GENETIC DIVERSITY ANALYSIS OF GREEN GRAM (*VIGNA RADIATA (L.) WILCZEK.*)

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ABSTRACT
Forty genotypes of green gram used to study the nature and magnitude of genetic divergence using Mahalanobis's D^2 Statistics. The data for ten important quantitative traits recorded from the genotypes raised in Randomized Block Design having three replications. The forty Green gram genotypes were grouped into thirteen clusters. Cluster III was largest with ten genotypes followed by cluster II with eight genotypes. The maximum inter-cluster distance was observed between cluster VIII and IV, suggesting that the genetic architecture of the genotypes in one cluster differ entirely from those included in other clusters. Three characters viz. Seed yield per plant (g), No. of pod per plant, and Pod length (cm) contributed maximum in manifestation of genetic diversity. Seed yield per plant had maximum Phenotypic and Genotypic Coefficient of Variation (PCV and GCV), followed by number of pods per plant. High magnitude of heritability (broad sense) was recorded for number of pod per plant. High heritability coupled with high genetic advance was observed for plant height and number of pod per plant suggesting that, the role of additive gene effect and possibilities of achieving high genetic progress through selection. The genotypes KM-09-152, KM-09-156, KM-09-183, BM-2005-1, Vaibhav, KM-09-187, KM-09-173 and KM-09-158 were identified as genetically diverse parents, which can be utilized for future crop improvement programme

INTRODUCTION

The green gram (*Vigna radiata* L. Wilczek) is one of the important pulse crop because of its adaptation to short growth duration, low water requirement, soil fertility and is favoured for consumption due to its easy digestibility and low production of flatulence (Shil and Bandopadhya, 2007). Average protein content in the seeds is around 24%. The protein is comparatively rich in lysine, an acid predominantly deficient in cereal grains (Baskaran *et al*., 2009). One of the constraints listed for lack of breakthrough in green gram production has been the lack of genetic variability for high yield potential (Ramanujam, 1978). Improvement in the grain yield of green gram is rather slow in comparison with other cereal grains. As green gram is a self-pollinated species, considerable variation exists among the green gram cultivars and within its related species (Bisht *et al*., 2005). Yield components are the primary objectives under study for crop improvement as because Grafius (1978) suggested that there may not be genes for yield *per se* but rather for the various components, the multiplicative interactions of which result in the artefact of yield. In any program aimed at genetic amelioration of yield, genetic diversity is the basic requirement. Effective hybridization program between genetically diverse parents will lead to considerable amount of heterotic response in F₁ hybrids and broad spectrum of variability in segregating generations. Mahalnobis D² statistics is a powerful tool in quantifying the degree of variability at the genotype level. The utility of multivariate analysis have greatly been emphasized (Murty and Arunachalam, 1966). Several workers studied

the genetic diversity, clustering pattern, relative contribution of different characters toward divergence and effectiveness of selection (Venkateswarlu, 2001; Manivannan *et al*., 2002; Patil *et al*., 2003; Bisht *et al*., 2005). So, the present experiment was formulated to study the genetic divergence and clustering pattern of the green gram genotypes for selection of suitable parents for utilizing in hybridization programme and to study the genetic parameters attributing to yield.

MATERIALS AND METHODS

The experimental material comprising forty genotypes of green gram was grown during *Kharif*, 2010 in a Randomized Block Design with three replication at Post Graduate Institute, Mahatma Phule Krishi Vidyapeeth, Rahuri. Data were recorded on five randomly tagged plants for *viz*., days to 50 per cent flowering, plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of clusters per plant, number of pods per plant, pod length, number of seeds per pod, 100 seed weight, and seed yield per plant. Wilks (1932) criteria was used to test the significance differences in mean values of all the ten characters.

Statistical analysis: Mahalanobis (1936) defined the distance between two populations as D^2, which was obtained by Tochers method, described by Rao (1952). Contribution of individual characters towards divergence was estimated according to the method described by Singh and Choudhary (1985). Grouping of variety into various clusters was done and average intra and inter cluster distance were estimated. The experimental data was analyzed statistically by the method

of analysis of variance for single factor (Gomez and Gomez, 1984) and lastly to find out the significance mean difference between varieties different genetic parameters were estimated.

RESULTS AND DISCUSSION

Significant differences were observed among forty genotypes of Green gram for all characters under study. The relative contribution of different characters towards divergence showed Seed yield per plant (g) contributed maximum towards divergence followed by number of pods per plant and Pod length (cm) which was also observed by Naidu and Satyanarayana (1991), Manivannan *et al.* (2002) and Raje and Rao (2000). Gupta and Singh (1970) found that the same characters are positively associated with yield and are the main yield components.

The parameters of genetic variability revealed high PCV and GCV values for seed yield per plant, number of pod per plant number of secondary branches per plant, number of cluster per plant and pod length respectively, indicating that these traits could be used as selection indices for yield improvement, similar finding were reported by Natarajan *et al.* (1998) and Makeen *et al.* (2007).

Number of pods per plant and Seed yield per plant (g) exhibited high values of heritability (in broad sense). Similar findings have been reported by Natarajan *et al.* (1988) for number of pods per plant and Venkuteshwarlu (2001) for seed yield per plant record high heritability. Number of pods per plant and plant height exhibited high heritability with high genetic advance; these results were in accordance with Das *et al.* (1998) for plant height, and number of pods per plant.

The forty genotypes studied were grouped into thirteen clusters by using Tocher's methods described by Rao (1952), cluster I with 7 genotypes, cluster II with 8 genotypes, cluster III with ten genotypes, cluster V with 4 genotypes, cluster XI with 3 genotypes and cluster IV, V, VI, VII, VIII, IX, XII, and XIII were monogenotypic. Highest inter cluster distance is observed between cluster VIII and IV (D = 11.46) followed by inter cluster VIII and V (D = 10.18), inter cluster XI and V (D = 10.10) and inter cluster VI and IV (D = 10.01) indicating wide divergence among the clusters. This also suggests that genetic architecture of the lines in one cluster differs entirely from those included in the other cluster. Cluster means were found highest for different characters (Table 2). Cluster ten showed highest mean performance for plant height, No. of secondary branches per plant and 100 Seed weight (g). Cluster IV recorded maximum performance for primary branches per plant and seed yield per plant, Cluster V showed higher mean performance for number of clusters per plant and number of pod per plant, Cluster XIII for pod length and seed per pod and clusters VII for days to 50% flowering.

Average intra and inter cluster D^2 values among forty genotypes revealed that cluster IV, VI, VII, VIII, IX, X, XII and XIII showed no intra-cluster D^2 value as it had only one genotypes each (Table 3). The cluster V showed maximum intra cluster D^2 value (4.56) followed by cluster II (3.81), cluster III (3.75) and cluster XI (3.66) revealing the inclusion of diversion of diverse genotypes in these clusters. In the present investigation, D^2 values between all possible selections of forty genotypes ranged between 2.92 (Between genotype AKM-9914 and Km-09-178) to 124.69 (between genotype Km-09-187 and Vaibhav). This high range of D^2 values showed the presence of good amount of diversity in the material used for the present study. Minimum inter cluster D^2 value was observed between cluster VI and VIII (3.28) indicating the close relationship among the genotypes included in these two clusters. As the D^2 values represent the index of genetic diversity among the cluster, it would be more appropriate to make cross between genotypes separated by high estimates of statistical distance. Bhat (1970) and Raman and Singh (1987) suggested that genotypes belonging to clusters separated by high genetic distance may be used in hybridization program to obtain a wide spectrum of variation among the segregates and in the present study similar suggestion had been made. The genotypes included in the diverse clusters namely, IV, V, VI, VII, VIII and XI hold good promise as parents for obtaining potential hybrids and thereby creating greater variability of these characters to improve the yield.

So from the above result it can be concluded that the genetic diversity was not related to geographic diversity. Among the 40 genotypes, Km-09-183 belonging to cluster VIII and Km-09-152 belonging to cluster IV has the highest intercluster distance and can be used for hybridization program to obtain better transgressive seregants. Two characters viz. Number

Table 1: Distribution of forty genotypes of green gram into different clusters

Cluster No.	No. of genotypes included	Name of genotypes
C1	7	Akm-9914, Km-09-178, Km-09-167, Km-09-177, Pm-2, Pm-202-10, Akm-07-204
C2	8	Kopergaon, Pm-203-13, Km-09-181, Akm-9911, Km-09-159, Pm-2002-23, Pm-2007-9, Km-09-155
C3	10	Km-09-188, Akm-9910, Akm-8802, Km-09-161, Km-09-169, Km-09-184, Pm-2002-48, Bm-2002-1, Bpmr-145, Km-09-157
C4	1	Km-09-152
C5	4	Bm-2005-1, Vaibhav, JLM-7, Akm-08-01
C6	1	Km-09-156
C7	1	Km-09-158
C8	1	Km-09-183
C9	1	Bm-2003-2
C10	1	Bm-2004
C11	3	Km-09-187, Km-09-173, Akm-07-227
C12	1	Km-09-166
C13	1	Akm-603

Table 2: Mean performance of clusters for 10 characters in green gram

Sr.No.	Cluster	Day to 50 % flowering	Plant height (cm)	No. of primary branches per plant	No. of secondary branches per plant	No. of cluster per plant	No. of pod per plant	Pod length (cm)	No. of seed per pod	100 seed weight (g)	Seed yield per plant (g)
1.	C1	40.81	43.10	2.58	5.92	7.29	18.68	8.47	11.32	3.44	7.87
2.	C2	45.38	48.04	2.88	5.65	7.83	19.98	6.86	10.52	3.72	6.96
3.	C3	42.40	41.80	2.68	5.29	5.56	13.11	8.32	10.46	3.73	5.26
4.	C4	41.33	49.03	3.17	6.27	7.73	20.50	9.03	11.10	2.80	9.87
5.	C5	41.17	47.70	3.13	6.18	9.53	24.68	8.77	12.15	3.88	8.71
6.	C6	41.33	40.90	2.13	3.70	4.70	9.63	6.73	8.47	2.43	2.70
7.	C7	52.33	50.00	2.83	5.57	5.23	9.97	5.50	7.83	2.47	2.57
8.	C8	51.67	48.90	1.70	2.47	5.67	11.43	6.00	8.60	3.67	2.57
9.	C9	46.00	38.07	2.27	3.70	6.70	20.27	6.57	7.60	4.90	7.73
10.	C10	39.00	55.23	2.93	6.40	7.63	16.53	10.33	11.43	5.13	6.70
11.	C11	40.00	32.10	2.38	3.39	5.23	11.77	6.44	7.86	4.08	5.61
12.	C12	37.67	38.53	3.00	3.23	7.67	21.73	7.23	9.30	3.47	8.20
13.	C13	46.67	33.60	2.27	3.17	5.53	11.53	10.70	12.37	3.50	4.73

Table 3: Average intra and inter cluster D² values from 40 genotypes of green gram

Sr.No.	Cluster	C1	C2	C3	C4	C5	C6	C7	C8	C9	C10	C11	C12	C13
1.	C1	3.36	4.44	5.14	4.25	5.22	7.24	6.58	8.62	6.46	5.08	7.45	5.74	7.30
2.	C2		3.81	5.93	5.95	4.78	7.18	5.89	7.75	5.92	6.08	7.85	5.20	8.25
3.	C3			3.75	7.55	7.71	4.67	4.85	6.29	6.72	4.80	5.74	7.01	4.74
4.	C4				0.00	5.60	10.01	9.00	11.46	8.15	6.80	9.67	6.81	9.84
5.	C5					4.56	9.51	8.33	10.18	7.95	6.73	10.10	6.34	9.81
6.	C6						0.00	3.82	3.28	6.73	7.28	4.92	7.25	4.57
7.	C7							0.00	4.86	7.11	6.57	6.71	7.75	6.65
8.	C8								0.00	6.83	8.35	6.02	7.86	5.98
9.	C9									0.00	8.58	5.01	3.69	8.33
10.	C10										0.00	8.38	8.38	6.53
11.	C11											3.66	6.44	6.07
12.	C12												0.00	8.40
13.	C13													0.00

of pods per plant and Seed yield per plant (g) exhibited high heritability estimates (in broad sense). These characters should be given importance for further improvement of yield and yield components.

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