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Research Article

ASSESSMENT OF GENETIC DIVERSITY IN MUNGBEAN [*Vigna radiata* L Wilczek] GENOTYPES

SHARMA S.R.*[1], SINGH D.[2], PAWAN KUMAR[3], KHEDAR O.P.[4] AND VARSHNAY N.[5]

[1,3,4]Division of Plant Breeding and Genetics, Rajasthan Agricultural Research Institute, Durgapura, 302018, Sri Karan Narendra Agriculture University, Jobner, 303329 Rajasthan, India

[2,5]ICAR-Indian Agricultural Statistical Research Institute, New Delhi, 110012, India

*Corresponding Author: Email - sheetalraj.sharma@gmail.com

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Abstract- Sixtyfour mungbean genotypes consisting breeding lines, advanced breeding lines and released varieties were evaluated to explore the extent of genetic diversity. Wilks (statistic) criterion was used to test the significant differences between the genotypes based on the pooled effect of all the characters. The genotypes under investigation demonstrated a wide range of diversity for considered traits. The cluster analysis through Tocher's method distributed the genotypes into eight clusters. Cluster I was largest with maximum 29 genotypes, followed by Cluster III, II and V comprising 9, 8 and 8 genotypes, respectively. The maximum inter cluster D^2 value (20.56) was recorded between cluster VII and VI, while the minimum D^2 value (10.26) was found between cluster VIII and VII. The grain yield/plant was found to be maximum in cluster VI which indicated importance of this cluster in improvement of yield in mungbean. Among all the traits studied 100-seed weight contributed maximum to the diversity, followed by number of clusters/plant, days to flowering (50%) and days to maturity. In the present study, mixed response was observed as the genotypes originating from different eco-geographical regions were grouped together into different clusters as well as in same clusters. It is suggested that diverse parents should be used to produce desirable recombinants for developing new improved mungbean varieties.

Key words- *Mungbean, Cluster analysis, Diversity analysis and Wilks statistics*

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Introduction

Mungbean is self-pollinated legume crop and belongs the family Leguminosae, sub-family Papilionaceae with chromosome number 2n = 2x = 22. It is consumed as dal, halwa, namkeen, snacks and so many other preparations. It is third most important pulse in South Asia after chickpea and pigeonpea. It is cultivated throughout the Southern Asia including India, Pakistan, Bangladesh, Sri Lanka, Cambodia, Vietnam, Indonesia, Malaysia and China. Asia alone contributes 90 percent of mungbean production in the world. In India, an area of 4.32 mha is covered under mungbean with an average production of 2.17 m tonnes and productivity of 502 kg/ha [1]. Genetic divergence among the genotypes is key to successful breeding programmes for yield enhancement. It is clear from divergence studies that the maximum genetic improvement is possible if crosses will be made between the parents with maximum genetic divergence. The divergent parents offer substantial variability that reflects in segregating generations through the production of transgressive segregants. Therefore, grouping of germplasm accessions through cluster analysis will be helpful to categorize the genotypes in different groups according to diversity between them. Such type grouping may help mungbean breeders to identify better combinations of parents to breed high yielding varieties. Thus, in the present experiment was conducted to study genetic divergence between sixty four mungbean genotypes.

Material and methods

In present experiment sixty four mungbean genotypes were grown in randomized block design with three replications at research farm of Rajasthan Agricultural Research Institute, Durgapura, Jaipur, Rajasthan. Three rows of 4 m length were grown with 30 cm of inter row distance with 10 cm inter plant distance.

This experiment was performed to assess genetic divergence among genotypes and nineteen different phenological, morphological, physiological, yield and related traits were recorded. Data of traits like; days to first flower, days to flowering (50%), days to maturity and plot yield were taken on plot basis. Five randomly selected plants were used to record data on traits like; plant height (cm), biomass/plant (g), number of secondary branches, number of clusters/plant, number of pods/cluster, pod length (cm), number of seed/pod, percent flower shed and grain yield/plant. Canopy temperature (˚C) and chlorophyll content was recorded with instruments namely; inferred thermometer and soil plant analyses development 502 (SPAD-502) leaf chlorophyll meter. Relative water content (RWC) and membrane stability index (MSI) was measured in laboratory as per method suggested by Weatherley (1950) [2] and Fletcher and Drexlure (1980) [3] respectively. The data obtained from all traits was analysed in statistical software Indo_Stat.

Results and Discussion

Wilks statistic criterion was used to test the significant differences between the genotypes based on the pooled effects of all the characters which indicated that these sixty four genotypes differed significantly when all the characters were considered simultaneously [Table-1]. The mean values of sixty four genotypes were transformed into standardized uncorrelated mean values using pivotal condensation method. The D^2 values were computed for all the possible pairs of genotypes. Sixty four mungbean genotypes were grouped into eight distinct non over lapping clusters using Tocher's method [4] and distribution of genotypes into each of eight clusters is presented in [Table-2] and illustrated in [Fig-1].

Table-1 Analysis of variance for dispersion in genotypes of mungbean

Source of variation	d.f.	Sum of square	mean square	F ratio	Probability
Genotypes	63	6.70E+21	1.06E+20	1.00E+04	0.000***
Error	125	4.61E+05	3.69E+05		
Total	188	6.70E+21	3.57E+19		

Table-2 Cluster composition of mungbean genotypes (Tocher's method)

SN	Cluster	Number of genotypes	Name of genotypes
1	Cluster I	29	MH-421, SML-832, SKNM-13-06, PAU-911, RMG-1091, SML-832, K-851, SKNM-12-08, SKNM-13-04, SML-134, RMG-975, SKNM-13-07, SKNM-13-03, RMG-1097, Pusa-9531, MH-560, Pusa-871, MH-729, IPM-02-3, MH-805, MH-810, MH-921, MSJ-118, MH-1128, RMG-492, MH-929, Samrat, MH-906, MH-1012
2	Cluster II	8	SKNM-1503, SKNM-1505, SKNM-1506, SKNM-1507, SKNM-12-02, SKNM 12-07, GM-3, GM-4
3	Cluster III	9	SKNM-13-05, SKNM-1501, SKNM-12-14, MUM-2, SML-668, Pant M-5, Pusa Vishal, RMG-1023, SKNM-13-02
4	Cluster IV	1	MH-1113
5	Cluster V	8	IPM 205-7, IPM 409-4, IPM-06-5, HUM-16, MH 1007, MH-318, Sattya, SKNM-1308
6	Cluster VI	7	ML-131, ML-818, ML-613, ML-5, ML-267, SKNM-1509, SML 95-1A
7	Cluster VII	1	GM-06-08
8	Cluster VIII	1	SKNM-13-10

Table-3 Intra-cluster (diagonal) and inter-cluster distances for five clusters in mungbean

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII
Cluster I	9.90	14.26	13.95	11.33	12.51	15.30	14.68	14.20
Cluster II		9.62	14.73	16.65	19.29	15.70	15.94	18.09
Cluster III			11.57	18.99	17.82	19.63	17.17	18.27
Cluster IV				0.00	11.66	13.95	17.02	14.18
Cluster V					12.94	18.96	17.25	15.93
Cluster VI						13.10	20.56	18.41
Cluster VII							0.00	10.26
Cluster VIII								0.00

Table-4 Mean performance of the clusters with respect to different traits

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII
DFF	32.57	35.75	32.30	33.00	31.25	34.43	33.33	32.33
DF (50%)	38.03	42.71	37.41	39.33	36.50	40.71	39.67	37.33
DM	71.06	74.08	72.78	69.67	66.38	79.62	70.67	74.00
PH	55.81	48.45	57.58	63.53	58.45	65.25	47.03	46.03
BM/Pt	24.88	28.08	29.48	17.90	21.17	24.43	27.30	33.13
CT	32.43	30.99	31.69	32.27	33.01	31.83	33.20	33.77
Chl.	382.18	411.83	371.37	323.00	354.33	425.00	438.67	355.00
RWC	81.66	79.61	80.89	77.50	81.15	81.43	78.60	80.83
MSI	80.09	81.22	79.35	82.70	80.24	78.93	79.30	79.60
100-SW	4.07	4.68	4.95	3.56	3.82	3.61	5.34	4.88
NSB	4.25	4.36	4.36	4.13	4.27	3.99	4.07	3.87
NC/Pt	4.43	4.89	5.23	4.13	4.18	4.60	2.80	2.77
NP/C	4.23	3.96	3.32	5.77	4.66	5.08	4.93	6.73
PL	7.91	7.73	8.23	7.90	8.07	8.23	7.60	8.10
NS/P	11.20	10.59	11.57	10.60	11.14	11.91	11.30	10.40
NP/Pt	17.53	17.76	15.43	21.67	18.31	20.71	12.60	16.90
% FD	11.57	11.28	12.10	11.40	11.73	11.77	11.20	12.10
GY/Pt	6.39	7.35	7.19	6.78	6.28	7.56	6.19	7.18
PY	419.04	475.16	466.11	435.97	416.00	475.41	408.80	478.40

Table-5 Contribution of different quantitative traits to diversity in mungbean

SN	Traits	Times Ranked 1st	% Contribution
1	Days to first flower	0	0.00
2	Days to flowering (50%)	352	17.46
3	Days to maturity	311	15.43
4	Plant height	9	0.45
5	Biomass/plant	97	4.81
6	Canopy temperature	0	0.00
7	Chlorophyll	51	2.53
8	RWC	0	0.00
9	MSI	0	0.00
10	100-seed weight	529	26.24
11	No. of secondary branches	7	0.35
12	No. of clusters/plant	507	25.15
13	No. of pods/cluster	90	4.46
14	Pod length	0	0.00
15	No. of seed/pod	5	0.25
16	No. of pods/plant	49	2.43
17	% Flower shed	1	0.05
18	Grain yield/plant	5	0.25
19	Plot yield	3	0.15

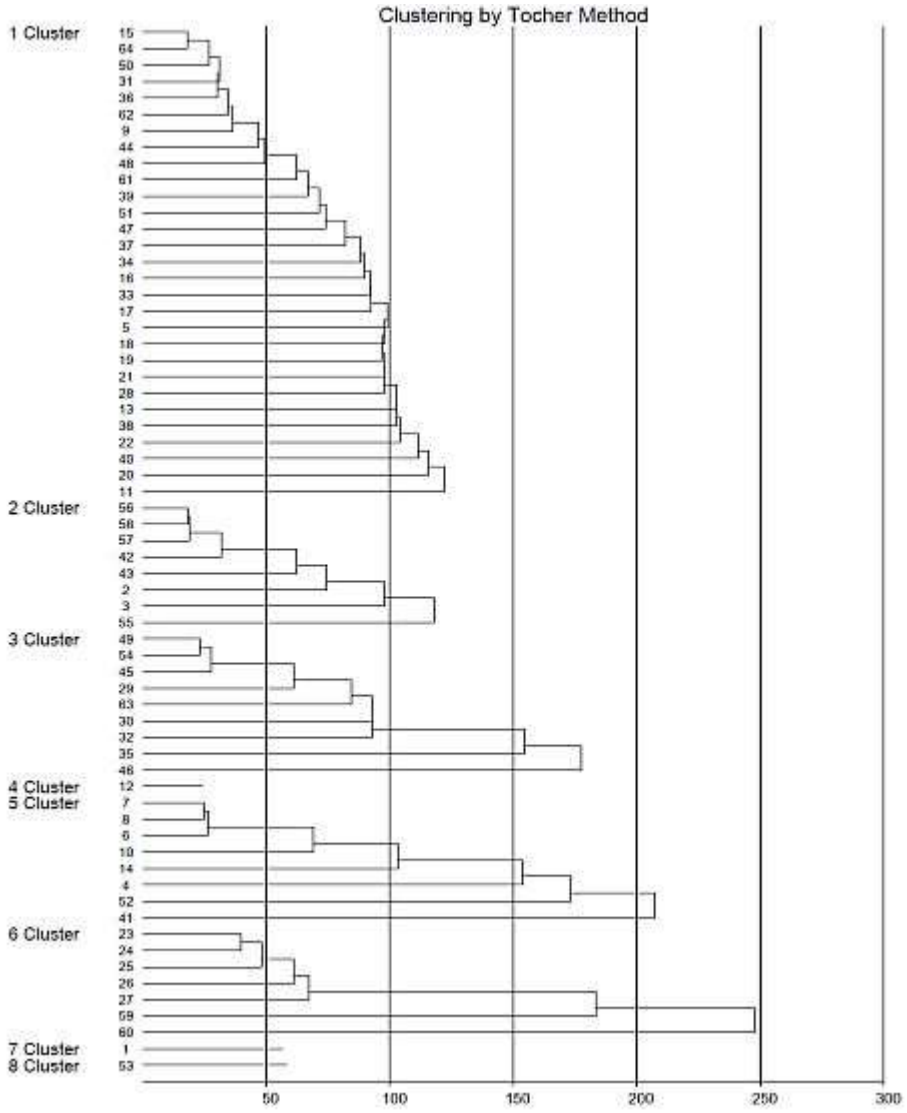

Fig-1 Cluster diagram of mungbean genotypes by Tocher's method

Cluster I was the largest with twenty nine genotypes followed by cluster III with nine genotypes, while the clusters IV, VII and VIII were solitary cluster consisting one genotype. Among the clusters, cluster VI had the maximum intra cluster distance (13.10), while the clusters IV, VII and VIII recorded zero values as they were solitary clusters. The maximum inter cluster D^2 value was recorded between cluster VII and VI (20.56), while the minimum D^2 value was found between cluster VIII and VII (10.26), [Table-3]. The maximum inter-cluster distance suggesting highest genetic divergence obtainable between the genotypes of these clusters and expected to give greater frequency of better transgressive segregants or anticipated combinations for development of useful genetic stocks or varieties. Similar outcomes were also reported by Gadakh *et al*. (2013) [5], Singh *et al*. (2014) [6] and Madhuri *et al*. (2017) [7]. It is generally assume that the parents with more diversity involved in crossing programme give more heterosis than the closely ones (Singh, 1991) [8]. Several researchers' *viz*., Abna *et al*. (2012) [9] and Patel and Patel (2012) [10] also gave emphasis on need of high genetic diversity to create the high genetic variation and genetic gain under selection. Considerable differences were observed between clusters means for all the traits under study. Cluster II was late to first flower, 50% flowering and maturity (35.75, 42.71 and 74.08 days), while cluster V was earliest (31.25, 36.50 and 66.38 days) similarly cluster VI was tallest (65.25 cm), while cluster VIII was smallest to plant height (46.03 cm). The genotypes in cluster IV had maximum pods/plant (21.07) while, cluster VII had minimum (12.60). Likewise grain yield/plant was found to be maximum and minimum in cluster II (7.19 g) and VII (6.19 g) while the cluster mean for plot yield was highest in cluster VIII (478.40 g) and lowest in cluster VII (408.80 g), [Table-4]. The selection and choice of parents mainly depend upon contribution of traits towards divergence. The number of times that each of the nineteen traits appeared in first rank and its respective percent contribution towards diversity is presented in [Table-5]. Among all the traits studied 100-seed weight contributed maximum (26.24%) to the diversity by taking first rank in 529 times out of 2016 combinations, followed by number of clusters/plant (25.15% with 507 times ranked first), days to 50% flowering (17.46% with 352 times ranked first) and days to maturity (15.43% with 311 times ranked first). Since these traits are important in contributing maximum towards divergence in mungbean, these traits could be exploited maximum in order to get the superior varieties with high yield [Table-5]. Similar pattern of results were also reported earlier by Tiwari *et al*. (2012) [11] for days to maturity and seed yield; Garje *et al*. (2013) [12] for seed yield; Prakash and Shekhawat (2012) [13] for days to 50% flowering and days to maturity; Prasanna *et al*. (2013) [14] for seed yield and days to maturity and Swathi (2013) [15] for seed yield and relative injury. On contrary, days to first flower, canopy temperature, RWC, MSI and pod length had negligible contribution towards genetic divergence. In the present study, mixed response was observed as the genotypes originating from different eco-geographical regions were grouped together into different clusters as well as in same clusters. The genotypes originating from Rajasthan, Uttar Pradesh, Gujarat, Punjab and Haryana have been grouped together into same cluster I [Table-2]. On contrary, the genotypes originating from Vadodara and Sardar Krushi Nagar of Gujarat have been distributed into different clusters indicating that geographic diversity though important may not necessarily be the only factor in determining genetic diversity. Hence, the clustering pattern obtained in the present study designated that the genotypes originating from different geographical regions grouped together into

different clusters show no or little relationship between genetic diversity and geographical distribution. Genetic drift and selection in different environments might have caused greater diversity than geographical distance. These results were also in confirmity with Patel and Patel (2012) [10], Garje *et al*. (2013) [12], Prasanna *et al*. (2013) [14] and Madhuri *et al*. (2017) [7]. This implies that the selection of parents for hybridization based on geographical origin would be arbitrary. The pattern of grouping in genotypes from same source into different clusters as observed in present investigation may be due to free exchange of breeding material among different regions, there by the character assemblage associated with a particular region, in nature lose their individuality under human interference.

Conclusion

Sixty four mungbean genotypes were grouped into eight clusters through Tocher's method. Cluster I was largest with maximum 29 genotypes, followed by Cluster III, II and V comprising 9, 8 and 8 genotypes, respectively. The maximum inter cluster D2 value (20.56) was recorded between cluster VII and VI so crosses will be most productive among these clusters. 100-seed weight contributed maximum to the diversity. In the present study, mixed response was observed as the genotypes originating from different eco-geographical regions were grouped together into different clusters as well as in same clusters.

Application of research: Diversity analysis is key for successful plant breeding programmes. Crosses among most divergent clusters will be more productive.

Research Category: Plant Breeding and Genetics

Abbreviations: DFF- days to first flower, DF (50%)- days to flowering (50%), DM- days to maturity, PH- plant height, BM/Pt- biomass/plant, CT- canopy temperature, Chl.- chlorophyll content, RWC- relative water content, MSI- membrane stability index, 100-SW- 100-seed weight, NSB- number of secondary branches, NC/Pt- number of clusters/plant, NP/C- number of pods/cluster, PL- pod length, NS/P- number of seed/pod, NP/Pt- number of pods/plant, % FW- percent flower shed, GY/Pt grain yield/plant and PY- Plot yield.

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