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Genetic diversity for yield and its component traits in green gram [*Vigna radiata* (L.) Wilczek]

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ABSTRACT

Genetic diversity analysis is a powerful tool in quantifying the degree of divergence between biological populations and to assess the relative contribution of different components of total divergence. The present investigation aimed to study the genetic divergence and clustering pattern of 50 genotypes of Green gram (Vigna radiata L. Wilczek) for selection of suitable parents that can be utilized in hybridization programme and to study the genetic parameters attributing to yield. The crosses of genotypes from cluster I, i.e. Kopergaon, Vaibhav, BM-4 and BM-2005-1 with those of genotypes BM-2003-2, PM-203-18, AKM-9907 and AKM-08-01 belonging to cluster III and RVSM-11, PM-201-19, ML-1354, AKM-0603 belonging to cluster II has the highest intercluster distance and might produce high level of segregating population in regards to yield as well as earliness. Among the thirteen characters the protein content contributed maximum amount towards divergence. High heritability estimates coupled with high genetic advance was observed for harvest index and biological yield per plant resembling the action of additive genes in controlling these particular characters and selection would be rewarding for yield improvement.

Keywords: Cluster, D^2 technique, genetic diversity, green gram

Pulses are extensively grown in tropical regions of the world as a major protein rich crop bringing considerable improvement in human diet. 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 favored for consumption due to its easy digestibility and low production of flatulence (Shil and Bandopadhyay, 2007). Creation of variability and selection of superior recombinants among the variants are the major objective of any plant breeding programme. As green gram is a self pollinated species considerable variation exists among the green gram cultivars and also 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 artifact 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. The utility of multivariate analysis have greatly been emphasized (Murty and Arunachalam, 1966). 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.

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MATERIALS AND METHODS

The experiment was conducted in the Botany farm of College of Agriculture, Latur, Maharashtra, India during 2010-2011. The experimental site is 18°24' N latitude and 76°36' E longitude with an altitude of 633.85 m above the mean sea level and topographically the land is medium low. The soil of the experimental field was found typical alluvial soil (Vertisol) having clay loam texture, neutral in reaction and moderate in soil fertility status. Fifty genotypes of green gram were collected from all over India and grown in a Randomized Block Design with three replications in a plot size of 18.2 × 3 m^2 for *kharif* season. Observations were recorded from five plants from the middle rows of the plot excluding the border plants, regarding fifteen characters, namely days to 50% flowering, days to 50% maturity, plant height, plant spread, number of primary branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, number of seeds per pod, length of pod, biological yield per plant, harvest index, 100-seed weight, grain yield per plant and protein content.

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 Chandhary (1985). 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

The analysis of variance revealed significant difference among the accession for all the characters studied indicating the existence of a wide genetic divergence among them. Based on D2 values, 50 genotypes were grouped into 7 clusters on the assumption that genotypes within the cluster have similar D2 values among themselves than those from groups belonging to two different clusters (Table 1). Cluster I has the highest number of genotypes *i.e*., 22. Cluster II has 18 genotypes, followed by cluster III which has 5 genotypes. Clusters VII have 2 genotypes. The mono-genotypic cluster was cluster IV, V and VI. Wide diversity was also reported by earlier workers, where Raman and Singh (1987) grouped 39 genotypes into 8 clusters. Similarly, Loganathan *et al.* (2001a) grouped 42 F3 and eight varietal genotypes into seven clusters; Das *et al.* (2010) grouped 23 genotypes in 8 clusters. The clustering pattern of the genotypes showed that genetic diversity was not related to geographic diversity. Such a type of constellation of germplasm proves that the collection made were genetically viable for different characters. The clustering pattern of the strains revealed that there was no close correspondence between geographical distribution and genetic divergence as estimated by the D^2 statistic.

Table 1: Distribution of fifty genotypes in to different clusters

Cluster No.	No. of genotypes included	Genotypes
I	BPMR-156, MGG-359, KM-2268, CGG-973, AKM-9911, PUSA-971, BM-4, ML-1472, AKM-8802, PM-2001-23, AKM-07-204, AKM-07-227, PM-203-13, PM-207-9, MGG-360, Kopergaon, BM-2005-1, BPMR-48, Vaibhav, AKM-9914, IPM-02-09-3, NDMZ-09-18	22
II	ML-131, KM-2272, PM-201-5, PM-2, PM-201-19, AKM-0603, ML-1354, SG-33-05, GM-05-08, PM-2001-48, AKM-08-02, GM-04-02, RMG-987, AKM-9910, MH-709, BM-2002-1, RVSM-11, JLM-7	18
III	BM-2003-2, BM-2004, PM-203-18, AKM-9907, AKM-08-01	5
IV	PUSA-0972	1
V	BPMR-75	1
VI	SG-63-14	1
VII	BPMR-145, PM-2001-19	2

Table 2: Intra and inter cluster D^2 and D values of seven clusters from fifty genotypes of green gram

Clusters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
Cluster I	**15.086**	21.829	39.236	18.385	18.149	23.864	19.666
	(3.884)	(4.672)	(6.264)	(4.288)	(4.280)	(4.885)	(4.435)
Cluster II		**15.582**	26.212	29.96	23.928	21.237	23.349
		(3.947)	(5.120)	(5.474)	(4.892)	(4.608)	(4.832)
Cluster III			**13.052**	46.127	39.736	27.822	38.025
			(3.613)	(6.792)	(6.304)	(5.271)	(6.166)
Cluster IV				**0.00**	18.241	25.04	22.036
				(0.00)	(4.271)	(5.004)	(4.694)
Cluster V					**0.00**	17.605	17.872
					(0.00)	(4.196)	(4.228)
Cluster VI						**0.00**	22.814
						(0.00)	(4.776)
Cluster VII							**14.22**
							(3.771)

Note: Diagonal figures indicate intra cluster distance. Figures in parentheses indicate the 'D' value.

The intra and inter cluster D2 value among 7 clusters are presented in table- 2. The maximum intra cluster distance was observed in the cluster II (D=3.947), followed by cluster I (D=3.884), cluster VII (D=3.771) and cluster III (3.613) suggesting that genotypes included in these clusters might have different genetical architecture. Further maximum inter-cluster distance was observed between the cluster III and IV (D=6.792) followed by cluster III and V (D=6.304), cluster I and III (D=6.264) and cluster III and VII (D=6.166), indicating wide divergence among these clusters (Figure 1). This also suggests that the genetic architecture of the genotypes in one cluster differs entirely from those included in the other cluster. The minimum inter cluster distance was observed between cluster V and VI (D=4.196)

followed by cluster V and VII (D=4.228) and cluster IV and V (D=4.271). The lower D value between their characters suggested that the genetic constitutions of these genotypes in one cluster were in close proximity with those genotypes in other clusters. The three mono selection clusters showed zero index cluster distance. Similar results were reported earlier by Natarajan *et al.* (1988) with only one monogenotypic cluster and also Naidu and Sathyanarayana (1991) reported 7 mono-genotypic clusters, suggesting parallelism with the present study.

The relative contribution of different characters towards divergence showed protein content (57.47%) contributed maximum towards divergence followed by biological yield per plant (14.69%), number of primary branches per plant (9.71%), plant height (4.65%), length of pod (4.16%) and grain yield per plant (3.35%) which was also observed by Naidu and Satyanarayana (1991), Manivannan *et al.* (2002) and Raje and Rao (2000). Gupta and Singh (1970) found that these characters are positively associated with yield and are the main yield components.

Considering the clustering pattern, PUSA-0972 were found to be genetically divergent from BM-2003-2, BM-2004, PM-203-18, AKM-9907 and AKM-08-01. Again, BPMR-75 the only variety in cluster V was genetically divergent from BPMR-145 and PM-2001-19. The genotypes BM-2003-2, BM-2004, PM-203-18, AKM-9907 and AKM-08-01 belonging to cluster III and PUSA-0972 belonging to cluster IV has the highest intercluster distance (46.12) and can be used for hybridization programme (Table 2).

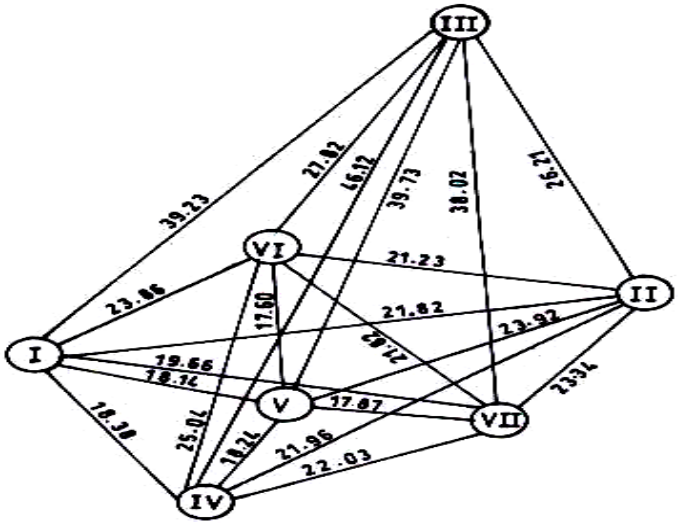

Fig. 1: Cluster diagram showing interrelationship among seven clusters using D^2 analysis (not to scale)

Table 3: Mean performance of different clusters for different characters in green gram

Cluster No.	Days to 50 % flowering	Days to maturity	Plant height (cm)	Plant spread (cm)	Primary branches plant--1	No. of clusters	No. of pods cluster^{-1}	No. of pods
I	39.17	68.68	74.26	36.51	1.83	5.78	3.47	20.12
II	39.06	68.76	74.56	36.51	1.92	5.25	3.42	18.27
III	38.73	68.00	75.13	36.38	1.48	6.03	3.45	19.97
IV	39.00	69.00	64.97	37.10	1.33	6.78	3.10	18.87
V	40.67	71.33	77.17	39.63	2.17	4.87	3.63	18.53
VI	39.00	69.00	80.10	37.37	1.77	6.63	3.63	20.87
VII	39.67	70.00	76.70	37.20	1.58	6.23	2.77	15.42

Table 4: Mean performance of different clusters for different characters in green gram

Cluster No.	Seeds pod^{-1}	Length of pod (cm)	Biological yield plant^{-1} (g)	Harvest index (%)	100 seed weight (g)	Protein content (%)	Seed yield plant^{-1} (g)
I	11.26	7.93	50.74	7.51	2.71	24.9713	3.63
II	11.48	8.33	42.69	8.91	2.85	22.07	3.41
III	11.69	8.50	46.47	8.14	3.11	17.71	3.55
IV	11.17	7.07	66.50	4.77	2.30	26.45	3.17
V	12.30	8.23	81.33	3.94	3.30	24.51	3.21
VI	11.17	7.78	76.00	3.47	2.00	21.58	2.63
VII	12.20	10.32	60.83	4.73	3.92	24.60	2.85

The existance of diversity among the genotypes was also assessed by considerable amount of variation in cluster mean for different characters (Table 3, 4). The genotypes in cluster III, I and II were the early maturing. The genotypes in cluster VI, V and VII were tallest and cluster IV had the dwarf genotype. The cluster mean for length of pod ranged from 7.1cm to 10.3cm, which were attained by cluster IV and VII respectively. The maximum number of pods per plant was noticed in cluster VI (20.8) while minimum was observed in cluster VII (15.4). Less number of primary branches per plant was recorded by the individual in the cluster IV (1.33), while more number was seen in cluster V (2.1). The minimum grain yield per plant was produced by the genotypes in clusters VI (2.6 g). The higher grain yield per plant was recorde by the genotypes in clusters I (3.6 g). So from the above result it can be concluded that the genetic diversity was not related to geographic diversity. Among the 50 genotypes, the genotypes from cluster I, *i.e.* Kopergaon, Vaibhav, BM-4 and BM-2005-1 with those of genotypes from cluster I, *i.e*. Kopergaon, Vaibhav, BM-4 and BM-2005-1 with those of genotypes BM-2003-2, PM-203-18, AKM-9907 and AKM-08-01 belonging to cluster III and RVSM-11, PM-201-19, ML-1354, AKM-0603 belonging to cluster II has the highest inter cluster distance and might produce high level of segregating population in regards to yield as well as earliness. Two characters *viz*., biological yield per plant and plant height exhibited high heritability estimates coupled with high genetic advance which resembles the action of additive genes in controlling these particular characters. These characters should be given importance for further improvement of yield and yield components.

REFERENCES

Bisht, I. S., Bhat, K.V., Lakhanpaul, S., Latha, M., Jayan, P. K., Biswas B. K. and Singh, A. K. 2005. Diversity and genetic resources of wild vigna species in India. *Genet. Resour.*, **52:** 53-68.

Das, A.M., Biswas and Dastidar, K.K.G. 2010. Genetic divergence in greengram (*Vigna radiate* L. Wilczek). *Scialert.net/abstract/doi : J.* 2010. 126-30.

Gomez, K. A. and Gomez, A. A. 1984. *Statistical Procedure for Agricultural Research.* 2nd Edn., Wiley Interscience, New York.

Grafius, J. E., 1978. Multiple characters and correlated response. *Crop Sci.,* **18:** 931-34.

Gupta, M.P. and Singh, K.B. 1970. Genetic divergence for yield and its components in green gram. *Indian J. Genet.,* **30:** 212-21.

Loganathan, P., Saravanan, K. and Ganesan, J. 2001a. Genetic variability in green gram (*Vigna radiata* L.) Wilczek). *Res. Crops,* **2**: 396-97.

Mahalanobis, P.C. 1936. On the generalized distance in statistics. *Proc. Nat. Inst. Sci.,* **2:**49-55.

Manivannan, N. 2002. Genetic Diversity in cross derivatives of green gram. *Legume Res*., **25:**50-52.

Murty, B.R. and Arunachalam, V. 1966. The nature of genetic divergence in relation to breeding system in crop plants. *Indian J. Genet*., **26:** 188-98.

Naidu, N.V. and Satyanarayana, A. 1991. Studies on genetic divergence over environments in mung bean (*Vigna radiata* L. Wilczek). *Indian J. Genet.*, **51:** 454-60.

Natarajan, C., Thiyagarajan, K. and Rathnaswamy, R. 1988. Association and genetic diversity studies in green gram [*Vigna radiata* (L.) Wilczek]. *Madras Agric. J*., **75:**238-45.

Raje, R.S. and Rao, S.K. 2000. Association analysis for yield and its components in mung bean (*Vigna radiata* (L.) Wilczek) in mung bean. *Legume Res.,* **23:** 42-48.

Raman, M.V. and Singh, D.P. 1987. Genetic divergence in mung bean [*Vigna radiata* (L.) Wilczek]. *Genome*, **30:** 835-37.

Rao, C. R., 1952. *Advanced Statistical Methods in Biometrical Research*. John Wiley and Sons, New York.

Shil, S. and Bandopadhyay, P.K. 2007. Retaining seed vigour and viability of mung bean by dry dressing treatments. *J. Food Legumes*, **20:** 173-75.

Singh, R.K. and Chaudhury, B.D. 1985. Biometrical methods of quantitative genetic analysis. *Haryana J. Hort. Sci*., **12:**151-58.