detect phenotypic diversity. The first seven principal component analyses detected the major contributing traits accounted for 80.1% of total variations and are informative enough to discriminate against 60 mung bean genotypes. The total genotypes were clustered into four distinct groups and the highest inter-cluster $D^2$ was recorded between cluster I and cluster IV followed by cluster I and cluster III, indicating that the inter-cluster distances were more genetically divergent from each other. The range of intra and inter-cluster distances was 3.53 to 6.49 units and 12.16 to 43.16 units, respectively. Hence, the high genetic distance exhibited within and among clusters.
ters has to be exploited through the crossing and selection of the most divergent parents for future mung bean breeding programs.

Intra cluster distance was much lesser than inter-cluster distance showing the presence of high genetic divergence among the clusters. Seed yield per hectare, pods per plant, seeds per pod, and harvest index were the most discriminate traits for grouping the entire genotype into different clusters. In general, the present investigation indicated that high genetic distances exhibited within and among clusters are an opportunity to exploit through breeding via crossing and selection of the most divergent parents from the clusters.

Furthermore, the adoption of biochemical and molecular approaches might show enough genetic diversity among mung bean genotypes for further variety development.

References


dorum. Euphytica, 32: 575-584.
38. Raji, A. A. (2002). Assessment of genetic diversity and hetro-
uation and identification of genetic donors in blackgram (Vi-
bean accessions based on quantitative characters. In Baltika-
netic diversity of mungbean (Vigna radiata L. Wilczek) in Malaysian tropical environment. African Journal of Microbi-
ology Research, 6(8), 1770-1775.