

Research Article



Genetic Analysis of Yield and Yield Components for the Improvement of Mungbean Germplasm

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Abstract | Mungbean is an important pulse crop and gaining popularity in the farming community of Pakistan. Improvement of mungbean germplasm for high seed yield requires information on genetic variability and correlation of traits. For this purpose, fifty eight exotic and indigenous diverse mungbean genotypes were evaluated for seed yield and other related traits. The genetic analysis of mungbean germplasm revealed high genotypic (GCV) and phenotypic (PCV) coefficients of variability for biological yield (GCV% = 31.70, PCV% = 33.58), harvest index (GCV% = 27.80, PCV% = 30.16) and seed yield (GCV% = 25.28, PCV% = 27.54). While heritability estimates were high for all the traits except days to maturity and clusters per plant. Biological yield, harvest index and seed yield depicted high estimates of heritability (0.89, 0.85 and 0.84, respectively) coupled with greater genetic advance (61.57, 52.81 and 47.82, respectively) indicating the involvement of additive type of genes, and selection based on these traits may help to improve the germplasm. Seed yield showed positive and significant genotypic and phenotypic correlations with clusters per plant ($r_g = 0.322$), pods per plant ($r_g = 0.276$), biological yield ($r_g = 0.470$) and harvest index ($r_g = 0.264$). These traits also showed high positive direct effects on seed yield. Hence, indirect selection for these traits may facilitate for developing high yielding genotypes. The diversity analysis categorized fifty-eight genotypes into four clusters. Clustering pattern did not show any relation to the geographic origin. Cluster-I with three genotypes (Thailand: 2; Sri Lanka: 1) and Cluster-II with seventeen genotypes (Thailand: 12, Pakistan: 3, India: 2) showed the highest values for yield and yield contributing traits. Three distant genotypes were identified; a genotype, VC3012B was found high yielding, NIMB-101 had high biological yield and number of clusters per plant and VC 3404 had high 100-seed weight. These genotypes may be used for the incorporation of genes for high seed yield, biological yield, clusters per plant and seed weight into well adapted germplasm.

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Keywords | Mungbean, Germplasm, Heritability, Correlation, Path coefficients, Genetic diversity

Introduction

Mungbean (*Vigna radiata* L. Wilczek) occupies an important position among pulses due to its ability to restore soil fertility through biological nitrogen fixation (Makeen et al., 2007) and high protein

concentration (Malik, 1994). Its protein source is preferred due to its easy digestibility and less expensive as compared to animal proteins. In Pakistan, mungbean area increased from 146.3 thousand hectares to 178.8 thousand hectares while production increased from 102.1 to 130.1 thousand tones (Anonymous,

2016-17). But this trend may differ from year to year and decline in mungbean crop may occur due to different diseases (Akhtar et al., 2009; 2010; 2011; 2012) and uncertain global geographical changes.

The only solution to this problem is to evolve high yielding, good quality and disease resistant varieties which depend upon the selection of suitable genotypes to be utilized in breeding programme. There is also a need to search new genes and improved genetic recombinants not already found either in the cultivated varieties or their relatives. The success of a plant breeding programme primarily depends upon the magnitude of genetic variability present in the breeding material. A successful selection also depends upon the information on association of traits amenable to visual selection. The understanding of such associations among various developmental and reproductive traits is necessary for framing an effective breeding program. And contribution of genetic factors in the development of a trait is revealed by its heritability. The study of genetic diversity among genotypes is also necessary in this context (Asghar et al., 2010; Abbas et al., 2010). Path co-efficient analysis separates the direct effects from indirect effects by partitioning correlation co-efficients (Dewey and Lu, 1959). Abbas et al. (2005) and Sadiq et al. (2005) reported positive correlation of seed yield with its components.

Keeping this in view, local as well as exotic genotypes were studied with the objectives, to generate information on genetic variability, correlation and to select diverse genotypes for breeding programme for producing good recombinants.

Materials and Methods

Fifty eight genotypes of mungbean originating from Pakistan, Thailand, India, Bangladesh and Sri Lanka were studied in this experiment. The detail of genotypes and their origin are given in Table 1. The experiment was laid out at NIAB, Faisalabad during the summer season of 2015 in a Randomized Complete Block Design (RCBD) with three replications having plot size of 4.8 m² by keeping row to row distance of 30 cm and plant to plant distance of 10 cm. Four plant rows were sown per entry. Normal agronomic practices were followed. At maturity five randomly selected guarded plants from each genotype in each replication were used to collect the data on different traits. Biological yield was recorded after sun dry-

ing the harvested material for seven days (constant weight).

Table 1: *Mungbean genotypes included in present study and their origin.*

| S. No. | Genotypes | Origin | S. No. | Genotypes | Origin |
|--------|---------------|----------|--------|---------------|------------|
| 1 | NM 92 | Pakistan | 30 | VC 3404 | Thailand |
| 2 | NM 2006 | Pakistan | 31 | VC 1968 | Thailand |
| 3 | NM 98 | Pakistan | 32 | VC 1628C | Thailand |
| 4 | NM 51 | Pakistan | 33 | VC 1682C | Thailand |
| 5 | NM 54 | Pakistan | 34 | VC 1502A | Thailand |
| 6 | NM 121-25 | Pakistan | 35 | VC 1945A | Thailand |
| 7 | NM 20-21 | Pakistan | 36 | VC 2709 | Thailand |
| 8 | NM 19-19 | Pakistan | 37 | VC 1000C | Thailand |
| 9 | NM 13-1 | Pakistan | 38 | VC 2755A | Thailand |
| 10 | NM 28 | Pakistan | 39 | VC 1381 | Thailand |
| 11 | VAR.6601 | Pakistan | 40 | VC 2778B | Thailand |
| 12 | NM 42-11-4 -1 | Pakistan | 41 | VC 1168B | Thailand |
| 13 | NM 43-41-3 | Pakistan | 42 | VC 1973A | Thailand |
| 14 | NM 42-39-4 -1 | Pakistan | 43 | VC 686 | Thailand |
| 15 | VC 1560D | Thailand | 44 | VC 1177B | Thailand |
| 16 | VC 2010 | Thailand | 45 | VC 2764A | Thailand |
| 17 | VC 6017 | Thailand | 46 | VC 2778A | Thailand |
| 18 | VC 5197A | Thailand | 47 | VC 3300A | Thailand |
| 19 | VC 1647B | Thailand | 48 | SML-32 | India |
| 20 | VC 3178A | Thailand | 49 | Pusa 9171 | India |
| 21 | VC 4420 | Thailand | 50 | Pusa 105 | India |
| 22 | VC 3528A | Thailand | 51 | Pusa 101 | India |
| 23 | VC 3012A | Thailand | 52 | L-24-2 | India |
| 24 | VC 2272 | Thailand | 53 | ML-5 | India |
| 25 | VC 3484 | Thailand | 54 | Shanuha Sp-92 | India |
| 26 | VC 3004A | Thailand | 55 | Shanuha Sp-93 | India |
| 27 | VC 3012B | Thailand | 56 | Bari Mung-2 | Bangladesh |
| 28 | VC 4403 | Thailand | 57 | Bari Mung-4 | Bangladesh |
| 29 | VC 2764B | Thailand | 58 | NIMB-101 | Sri Lanka |

NM: *NIAB Mung*; **VC:** *AVRDC (Asian Vegetable Research and Development Corporation).*

The mean data were subjected to the analysis of variance as described by Steel et al. (1997). Heritability was calculated by following Cochran and Cox (1957) and genetic advance was estimated according to Allard (1960). Correlation coefficient analysis was performed as described by Singh and Chaudhary (1999) for the estimation of genotypic and phenotypic variances, genotypic and phenotypic coefficient of variability, heritability and genetic advance. Path analysis was performed by using the method reported

by Dewey and Lu (1959) for seed yield and its components by keeping seed yield as resultant variable and other traits as causal variables. Cluster analysis was performed by using the STATISTICA software. Classificatory techniques were used to quantify the genetic divergence of mungbean genotypes as outlined by Bish et al. (1998) and Sharma et al. (1996).

Results and Discussion

Genetic parameters

Highly significant differences were observed among the genotypes for all the traits under study (Table 2). Mean values depicted that genotypes were generally medium seeded and had good harvest index. Genetic parameters i.e. genetic variance (V_G), phenotypic variance (V_P), genotypic and phenotypic coefficients of variation (GCV% and PCV%, respectively), heritability and genetic advance are presented in Table 3. In general, phenotypic coefficients of variability had higher values as compared to their corresponding genotypic coefficients for all traits under study which revealed the role of environment on the expression of traits. Higher PCV values for different traits have been reported by several workers (Siddique et al., 2006; Makeen et al., 2007; Sadiq et al., 2005). Higher magnitudes of heritability were observed for 100-seed weight (0.97), plant height (0.94), biological yield (0.89), pods per plant (0.83), harvest index (0.85) and seed yield (0.84) that coincided with the findings reported earlier (Rohman and Hussain, 2003; Siddique et al., 2006; Idrees et al., 2006). Heritability estimates coupled with genetic advance are more appropriate in predicting the gain under selection than heritability estimates alone (Johnson et al., 1955). In this study, it was observed that traits like biological yield, harvest index and seed yield were mainly controlled by additive types of genes because these traits showed high heritability coupled with high genetic advance. Other traits except days to maturity showed high heritability but low genetic advance, therefore, controlled by non-additive genes. Days to maturity reveals low heritability and genetic advance and indicates that the character is highly influenced by environmental effects. Therefore there seems to be a limited scope for the improvement of such traits controlled by non-additive genes and those influenced by environmental effects by direct selection. Panse (1957) and Siddique et al. (2006) have mentioned the importance of additive type of genes and demonstrated that genetic advance accompanied with high values of heritability

was more advantageous as compared to heritability alone in formulating the selection criterion.

Table 2: Range, mean and mean square of different traits.

| Characters | Range | Mean | Mean Square |
|---------------------------|------------|--------|-------------|
| Days to maturity | 52-89 | 75.00 | 95.73** |
| Plant height (cm) | 35-69 | 48.59 | 116.36** |
| Clusters/Plant | 6-12 | 9.00 | 6.69** |
| Pods/Plant | 15-49 | 25.00 | 78.85** |
| 100-seed weight (g) | 3.33-6.79 | 4.99 | 2.55** |
| Biological yield (g/plot) | 400-1900 | 975.57 | 298652.90** |
| Harvest Index | 6.33-51.67 | 23.91 | 140.39** |
| Seed yield (g/plot) | 117-327 | 219.54 | 9816.90** |

Correlation coefficients

Genotypic and phenotypic correlations among different traits are presented in Table 4. The results indicated that the magnitudes of genotypic correlation were higher as compared to their corresponding phenotypic correlation for most of the traits indicating the preponderance of genetic variance in the expression of characters (Nazir et al., 2005; Biradar et al., 2007). Biological yield had highly significant and positive correlation with seed yield at the both genotypic and phenotypic levels. Similarly, harvest index, clusters per plant and pods per plant showed positive and significant genotypic correlation with seed yield. Positive and significant correlations of clusters per plant, harvest index and pods per plant with seed yield have been reported (Venkatrishana et al., 2002; Haritha et al., 2002; Rajan et al., 2002; Abbas et al., 2005) which implied that selection of genotypes having higher biological yield or harvest index coupled with more clusters and pods per plant might improve yield considerably.

Days to maturity showed positive correlations with plant height, biological yield and harvest index at both genotypic and phenotypic levels. Hence it can be concluded that the late maturing tall plants may bear more clusters and produce higher biomass and grain yield. The positive genotypic and phenotypic correlation of plant height with other traits showed that selection of tall plants may favor to boost the yield of mungbean subject to the balance maintaining among biomass, harvest index and grain yield. Present findings are in conformity with Sarwar et al. (2002). However, plant height had negative and significant genetic and phenotypic correlation with harvest index which

Table 3: Genetic parameters of different morphological and economic traits of mungbean.

| Character | Genetic variance (V_g) | Phenotypic variance (V_p) | Genetic coefficient of variation (GCV%) | Phenotypic coefficient of variation (PCV%) | Heritability (h^2) | Genetic Advancement (% of mean) |
|---------------------------|----------------------------|-------------------------------|---|--|------------------------|---------------------------------|
| Days to maturity | 22.37 | 55.99 | 6.30 | 9.52 | 0.44 | 8.60 |
| Plant height (cm) | 38.01 | 40.33 | 12.69 | 13.07 | 0.94 | 25.37 |
| Clusters/Plant | 1.92 | 2.85 | 14.75 | 17.98 | 0.67 | 24.92 |
| Pods/Plant | 24.61 | 29.63 | 19.74 | 21.66 | 0.83 | 37.07 |
| 100-seed weight (g) | 0.84 | 0.87 | 18.35 | 18.67 | 0.97 | 37.18 |
| Biological yield (g/plot) | 95652.53 | 107347.80 | 31.70 | 33.58 | 0.89 | 61.57 |
| Harvest Index | 44.19 | 52.00 | 27.80 | 30.16 | 0.85 | 52.81 |
| Seed yield (g/plot) | 3080.99 | 3654.91 | 25.28 | 27.54 | 0.84 | 47.82 |

Table 4: Genetic (top figures) and phenotypic (bottom figures) correlation coefficients among mungbean genotypes.

| Characters | | Days to mature | Plant height | Clusters /plant | Pods /plant | 100-Seed weight | Biological yield | Harvest Index |
|--------------------------|-------|----------------------|----------------------|----------------------|----------------------|-----------------|----------------------|---------------------|
| Plant height(cm) | r_g | 0.583 ⁺ | | | | | | |
| | r_p | 0.367 ^{**} | | | | | | |
| Clusters /plant | r_g | 0.374 | 0.419 ⁺ | | | | | |
| | r_p | 0.287 ^{**} | 0.353 ^{**} | | | | | |
| Pods /plant | r_g | 0.009 | 0.228 ⁺ | 0.422 ⁺ | | | | |
| | r_p | 0.001 | 0.207 ^{**} | 0.408 ^{**} | | | | |
| 100-seed weight (g) | r_g | 0.040 | -0.153 ⁺ | -0.126 | -0.538 ⁺ | | | |
| | r_p | 0.034 | -0.150 ⁺ | -0.114 ⁺ | -0.483 ^{**} | | | |
| Biological yield(g/plot) | r_g | 0.503 ⁺ | 0.503 ⁺ | 0.295 ⁺ | 0.030 | 0.078 | | |
| | r_p | 0.285 ^{**} | 0.465 ^{**} | 0.222 ^{**} | 0.031 | 0.070 | | |
| Harvest Index | r_g | -0.567 ⁺ | -0.608 ⁺ | -0.208 ⁺ | 0.140 | -0.008 | 0.001 | |
| | r_p | -0.327 ^{**} | -0.550 ^{**} | -0.163 ^{**} | 0.125 ⁺ | -0.081 | -0.600 ^{**} | |
| Seed yield (g/plot) | r_g | -0.012 | -0.108 | 0.322 ⁺ | 0.276 ⁺ | -0.002 | 0.470 ⁺ | 0.264 ⁺ |
| | r_p | -0.038 | -0.096 | 0.221 ^{**} | 0.253 ^{**} | -0.007 | 0.475 ^{**} | 0.273 ^{**} |

r_g : Genetic correlation; r_p : Phenotypic correlation; +: Genetic correlation coefficient differs significantly from zero as its absolute magnitude exceeded twice its standard error; *, **: Significant at 0.05 and 0.01 probability levels, respectively.

indicates that tall plants are generally low yielding. Clusters per plant had positive and highly significant genotypic and phenotypic correlations with pods per plant, biological yield, harvest index and seed yield. Thus plants having more clusters would bear more pods and increase yield. Similar results were found by Sarwar et al. (2002) and Sadiq et al. (2004). Pods per plant showed positive and significant genotypic and phenotypic correlations with 100-seed weight and seed yield. This would mean that selection of genotypes having more pods may improve seed size and seed yield. These results are in agreement with those of Abbas et al. (2005).

Path coefficients

The estimates of direct and indirect effects of different traits are given in Table 5. Positive direct effects of clusters per plant, pods per plant, 100-seed weight, biological yield and harvest index on seed yield were

observed. Clusters per plant, pods per plant, biological yield and harvest index also had positive genotypic correlation with seed yield. Some of the workers have reported positive direct effects of cluster per plant on seed yield (Rohman and Hussain, 2003; Celal, 2004; Makeen et al., 2007; Rao et al., 2006; Nazir et al., 2005; Hakim, 2008) and positive direct effect of pods per plant (Abbas et al., 2005). Days to maturity affected positively and indirectly through clusters per plant, pods per plant, 100-seed weight and biological yield. Likewise, positive indirect effect of plant height on seed yield had been observed through clusters per plant, pods per plant and biological yield. Clusters per plant affected positively and indirectly via pods per plant and biological yield. Positive indirect effects of pods per plant through clusters per plant, biological yield and harvest index were also observed. Hundred seed weight affected positively and indirectly via plant height and biological yield. Positive indirect

Table 5: Direct and indirect effects of different traits on seed yield of mungbean genotypes.

| Characters | Days to maturity | Plant height | Clusters /plant | Pods /plant | 100-Seed weight(g) | Biological yield (g) | Harvest Index (%) | Seed Yield (g) |
|---------------------------|------------------|--------------|-----------------|-------------|--------------------|----------------------|-------------------|----------------|
| Days to maturity | -0.039 | -0.153 | 0.009 | 0.001 | 0.0016 | 0.509 | -0.430 | -0.012 |
| Plant height (cm) | -0.023 | -0.263 | 0.111 | 0.025 | -0.006 | 0.509 | -0.461 | -0.108 |
| Clusters /plant | -0.015 | -0.110 | 0.265 | 0.047 | -0.005 | 0.298 | -0.158 | 0.322 |
| Pods /plant | -0.001 | -0.060 | 0.119 | 0.111 | -0.218 | 0.031 | 0.106 | 0.276 |
| 100-seed weight (g) | -0.002 | 0.040 | -0.033 | -0.060 | 0.040 | 0.007 | -0.067 | -0.002 |
| Biological yield (g/plot) | -0.020 | -0.132 | 0.078 | 0.003 | 0.003 | 1.012 | -0.474 | 0.470 |
| Harvest Index | 0.022 | 0.160 | -0.055 | 0.015 | -0.004 | -0.634 | 0.758 | 0.264 |

Table 6: Mean and standard deviation of four clusters of fifty eight mungbean genotypes for eight characters.

| Traits | Cluster I | | Cluster II | | Cluster III | | Cluster IV | |
|----------------------------------|-----------|--------|------------|---------|-------------|--------|------------|--------|
| | Mean | STDEV | Mean | STDEV | Mean | STDEV | Mean | STDEV |
| Days to maturity | 76.00 | ±0.00 | 77.12 | ±4.87 | 75.78 | ±3.92 | 73.07 | ±5.39 |
| Plant height (cm) | 49.00 | ±3.61 | 50.94 | ±6.20 | 49.35 | ±6.45 | 44.60 | ±4.79 |
| Clusters per plant | 10.33 | ±1.53 | 9.82 | ±1.51 | 9.35 | ±1.56 | 8.67 | ±1.63 |
| Pods per plant | 23.33 | ±2.08 | 26.06 | ±7.48 | 25.13 | ±4.21 | 24.40 | ±3.42 |
| 100 seed weight (g) | 5.40 | ±0.43 | 5.17 | ±0.91 | 4.87 | ±1.02 | 4.91 | ±0.88 |
| Biological yield (g/plot) | 1655.33 | ±38.68 | 1212.12 | ±129.25 | 919.57 | ±93.25 | 617.93 | ±91.74 |
| Seed yield (g/plot) | 283.00 | ±78.10 | 261.35 | ±59.39 | 214.70 | ±45.63 | 172.73 | ±37.24 |
| Harvest index (%) | 17.27 | ±4.68 | 21.28 | ±5.36 | 23.59 | ±5.02 | 28.03 | ±7.94 |
| No. of genotypes in each cluster | | 3 | | 17 | | 23 | | 15 |
| Origin | Thailand | 2 | Thailand | 12 | Thailand | 13 | Thailand | 6 |
| | Sri Lanka | 1 | Pakistan | 3 | Pakistan | 5 | Pakistan | 6 |
| | | | India | 2 | India | 3 | India | 3 |
| | | | | | Bangladesh | 2 | | |

effects of biological yield on seed yield were observed through clusters per plant, pods per plant and 100-seed weight. Harvest index affected positively and indirectly through days to maturity, plant height and pods per plant.

Negative direct effects of days to maturity and plant height were observed on seed yield. Days to maturity showed negative indirect effects on seed yield through harvest index. Negative indirect effects of plant height on seed yield were observed through days to maturity, 100-seed weight and harvest index. Clusters per plant affected indirectly and negatively through days to maturity, plant height, 100-seed weight and harvest index. Pods per plant had negative indirect effects on seed yield via days to maturity, plant height and 100-seed weight. Negative indirect effects observed on seed yield were also of 100-seed weight through the traits like days to maturity, clusters per plant and harvest index. Biological yield affected seed yield indirectly and negatively through the traits like days to

maturity, plant height and harvest index. Harvest index affected negatively and indirectly through clusters per plant, 100-seed weight and biological yield. Days to maturity and plant height had negative genotypic correlation with seed yield. Positive direct effects of pods per plant pods per cluster, pod length, 100 seed weight and harvest index confirmed the findings of [Rohman and Hussain \(2003\)](#).

The traits clusters per plant, pods per plant, biological yield and harvest index showing positive direct effects along with positive genotypic correlations with seed yield indicated strong associations. Therefore, direct selection for these traits may prove effective for the improvement of seed yield in the germplasm under study. If the correlation is positive but the direct effect is negative or negligible, the trait may be selected on the basis of high indirect effect.

Genetic diversity

Parameters of cluster analysis are given in [Table 6](#).

Analysis of genetic divergence through clustering is presented in Figure 1. Cluster diagram based on Euclidean dissimilarity using complete linkage method categorized the germplasm into four clusters. Cluster-I consisted of only three exotic genotypes (Thailand: 2 and Sri Lanka: 1), cluster-II had seventeen local and exotic genotypes (Thailand: 12, Pakistan: 3 and India: 2), cluster-III had twenty three local and exotic genotypes (Thailand: 13, Pakistan: 5, India: 3 and Bangladesh: 2) and cluster-IV with fifteen local and exotic genotypes (Thailand: 6, Pakistan: 6 and India: 3). The four clusters were analyzed for mean and Standard Deviation (Table 6). Distribution pattern of the genotypes into various clusters showed the presence of considerable genetic divergence in the germplasm for most of the traits under study. Maximum and minimum genetic distances were observed within cluster-II and cluster-IV. The presence of only three genotypes (2 of Thailand and 1 of Sri Lanka) in cluster-I revealed that these genotypes had not been used in Pakistan. The remaining clusters had genotypes belonging to Pakistan, India, Thailand and Bangladesh. The grouping of genotypes of Pakistan, Thailand and India indicated the gene flow from India and Thailand to the Pakistani genotypes, because most of the Pakistani varieties/lines have been developed by using AVRDC germplasm. There is partial relationship between the geographic origin and their divergence on the basis of all the morphological and economic traits

studied. Genetic divergence among the genotypes had been reported by Sharma et al. (1996) and Sadiq et al. (2004). The genotypes in cluster-I had higher number of cluster per plant (10.33), 100-seed weight (5.40 g), biological yield (1655.33 g/plot) and seed yield (283.00 g/plot) as compared to other clusters. Three genotype, VC3012B: high yielding, NIMB-101: high biomass and clusters and VC 3404: high seed weight, were observed for their utilization in the conventional breeding process by introgression the desired genes for biomass, seed weight and grain yield.

Conclusion

The traits biological yield, harvest index and seed yield were mainly controlled by additive types of genes and may be used as selection criteria for the improvement of mungbean. Direct selection for traits like number of clusters per plant, pods per plant, biological yield and harvest index is effective for the improvement of seed yield in mungbean. Indirect selection through clusters, pods, biological yield and harvest index may improve mungbean yield to evolve high yielding mungbean varieties. The studies showed that three genotypes viz; VC3012B, NIMB-101 and VC 3404 may be used for the incorporation of genes for high seed yield, biological yield, clusters per plant and 100-seed weight into well adapted germplasm.

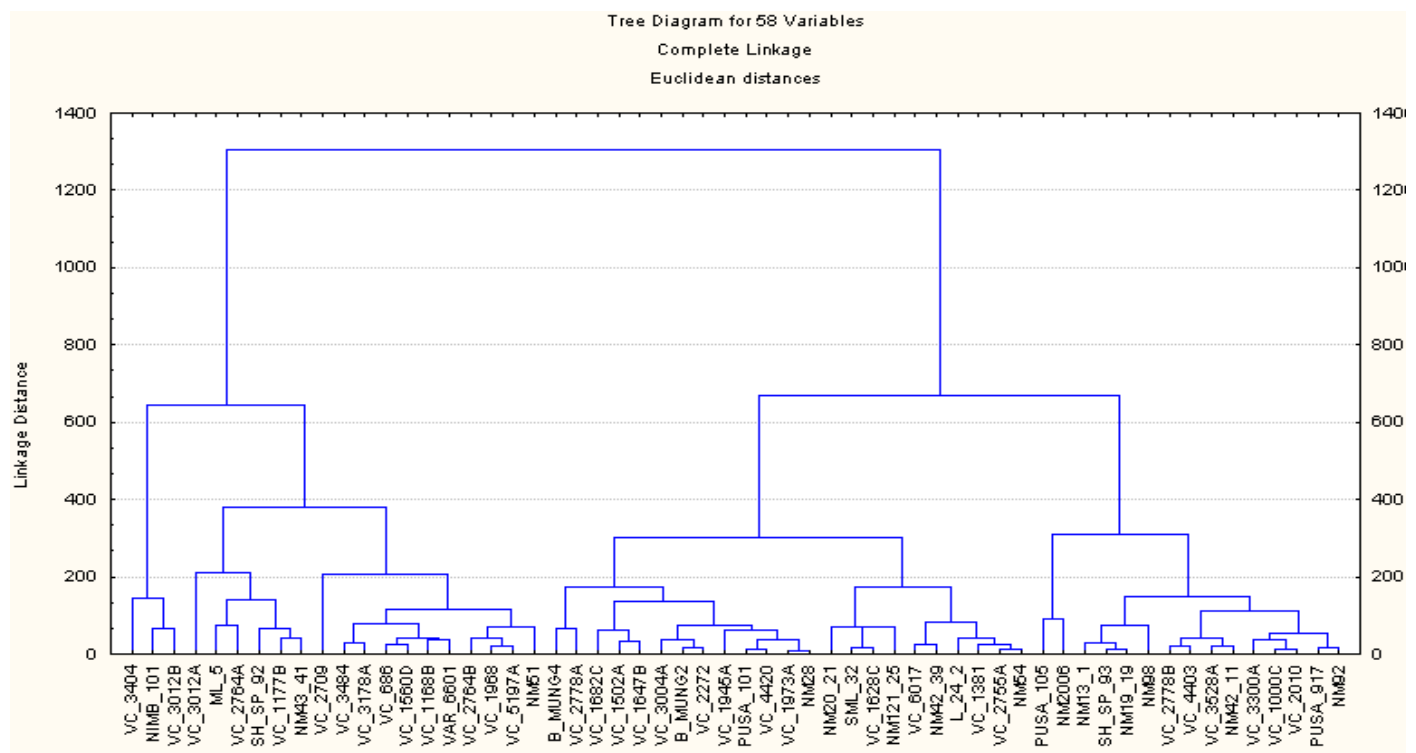


Figure 1: Cluster diagram of 58 mungbean genotypes based on eight characters.

Author's Contribution

GA and MJA developed the basic idea and prepared the manuscript draft. FA recorded the data. MA and JH performed the statistical analysis. MR helped in the execution of experiment, writing of manuscript and did proofreading and necessary corrections.

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