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Genetic diversity studies for quantitative characters in green gram (*Vigna radiata* (L.) Wilczek)

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Abstract
The present investigation was undertaken to examine the genetic divergence in 41 germplasm lines including one check *viz*.BM-2003-2 for 11 yield and yield contributing characters using Mahalanobis D^2 statistics for selection of suitable parents that can be utilized in hybridization programme. The experiment was carried out at Agricultural Research Station, Badnapur during *kharif* 2016-17. Observations were recorded on 11 characters *viz.* days to 50% flowering, days to maturity, plant height, number of clusters per plant, number of pods per cluster, number of pods per plant, pod length, number of seeds per pod, 100 seed weight, protein content and seed yield per plant. All the 41 genotypes evaluated were grouped in to seven clusters. Cluster I with 22 genotypes emerged as largest cluster followed by cluster IV and clusters VI with six genotypes each and cluster V with four genotypes. The clusters II, III and VII had single genotype. The maximum intra clusters distance was observed for cluster V followed by cluster VI, cluster IV and cluster I. Suggesting the genotypes present in these clusters possessing varied genetic architecture and might have originated from different genetic pool. The maximum inter-cluster distance was observed between cluster VII and cluster VI, suggesting that the genetic architecture of the genotypes in one cluster differ entirely from those included in other clusters. The crosses involving parents from these divergent clusters are expected to yield good amount of heterosis in F_1 and desirable segregants and genetic variability in subsequent generations. Among the eleven characters, the pods per plant contributed maximum amount towards divergence.

Keywords: Germplasm, divergence, D^2 statistics

Introduction
Green gram (*Vigna radiata* (L.) Wilczek) is one of the most important pulse crop in India. The origin of green gram is supposed to be India (De candolle, 1886; Vavilov, 1926; and Zukoveskij 1962) [3, 16, 18]. It is cultivated in three seasons *viz. Kharif, Rabbi and Summer* as a sole crop or an intercrop. It improves the nutritional status of soil (Asthana, 1998) [2] by atmospheric nitrogen fixation. Green gram is a cheap and rich source of digestible protein for vegetarians as compared to meat, fish and eggs. It is also a source of vitamin B and essential amino acids and sprouts are rich in vitamin C and E. It is an important part of daily diet of human being because of its nutritional properties. During the year 2015-16 in India area under green gram cultivation is 2.45 m ha and annual production of green gram is 2.13 m tonnes with an average yield of 632 kg/ha. In Maharashtra 5.11 lakh ha area is under cultivation and 2.89 lakh tonnes production with average productivity of 566 Kg/ha. Maharashtra contributes 16.19 per cent area with 13.46 per cent production as a part of the nation (average of last ten years) (Anonymous 2015-16) [1]. Andhra Pradesh, Telangana, Maharashtra, Gujrat, Orrisa and Tamilnadu are the major green gram producing states.

Genetic divergence, which is due to genetic factors, is the basis for heritable improvement. It is one of the criteria of parent selection for hybridization programme. For effective breeding programme, prescribed information about genetic divergence is important. The genetically diverse parents are known to produce higher heterotic effects and consqently give desirable recombinations in the breeding material. To determine the genetic diversity through biometrical procedures such as Mahalanobis's D^2 Statistic has made possible to choose genetically diverse parents. It is observed that Mahalanobis's generalized distance is an efficient tool in quantitative estimation of genetic diversity (Mahalanobis, 1936) [6]. Therefore, the present investigation was undertaken for identification, classification of genotypes through D^2 analysis for yield and yield components, to identify the diverse parents and to group various genotypes into suitable clusters.

Materials and Methods

The present investigation is carried out to study the genetic diversity in Green gram (*Vigna radiata* (L.) Wilczek) with 40 germplasm lines of green gram and one check *viz*. BM 2003-2 during *Kharif* 2016-17 at Agricultural Research Station, Badnapur. The experimental material comprised of 41 genotypes including one check *viz*.BM 2003-2 received from Agricultural Research Station, Badnapur were grown in a randomized block design with two replications during *Kharif* 2016-17. The standard packages of practices were followed to raise a good crop. At maturity data were recorded on five randomly selected plants from each replication for eleven different characters *viz.*, days to 50% flowering, days to maturity, plant height, number of clusters per plant, number of pods per cluster, number of pods per plant, pod length, number of seeds per pod, 100 seed weight, protein content and seed yield per plant. For analysis of variance standard statistical method was used. Genetic diversity was found through cluster analysis by following Tocher's method as described by Singh and Chaudhary, (1977) [14] and D^2 statistics proposed by Mahalanobis (1936) [6] as described by Rao (1952) [12].

Results and Discussion

The analysis of variance showed significant differences for all the characters studied indicating wide genetic divergence among them. Based on D^2 values, forty one genotypes were grouped into seven clusters (Table 1). The cluster I was with the highest number of genotypes (22 genotypes) followed by cluster IV and clusters VI both were with 06 genotypes each and cluster V with 04 genotypes. The clusters II, III and VII had single genotype. The clustering pattern of genotypes showed that genetic diversity was not related to geographic diversity suggesting that collection of germplasm genetically viable for different characters. Wide diversity also reported by earlier workers where Ramana and Singh (1987) [11] grouped 39 genotypes into 8 clusters. Similarlly Manivannan (1998) [7] grouped 30 genotypes into 8 clusters. However, Venkatakrishna *et al.* (2000a) [17] grouped 40 genotypes into 8 clusters and Shweta (2013) [13] grouped 77 genotypes into 9 clusters.

The average intra and inter cluster D^2 was presented in Table 2.The highest intra cluster distance was observed for cluster V (D=9.65) followed by cluster VI (D=9.53), cluster IV (D=8.82) and cluster I (D=6.69). The maximum inter cluster distance (D =21.26) was observed between cluster VII and cluster VI, followed by cluster VI and V (D = 15.89), cluster VII and cluster V (D=15.88), cluster V and cluster III (D = 14.65). Parents selected from these individual groups showing maximum inter cluster distance are likely to produce superior recombinatants. Natrajan *et al.* (1988) [9] have also opined that selection of parents for hybridization should be done based on the inter cluster distance to get maximum variability. The minimum inter cluster distance (D = 3.83) was between cluster III and II followed by cluster IV and cluster II (D=6.84). The minimum inter cluster distance (D = 3.83) between III and II indicating that this cluster is less divergent. Similar results were also observed by Murthy and Arunachalam (1966) [8].

The cluster mean for the eleven characters are presented in Table 3.The cluster mean for days to 50 per cent flowering lowest for cluster VII (36.00) and highest for cluster VI (42.50). Days to maturity was lowest in cluster VII (53.00) and highest in cluster VI (70.17). The highest cluster mean for plant height was 66.20 cm, which was observed in cluster III and lowest for cluster VI (44.25cm). The cluster mean for the number of clusters per plant ranged from 6.95 (cluster I) to 10.01 (cluster V). The cluster mean for pods per cluster ranged between 3.57 (cluster VI) and 4.95 (cluster II). The cluster mean for number of pods per plant was maximum in cluster V (34.56) and it was minimum in cluster I (21.49). The cluster mean for pod length recorded lowest in cluster III (6.05) and recorded highest in cluster I (10.09). The cluster mean for number of seeds per pod was maximum in cluster V (13.13) and it was minimum in cluster VI (10.07). The cluster mean for 100 seed weight was minimum in cluster II (3.11 g) and it was maximum in cluster I (4.75 g). The cluster mean for seed yield per plant was lowest for cluster III (7.82g) and highest for cluster V (16.82 g). The cluster mean for protein content was maximum in cluster VI (23.97%) and minimum in case of cluster III (20.48%).

The per cent contribution of eleven characters studied, towards total divergence represented in Fig. 1. It was observed that among all the traits, number of pods per plant (26.34%) contributed highest for divergence followed by pod length (17.32%), seed yield per plant (14.51%), days to 50% flowering (9.76%), protein content (8.66%), plant height (8.17%), days to maturity (5.37%), number of pods per cluster (3.41%), number of seeds per pod (3.05%), 100 seed weight (2.56%) number of clusters per plant (0.85%). Similar results were observed by Ghaderi *et al.* (1979) [4], Thulsidas (1984) [15], Venkatakrishna *et al*. (2000) [17] and Pandey (2007) [5] for number of pods per plant contributed maximum to diversity. Selection based on this will be useful for improving seed yield in green gram.

Table 1: Disribution of forty one green gram genotypes into different clusters

Cluster No.	No. of genotypes	Genotypes included in the cluster
I	22	BMG 4-9-2, BMG 11-1, BMG 14-1,BMG 31-1, BMG 43-1, BMG 43-2, BMG 44, BMG 45, BMG 45-2, BMG 59-1, BMG 60-1, BMG 63, BMG 64, BMG 64-2, BMG 64-3, BMG 65, BMG 66, BWMCD 51,BWMT 42-1-2, BWMF 3-1,BWMF 16, BM 2003-2
II	1	BMG 37
III	1	BMG 62
IV	6	BMG 42-1, BMG61-2, BMG 69-1, BWMCD 6-39, BWMCD 61, BWMUC 8-1
V	4	BMG 1-3, BWMCD1-6, BWMT 40-1-6, BWMF1-3
VI	6	BWMT 2-1, BWMT 40-1-10, BWMF 2-1, BWMUC 5-1-8, BWMUC 6-1, BWMUC 22-1-2-1
VII	1	BMG 54-2

Table 2: Average intra and inter cluster distance (D^2) values for 41 genotypes in green gram

Cluster No.	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
Cluster I	44.76	91.78	103.43	122.77	111.72	193.77	182.52
Cluster II		0.000	14.67	46.79	187.70	140.42	170.56
Cluster III			0.00	60.84	214.62	169.00	162.82
Cluster IV				77.79	209.96	179.56	160.78
Cluster V					93.12	252.49	252.17
Cluster VI						90.82	451.99
Cluster VII							0.000

Table 3: Mean performance of different clusters for different yield and yield component traits in green gram

Character	Days to 50% flowering	Days to maturity	Plant height	Number of clusters per plant	Number of pods per clusters	Number of pods per plant	Pod length	Number of seeds per pod	100 seed weight	Seed yield per plant	Protein content
Cluster I	38.82	62.27	59.33	6.95	3.71	21.49	10.09	12.77	4.75	10.52	21.58
Cluster II	40.00	66.50	62.00	7.31	4.95	29.26	6.75	11.70	3.11	8.26	21.44
Cluster III	41.50	64.00	66.20	7.20	4.30	27.16	6.05	12.00	3.28	7.82	20.48
Cluster IV	39.75	63.42	51.07	7.06	4.61	25.68	6.98	11.53	3.32	9.20	21.75
Cluster V	40.00	63.00	49.98	10.01	3.98	34.56	9.38	13.13	4.35	16.82	22.47
Cluster VI	42.50	70.17	44.25	8.14	3.57	25.48	7.52	10.07	4.42	9.90	23.97
Cluster VII	36.00	53.00	49.20	7.51	4.95	27.58	6.40	12.70	3.42	10.17	22.23

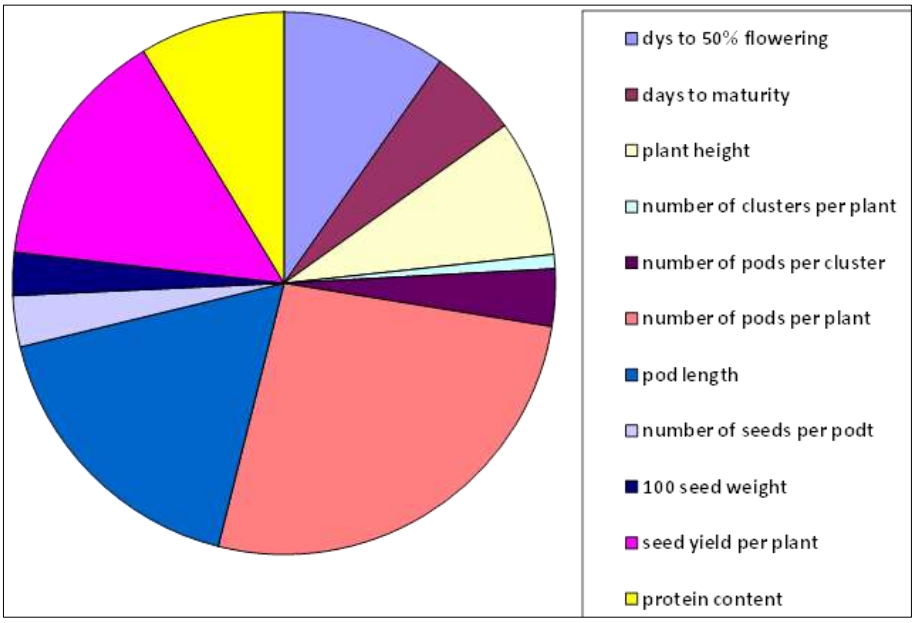

Fig 1: Percent contribution of eleven characters to the total diversity in mungbean

Conclusion

It can be concluded from the findings that the genotypes falling in the cluster V, VI, IV and I were highly divergent from each other implying large amount of diversity within and between groups, which is helpful in breeding programmes. The present study suggest that inter cluster distance is an important factor while selecting parents for hybridization that may provide wide spectrum of variation in the segregating generations and crosses involving parents from these divergent clusters are expected to yield good amount of heterosis in F_1.

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