



Assessment of Genetic Diversity in Mungbean (*Vigna radiata* L.)

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

Article Information

DOI: 10.9734/JABB/2024/v27i6870

Open Peer Review History:

This journal follows the Advanced Open Peer Review policy. Identity of the Reviewers, Editor(s) and additional Reviewers, peer review comments, different versions of the manuscript, comments of the editors, etc are available here: <https://www.sdiarticle5.com/review-history/116259>

Original Research Article

Received: 28/02/2024

Accepted: 02/05/2024

Published: 07/05/2024

ABSTRACT

The present study on genetic divergence among 33 genotypes in mungbean was carried out using Mahalanobis D² statistics for yield and its contributing traits, and a total of six clusters were formed. Cluster VI contains the highest number of genotypes (17), followed by clusters I, II, and V with 7, 4, and 3 genotypes, respectively, and clusters III and VI are monogenotypic. The inter-cluster distance was highest between clusters I and VI (250.89) and lowest between clusters I and III (57.74), whereas the intra-cluster distance was highest in cluster IV (63.97) and lowest for clusters III and VI (0.00), which have only one genotype. Cluster III records the highest mean for seed yield per plant, number of pods per plant, and lowest days to maturity, and Cluster VI also records the second highest mean for seed yield per plant, highest seed germination%, speed of germination, and seed viability. The maximum contribution towards genetic diversity was determined by the number of primary branches per plant (12.12%), followed by the number of secondary branches

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per plant. Genotypes belonging to clusters III and VI may be taken for a hybridization breeding program. Therefore, from the analysis, it was also concluded that genotypes belonging to different clusters separated by a high statistical distance may be used for developing new recombinants and desired traits.

Keywords: Clustering; D2 analysis; genetic divergence; genetic variability; mungbean; seed yield.

1. INTRODUCTION

“The Mungbean (*Vigna radiata* L.) Wilzeck is one of the most important edible legume crops. It belongs to the family Leguminosae/Fabaceae and the sub-family Papilionaceae, with chromosome number $2n = 2x = 22$. In India, mung bean is grown as the third most important pulse crop and is also known as green gram, golden gram, and moong” [1]. “It is a major pulse crop in many Asian countries, including India, where the diet is mostly cereal-based. Green gram has a special role in the diversification of Indian agriculture and the fight against malnutrition among the nation's vegetarian population” [2]. The average percentage of nutrients found in mungbean is protein (22.9 g), fat (1.2 g), total carbohydrate (61.8 g), crude fiber (4.4 g), and ash (3.5 g) per 100 g of sample [3] and provides 334–344 kcal of energy [4]. “Production has increased from 0.53 million metric tons in 1965–66 to 3.09 million metric tons with an area of 7.13 million hectares and a productivity of 601 kg/hectare” [5]. The biggest producers of green gram in India are the states of Rajasthan (19.69 lakh ha), Karnataka (4.14 lakh ha), Maharashtra (3.68 lakh ha), and Madhya Pradesh (1.60 lakh ha) [6].

Evaluation of diversity is an effective biometrical tool to assess the genetic diversity present among the population. A diverse plant population assures better crop improvement and the chances of obtaining a better hybrid through a hybridization program. Mung bean has high genetic variation [7,8], indicating possibilities for crop improvements. Genetic diversity is commonly studied in breeding programs by traditional methods such as Mahalanobis D^2 statistics, cluster analysis, or molecular biology technologies. The present paper examined 33 green gram genotypes using the former method to evaluate their genetic diversity and potential for future hybridization programs.

2. MATERIALS AND METHODS

The experiment material consists of 33 mungbean genotypes, including three check

varieties, namely NDM-1, NDM-95-3, and NDM-95-5. The experiment was carried out in a randomized block design during kharif 2021-2022 at the Genetics and Plant Breeding Farm, and seed quality parameters were tested in the seed technology laboratory at Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya (UP). Each genotype was sown with a spacing of 30 x 10 cm, replicated three times, and recommended agronomic and plant protection practices were followed to raise a healthy crop. At maturity, five guarded plants were selected at random from every genotype except for days to 50% flowering and days to maturity, which were recorded on a plot basis, and in each replication, data on different traits were recorded. The observations were recorded on fourteen quantitative characters, viz., Days to 50% flowering (DFF), Days on maturity (DM), Plant Height (PH), Number of primary branches per plant (PBPP), Number of secondary branches per plant (SBPP), Number of pods per plant (PPP), Number of seeds per pod (SPP), 100-seed weight (100-SW), Seed Germination% (SG%), Speed of Germination (SoG), Seedling length (cm) (SL), Seed viability (SV), Vigour Index-I (VI), and Seed yield per plant (SYPP). The data were subjected to Mahalanobis D^2 statistics as per the Mahalanobis [9] method, and genotypes were grouped into different clusters following Toucher's method as suggested by Rao [10].

3. RESULTS AND DISCUSSION

The statistical evaluation of variance shows significant variation within mungbean genotypes for all the characters under study. All the 33 genotypes were grouped into six clusters (Table 1). The maximum number of genotypes was found in cluster VI (17 genotypes), followed by cluster I (7 genotypes), cluster II (4 genotypes), and cluster V (3 genotypes). The remaining two clusters are monogenotypic. Monogenotypic clustering shows that such genotypes may have a completely different genetic makeup from the remaining genotypes, resulting in the formation of a distinct cluster, while genotypes belonging to the same cluster show a close relationship between them.

The intra-cluster distance among 33 genotypes ranged from 0.00 to 63.97 (Table 2). The intra-cluster distance values show the closeness of genotypes inside the same cluster. High intra-cluster D^2 values show that there is more genetic divergence between genotypes belonging to the same cluster and therefore more heterogeneity than that with an intra-cluster distance of 0.00, which shows that they are monogenotypic and less heterogenous. Among the formed clusters, cluster IV possessed the highest intra-cluster distance (63.97), followed by cluster II (45.19), cluster I (35.26) and cluster V (27.52). Murty and Arunachalam [11] found that the success of hybridization and selection is heavily influenced by selecting parents with significant genetic diversity for desired features. The current experiment found intra-cluster variation among constituent genotypes, which could be

used to select parents for recombination breeding.

The average inter-cluster distance among genotypes varied from 57.74 to 250.89. The highest inter-cluster distance was between clusters I and VI, followed by clusters IV and VI, cluster III and VI, cluster II and VI, and cluster II and VI. It implies that, with regard to the characteristics under investigation, the genotypic composition of these cluster pairs comprised the genes from the majority of their parents who were most distantly related. The genotypes from various clusters separated by a high estimated statistical distance can be used to examine the inheritance pattern of many mung bean characters and to improve crop yield through hybridization. Similar results were reported by Kumaret al. [12], Sen and De [13], and Gadakh et al. [14].

Table 1. Grouping of 33 mungbean genotypes in different clusters

Cluster	No. of Genotype	Genotype Name
I	7	IPM 1704-14, OBGG 106, PM 1918, BCM 20-73, Pusa M 2271 PMS 8, AKM 1606
II	4	NDM-95-3©, NDM-95-5©, NDM-1©, BM 2021-2
III	1	ML 2748
IV	17	MGG 519, IGKM 05-06-27, RMG 1188, ML 2738, RVSM 22-7, AKM 12-12, RVSM 22-4, VGG 20-225, IPM 1205-2, IGKM 06-10-7, OBGG 112, KM 2417, MH 1908, SGC 25, BCM 20-56, VGG 20-153, PM 1903
V	3	SVM 106, JLPM 707-27, RMG 1183
VI	1	LGG 628

Table 2. Estimates of average intra (bold) and inter cluster distance for 6 clusters in genotypes

Cluster Number	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
Cluster I	35.26	83.39	57.74	102.25	66.41	250.89
Cluster II		45.19	116.69	137.98	81.66	142.42
Cluster III			0.00	135.84	75.18	228.62
Cluster IV				63.97	123.76	231.19
Cluster V					27.52	180.98
Cluster VI						0.00

Table 3. Cluster means for 6 clusters in mungbean genotypes

Characters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
DFF	43.24	43.48	40.22	51.33	42.00	45.33
DM	64.50	63.10	61.00	71.67	64.00	65.00
PH	72.91	72.10	78.67	82.00	52.00	72.67
PBPP	1.01	1.05	1.08	1.11	1.57	1.00
SBPP	1.95	2.10	2.40	2.01	2.93	2.57
PPP	14.64	15.63	16.33	11.27	15.50	15.13
SPP	9.21	10.91	9.66	9.96	8.63	10.40
100-SW	3.97	4.17	3.10	3.31	3.20	3.25
SG%	80.41	82.75	79.40	81.00	80.33	83.33
SoG	33.14	51.96	30.85	39.79	42.35	66.69
SL	29.38	29.62	24.19	29.02	25.27	12.47
SV	82.15	84.52	80.44	82.22	81.33	85.33
VI	2363.42	2446.08	1922.04	2348.79	2029.33	1039.80
SYPP	10.02	9.79	10.83	9.10	10.67	10.77

To improve yield and related characteristics in breeding programs, cluster means for seed yield per plant and key components should be considered while selecting genotypes. The mean number of pods per plant varied from 11.27 in cluster IV to 16.33 in cluster III (Table 3). The number of seeds per pod varied from 8.63 in cluster V to 10.91 in cluster II. Seed germination%, speed of germination, and seed viability were recorded to be highest in cluster VI, comprising genotype LGG 628. The highest yield was recorded in cluster III with genotype ML 2748, followed by cluster VI with genotype LGG 628. 100 seed weight, seedling

length, and vigor index were recorded to be highest in cluster II, comprising check varieties NDM-1, NDM-95-3, and NDM-95-5 and genotype BM2021-2. Cluster VI had the highest mean for days to 50% flowering, days to maturity, and plant height. Similar results were reported by [15]^a, [16] and [17]^a. The aforementioned results indicate that there was no cluster with genotypes with all of the necessary characteristics that could be directly selected and used. Interestingly, the majority of the minimum and maximum mean values were spread in rather distant clusters. [18] recommended recombination breeding between genotypes from distinct clusters.

Table 4. Contribution of 14 morphological characters towards divergence (Rank and % contribution) in mungbean

Sources	Time ranked 1 st	Contribution (%)
Days to flowering	26	4.92
Days to maturity	28	5.30
Plant height	30	5.68
No. of primary branches per plant	64	12.12
No. of secondary branches per plant	53	10.04
Number of pods per plant	44	8.33
Number of seeds per pod	53	10.04
100 - seeds weight	34	6.44
Seed germination (%)	47	8.90
Speed of germination	41	7.77
Seedling length (cm)	22	4.17
Seed viability	42	7.95
Vigour Index I	13	2.46
Seed yield per plant (g)	31	5.87

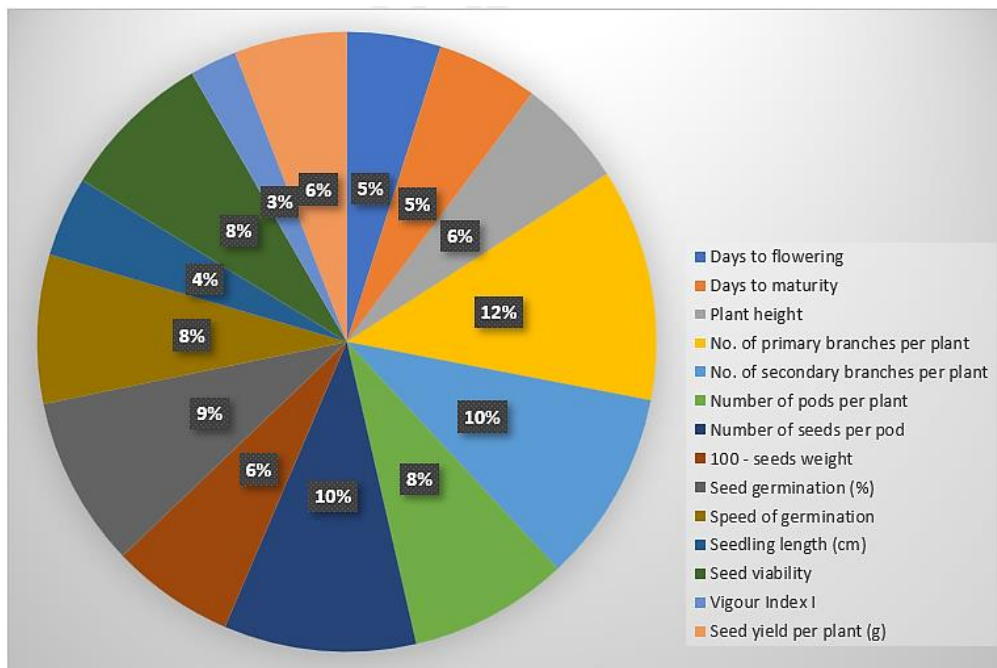


Fig. 1. Contribution of 14 morphological characters towards genetic divergence in mungbean

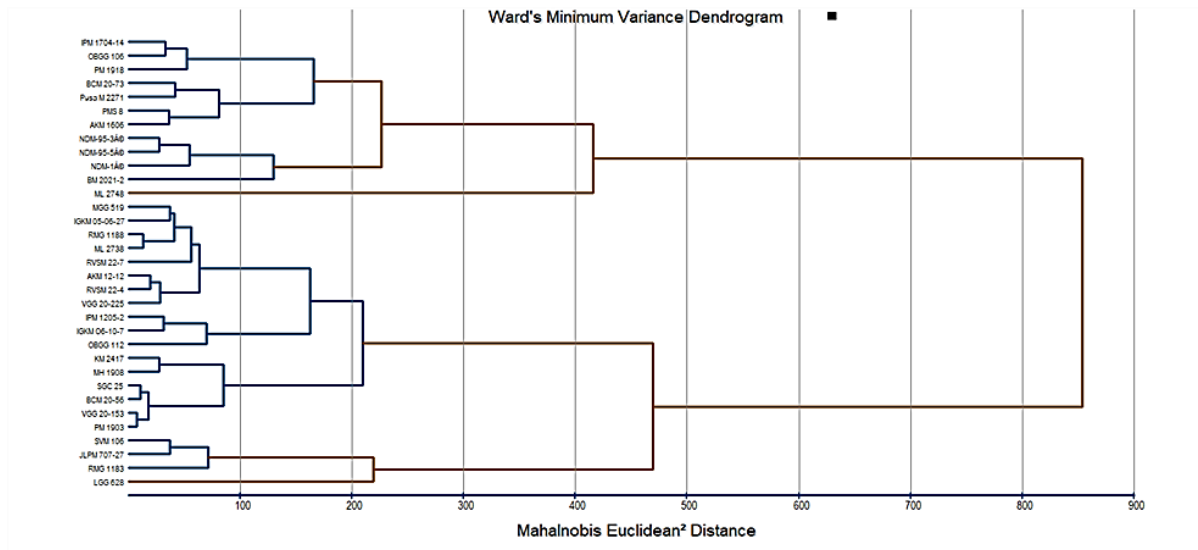


Fig. 2. Cluster analysis of the genotypes represented by dendrogram

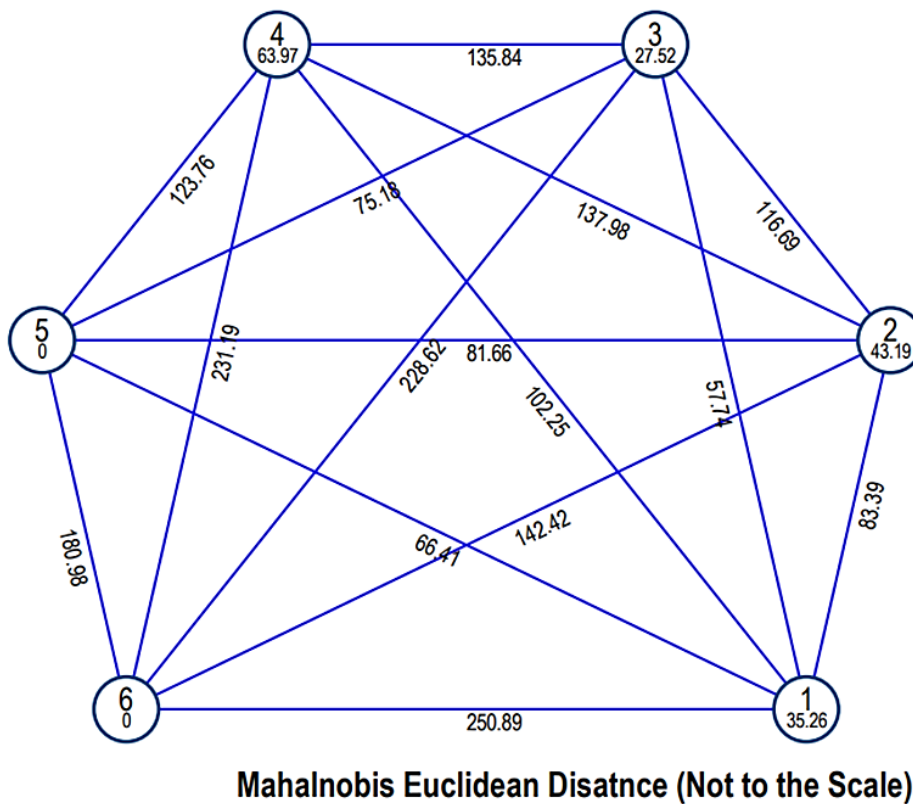


Fig. 3. Graphical representation of inter and intra cluster distance among six clusters

Improvement in yield and other relevant characteristics is a fundamental goal of any breeding program. The selection and choice of parents are mostly determined by the contribution of character to divergence [19], and the contribution to genetic divergence is

illustrated in Table 4. Among the given traits, the highest contribution towards genetic divergence was by the number of primary branches per plant (12.12%), followed by the number of secondary branches per plant and the number of seeds per pod, which have similar contributions (10.04%),

while the minimum contribution towards divergence was by Vigor Index I. Ram et al. [15]^b, Kunda et al. [17]^b and Joshi et al. [20] also reported similar findings. The above-mentioned characters appeared more frequently in the top rank and provided a much higher proportion of divergence toward the total divergence in the D² statistics. A pie diagram shows the percentage contribution of each character to the divergence D² statistics (Fig. 1).

4. CONCLUSION

In order to produce a large number of segregants in the next generation, heterosis breeding may benefit from the selection of divergent parents based on the above characteristics. The present study indicates that parental lines selected from cluster III (ML 2748) for seed yield per plant and number of pods per plant, cluster VI (LGG 628) for seed yield per plant, seed germination%, speed of germination, and seed viability, and from cluster V (SVM 106, JLPM 707-27, RMG 1183) for seed yield and number of primary and secondary branches per plant would be useful in future breeding programs for desired segregants.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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DOI:10.18805/LR-4836

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