# Genetic Diversity for Yield and its Component Traits in Mungbean [*Vigna radiata* (L.) Wilczek

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**Abstract:** *Genetic diversity analysis is a powerful tool in quantifying the degree of divergence between biological populations and to assess the relative contribution of different components of total divergence. The aim of present investigation is to study the genetic divergence and clustering pattern of 40 genotypes of Mungbean [Vigna radiata (L.) Wilczek] for selection of suitable parents that can be utilized in hybridization programme and to study the genetic parameters attributing to yield. The crosses of genotypes from cluster II, i.e. PLM-818, PLM-829, PLM-841, PLM-884, PLM-891 with those of genotypes belonging to cluster V i.e. EC-206971, EC-206979, EC-206975, EC-206973, IC-08592-3, IC-10492, PLM-0003, PLM-0021, PLM-0032, IC-10497 has the highest inter cluster distance and might produce high level heterotic response of segregating population with regard to yield. High heritability estimates coupled with high genetic advance was observed for plant height and number of pods per plant resembling the action of additive genes in controlling these particular characters and selection would be rewarding for yield improvement.*

**Keywords:** Cluster, $D^2$ technique, Genetic diversity, Genetic distance, Genotypes, Hybridization

## 1. Introduction

Pulses are extensively grown in tropical regions of the world as a major protein rich crop bringing considerable improvement in human diet. Creation of variability and selection of superior recombinants among the variants is major objective of any plant breeding programme. Since Mungbean is a self pollinated species considerable variation exists among the green gram cultivars and also within its related species (Bisht *et al*., 2005). Yield components are the primary objectives of plant breeders for crop improvement. Grafius (1978) has suggested that there may not be genes for yield per se but rather for various components, the multiplicative interactions results in the augmentation of yield. Any breeding program which has been focused on genetic amelioration of yield, genetic diversity is the basic requirement. Effective hybridization program between genetically diverse parents will lead to considerable amount of heterotic response in $F_1$ hybrids and broad spectrum of variability in segregating generations. The utility of multivariate analysis has been emphasized by Murty and Arunachalam, 1966. Even when breeding programmes emphasize to involve diverse sources as parental lines, the plant breeders generally limit their efforts to a narrow range of adapted lines for genetic improvement, leading to erosion of genetic diversity in long run. Assessment of genetic diversity in available cultivars has important implication in understanding the progress made in any breeding programme. Morphological markers are routinely used for estimating the genetic diversity (Subhojit Datta *et al*. 2012). Therefore, the present experiment has been formulated to study the genetic divergence and clustering pattern of the Mungbean genotypes for selection of suitable parents for utilizing in hybridization programme and to study the genetic parameters attributing to yield and its contributing characters.

## 2. Materials and Methods

The present investigation was carried out during spring season of 2010 at the Research Farm of Kisan PG College, Simbhaoli, Hapur, Uttar Pradesh affiliated to CCS University, Meerut, India. The materials for this study comprising 40 genotypes of Mungbean were obtained from NBPGR, New Delhi. The experiment was conducted in a randomized block design (RBD) with three replications. The spacing of 30cm row to row and 10cm for plant to plant was maintained. Recommended packages of practice and plant protection measures were attempted in order to raise a healthy crop. The observations were recorded on five randomly selected plants in each replication for ten quantitative characters, namely; Plant height (cm), Number of branches per plant, Days to 50% flowering, Number of pods per plant, Days to maturity, Number of seeds per pod, 100-seed weight, Seed yield per plant (g), Biological yield (g) and Harvest index (%). Mahalanobis (1936) defined the distance between two populations as $D^2$ which was obtained by Tochers method, described by Rao (1952). Contribution of individual characters towards divergence was estimated according to the method described by Singh and Chaudhary (1985). The experimental data were analyzed statistically following the method of analysis of variance for single factor (Gomez and Gomez, 1984).

## 3. Results and Discussion

The analysis of variance revealed significant difference among the accession for all the characters studied indicating the existence of a wide genetic divergence among them. Based on $D^2$ values, 40 genotypes were grouped into 6 clusters on the assumption that genotypes within cluster have similar $D^2$ values among themselves than those from groups belonging to two different clusters (Table 1). Cluster IV has the highest number of genotypes i.e., 12. Cluster V

has 10 genotypes, followed by cluster I which has 6 genotypes. Cluster II have 5 genotypes. Wide diversity was also reported by earlier workers. Raman and Singh (1987) grouped 39 genotypes into 8 clusters. Similarly, Loganathan *et al.*, (2001a) grouped 42 $F_3$ and eight varietal genotypes into seven clusters. Das *et al.*, (2010) grouped 23 genotypes into 8 clusters. The clustering pattern of the genotypes showed that genetic diversity was not related geographic diversity. Such a type of constellation of germplasm proves that the collection made were genetically viable for different characters.

The clustering pattern of the stains revealed that there was no close correspondence between geographical distribution and genetic divergence as estimated by the $D^2$ statistic. The intra and inter cluster $D^2$ value among 6 clusters are presented in table-1. The maximum intra cluster distance was observed in the cluster II (D=2.279), followed by cluster V (D=2.054) and cluster I (D=2.002) suggesting that genotypes included in these clusters might have different genetical architecture. Further maximum inter-cluster distance was observed between the cluster I and VI (D=5.530) followed by cluster I and III (D=5.449) and cluster I and II (D=5.241) indicating wide divergence among these clusters (Figure 1). This also suggests that the genetic architecture of the genotypes in one cluster differs entirely from those included in the other cluster. The minimum inter cluster distance was observed between cluster IV and V (D=2.422) followed by cluster IV and VI (D=2.712). The lower D value between their characters suggested that the genetic constitutions of these genotypes in one cluster were in close proximity with those genotypes in other clusters.

Considering the clustering pattern, presented in table 2 revealed that cluster IV has highest number of genotypes (12) followed by cluster V having 10 genotypes however, minimum number of 3 genotypes were grouped in to III cluster. The genotypes belonging to cluster I (EC.2513-3, EC-206977, IC-39327, IC-73536, PLM-759, PLM-777) and genotypes belonging to cluster VI (IC-00114, IC-00557, IC-00615-5, EC-206972) have highest inter cluster distance (5.530) and therefore can be used for hybridization programme (Table 1).

The existence of diversity among the genotypes was also assessed by considerable amount of variation in cluster mean for different characters (Table 3). The maximum number of pods per plant was noticed in cluster IV (59.97) while minimum was observed in cluster I (49.10). The maximum number of seed yield per plant was recorded by the

genotypes in cluster VI (70.71) and minimum in cluster III (16.39). Therefore, from the above findings it can be concluded that the genetic diversity was not related to geographical diversity.

Among the 40 genotypes, the genotypes from cluster I, i.e. EC-2513-3, EC-206977, IC-39327, IC-73536, PLM-759, PLM-777 with those of genotypes belonging to cluster VI i.e. IC-00114, IC-00557, IC-00615-5, EC-206972 have the highest inter cluster distance and might produce higher magnitude of heterosis with regard to yield. Two characters viz., plant height and number of pods per plant exhibited high heritability estimates coupled with high genetic advance which resembles the action of additive genes in controlling these particular characters. The characters should be given importance for further improvement of yield and its components. The present findings are in conformity with the findings of Sirohi *et al.* 2006 and Gadakh *et al.* 2013.

**Table 1:** Estimates of average inter and intra cluster (bold values) involving 40 genotypes.

| I | II | III | IV | V | VI |
|---|---|---|---|---|---|
| **2.002** | 5.241 | 5.449 | 5.074 | 3.095 | 5.530 |
| | **2.279** | 4.782 | 4.001 | 4.362 | 4.494 |
| | | **1.496** | 3.066 | 3.856 | 3.748 |
| | | | **1.733** | 2.442 | 2.712 |
| | | | | **2.054** | 3.208 |
| | | | | | **1.936** |

**Table 2:** Distribution of 40 genotypes of Mungbean for six clusters

| Clusters | No. of genotypes | Name of genotypes |
|---|---|---|
| **I** | 6 | EC-2513-3, EC-206977, IC-73536, PLM-759, PLM-777 |
| **II** | 5 | PLM-818, PLM-829, PLM-841, PLM-884, PLM-891 |
| **III** | 3 | IC-08917, PLM-924, PLM-953 |
| **IV** | 12 | EC-206976, EC-206978, EC-206974, EC-206980, IC-11303, PLM-0345, PLM-0380, PLM-391-A, PLM-726, PLM-748, PLM-904, IC-02056-2 |
| **V** | 10 | EC-206971, EC-206979, EC-206975, EC-206973, IC-08592, IC-10492 PLM-0003, PLM-0021, PLM-0032, IC-10497 |
| **VI** | 4 | IC-00114, IC-00557, IC-00615-5, EC-206972 |

**Table 3:** Average performance of different clusters for yield and its contributing traits in Mungbean

| Cluster | Days to 75% flowering | Days to Maturity | Plant Height (cm) | Number of branches per plant | Number of pods per plant | Number of seeds per plant | Seed yield per plant(g) | Biological yield per plant (g) | Seed weight (g) | Harvest Index |
|---|---|---|---|---|---|---|---|---|---|---|
| I | 37.42 | 8.39 | 54.68 | 11.73 | 49.10 | 9.43 | 15.38 | 47.53 | 3.17 | 32.19 |
| II | 43.99 | 48.14 | 59.75 | 17.20 | 53.15 | 10.24 | 22.14 | 73.88 | 3.44 | 31.80 |
| III | 36.08 | 87.77 | 65.32 | 18.17 | 58.30 | 11.29 | 16.39 | 53.71 | 3.70 | 30.35 |
| IV | 37.75 | 88.07 | 67.95 | 16.69 | 59.97 | 9.78 | 19.06 | 57.8 | 3.37 | 33.05 |
| V | 36.65 | 85.78 | 62.49 | 14.92 | 53.50 | 9.60 | 17.65 | 52.72 | 3.09 | 33.68 |
| VI | 35.24 | 87.52 | 61.55 | 17.16 | 59.39 | 10.66 | 70.71 | 58.03 | 3.67 | 35.80 |
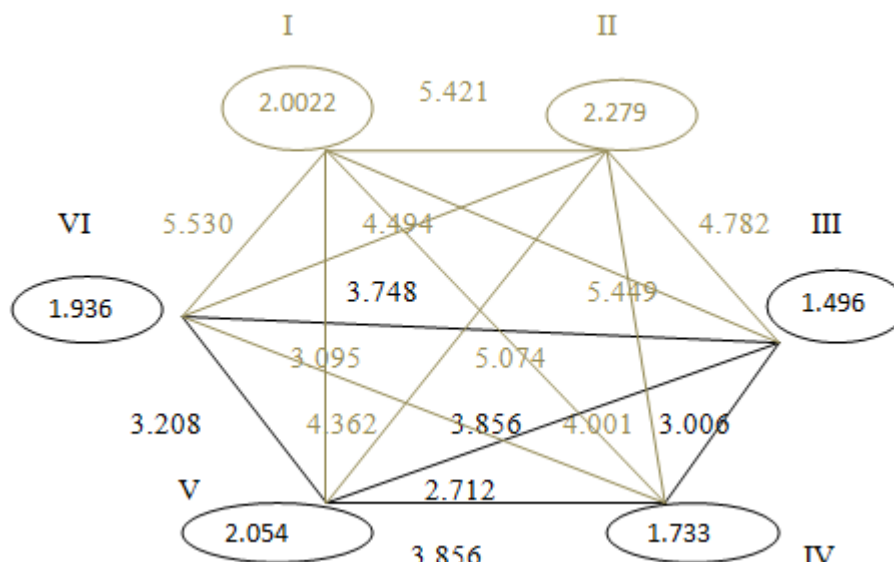
**Figure 1:** Cluster diagram showing intra and inter cluster distances for six clusters

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