Characterization and Evaluation of Mungbean [\textit{Vigna radiata} (L.) Wilczek] Germplasm through Morphological and Agronomic Characters

K.S. Win¹, S. Win¹, T.M. Htun², N.K.K. Win³

ABSTRACT

The study was conducted to assess the genetic diversity based on morphological and agronomic characters among 185 mungbean accessions by multivariate analysis such as cluster analysis and principal component analysis. The results exhibited that hierarchical cluster analysis divided into 7 clusters among the germplasm. The maximum number of accessions was observed in Cluster I with 60 accessions followed by Cluster II and Cluster III consists of 42 and 38 accessions, respectively. Cluster IV and VI comprised 18 accessions each whereas each of Cluster V and VII involved 5 accessions. Principal component analysis provided that the first three principal components accounted for 78.06% of the total variability of agronomic characters. Among the study of agronomic characters, days to 50% flowering, days to maturity, plant height at flowering, plant height at maturity, number of pod bearing branches per plant and 100 seed weight were contributed with the first principal component (PC1) whereas were the number of cluster per plant, pod per plant and yield per plant with PC2 and seed per pod and pod length with PC3, respectively. According to the findings of this research, the significant presence of genetic diversity was presented among the tested mungbean accessions and provides a good chance for the selection of parents for the improvement program.

Key words: Cluster analysis, Germplasm, Multivariate analysis, Mungbean, Principal component analysis.

INTRODUCTION

Mungbean is a warm-season crop and providing a good opportunity for diversifying cropping systems due to the ability of short growth duration which allows adaptation with many cropping systems and rotations of crops (Shanmugasundaram et al., 2010). Currently, the global annual growing and production is about 6 million hectares worldwide and global 3 million tonnes, respectively. India leads the production of mungbean worldwide followed by China and Myanmar (Nair et al., 2014).

The key factor of major constraints in mungbean improvement program is the lack of genetic diversity in the primary gene pool (Kumar et al., 2011 and Evgenidis et al., 2011). Genetic diversity provides a good opportunity for plant breeders to develop new and improved cultivars with desirable characteristics (Bhandari et al., 2017). Assessment of phenotypic diversity or characterization of morphological and agronomical characters is the important role for the selection of proper parents in the genetic improvement or plant breeding program (Abna et al., 2012; Basnet et al., 2014; NB et al., 2015).

Multivariate statistics are very useful techniques to estimated genetic diversity and provide the most reliable evidence regarding the actual genetic distances between the tested genotypes. Some of the multivariate techniques which are used to estimate the genetic diversity are metroglyph analysis, D² statistics, cluster analysis, principal component analysis, principal coordinate analysis, canonical analysis, factor analysis and correspondence analysis (Singh and Pawar, 2005). Among the techniques of multivariate, cluster analysis and principal component analysis are the most common techniques to estimate the variability of quantitative traits and identify the superior genotypes (Jeberson et al., 2017). Therefore, this research was conducted to assess the genetic diversity based on morphological and agronomic characters among the tested mungbean accessions, classify the similar group of accessions by cluster analysis and principal component analysis and select the superior genotypes for the utilization of parent varieties in the future breeding program.

MATERIALS AND METHODS

This research was conducted at Food Legumes Section,

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Department of Agricultural Research (DAR), Yezin, Myanmar (19°51’N latitude and 96°7’E longitude at 97 m altitude) in monsoon season (May-July) of 2018. A total of 196 germplasm accessions from 15 diverse locations were used for the study of genetic diversity based on morphological and agronomic characters between the tested mungbean accessions (Table 1). A randomized complete block design with three replications was used in this study. Seeds of each germplasm were sown in a single row of 3 m long with 12.5 cm intra-row and 50 cm inter-row spacing (30 plants/row). The fertilizers were applied in soil preparation at the rate of 62 kg per hectare of triple superphosphate, 62 kg per hectare of muriate of potash. The operation of thinning was followed 12 days after sowing and left one plant on a hill. All recommended agronomic practices were followed as usual.

The 25 morphological characters and 11 agronomic characters, which are presented in Table 2, were documented on five randomly selected plants from each genotype in each replication according to International Plant Genetic Resources Institute (IPGRI) descriptor (IPBGR 1980). Among 196 accessions, 11 accessions (4183, 4188, 4189, 4190, 4197, 4198, 7350, 7359, 7364, 7380 and 8961) were provided no information due to the effect of non-photoperiod sensitive. The recorded data were analyzed for descriptive statistics (minimum, maximum, mean, standard deviation and coefficient of variation) of agronomic traits and frequency distribution of morphological characters by using the methods of Steel and Torrie (1980). Hierarchical cluster analysis and principal component analysis were performed by Statistical Tool for Agricultural Research (STAR) program, Version 2.0.1 following the methods of Ward (1963) and Sneath and Sokal, (1973), respectively to estimate the genetic diversity of mungbean germplasm.

**RESULTS AND DISCUSSION**

The hierarchical clustering method performed by Ward’s minimum variance on Euclidian distance is presented with the distribution of 185 mungbean germplasm in different clusters and dendrogram in Table 3 and Fig 1. The accessions in this observation were clustered into 7 clusters based on 25 morphological and 11 agronomic characters. The maximum number of accessions was observed in Cluster I with 60 accessions followed by Cluster II and Cluster III consists of 42 and 38 accessions, respectively. Cluster IV and V comprised 18 accessions each whereas each of Cluster VI and VII involved 5 accessions. The finding of this research was very closely related with many investigations of Bhattacharya and Vijaylaxmi, 2005, Singh et al., 2009, Yimram et al., 2009, Gokulakrishnan et al., 2012, Pandiyan et al., 2012, Divyaramakrishnan and Savithramma., 2014, NB et al., 2015, Sarkar and Kundagrami, 2016, Jain et al., 2017 and Sen and De, 2017 who described that 10 clusters of 25 genotypes in mungbean, 11 cluster of 80 genotypes in mungbean, 6 clusters of 340 genotypes in mungbean, 6 clusters of 30 genotypes in mungbean, 8 clusters of 646 genotypes in Green gram, 8 clusters of 374 genotypes in mungbean, 13 clusters of 100 accessions in mungbean, 5 clusters of 23 genotypes in mungbean, 9 clusters of 24 genotypes in soybean and 6 cluster in 30 mungbean genotypes. This finding indicates the significant exiting of genetic diversity among the tested mungbean accessions and provides a good chance for the selection of parents for the improvement program.

The cluster mean and standard deviation of agronomic characters in different clusters have been presented in Table 4.

**Table 1:** Origin of 196 mungbean accessions.

| Origin       | No. of accession |
|--------------|------------------|
| Australia    | 7                |
| AVRDC        | 46               |
| China        | 4                |
| India        | 22               |
| Indonesia    | 4                |
| IRRI         | 5                |
| Korea        | 2                |
| Myanmar      | 55               |
| Pakistan     | 10               |
| Philippine   | 28               |
| SB, DAR      | 6                |
| Thailand     | 2                |
| USA          | 1                |
| Vietnam      | 1                |
| Unknown      | 3                |

**Table 2:** Morphological and Agronomic characters of mungbean germplasm.

| Morphological character | Agronomic character                 |
|------------------------|------------------------------------|
| Growth habit           | Days to 50% flowering              |
| Growth pattern         | Days to maturity                   |
| Hypocotyl color        | Plant height at flowering          |
| Primary leaf length    | Plant height at maturity           |
| Primary leaf width     | Cluster per plant                  |
| Terminal leaflet length| Pod bearing branches per plant     |
| Terminal leaflet width, leaf color | Pod per plant |
| Petiole color          | Seed per pod                       |
| Stem color, petiole length | Pod length                      |
| Raceme position        | 100 seed weight                    |
| Calyx color            | Yield per plant                    |
| Corolla color          | Immature pod color                 |
| Immature pod color     | Color of ventral structure of immature pod |
| Pod attachment         | Twining tendency                   |
| Length of peduncle     | Mature pod color                   |
| Mature pod color       | Pod cross-section                  |
| Constriction of pod between seeds | Seed shape                  |
| Seed shape             | Seed color                         |
| Seed color             | Lustre on seed surface             |

**Table 3:** Genetic diversity of mungbean germplasm through Morphological and...
Among the different clusters, cluster VI showed late-flowering accessions followed by cluster VII whereas the remaining 5 clusters revealed the early flowering accessions, respectively. Similarly, days to maturity showed the same trend as days to flowering among different clusters. The result showed that the plant height at flowering time and maturity had the highest range in the cluster VI and VII and the lowest range in the remaining 5 clusters (I, II, III, IV and V), respectively.

The highest number of cluster was observed in cluster II. The cluster VII, VI and II provided the highest number of pod bearing branches per plant. Cluster VII and II recorded with good information due to the presence of the maximum number of pod per plant. The highest range of pod length was classified in Cluster IV, V, I and III and whereas the lowest range of pod length was observed in cluster II, VI and VII, respectively. The average 100 seed weight with above 4.0 g was observed in cluster IV, V, I and III and the average 100 seed weight with 3.19 and below was found in clusters II, VI and VII. Among the different clusters, the maximum yield per plant existed in cluster II followed by cluster IV and the minimum yield per plant was recorded in cluster VI. This result was very closely related with the research of Yimram et al., 2009, Divyaramakrishnan and Savithramma, 2014, NB et al., 2015 and Jain et al., 2017 and indicated that mean performance of agronomic characters was very prominently diverse among different clusters. Therefore, the information of this result will be very useful with some interested characters for future plant breeding program and improvement of a new variety.

The results of descriptive statistics for 11 agronomic characters such as minimum, maximum, standard deviation and coefficient of variation were shown in Table 5. The highest coefficient variation was observed in pod per plant (33.29%) followed by pod bearing branches per plant (31.50%), yield per plant (28.57%), 100 seed weight (25.79) and plant height at flowering (25.49%). Moderate coefficient variation was found in plant height at maturity (18.85%), number of cluster per plant (14.40%), days to 50% flowering (13.42%) and pod length (12.73%). Days to maturity and seed per pod which are represented as low variability among tested mungbean germplasm with the coefficient of variation of 9.52% and 6.25%. Many research findings were most similar with this finding by Yimram et al., 2009, Abna et al., 2012, Sarkar 2014, Singh et al., 2014, Shyamalee et al., 2016, Hapsari et al., 2018, etc. This research showed significant diversity among the tested germplasm especially for yield and its related characters such as pod per plant, pod bearing branches and number of cluster per plant.

Comparison of eigenvectors and eigenvalues for the first three principal components among 185 mungbean accessions was presented in Table 6 and scree plot constructed for 11 agronomic characters of 11 principal components was shown in Fig 2. The values of principal component which are larger than unity (>1) were found in the first three principal components (PC1, PC2 and PC3) with the eigenvalue of 5.16, 2.31 and 1.12, respectively. The analysis based on standardized data revealed that the first three principal components accounted for 78.06 % of the total variability of agronomic characters. Among the first important three principal components, high proportion of total variance (46.91%) was recorded in PC1 and other two principal components PC2 and PC3 were observed with 20.98% and 10.26% of the total variance, respectively (Table 6 and Fig 2).

Among the study of agronomic characters, days to 50% flowering, days to maturity, plant height at flowering, plant height at maturity, number of pod bearing branches...
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Table 4: Mean and standard deviation of agronomic characters in different clusters.

| Character                        | Cluster I         | Cluster II        | Cluster III        | Cluster IV         | Cluster V         | Cluster VI        | Cluster VII        |
|---------------------------------|-------------------|-------------------|--------------------|--------------------|-------------------|-------------------|--------------------|
| Days to 50% flowering (days)    | 45.7±3.44         | 46.57±3.72        | 43.99±5.44         | 44.88±2.35         | 46.56±2.22        | 63.13±6.82        | 50.08±6.21         |
| Days to maturity (days)         | 69.04±2.62        | 70.27±3.72        | 67.54±3.50         | 67.98±1.67         | 67.78±1.24        | 90±7.28           | 76.08±11.50        |
| Plant height at flowering (cm)  | 31.38±4.4         | 32.84±7.81        | 30.98±5.01         | 31.35±3.81         | 32.66±5.44        | 53.46±10.67       | 44.19±13.95        |
| Plant height at maturity (cm)   | 62.76±9.59        | 67.98±9.74        | 61.15±9.89         | 60.69±5.30         | 62.42±8.39        | 87.03±13.85       | 77.79±16.90        |
| Cluster per plant (no.)         | 5.41±0.66         | 5.71±0.81         | 5.37±0.65          | 5.03±0.39          | 5.56±0.35         | 5.26±0.74         | 6.70±0.70          |
| Pod bearing branches per plant (no.) | 1.55±0.48       | 2.06±0.65         | 1.49±0.47          | 1.42±0.54          | 1.68±0.48         | 2.44±0.65         | 2.48±0.64          |
| Pod per plant (no.)             | 14.92±3.19        | 22.03±5.97        | 14.96±3.60         | 14.76±3.56         | 14.97±2.31        | 13.25±7.22        | 24.47±10.50        |
| Seed per pod (no.)              | 11.85±0.59        | 11.24±0.71        | 11.94±0.67         | 12.09±0.54         | 11.74±0.45        | 10.73±0.69        | 10.80±0.69         |
| Pod length (cm)                 | 9.32±0.75         | 7.69±0.65         | 9.29±0.76          | 9.92±0.61          | 9.36±0.35         | 7.41±0.73         | 7.00±0.80          |
| 100 seed weight (g)             | 4.71±0.73         | 3.19±0.74         | 4.4±0.72           | 4.97±0.71          | 4.72±0.84         | 2.72±0.35         | 2.19±0.34          |
| Yield per plant (g)             | 6.58±1.34         | 6.97±1.95         | 6.25±1.58          | 6.63±1.33          | 6.59±1.75         | 3.47±1.79         | 5.84±2.86          |

Fig 1: Ward’s minimum variance dendrogram of 185 mung bean accessions based on Euclidean distance.
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Table 5: Descriptive statistics for agronomic characters among 185 accessions of mungbean germplasm.

| Character                          | Minimum | Maximum | Mean  | SD    | CV %  |
|-----------------------------------|---------|---------|-------|-------|-------|
| Days to 50% flowering (days)      | 31.00   | 74.67   | 46.79 | 6.28  | 13.42 |
| Days to maturity (days)           | 59.67   | 98.00   | 70.48 | 6.71  | 9.52  |
| Plant height at flowering (cm)    | 21.03   | 68.66   | 33.46 | 8.53  | 25.49 |
| Plant height at maturity (cm)     | 42.47   | 109.73  | 65.47 | 11.88 | 18.15 |
| Cluster per plant (no.)           | 4.00    | 9.00    | 5.00  | 0.72  | 14.40 |
| Pod bearing branches per plant (no.) | 1.00    | 4.00    | 2.00  | 0.63  | 31.50 |
| Pod per plant (no.)               | 4.00    | 34.00   | 17.00 | 5.66  | 33.29 |
| Seed per pod (no.)                | 10.00   | 14.00   | 12.00 | 0.75  | 6.25  |
| Pod length (cm)                   | 5.91    | 10.88   | 8.80  | 1.12  | 12.73 |
| 100 seed weight (g)               | 1.80    | 6.31    | 4.11  | 1.06  | 25.79 |
| Yield per plant (g)               | 1.11    | 11.62   | 6.37  | 1.82  | 28.57 |

Fig 2: Scree plot constructed for 11 agronomic characters.

per plant and 100 seed weight were more related with the first principal component (PC1) with the eigenvector of 0.34, 0.37, 0.34, 0.37, 0.33, and 0.36. The characters which contributed more relatively with PC2 were the number of cluster per plant, pod per plant and yield per plant (0.35, 0.60, and 0.48). The third principal component (PC3) was generally associated with seed per pod and pod length with the eigenvector of 0.51 and 0.37, respectively. The coefficient of the appropriate vectors was considered by the criterion of Raji, 2002 who described that the criterion vector was greater than 0.3 which provides large effect to be considered important while the characters which have a lesser value than 0.3 were considered as non-important effects on overall variation. Principal component analysis is beneficial for the breeders to conduct specific breeding programs according to good information about the groups where certain traits are more important. The results of this study are more related with the characterization of germplasm by Yimram et al., 2009, Abna et al., 2012, Divyaramakrishnan and Savithramma, 2014, Singh et al., 2014, Sarkar and Kundagrami, 2016 and Hapsari et al., 2018 who described that five, three, four, three, five and five principal components with 68.9%, 84.04%, 79.00%, 63.87%, 73.22%, and 76.00% of total variance in mungbean.

Table 6: Comparison of eigenvectors and eigenvalues for the first three principal components among 185 mungbean accessions.

| Character                         | PC1     | PC2     | PC3     |
|-----------------------------------|---------|---------|---------|
| Days to 50% flowering (days)      | 0.34    | -0.29   | 0.15    |
| Days to maturity (days)           | 0.37    | -0.24   | 0.10    |
| Plant height at flowering (cm)    | 0.34    | -0.20   | 0.32    |
| Plant height at maturity (cm)     | 0.37    | 0.00    | 0.36    |
| Cluster per plant (no.)           | 0.16    | 0.35    | 0.21    |
| Pod bearing branches per plant (no.) | 0.33    | 0.12    | 0.23    |
| Pod per plant (no.)               | 0.09    | 0.60    | 0.03    |
| Seed per pod (no.)                | 0.29    | -0.06   | 0.51    |
| Pod length (cm)                   | 0.35    | -0.22   | 0.37    |
| 100 seed weight (g)               | 0.36    | -0.22   | 0.28    |
| Yield per plant (g)               | 0.15    | 0.48    | 0.40    |
| Eigen value                       | 5.16    | 2.31    | 1.12    |
| Variability (%)                   | 46.91   | 20.98   | 10.16   |
| Cumulative %                      | 46.91   | 67.89   | 78.06   |

**CONCLUSION**

Among the tested germplasm, existed genetic diversity was present with 7 clusters according to the result finding by hierarchical cluster analysis. Information from this research by descriptive statistics pointed that yield and its related
Characters such as pod per plant, pod bearing branches and number of cluster per plant represented as the important characters for classification of significant diversity among the tested germplasm. Moreover, principal component analysis provided good information for the estimation of genetic diversity with the more important agronomic characters. According to the findings of this research, the significant presence of genetic diversity was presented among the tested mungbean accessions and provides a good chance for the selection of parents for the improvement program. Therefore, the information of this result will be very useful with some interested characters for future plant breeding program and improvement of a new variety.

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