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Genetic Divergence Studies in Mungbean [*Vigna radiata* (L.) Wilzeck] Germplasm under Arid Environment

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Abstract: Field experiment with 79 genotypes of mungbean was conducted to study the genetic divergence in the mungbean genotypes at Swami Keshwanand Rajasthan Agricultural University, Bikaner, Rajasthan during *kharif* 2017-18. Significance difference was observed among all 11 characters studied. These genotypes were grouped into fifteen clusters which indicate the existence of an ample amount of genetic diversity in the genotypes and therefore, signify the scope of selection for genetic improvement of mungbean. The cluster-III was largest with 26 genotypes followed by cluster-II with 20 genotypes, cluster-I with 12 genotypes, cluster-IV with 9 genotypes and cluster-XI with 2 genotypes. The remaining 10 clusters were mono-genotypic. The maximum intra-cluster distance was found in cluster-IV and the maximum inter-cluster distance was observed between cluster-III and cluster-IX. D^2 analysis exhibited that days to 50 per cent flowering, 100-seed weight, biological yield per plant, number of branches per plant and number of pods per plant contributed 91.79 per cent towards total divergence.

Keywords: Cluster analysis, Genetic diversity, Germplasm, Mahalanobis's D^2 Statistics, Mungbean, Tocher's method

Mungbean [*Vigna radiata* (L.) Wilczek, 2n=22, Fabaceae) is an important pulse crop which is cultivated throughout India. It is a short day, hot season crop, mainly grown in arid and semi-arid regions (Anita et al 2024). 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 Can GM 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 3.17mt from an area of 5.50mha with the productivity of 570 kg per ha (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 6.3-7.5 is the best for mungbean cultivation (Sharma NK 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 79 genotypes of mungbean.

MATERIAL AND METHODS

The experiment was carried out at, Swami Keshwanand Rajasthan Agricultural University, Bikaner, Rajasthan during *Kharif*, 2017-18. The experimental site is situated at 28.01^0N latitude and 73.22^0E longitude at an altitude of 234.70 meters. According to National Planning Commission, Bikaner falls under Agro-climatic Zone XIV (Western Dry Region) of India. The average rainfall of the zone is 265 mm. The experimental material consisted of 79 genotypes (Table 1) and was sown on July 6, 2017 in randomized block design with three replications accommodating 3 meters long two rows per replication at 30 cm spacing under sprinkler irrigated situation. All recommended agronomic practices were adopted for raising a healthy crop. The data were recorded for 11 characters viz. days to 50% flowering and days to maturity on a whole plot basis whereas, plant height (cm), number of branches per plant, number of pods per plant, pod length (cm), number of seeds per pod, 100 seed weight (g), biological yield per plant (g), seed yield per plant (g) and harvest index (%) were measured on five competitive plants in each replication.

The statistical analysis was performed using INDOSTAT

Table 1. Mungbean genotypes used for present investigation

Name of germplasm	Year of collection	Source of procurement
Germplasm procured from NBPGR, Regional Station, Jodhpur		
IC-39269	1993	Jodhpur, Rajasthan
IC-39275	1993	Kherapa, Jodhpur, Rajasthan
IC-39279	1993	*
IC-39288	1993	Nimbojhai, Nagour, Rajasthan
IC-39293	1993	Kadampura, Nagour, Rajasthan
IC-39298	1993	Bambor,Jodhpur, Rajasthan
IC-39300	1993	Jaswasar, Bikaner, Rajasthan
IC-39328	1993	Lalela, Barmer, Rajasthan
IC-39333	1993	Dhawa, Barmer, Rajasthan
IC-39352	1993	Manduwa, Barmer, Rajasthan
IC-39368	1993	Lunawas, Jodhpur, Rajasthan
IC-39375	1993	Nibali, Barmer, Rajasthan
IC-39383	1993	Godan, Jalore, Rajasthan
IC-39395	1993	Aburoad, Sirohi, Rajasthan
IC-39399	1993	Jaspura, Palanpur, Gujarat
IC-39409	1993	Kapara, Banaskantha, Gujarat
IC-39420	1993	Nearsami, Patan, Gujarat
IC-39427	1993	Harij, Patan, Gujarat
IC-39451	1988	Lakhtarar, Surendranagar, Gujarat
IC-39454	1988	Surendranagar, Gujarat
IC-39465	1988	Kalyana, Patan, Gujarat
IC-39483	1988	Kalapur, Surendranagar, Gujarat
IC-39492	1988	Dudhai, Mahesana, Gujarat
IC-39495	1988	Chandrani, Kachchh, Gujarat
IC-39500	1988	Kishangarh, Gujarat
IC-39515	1988	Kauth, Gujarat
IC-39580	1992	Bachau, Kutch, Gujarat
IC-39582	1992	Chilora, Kheda, Gujarat
IC-39591	1992	Sevelia, Kheda, Gujarat
IC-39604	1992	Bholi, Rajasmand, Rajasthan
IC-39608	1992	Nevra, Jodhpur, Rajasthan
IC-39610	1992	Osian, Jodhpur, Rajasthan
IC-52073	1992	*
IC-52076	1992	*
IC-52078	1992	*
IC-52081	1992	*
IC-52082	1992	*
IC-52087	1992	*
IC-55069	1992	*
IC-102792	1986	Banar, Jodhpur, Rajasthan
IC-102821	1986	Gidani, Jaipur, Rajasthan

Cont...

Table 1. Mungbean genotypes used for present investigation

Name of germplasm	Year of collection	Source of procurement
IC-102857	1986	Khasur, Dholpur, Rajasthan
IC-102963	1986	Avikanagar, Tonk, Rajasthan
IC-103014	1986	Alampur, Kheda, Gujarat
IC-103059	1986	Krakas, Amreli, Gujarat
IC-103204	1987	Gangawar, Chittorgarh, Raj.
IC-103207	1987	Dhinva, Chittorgarh, Rajasthan
IC-103244	1986	Bhrwasa, Didwana, Nagaur, Raj.
IC-103245	1987	Odda, Banswara, Rajasthan
IC-103785	1989	Khemlo, Vishsana, Rajasthan
IC-103821	1989	Nagdhan, Santrampur, Gujarat
IC-103973	1989	Barvalbhipor, Bhavnagar, Gujarat
IC-324012	-	*
IC-338868	1990	Sanari, Barmer, Rajasthan
Varieties procured from Agriculture University, Jodhpur		
Sweta		CSAVAT, Kanpur
IPM-02-3		ICAR-IIPR, Kanpur
IPM-02-14		ICAR-IIPR, Kanpur
Samrat (PDM-139)		ICAR-IIPR, Kanpur
GM-4		AAU, Pulse Res.Station,Vadodara
MH 2-15		CCSHAU, Hisar
MH-421		CCSHAU, Hisar
IPM-205-7		ICAR-IIPR, Kanpur
IPM 99-125 (Meha)		ICAR-IIPR, Kanpur
IPM-409-4		ICAR-IIPR, Kanpur
GAM-5		AAU,PulseRes.Station, Vadodara
COGG-912		TNAU, Coimbatore
Varieties procured from RARI, Durgapura, Jaipur		
RMG-62		SKRAU-ARS, Durgapura, Jaipur
RMG-268		SKRAU-ARS, Durgapura, Jaipur
RMG-344		SKRAU-ARS, Durgapura, Jaipur
RMG-492		SKRAU-ARS, Durgapura, Jaipur
Keshwanand Mung-1 (RMG-975)		SKNAU-RARI, Durgapura, Jaipur
Keshwanand Mung-2 (MSJ-118)		SKNAU-RARI, Durgapura, Jaipur
Varieties procured from ARS, Sriganganagar		
Ganga-1		SKRAU-ARS, Sriganganagar
Ganga-8		SKRAU-ARS, Sriganganagar
MUM-2		CCS Meerut University, Meerut
SML-668		PAU, Ludhiana
SML-832		PAU, Ludhiana
ML-683		PAU, Ludhiana
ML-818		PAU, Ludhiana

*Source was not mentioned by NBPGR, Regional Station, Jodhpur, Rajasthan, India

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 (1985).

RESULTS AND DISCUSSION

There were significant differences among all the genotypes for all eleven traits studied that the material has sufficient genetic diversity to support the breeding programme for improving the seed yield of mungbean (Table 2). In this study, based on D^2 values using Tocher's method, 79 genotypes of mungbean were grouped into fifteen clusters (Table 3 & Fig. 1). The cluster-III contains maximum (26) genotypes followed by cluster-II with 20 genotypes, cluster-I with 12 genotypes and cluster-IV with 9 genotypes. Cluster-XI comprise only two genotypes; while the remaining ten clusters were mono genotypic indicating that these genotypes may be having completely different genetic makeup, thus leading to the formation of separate cluster.

Table 2. Analysis of variance for different characters of mungbean

Source of variation	d. f.	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of branches per plant	No. of pods per plant	No. of seeds per pod	Pod length (cm)	100-seed weight (g)	Biological yield per plant (g)	Harvest index (%)	Seed yield per plant (g)
Replications	2	0.34	4.81	27.06	0.362**	0.76	0.46	0.48	0.001	2.04	0.98	0.63
Genotypes	78	250.90**	159.74**	1057.98**	0.635**	572.79**	2.84**	2.91**	0.580**	1252.01**	316.13**	162.12**
Error	156	0.18	1.79	12.36	0.006	1.99	0.20	0.16	0.003	6.87	3.07	0.37

*Significant at P = 0.05
** Highly significant at P = 0.01

Table 3. Composition of mungbean genotypes into fifteen different clusters by Mahalanobis's D^2 statistic and their salient features

Cluster	No. of genotypes	Composition of cluster / Name of genotypes	Salient features of the cluster
I	12	MH 421, GAM 5, SML 832, IPM 205-7, ML 683, COGG 912, RMG 268, MH 2-15, ML 818, Samrat, RMG 344, GM-4	Early flowering, early maturity, higher harvest index, long pod length and more number of pods
II	20	IC-39275, IC-103207, IC-103204, IC-39395, IC-39399, IC-39279, IC-103785, IC-39293, IC-39383, IC-103821, IC-39500, IC-55069, IC-103245, IC-102857, IC-39492, IC-39454, IC-39352, IC-39333, IC-39495, IC-102821	More plant height, late flowering and late maturity
III	26	IC-39610, IC-55069, IC-39483, IC-39300, IC-39298, IC-39580, IC-39465, IC-102963, IC-39368, IC-102792, IC-39591, IC-39451, IC-39515, IC-103244, IC-39427, IC-39375, IC-39420, IC-52076, IC-39604, IC-39582, IC-52073, IC-324012, IC-52082, IC-338868, IC-103973, IC-39608	More plant height, late flowering and late maturity
IV	9	RMG-62, Ganga-8, Keshwanand Mung-2, IC-39409, IPM 99-125, IPM 409-4, Sweta, IPM 2-14, IC-52087	Early flowering, early maturity and higher harvest index
V	1	RMG-492	Early flowering, early maturity, higher seed and biological yield
VI	1	Keshwanand Mung-1	Early flowering, early maturity, higher seed and biological yield
VII	1	IC-52081	Early flowering and early maturity
VIII	1	IC-103014	Late flowering and late maturity
IX	1	MUM-2	Early flowering, early maturity, higher seed and biological yield, more number of pods per plant
X	1	IC-39269	Late flowering and late maturity
XI	2	IC-39288, IPM 02-3	Early flowering, early maturity and higher harvest index
XII	1	SML-668	Early flowering, early maturity, higher harvest index and more number of pods per plant
XIII	1	IC-39328	Late flowering and late maturity
XIV	1	IC-103059	Late flowering and late maturity
XV	1	Ganga-1	

The genotype which belongs to the same cluster indicates to be more closely related than those belonging to different clusters. Similar findings were observed by Wesly et al (2020), Sridhar et al (2022), Kingsly et al (2023) and Srivastava et al (2024).

Improvement in yield and other related characters is the basic objective in any breeding programme. So, cluster diversity for seed yield and its contributing attributes should to be considered for selection of genotypes. In present investigation considerable differences were observed among the clusters for most of the characters studied (Table 4 and Fig. 2). The maximum intra-cluster D^2 value was observed for cluster-IV (145.87) followed by cluster-II (105.50), cluster-III (98.50) and cluster-XI (60.26) indicating that maximum differences exists among the genotypes that fall in these clusters. Therefore, such intra-cluster heterogeneity among the constituent genotypes obtained in the present experiment might serve as guideline to choose

Table 4. Average intra (in bold) and inter cluster (D^2) value for seventy-nine genotypes of mungbean

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV
I	60.07	677.15	1606.57	227.82	115.92	127.23	684.92	856.99	220.64	438.28	502.11	140.82	899.04	988.44	280.05
II		105.50	393.13	474.87	775.82	927.18	341.21	149.43	1267.26	151.14	646.00	893.08	226.62	190.01	1020.94
III			98.50	1365.13	1731.46	1892.61	1030.80	463.01	2356.28	571.20	1497.69	1910.63	441.46	341.36	1779.50
IV				145.87	278.51	376.37	336.13	598.90	539.33	323.20	442.56	317.84	609.36	752.78	617.50
V					0.00	31.36	802.10	972.87	157.48	536.13	869.06	157.25	810.23	1121.39	256.62
VI						0.00	1056.73	1152.41	56.38	598.28	981.79	97.71	969.22	1287.33	130.86
VII							0.00	384.45	1424.19	466.79	392.85	1000.13	545.16	495.18	1442.52
VIII								0.00	1507.81	290.20	747.97	1037.36	346.82	117.43	1271.57
IX									0.00	810.00	1163.35	85.80	1336.46	1659.49	114.23
X										0.00	583.34	521.12	249.63	313.77	610.46
XI											60.26	825.85	1215.51	848.73	1191.46
XII												0.00	994.73	1221.79	163.11
XIII													0.00	397.50	1050.97
XIV														0.00	1321.38
XV															0.00

Table 5. Mean values for seed yield and component characters of mungbean

Cluster	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of branches per plant	Number of pods per plant	Number of seeds per pod	Pod length (cm)	100-seed weight (gm)	Biological yield per plant	Harvest index	Seed yield per plant (gm)
I	37.00	67.00	57.32	1.93	37.46	10.75	7.88	1.91^{L}	72.31	28.57	20.46
II	47.00	74.00	87.35	2.37	17.51	10.30	7.69	3.58	33.31	18.13	5.92
III	59.00^{H}	83.00^{H}	89.70	2.54	9.58	9.50	6.86	3.51	35.70	9.10	3.21
IV	37.00	67.00	55.14	2.21	35.70	10.52	7.76	3.56	39.84	31.37	12.00
V	37.00	67.00	63.77	1.80	38.33	11.33^{H}	7.07	3.05	82.90	24.52	20.33
VI	38.00	67.00	64.87	2.10	44.60	11.33^{H}	7.31	3.27	92.13	25.27	23.27
VII	38.00	65.00	45.47^{L}	1.80	12.47	11.00	7.29	3.52	12.20^{L}	32.81	4.00
VIII	45.00	71.00	106.73^{H}	2.97	4.60	8.33^{L}	7.83	3.43	24.80	5.70	1.40
IX	36.00^{L}	67.00	62.83	2.50	55.60^{H}	10.67	7.56	3.56	96.70	26.14	25.27
X	47.00	74.00	92.53	2.60	35.67	11.00	6.88	3.84	39.67	23.55	9.33
XI	36.00^{L}	68.00	52.53	1.70^{L}	24.00	11.17	9.69^{H}	5.28^{H}	35.48	31.45	10.93
XII	36.00^{L}	64.00^{L}	66.03	3.00^{H}	46.80	11.00	7.93	3.65	66.43	33.33^{H}	22.17
XIII	49.00	82.00	85.53	2.70	23.60	11.33^{H}	7.35	2.45	24.93	29.18	7.20
XIV	49.00	75.00	90.40	3.00^{H}	1.53^{L}	9.00	2.46^{L}	3.64	43.20	1.10^{L}	0.47^{L}
XV	42.00	76.00	70.53	2.90	48.27	9.67	7.64	3.66	104.33^{H}	24.99	26.07^{H}

parents for the recombination breeding programme. The cluster-III and cluster-IX showed maximum inter-cluster distance of 2356.28 followed by cluster III and cluster XII (1910.63), cluster III and cluster VI (1892.61) and cluster III and cluster XV (1779.50) indicating that genotypes included in these clusters are genetically diverse. It indicated that these cluster pairs were most divergent and can be utilized in the hybridization programme for crop improvement as well as for studying the inheritance pattern of different characters in mungbean (Talukdar et al 2020, Goyal et al 2021, Sridhar et al 2022 , Gupta et al 2023 , Anita et al 2024).

The comparison of cluster mean values (Table 5) in mungbean genotypes indicated that cluster-XV had highest mean value for seed yield per plant (26.07) and biological yield per plant (104.33). Cluster-IX had highest value for number of pods per plant (55.60) and the lowest value for days to 50 per cent flowering (36), which is a desirable trait for arid zone. Cluster-VI had maximum mean value for number of seeds per pod (11.33). Cluster-XII had maximum value for harvest index (33.33), number of branches per plant (3.00) and the lowest value for days to 50 per cent flowering (36.00) and days to maturity (64.00); which is a desirable trait for arid zone. Cluster-III had highest value for days to 50 per cent flowering (59.00) and days to maturity (83.00). This comparison indicates that cluster XV, IX, VI, XII and III had better cluster means for most of the characters. Therefore, these clusters may be considered better for selecting genotypes with desirable characters. Similar findings were earlier reported by Goyal et al (2021), Sridhar et al (2022) and Gupta et al (2023) and Anita et al (2024). Amongst the characters, days to 50 per cent flowering contributed highest towards genetic divergence (61.60%) followed by 100-seed weight, biological yield per plant, number of branches per plant, number of pods per plant and seed yield per plant; while the remaining characters contributed little to genetic divergence (Table 3). Consequently, considering both cluster mean and per cent contribution of each character, genotypes belonging to cluster XV, IX, VI, XII and III found promising for use as breeding material in future hybridization programme. Similar results were also earlier reported by Mathankumar et al (2020), Tiwari et al (2022), Gupta et al (2023) and Srivastava et al (2024).

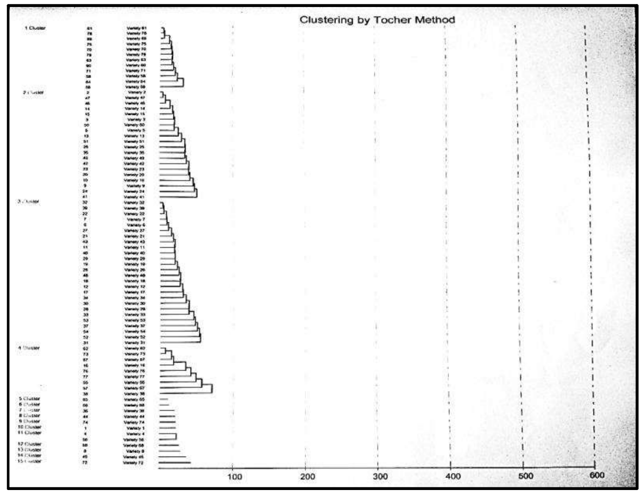

Fig. 1. Clustering pattern of seventy nine mungbean genotypes by Tocher's method

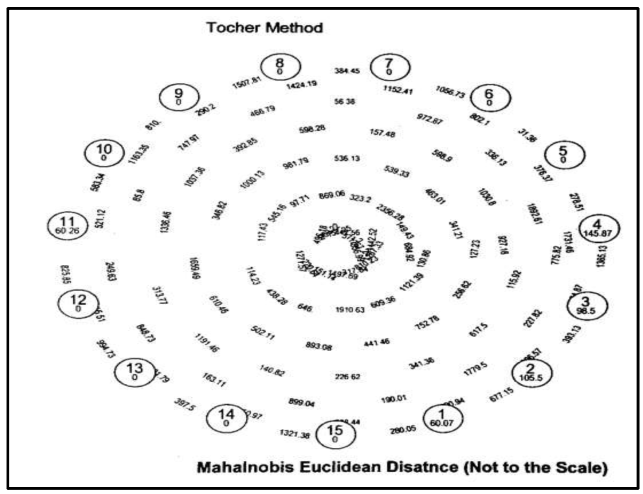

Fig. 2. Divergence average intra and inter cluster distance among grouped seventy nine mungbean genotypes

Table 6. Contribution of eleven characters towards total genetic divergence in mungbean

Name of characters	Per cent contribution of characters
Days to 50% flowering	61.6
Days to maturity	0.19
Plant height	1.59
Number of branches per plant	6.62
Number of pods per plant	4.45
Number of seeds per pod	0.16
Pod length	0.39
100-seed weight	10.00
Biological yield per plant	9.12
Harvest index	2.50
Seed yield per plant	3.38

CONCLUSON

The percentage contribution towards genetic divergence was found high for days to 50 per cent flowering followed 100 seed weight and biological yield per plant. The genotypes of cluster XV, IX, VI, XII and III had maximum inter-cluster distances as well as maximum cluster means for most of the yield component traits indicated that these genotypes were most diverse and good recombinants can be obtain by mating between these genotypes. Hence, these genotypes would be used as parental source for upcoming mungbean breeding programmes.

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