



Genetic Diversity Analysis of Mungbean [*Vigna radiata* (L.) Wilczek] Genotypes under Rainfed Condition of Thar Desert

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Abstract: Field experiment with 38 varieties was conducted to study the genetic divergence in the mungbean variety at Agricultural University, Jodhpur during *Kharif* 2019. Significance difference was observed among all 11 characters studied. These genotypes were grouped into nine clusters which indicate the existence of an ample amount of genetic diversity in the variety and therefore signify the scope of selection for genetic improvement of mungbean. The maximum intra-cluster distance was exhibited in cluster I, while the maximum inter-cluster distance was exhibited between II and XI. The greater distance between two clusters indicates the presence of wider genetic diversity among the genotypes of those clusters. Therefore, genotypes belonging to diversified clusters may be used in a hybridization programme for developing the high-yielding variety in mungbean.

Keywords: Genetic divergence, Clusters, Mungbean, Seed yield

Mungbean (*Vigna radiata* L. Wilczek, $2n=22$, *Fabaceae*) is an important pulse crop which is broad cultivated throughout India. Mungbean is a short day, hot season crop, mainly grown in arid and semi-arid regions. Mungbean has 22 chromosomes in the $2n$ set and a relatively modest (579 Mb) genome (Kang et al 2014). The names greensoy, green gram, green bean, mash bean, and gold engram are also used to describe it (Markam et al 2018). Mungbean has become an extremely valuable short-lived grain legume crop with many desirable characteristics, such as wide adaptability, low input requirements and the ability to improve soil fertility (Pooran and G. M., Can 2021). According to 3rd advance estimates for 2021-2022, the overall production of pulses in India to be 27.75 million tonnes. In India, a total of 2.85mt mungbean productions including 1.48mt in *kharif* and 1.37mt in *rabi*, accounting for 10% of all pulse production (Directorate of Economics and Statistics, Ministry of Agriculture and Farmers Welfare 2022). India is the principle producer of mungbean in the world with an annual production of 3.17 mt from an area of 5.50 mha with the productivity of 570 kg per ha and contributing 10.30 per cent to the total pulses production (Anonymous 2022-23). It is a drought hardy crop with ability to grow under harsh climate and medium to low rainfall conditions and grows on a variety of soils including black, red lateritic, gravelly and sandy soils. Well drained fertile sandy loam soil with a pH between 6.3 - 7.5 is the best for mungbean cultivation (Sharma 2016). Genetic diversity is a dominant factor and also a precondition

in any hybridization programme. Introduction of diverse parents in hybridization programme serves the purpose of combining advisable recombination. Multivariate analysis by means of Mahalanobis D^2 statistic is a dominant tool in quantifying the degree of divergence at genotypic level. Therefore, an attempt has been made in the present inspection with a view to approximate genetic divergence among a set of 38 genotypes of mungbean.

MATERIAL AND METHODS

The present study was carried out during *Kharif*, 2019 at Agriculture University, Mandor, Jodhpur. The experimental material consisted of 38 genotypes (Table 1) and was sown on July 23, 2019 in RBD design with three replications. The data were recorded for 11 characters viz. days to 50% flowering, days to maturity, 100 seed weight (g) and protein content (%) on a whole plot basis whereas, plant height (cm), pods per plant, pod length (cm), branches per plant, seeds per pod, seed yield per plant (g) and harvest index (%) were measured on five competitive plants in each replication. The statistical analysis was performed using INDOSTAT 8.1 and XLSTAT 2021.2.2 software. Diversity analysis (D^2) was done by following the method of Mahalanobis (1936) and grouped into separate clusters following the Toucher's method as suggested by Rao (1952). Average intra and inter-cluster distances were determined using GENRES version 3.11, 1994 Pascal Intl. Software as suggested by Singh and Chaudhary (1977).

RESULTS AND DISCUSSION

There were significant differences among genotypes for all 11 characters recommended that the material has sufficient genetic diversity to support the breeding programme for improving the seed yield of mungbean. In this study, 38 genotypes were assembled into nine clusters based on D^2 values using Tocher's method. The cluster-I contains maximum (29) genotypes, followed by cluster-II with two, while cluster-III, IV, V, VI, VII, VIII and IX were monogenotypic (Table 2 and Fig. 1). Similar findings were observed by Markam et al (2018), Talukdar et al (2020), Wesly et al (2020), Gupta et al (2021), Sridhar et al (2022), Kingsly et al. (2023) and Srivastava et al (2024).

Amongst the characters, plant height contributed highest towards genetic divergence (45.38%) followed by pods per plant, 100-seed weight and days to 50% flowering (9.53%) while the remaining characters contributed little to genetic divergence [Markam et al 2018, Mathankumar et al 2020, Talukdar et al 2020, Gupta et al 2021, Tiwari et al 2022 and Srivastava et al 2024] (Table 3). The greatest intra-cluster distance was approximate in cluster-I (12.43) and cluster-II

(6.44) (Table 4). The highest inter-cluster distance was observed between cluster-II and IX (46.44) followed by cluster-II and VII, cluster-II and V, cluster-II and III, cluster-II and VII and cluster-II and VI suggesting broad diversity between genotypes of these clusters (Goyal et al 2021, Gupta et al 2021, Sridhar et al 2022). The diversity was also supported by the considerable amount of variation among the cluster means for distinct characters (Table 5). The data suggested that the cluster mean for days to 50% flowering

Table 1. List of mungbean genotypes used for present investigation

Source	Name of genotypes
IIPR, Kanpur, U.P. 02-	IPM 02-3, IPM 604-1, Virat, Shikha M
SDAU, S.K. Nagar, Gujarat	SKNM 1514, SKNM 1516, GM 6, GM 4
PAU, Ludhiana, Punjab	ML 818, ML 2483, SML 1901, SML 668
Hisar, Haryana	MH 2-15, MH 421, MH 1344, SVM 6262
NPRC, Vamban, T.N.	VGG 17-002, VGG 17-009, VGG 16-055
IARI, New Delhi	Pusa M 1871, Pusa M 1872 871
OUAT, Bhubaneswar, Odisha	OBGG 101, 1OBGG 102
IGKVV, Raipur, Chhattisgarh	IGKM 05-6-27, IGKM 06-18-3
GBPUA & T, Pant Nagar, Uttarakhand	PM 1511, PM 1522
Coimbatore, T.N.	CO-6, COGG-912
Anand, Gujarat	GAM 5
ARS, Lam, A.P.	LGG 630
ARS, Dharwad, Karnataka	DGGV-59
ARS, Madhira, Telangana	MGG 399
Agartala, Tripura, Bangladesh	TRCM 171-B-B-12-6
Berhampur, Odisha	OUM 11-5
MPKV, Jalgaon, M. H.	JLM 707-5
PDKV, Akola, M.H.	AKM- 1604
Srinagar, J & K	SKAU-M-365

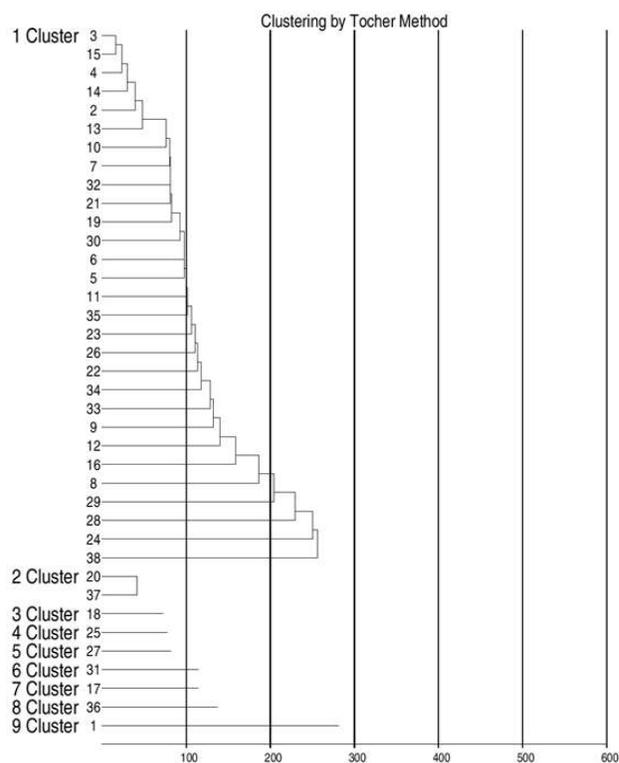
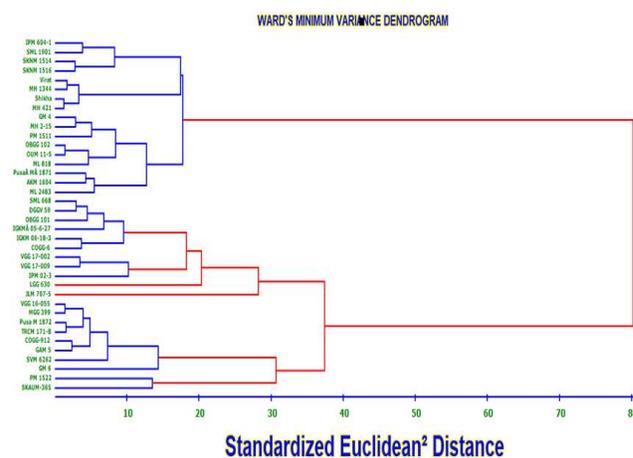


Fig. 1. Clustering pattern among 38 genotypes of mungbean (Tocher's method)

Table 2. Clustering pattern among 38 genotypes of mungbean (Tocher's method)

Cluster	Number of genotypes	Genotypes
I	29	Virat, MH1344, Shikha, MH421, IPM 604-1, MH2-15, ML 2483, GM-4, DGGV-59, PusaM-1872, VGG16-055, GAM-5, SKNM-1516, SKNM-1514, SML1901, DUM11-5, OBG G 102, PM 15 11, OBG G 101, TRCM171-B-B-12-6, MGG399, ML818, SML668, SVM6262, GM6, COGG-912, COGG-6, IGKM 05-6-27, SKAU-M-365
II	2	Pusa M-1871, AKM-1604
III	1	VGG17-009
IV	1	IGKM06-18-3
V	1	PM 1522
VI	1	LGG630
VII	1	VGG 17-002
VIII	1	JLM707-5
IX	1	IPM02-3

was maximum in cluster VI (57.00) and the minimum in cluster II (41.83). Days to maturity were show highest and lowest means in cluster VIII (82.67) and cluster I (74.33). Cluster IX exhibited highest mean for plant height (69.73 cm),

Table 3. Contribution of different characters towards genetic divergence in 38 mungbean genotypes

Source	Contribution (%)	Times ranked 1 st
Days to 50% flowering	9.53%	67
Days to maturity	0.57%	4
Plant height (cm)	45.38%	319
No. of pods per plant	16.79%	118
Pod length (cm)	0.14%	1
No. of branches per plant	2.70%	19
Number of seeds per pod	0.00%	0
100 seed weight (g)	16.50%	116
Seed yield per plant (g)	1.56%	11
Harvest Index (%)	6.54%	46
Protein content (%)	0.28%	2

Table 4. Intra (Diagonal) and inter-cluster average of D² values of 38 mungbean genotypes

Clusters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Cluster IX
Cluster I	12.43	21.47	16.88	17.58	23.14	20.32	22.36	17.84	28.78
Cluster II		6.44	33.03	30.71	37.78	30.76	38.43	30.92	46.44
Cluster III			0.00	15.07	17.24	18.31	10.70	15.08	16.77
Cluster IV				0.00	9.04	14.67	13.66	16.33	25.42
Cluster V					0.00	18.41	14.24	16.89	23.26
Cluster VI						0.00	18.01	21.25	28.07
Cluster VII							0.00	21.64	17.41
Cluster VIII								0.00	23.29
Cluster IX									0.00

Table 5. Cluster means for seed yield and yield attributing characters in 38 mungbean genotype

Clusters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Cluster IX
Days to 50% flowering	43.53	41.83 ^L	48	46	48.33	57 ^H	49.33	43.33	44
Days to maturity	74.33 ^L	76	81	74.67	75.67	80.33	78	82.67 ^H	77.33
Plant height (cm)	41.09	20.87 ^L	55.87	51.13	57.27	51.40	62.73	46.80	69.73 ^H
No. of pods per plant	13.13	12.30	12.60	22.73	25.53 ^H	18.27	16.27	19.93	11.87 ^L
Pod length (cm)	7.23	7.21	6.93	6.89	7.33 ^H	7.06	7.01	5.28 ^L	6.95
No. of branches per plant	1.52	1.40	1.20 ^L	1.60	2.27 ^H	2.07	1.33	2.07	1.80
Number of seeds per pod	9.89	9.57	9.40	10.53	11.07 ^H	8.80	10.07	8.60 ^L	10.07
100 seed weight (g)	4.51	4.41	4.53	3.79	4.15	3.94	3.40 ^L	5.85 ^H	4.85
Seed yield per plant (g)	7.71	5.27 ^L	7.77	10.37	11.65 ^H	6.23	6.75	9.93	6.27
Harvest Index (%)	29.31	30.65	32.43	30.33	34.60 ^H	12.60 ^L	33.50	28.27	20.23
Protein content (%)	24.28	25.12	22.27	25.43	24.57	26.33 ^H	21.97 ^L	22.63	24.80

while lowest was in cluster II (20.87 cm) (Jadhav et al 2021, Sridhar et al 2022, Kingsly et al 2023).

CONCLUSION

The percentage contribution towards genetic divergence was found high for plant height followed by pods per plant and 100 seed weight. Maximum inter cluster divergence was observed between cluster II and XI followed by cluster II and VII preferable that good recombinants can be obtain by mating between the genotypes. Out of 38 genotypes, PM 1522, GM-6, IGKM 06-18-3 and GM-4 were encouraging in seed yield and other characters. Hence, these genotypes would be used as parental source for upcoming breeding programmes.

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