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Estimation of Genetic Diversity in Mungbean [*Vigna radiata* (L.) Wilczek] Genotypes Grown in Gujarat

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ABSTRACT

Background: Genetically diverse parents give an increased chance of genetic recombination and superior expression of hybrid vigour. Mahalanobis D^2 statistics is an important tool for calculating the amount of genetic diversity in the populations and for assessing the relative contribution of various components to the total genetic divergence.

Methods: Thirty genotypes of mungbean [*Vigna radiata* (L.) Wilczek] were grown in a randomized block design with four replications at S.D.A.U., Gujarat during *kharif*, 2019 to study genetic diversity. By using Mahalanobis's D^2 statistics, all possible 435 pairs of thirty genotypes were computed for ten characters.

Result: D^2 analysis indicated that material was genetically diverse. Twelve clusters were formed by dividing the genotypes. To become highly genetically diverse, the inter-cluster distance should be high (Distance between cluster XI and cluster IX; cluster XI and cluster X), which can be used for hybridization programme. Cluster X followed by cluster I found appropriate for within group hybridization due to the presence of most heterogeneous genotypes indicating high intra-cluster value. Cluster data revealed that genotypes in cluster X, cluster VIII and cluster IV had desirable traits for yield improvement. These clusters could be directly selected for breeding programme. Contribution to total divergence was higher from number of branches per plant, pod length and 100-seed weight.

Key words: Cluster, D^2 analysis, Genetic diversity, Mahalanobis D^2, Mungbean.

INTRODUCTION

In India, pulses occupy second place next to cereal in terms of vegetarian diet. High protein of pulses makes it rich man's vegetable and poor man's meat. WHO (World Health Organization) recommends to consume 80 g pulses for a person in a day, but *per capita* availability is only 42 g/ person/day.

Mungbean is a diploid which has 2n = 2x = 22 chromosomes and self-polinating nature. It is also known as greengram, goldengram, greenbean, greensoy, moong and mashbean. The center of origin for mungbean is not known exactly, but it might have originated in Hindustan and Central Asiatic region. In the world, mungbean cultivation is carried out in countries like India, Pakistan, Burma, Nepal, Bangladesh, Sri Lanka, Thailand, Indonesia, Philippines and Africa continent. Maharashtra, Gujarat andhra Pradesh, Tamil Nadu, Uttar Pradesh and Bihar are the Indian states which cultivate mungbean (Singh *et al*., 2010; Inbasekar, 2014; Kumar and Kumar, 2014). Mungbean has nutrition like 24 to 25% protein, 1.3% fat, 3.5% minerals, 4.1% fiber, 56% carbohydrate, 124 mg/100 g calcium, 326 mg/100 g phosphorus, 7.3 mg/100 g iron, 334 kcal/100 g calorific value, 10 per cent moisture, 83 mg/ 100 g (Anonymous, 2017).

The major limiting factors for pulses production and productivity in our country are the non-availability of high yielding varieties which can tolerate environmental fluctuations to greater extent. Therefore, plant breeders want to study the genetic diversity in the varieties/germplasm. Genetically diverse parents generally produce high heterotic effects (Griffing and Lindston, 1954). For hybridization programme diverse genotype with broad genetic background should be selected as parents for bringing together higher frequency of desirable genes in a strain and to greater the possibility of generating broad spectrum of variability in segregating generation.

Selection of parents should be dependent on the number of important attributes collectively rather than individually for improving complex quantitative characters such as seed yield. Processes to measure divergence between population using Multivariate analysis are coefficient of racial likeness (Pearson, 1926), Discriminant function (Fisher, 1936), multiple regression (Hotelling, 1936) and D^2 statistics (Mahalanobis,1936). Among these, Mahalanobis (1936) D^2 statistics quantify the degree of divergence in populations at genetic level and assess the

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relative contribution of various components to the overall genetic divergence.

MATERIALS AND METHODS

Experiment season was *kharif*, 2019. Experiment site was Agronomy Instructional Farm, C.P. College of Agriculture, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar, Gujarat, India. The experimental site represents typical sub-tropical climate with semi-arid and arid condition. Total thirty genotypes of greengram were selected from the Pulses Research Station, S.D.A.U., Sardarkrushinagar (Table 1). Randomized block design (RBD) with four replications were used to grow complete sets of 30 genotypes. Inter raw spacing was 45 cm and intra-raw spacing was 10 cm as well as single plot of 3 m length was prepared for each genotype.

The observations were recorded as visual assessment and measurement on individual plants (five competitive randomly selected plants per genotype in each replication). Ten characters *viz*., days to flowering, days to maturity, plant height (cm), number of branches per plant, number of pods per plant, number of seeds per pod, pod length (cm), 100-seed weight (g), protein content (%) and seed yield per plant (g) were studied.

Genetic divergence was computed with the method of Mahanobis's D^2 (Mahalanobis, 1936). Tocher's method was used to group the genotypes in different clusters (Rao, 1952). Average intracluster distance and average intercluster distance were obtained by using the method suggested by Singh and Chaudhary, 1977.

RESULTS AND DISCUSSION

ANOVA (analysis of variance) showed that differences in the genotypes were highly significant for all the traits, which indicated an ample scope to identify desirable genotypes to improve various traits.

Mahalanobis's D^2 statistics computed 435 pairs by using data of ten characters of 30 genotypes. The generalized distance (D) between two populations varies from 0.00 (intra cluster) to 19.456 (inter cluster) which indicates that there was a considerable diversity existed in the genotypes studied for the majority of the characters.

Cluster composition

Total twelve clusters were formed and their compositions are given in Table 2. Largest cluster was Cluster I with 10 genotypes followed by cluster II (7 genotypes), clusters III, V and X (each with 2 genotypes) and clusters IV, VI, VII, VIII, IX, XI and XII were with one genotype each.

D^2 analysis was done by many workers in this crop. Based on divergence Rahim *et al*. (2010) found 3 clusters from 26 genotypes, Sunil *et al*. (2011) found 8 clusters from 129 genotypes, Titumeer *et al*. (2014) found six clusters from 50 genotypes, Abbas *et al*. (2018) grouped 58 genotypes into four clusters and Mahalingam *et al*. (2018) grouped 445 genotypes into three clusters.

Intra and inter-cluster distance

The result of intra and inter-cluster distance (D) between all possible pairs of twelve clusters are shown in Table 3. Also, cluster diagram (Fig 1) showing the interrelationship among clusters. Intracluster divergence means the divergence between the genotypes of the same cluster. Intercluster divergence indicates the divergence between the genotypes of the different clusters.

Result showed that the intercluster distance (D) ranged from 5.721 to 19.456. Minimum intercluster distance (D = 5.721) was observed between clusters XI and XII. It indicated the presence of similarity in the genetic architecture of the genotypes of one cluster and another cluster. Maximum intercluster distance (D = 19.456) was observed between clusters IX and XI. It indicated the entire differences in the genetic architecture of genotypes of one cluster to another cluster.

Considering the highest intercluster distance, LM-584 (belonging to cluster XI) was genetically divergent to LM-1 (belonging to cluster IX) and GM-4 and GAM-5 (belonging to cluster X) which can be used for hybridization programme.

Table 1: Details of the mungbean genotypes and their origin/source.

Name of genotypes	Source
Guj-1	
PIMS-1	
A-59-7	
A-61-1	
LAM-GG-127	
GP-229-B	
SML-68	
M.GP-124-B	
LM-141	
MBC-5	
LM-554	
LM-578	
No-223 (1)	
LM-584	Pulses Research Station, S.D.A.U., Sardarkrushinagar-385 506, District: Banaskantha, (Gujarat).
CM-512	
LM-2	
LM-1	
LM-389	
PS-10	
LM-7	
LM-359	
LM-34	
TT8E × 345	
LM-385	
LM-350	
LM-353	
Chaklama-2	
LM-309	
GM-4	
GAM-5	

Range of intra cluster distance (D) was 0.000 to 5.639. Highest intracluster value (D = 5.639) was noticed for cluster X followed by cluster I (D = 5.295) which indicated that genotypes of these clusters were most heterogeneous, probably have different genetic architecture and these clusters were the best for within group hybridization. Lowest intra cluster value (D = 4.199) was noticed for cluster III which proved that these accessions were passed through similar evolutionary factors than other cluster's genotypes. As the clusters IV, VI, VII, VIII, IX, XI and XII contains solitary genotype no intracluster distance has been worked out (D = 0.000 each). Earlier researchers like Singh *et al.* (2009) found five mono selection clusters, Gokulakrishnan *et al.* (2012) and Panigrahi and Baisakh (2014) each found two clusters with solitary genotype, Gadakh *et al.* (2013) and Ahmad *et al.* (2016) each found three mono selection clusters.

The result revealed wide divergence (Fig 1) and substantial genetic diversity in the studied material for majority of the characters. Singh *et al.* (2009), Gokulakrishnan *et al.* (2012), Panigrahi and Baisakh (2014), Sunil *et al.* (2011), Titumeer *et al.* (2014) also found significant genetic diversity in this crop.

In heterosis breeding, inter-crossing between parents belonging to most divergent clusters are assumed to

Table 2: The distribution of thirty mungbean genotypes to various clusters on the basis of D^2 statistic.

Clusters	Number of genotypes	Genotypes
I	10	LM-141, LM-353, LM-350, Guj-1, SML-68, M.GP-124-B, LM-34, LM-385, LM-7, LM-554
II	7	PIMS-1, A-59-7, LM-309, TT8E × 345, Chaklama-2, PS-10, LAM-GG-127
III	2	LM-578, No-223(1)
IV	1	GP-229-B
V	2	A-61-1, LM-389
VI	1	LM-359
VII	1	LM-2
VIII	1	MBC-5
IX	1	LM-1
X	2	GM-4, GAM-5
XI	1	LM-584
XII	1	CM-512

Table 3: Average intra (bold) and inter-cluster values (D^2 and D) ($D = \sqrt{D^2}$) for thirty genotypes of mungbean.

Clusters	Values	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII
I	D^2	28.042	55.444	82.842	33.400	58.141	78.122	65.900	47.401	168.349	130.648	89.174	63.266
	D	5.295	7.446	9.102	5.779	7.625	8.839	8.118	6.885	12.975	11.430	9.443	7.954
II	D^2		22.956	44.353	33.084	45.366	33.023	40.106	114.522	68.631	105.213	176.177	104.321
	D		4.791	6.660	5.752	6.735	5.747	6.333	10.701	8.284	10.257	13.273	10.214
III	D^2			17.630	68.497	98.770	50.783	83.144	169.398	53.137	144.267	229.991	181.053
	D			4.199	8.276	9.938	7.126	9.118	13.015	7.290	12.011	15.165	13.456
IV	D^2				0.000	43.551	42.230	39.836	52.422	123.359	93.794	129.923	65.220
	D				0.000	6.599	6.498	6.312	7.240	11.107	9.685	11.398	8.076
V	D^2					19.266	87.265	33.010	81.611	118.709	80.139	129.882	54.718
	D					4.389	9.342	5.745	9.034	10.895	8.952	11.397	7.397
VI	D^2						0.000	56.689	146.427	74.021	161.340	234.687	158.695
	D						0.000	7.529	12.101	8.604	12.702	15.319	12.597
VII	D^2							0.000	110.385	79.564	50.460	215.148	118.622
	D							0.000	10.506	8.920	7.104	14.668	10.891
VIII	D^2								0.000	292.722	160.164	76.075	52.051
	D								0.000	17.109	12.656	8.722	7.215
IX	D^2									0.000	121.941	378.521	268.078
	D									0.000	11.043	19.456	16.373
X	D^2										31.800	295.904	180.682
	D										5.639	17.202	13.442
XI	D^2											0.000	32.735
	D											0.000	5.721
XII	D^2												0.000
	D												0.000

produce maximum amount of heterosis. However, to improve a specific character in breeding programme, it is advised to choose the donor from an appropriate cluster.

Cluster means of various quantitative traits

Cluster means of ten traits of thirty genotypes are shown in Table 4. Cluster data showed that genotypes in cluster X had medium pod (8.22), maximum 100-seed weight (4.37), maximum protein content (21.88) and maximum seed yield per plant (5.19); genotypes in cluster VIII had maximum number of branches per plant (1.00) and more number of pods per plant (20.36); genotypes in cluster XI had maximum number of branches per plant (1.00), late flowering (55.75), lowest number of pods per plant (10.35) and minimum seed yield (2.10); genotypes in cluster XII were late maturing (84.75) and tallest (98.90); genotypes in cluster III were early maturing (59.38), medium heighted (53.85) and with minimum number of seeds per pod (10.09); genotypes in cluster IV had the highest mean value for number of seeds per pod (12.08); genotypes in cluster V had the lowest protein content (20.14); genotypes in cluster VI were short podded (6.46) and with lowest 100-seed weight (2.56); genotypes in cluster IX were early flowering (38.75) and with lowest number of branches per plant (0.00).

These results indicated that cluster X which contained the popular check varieties GM-4 and GAM-5 with most desirable characters, could be directly selected and utilized

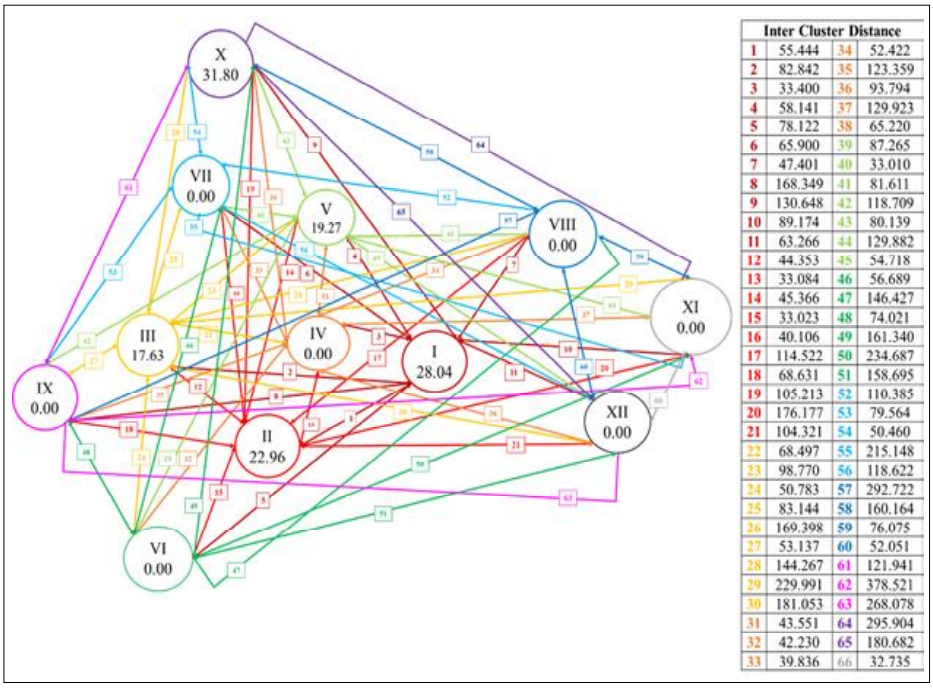

Fig 1: Cluster diagram indicating interrelationship between twelve clusters using D^2 analysis (D^2 value) (not to scale).

Table 4: Cluster means for ten traits in thirty genotypes of mungbean.

Clusters	Days to flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of pods per plant	Number of seeds per pod	Pod length (cm)	100-seed weight (g)	Protein content (%)	Seed yield per plant (g)
I	45.15	72.80	74.04	0.72	15.72	10.59	6.90	2.90	21.84	3.33
II	44.54	70.14	77.81	0.37	15.26	10.19	6.78	3.10	21.69	3.50
III	39.25	59.38	53.85	0.40	11.50	10.09	6.60	3.08	21.30	2.80
IV	48.75	73.75	68.40	0.50	15.30	12.08	6.90	3.16	20.70	3.95
V	46.63	74.38	89.93	0.53	15.06	10.26	7.33	3.40	20.14	3.65
VI	45.00	73.25	61.20	0.20	17.18	11.04	6.46	2.56	20.76	3.00
VII	42.50	74.00	75.75	0.40	17.39	10.89	7.66	3.28	20.67	4.70
VIII	47.25	75.75	77.50	1.00	20.36	10.51	6.60	3.12	21.14	4.27
IX	38.75	60.00	64.45	0.00	11.56	10.50	7.44	3.48	21.09	2.88
X	41.00	66.25	74.25	0.50	16.07	10.71	8.22	4.37	21.88	5.19
XI	55.75	80.25	93.30	1.00	10.35	10.96	6.75	2.65	21.03	2.10
XII	54.50	84.75	98.90	0.75	11.94	11.25	6.92	3.11	20.38	3.22

Table 5: Per cent contribution of various traits to the total genetic divergence.

Characters	Number of times characters ranked first	Per cent contribution
Days to flowering	6	1.38
Days to maturity	20	4.60
Plant height (cm)	26	5.98
Number of branches per plant	208	47.81
Number of pods per plant	14	3.22
Number of seeds per pod	7	1.61
Pod length (cm)	77	17.70
100-seed weight (g)	55	12.64
Protein content (%)	21	4.83
Seed yield per plant (g)	1	0.23
Total	435	100.00

for breeding programme. Also, it is advised to cross between genotypes from most distance clusters with high mean performance to achieve desirable transgressive segregants.

Per cent contribution of different traits towards divergence

The selection of parents mostly depends on contribution of various traits towards divergence. The component of D^2s (because of each character variable) were ranked in descending order of magnitude (highest value has given rank I). The component of D^2 is the squares of difference in the transformed uncorrelated mean values related to that character variable. The total of these ranks in all possible 435 combinations provides indirect knowledge of the order of priority in the forms of percentage contribution of the trait to the total divergence. This per cent contribution of various traits towards divergence is shown in Table 5.

Number of branches per plant was the greatest contributor to the total divergence *i.e.,* 208 times (47.81 %) out of 435 . The next larger contributors are pod length (77 cases or 17.70 %) followed by 100-seed weight (55 cases or 12.64 %), plant height (26 cases or 5.98 %), protein content (21 cases or 4.83 %), days to maturity (20 cases or 4.60 %), number of pods per plant (14 cases or 3.22 %), number of seeds per pod (7 cases or1.61 %), days to flowering (6 cases or 1.38 %) and seed yield per plant (1 cases or 0.23 %). Similar trend noticed by Singh *et al.* (2009) and Rekha *et al.* (2015) for 100-seed weight.

CONCLUSION

Genetic diversity using D^2 analysis indicated that material studied was genetically diverse. The genotypes were partitioned into twelve clusters. Considering the highest inter-cluster distance, LM-584 (belonging to cluster XI) was genetically divergent with LM-1 (belonging to cluster IX) and with GM-4 and GAM-5 (belonging to cluster X) which can be used for hybridization programme. Intra-cluster value was highest for cluster X followed by cluster I which indicated that genotypes of these clusters were most heterogeneous and these clusters were the best for within group hybridization.

Cluster data revealed that genotypes in cluster X (GM-4 and GAM-5) had medium pod (8.22 cm), maximum 100-seed-weight (4.37 g), maximum protein content (21.88 per cent) and maximum seed yield per plant (5.19 g); genotypes in cluster VIII (MBC-5) had maximum number of branches per plant (1.00) and more number of pods per plant (20.36); cluster IV (GP-229-B) had the highest mean value for number of seeds per pod (12.08). These clusters could be directly selected and utilized for breeding programme. Traits like number of branches per plant, pod length and 100-seed weight were found greater contributors to total morphological divergence.

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