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Genetic Divergence in Green Gram (*Vigna radiata* L. Wilczek)

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Abstract: An experiment was carried out at Bidhan Chandra Krishi Viswavidyalaya, Nadia, India to study the genetic divergence and clustering pattern of 23 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. All the genotypes were grown in RBD in three replications and observations were recorded from ten plants regarding six characters namely days to first flower, Number of pods per plant, Number of seeds per pod, days at 80% maturity, seed yield per plant (g) and 100 seed weight (g). Grouping of genotypes into various clusters was done by Mahalnobis D^2 statistics. The experimental data was analyzed statistically by the method of analysis of variance for single factor and lastly to find out the significance mean difference between varieties, different genetic parameters were estimated. The analysis of variance for all characters revealed highly significant differences among all genotypes suggesting the presence of substantial genetic variability. The 23 strains were grouped into 8 clusters with genotypes SML-175, Malda-95-22 belonging to cluster VII and T-44 and SML-286 belonging to cluster V has the highest intercluster distance and can be used for hybridization programme. Among the six characters the number of seeds per pod contributed maximum amount towards divergence. High heritability estimates coupled with high genetic advance was observed for seed yield per plant and number of seeds per pod resembling the action of additive genes in controlling these particular characters and selection would be rewarding for yield improvement.

Key words: Genetic diversity, genetic parameters, transgressive segregants, yield, heterosis

INTRODUCTION

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 Bandopadhya, 2007). Average protein content in the seeds is around 24%. The protein is comparatively rich in lysine, an amino acid predominantly deficient in cereal grains (Baskaran *et al*., 2009).

Creation of variability and selection of superior recombinants among the variants are the major objective of any plant breeding programme. One of the constraints listed for lack of break through 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 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 F_1 hybrids and broad spectrum of variability in segregating generations. Mahalnobis D^2 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, 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.

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MATERIALS AND METHODS

Experimental material and design: The experiment was conducted in the Mondouri farm of Bidhan Chandra Krishi Viswavidyalaya, West Bengal, India during 2002-2003. The experimental site is 22° N latitude and 89° E longitude with an altitude of 9.75 m above the mean sea level and topographically the land is medium low. The soil of the experimental field was found typical alluvial soil (Entisol) having clay loam texture, neutral in reaction and moderate in soil fertility status. Twenty three germplasms of green gram (MM-6, SML-264, SML-32, A-264, SML-134, 83-M (S), 83-M, BM-18 (S), BM-18, LM-23 (S), Sheela, T-44, Midnapur Local, A-89 (S), SML-175, Malda-95-22, SML-286, MM-25 (S), BR-3, RI-64, RI-65, Datan Chaitali and Datan Sonamung) were collected from all over India and grown in a Randomized Block Design with three replications in a plot size of 10×5 m for two seasons. Observations were recorded from ten plants from the middle rows of the plot excluding the border plants, regarding six characters namely days to first flower, no. of pods per plant, no. of seeds per pod, days at 80% maturity, seed yield per plant (g) and 100 seed weight (g).

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 Chandhary (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

The analysis of variance for all characters revealed highly significant differences among all genotypes suggesting the presence of substantial genetic variability. From the study of mean performance of the genotypes it was found that SML-175 (12.20), Malda-95-22 (11.33), A-89 (S) (10.50) and LM-23 (S) (9.38) had more no. of seeds per pod (Table 1). No of pods per plant was highest in Datan Chaitali (48.68), followed by T-44 (42.83), RI-64 (42.80) and SML-264 (41.33). Genotypes Sheela and MM-6 required minimum times for 80% maturity among the other genotypes.

Regarding grouping of genotypes all the 23 genotypes were grouped into 8 clusters on the assumption that germplasms within the cluster have similar D^2 values among themselves than those from groups belonging to two different clusters (Table 2). Cluster I has the highest number of genotypes i.e., 6. Cluster II has 5 genotypes, followed by cluster IV which has 3 genotypes. Clusters III, V, VI and VII have 2 genotypes each. The only monogenotypic cluster was cluster VIII (83-M). The clustering pattern of the

Table 1: Mean performance of six characters of 23 genotypes of Green gram

Genotypes	Days to first flower	No. of pods per plant	No. of seeds per pod	Days at 80% maturity	Seed yield/plant (g)	100 seed weight (g)
MM-6	35.85	36.78	4.53	57.12	4.4	2.68
SML-264	37.75	41.33	7.57	73.02	7.28	2.3
SML-32	45.33	27.48	7.57	72.18	6.62	3.03
A-264	34.6	34.08	8.05	74.4	7.1	2.53
SML-134	37.75	35.9	6.5	70.18	9.83	2.2
83-M(S)	35.28	35.42	5.05	70.07	4.57	2.55
83-M	36.55	18.08	4.43	67.53	2.4	3.07
BM-18(S)	38.28	17.9	6.8	64.45	3.5	3.07
BM-18	43.78	26.67	8.52	75.32	6.52	2.88
LM-23(S)	38.07	31.95	9.38	64.45	8.43	2.88
Sheela	37.2	12.77	5.7	56.7	1.77	2.57
T-44	43.62	42.83	4.12	81.77	5.2	3.07
Midnapur local	46.18	21.35	6.78	71.1	4.9	3.05
A-89(S)	38.12	33.65	10.5	69.43	10.02	2.57
SML-175	48.32	28.5	12.2	73.57	7.35	2.18
Malda-95-22	45.35	21.85	11.33	82.88	50.53	2.28
SML-286	36.43	35.78	4.52	79.95	5.75	3.3
MM-25(S)	50.1	40.45	8.23	77.05	10.5	3.03
BR-3	45.78	26.85	8.33	68.78	5.62	2.72
RI-64	37.1	42.8	5.47	69.57	7.25	3.05
RI-65	41.05	25.65	8.17	74.75	5.95	2.95
Datan Chaitali	37.42	48.68	8.38	74.85	10.85	2.65
Datan Sonamung	42.22	37.12	9.27	73.15	10.4	3.28
SE	0.623	0.353	0.055	0.455	0.122	0.029
CD	1.304	0.739	0.115	0.952	0.255	0.06

Table 2: Grouping of genotypes into different clusters

Clusters	No. of genotypes	Genotypes	Source
I	6	BM-18, RI-65, BR-3, SML-32, A-267, Midnapur Local	Maharastra, West Bengal, Gujrat, Punjab, Rajasthan, West Bengal,
II	5	SML-264, SML-134, Datan Chaitali, MM-25(S), Datan Sonamung	Punjab, Punjab, West Bengal, Mayanmar, West Bengal
III	2	BM-18(S), Sheela	Maharashtra, West Bengal
IV	3	83-M(S), MM-6, RI-64	Gujrat, Mayanmar, Tripura,
V	2	SML-286, T-44	Punjab, Maharashtra
VI	2	LM-23(S), A-89(S)	Tripura, West Bengal
VII	2	SML-175, Malda-95-22	Punjab, West Bengal
VIII	1	83-M	Rajasthan

Table 3: Average intra and inter cluster distance (D^2) values

Cluster	I	II	III	IV	V	VI	VII	VIII
I	33.171	57.740	55.080	86.703	133.8340	79.158	112.036	90.664
II		44.246	93.615	86.556	133.6610	80.214	125.567	115.79
III			29.751	91.052	137.6680	107.158	134.07	69.081
IV				34.406	68.8260	144.556	187.66	64.105
V					32.4510	198.744	236.837	82.24
VI						35.86	68.45	160.168
VII							46.529	181.168
VIII								0

Table 4: Estimation of genetic parameters and percentage contribution of different characters towards genetic divergence

Characters	Genotypic coefficient of variation (GCV)	Phenotypic coefficients of variation (PCV)	Heritability (Broad sense)	Genetic advance	Genetic advance as % over mean	% contribution of different characters towards divergence
Days to first flower	11.27	11.38	0.982	9.32	22.99	0.00
No. of pods per plant	29.29	29.29	0.999	18.96	60.24	25.30
No. of seeds per pod	30.01	30.01	0.999	4.60	61.72	36.76
Days at 80% maturity	9.20	9.22	0.995	13.50	18.90	10.28
Seed yield per plant (g)	38.54	38.59	0.998	5.23	79.26	3.16
100 seed weight (g)	12.16	12.21	0.992	0.69	24.85	24.51

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.

Considering the clustering pattern, SML-286 and T-44 were found to be genetically divergent from LM-23 (S), A-89 (S), SML-175 and Malda-95-22. Again, 83-M the only variety in cluster VIII was genetically divergent from SML-175 and Malda-95-22. The genotypes SML-175, Malda-95-22 belonging to cluster VII and T-44 and SML-286 belonging to cluster V has the highest intercluster distance (236.83) and can be used for hybridization programme (Table 3). A-89 (S) and LM-23(S) can also be used for crossing with 83-M and MM-6 to get better transgressive segregants.

The analysis of variance indicated that significant variability exists among genotypes under study for all characters except 100 seed weight (g), though the amount of variability differed from character to character (Table 4). The genotypic coefficients of variation (GCV) was highest for seed yield per plant (38.54%), number of seeds per pod (30.01%) and number of pods per plant (29.27%). The genetic advance as percentage of mean was found to be maximum for seed yield per plant (79.26%) followed by number of seeds per pod (61.72%) and number of pods per plant (60.24%). In the present study high heritability estimates coupled with high genetic advance was observed for seed yield per plant and number of seeds per pod which suggested the action of additive genes in controlling that particular characters (Panse and Sukhatme, 1967). These characters may be given importance for further improvement of yield and yield components. Phenotypic Coefficient of Variation (PCV) was high for total plant harvest (38.59%). All the characters in this study showed high heritability values. The relative contribution of different characters towards divergence showed number of seeds per pod contributed maximum towards divergence (36.76%) followed by number of pods per plant (25.30%) and 100 seed weight (24.51%).

DISCUSSION

The knowledge of genetic diversity is a useful tool in gene bank management and breeding experiments like tagging of germplasm, identification and or elimination of duplicates in the gene stock and establishment of core collections (Dwevedi and Gaibriyal, 2009). Genotypes from distinct geographic regions are usually selected for

hybridization programme presuming the presence of considerable genetic diversity among them. However there was no association between eco-geographical distribution of genotypes and genetic diversity as genotypes selected under diverse locations, get cluster together. In the present study the concomitant finding was revealed. Murthy *et al.* (1965) in Brassica, Arunachalam and Ram (1967) in sorghum, Singh and Bains (1968) in cotton, Gupta and Singh (1970), Malhotra *et al.* (1974) and Venkateswarlu (2001) in Green gram have also indicated the similar finding that geographic diversity can not always be used as an index of genetic diversity. So, it can be stated that this kind of genetic diversity might be due to differential adoption, selection criteria, selection pressure and environment (Vivekananda and Subramanian, 1993). This indicated that genetic drift produce greater diversity than the geographic diversity (Singh and Chaudhury, 1985; Selvakumar *et al.*, 1989). This prompted to select parents for green gram hybridization on the basis of genetic diversity and not merely on the basis of eco-geographical isolation. 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. Regarding presence of genetic variation for different characters Natarajan *et al.* (1998) showed that seed yield per plant, no. of pods per plant and plant height has high genotypic co-efficient of variation which was similar with the present finding. The genetic advance as percentage of mean was found to be maximum for seed yield per plant followed by number of seeds per pod and number of pods per plant which was supported by the report of Venkateswarlu (2001). Makeen *et al.* (2007) reported that additive gene effects were detected for pods per plant and seeds per pod, indicating that improvement of these traits may be achieved by phenotypic selection which was corroborated with the present finding. But Makeen *et al.* (2007) reported that plant height and 100 seed weight were also governed by additive gene action which was not detected in the present finding. These characters may be given importance for further improvement of yield and yield components. Contradictory with the present finding Makeen *et al.* (2007) reported high phenotypic coefficient of variation (PCV) value for seed yield and no. of pods per plant. The relative contribution of different characters towards divergence showed number of seeds per pod contributed maximum towards divergence followed by number of pods per plant and 100 seed weight which was also observed by Naidu and Satyanarayana (1991), Manivannan (2002) and Raje and Rao (2000). Gupta and Singh (1970) found that the same three characters are positively associated with yield and are the main yield components.

CONCLUSION

So from the above result it can be concluded that the genetic diversity was not related to geographic diversity. Among the 23 genotypes SML-175, Malda-95-22 belonging to cluster VII and T-44, SML-286 belonging to cluster V has the highest intercluster distance and can be used for hybridization program to obtain better transgressive segregants. Two characters viz. seed yield per plant and number of seeds per pod 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.

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