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Genetic Variability Study of Yield and Yield Related Characters in Green Gram *(Vignaradiata* (L.) Wilczek)

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Abstract

Fifty green gram genotypes were evaluated for 10 quantitative characters viz., days to 50% flowering, days to maturity, plant height, number of primary 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. The ANOVA test revealed significant differences among 50 genotypes for all the 10 characters studied. High PCV and GCV was observed for number of primary branches per plant, seed yield per plant, number of pods per plant and 100 seed weight. High heritability coupled with high genetic advance as per cent of mean was recorded for all the characters except days to maturity and days to 50% flowering, indicating the preponderance of additive gene action. The genetic diversity study using Mahanolobis D^2 statistics grouped 50 green gram genotypes into 10 clusters. Cluster I and cluster II were the largest clusters having 17 genotypes each. Clusters IV and V were found as highly divergent clusters. Cluster I recorded highest mean for seed yield per plant and Cluster IX recorded highest mean value for number of clusters per plant, number of pods per plant and number of seeds per pod. The 100 seed weight contributed maximum towards genetic divergence followed by number of primary branches per plant and number of clusters per plant.

Key words: *Green gram, Variability, Genetic diversity, Heritability, D^2, Cluster*

Introduction

Green gram (***Vignaradiata*** (L.) Wilczek)is a popular short duration legume crop which can be cultivated throughout the seasons in almost all parts of the country. It is suitable for different multiple and intercropping systems of cultivation. Green gram is an excellent source of high quality easily digestible protein. The germinated seeds have high nutritional value which is comparable with that of asparagus or mushroom and thus green gram is called as "poor man's meat". The green gram seeds contain approximately 25-28% protein, 1.0-1.5% oil, 3.5-4.5% fiber, 4.5–5.5% ash and 62–65% carbohydrates on dry weight basis. Green gram is also used as a green fodder crop and is grown as cover crop for enriching soil fertility. Green gram is cultivated in Asia, Tropical and Sub-tropical Africa, Australia, West Indies, South and North America. In India, it ranks third in production after chickpea and pigeon pea (Dixit, 2005) and thus accounts for 65% of the world acreage and 54% of the world production.

Selection of green gram genotypes with high yield and desirable traits from a set of germplasm depends upon the availability of variability among germplasm for different traits.The variability within these germplasm has to be studied before planning a breeding programme. This helps breeder to get a clear idea on the extent of variability for utilization of the desirable genotypes in breeding programme from a set of germplasm. The quantitative estimation of variability reveals the potentiality of germplasm and improves the efficiency of selection of desirable genotypes for improvement of yield and other desirable characters.

The variability parameters like mean, range and coefficients of variation provides an insight on the presence of variability within a set of germplasm. The phenotypic (observed) variance is the sum total of genetic and environmental variances. But genetic variance is only the heritable component of variance which is transmitted to progenies. Heritability estimation gives an idea of the transmission of a character. Broad sense

heritability (h^2) is expressed as ratio of genetic variance to phenotypic variance. If h^2estimate is ≥80%, selection for that character will be effective as phenotypes represent its genotype. Genetic advance as per cent of mean (GAM) is the improvement employed in a population through selection. Both these parameters are considered together for predicting the environmental influence of a character. The character with high h^2 and GAM can be used for indirect selection.

Genetic diversity is the base for any plant breeding programmes. The plant genetic resources are the base populations with enormous variability which possess many useful genes. Diversity in the plant genetic resources for desirable traits helps in the development of improved varieties. The hybridization between genetic diverse parents produces superior recombinants. Thus genetic diversity in the population has to be studied before planning of any recombination breeding programme. In this context, the present study was done with an objective to estimate the variance within a set of green gram germplasm accessions and to assess the genetic diversity among the green gram genotypes.

Materials and methods

The present investigation was carried out at Department of Plant Breeding and Genetics, OUAT, Bhubaneswar, Odisha, during Kharif 2016. Fifty green gram genotypes were grown in randomized complete block design with 3 replications in rows of two-meter length with 30 cm x 10 cm spacing. All the recommended agronomic practices and need based plant protection measures were done in the experimental site to raise a good crop. The data was recorded on ten yield and yield contributing characters *viz*., days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of clusters per plant, number of pods per plant, pod length (cm), number of seeds per pod, 100 seed weight (g) and seed yield per plant (g). The observations were recorded from five randomly selected plants of each genotype from three replications and the mean value was calculated. The statistical analysis of the data was done using Indostat software. The analysis of variance for different characters in RBD design was carried out as suggested by Panse and Sukhatme (1985) to understand whether the genotypes differ significantly for the characters studied. The various genetic parameters like phenotypic and genotypic coefficients of variation as suggested by Burton (1952), broad sense heritability (Allard, 1960) and genetic advance as per cent of mean (Johnson *et al*., 1955) was calculated for these genotypes. The genetic diversity among 50 germplasm accessions for 10 characters was studied using D^2 analysis as suggested by Mahalanobis (1928).

Results and discussion

The analysis of variance was done using mean data on 10 quantitative characters of 50 green gram genotypes. It was observed that all the genotypes varied significantly for all the characters studied, indicating the existence of wide genetic variation within the green gram germplasm for these characters. The presence of variability in the germplasm indicates that selection can be made for these characters. Khairnar *et al*., 2003, Siddique *et al*., 2006 and Rao *et al*., 2006 also reported considerable variation among different green gram genotypes for different characters.

The mean, range, PCV, GCV, broad sense heritability and genetic advance as per cent of mean were calculated and presented in Table 1. It was observed that days to 50% flowering ranged from 31 (OUM 11-05) to 40 days (BKG) with a mean of 35.15 days. Days to maturity varied from 62 (OUM 11-05) to 71 days (Ambagaon local and OBGG 177) with a mean of 66.14 days. The plant height ranged from 24.20 cm (Pusa Vishal) to 49.51cm (ML 818) with a mean value of 39.55 cm. The number of primary branches varied from 0 (EC 693369, ML 1666 and NM 94) to 2.94 (OBGG 52) with a mean value of 1.51. The number of clusters per plant ranged from 1.50 (BKG) to 6.10 (EC 693367) with a mean of 4.34. The pod number ranged from 4.50 (BKG) to 27.80 (T 43-1-3) with a mean of 15.12. The pod length ranged from 5.30 cm (Jharsuguda local) to 12.44 cm (BKG) with a mean value of 6.79 cm. The number of seeds per pod ranged from 6.70 (Pusa Vishal) to 12.30 (EC 693367 and EC 693358) with a mean value of 10.54. The 100 seed weight ranged from 2.24 g (EC 693363) to 7.38 g (BKG) with a mean value of 3.43 g. Seed yield per plant ranged from1.72 g (EC 693363) to 6.49 g (IPM 02-03) with a mean value of 4.23 g.

Table 1: Estimate of variability, heritability and genetic advance as per cent ofmean for 10 characters in 50 green gram genotypes

Characters	Range		Mean	PCV (%)	GCV (%)	h^2(BS) (%)	GAM
	Min.	Max.					
Days to 50% flowering	31.00	40.00	35.15	7.55	6.94	84.61	13.16
Days to maturity	62.00	71.00	66.14	3.96	3.64	84.61	6.91
Plant height (cm)	24.20	49.51	39.55	16.22	14.79	83.14	27.78
No of primary branches	0.00	2.94	1.51	52.57	50.42	91.99	99.62
No of clusters per plant	1.5	6.10	4.34	19.38	18.59	91.96	36.72
No of pods per plant	4.50	27.8	15.12	29.31	27.51	87.75	53.09
Pod length (cm)	5.30	12.44	6.79	17.85	16.87	89.32	32.84
No of seeds per pod	6.70	12.3	10.54	14.22	13.18	86.00	25.18
100 seed weight (g)	2.24	7.38	3.43	23.35	23.22	98.89	47.58
Seed yield per plant (g)	1.72	6.49	4.13	28.62	25.05	76.62	45.17

Phenotypic coefficient of variation (PCV) was found higher than genotypic coefficient of variation (GCV) for all the ten characters, indicating the involvement of environment in expression of these characters. Hence, the selection for such traits will be often misleading. Similar trends in coefficient of variation in green gram genotypes were reported by Singh *et al*. (2009), Gadakh *et al.* (2013), Kumar *et al.* (2013), Garje *et al*. (2013) and Degefa *et al*. (2014). PCV and GCV ranged from 3.96 and 3.64 (days to maturity) to 52.57 and 50.42% (number of primary branches per plant) respectively. High PCV and GCV was observed for number of primary branches per plant, seed yield per plant, number of pods per plant and 100 seed weight. The estimates of broad sense heritability ranged from 76.62% (seed yield per plant) to 98.89% (100 seed weight). Genetic advance as per cent of mean ranged from 6.91 (days to maturity) to 99.62 (number of primary branches per plant). Thus high heritability coupled with high genetic advance was observed in all the characters except days to maturity and days to 50% flowering. High heritability along with higher genetic advance indicates additive gene action and thus these characters can be improved through simple selection methods.

Genetic Diversity

The genetic diversity among the 50 green gram genotypes for 10 quantitative characters has been studied using Mahalanobis D^2statistics. The cluster analysis revealed wide diversity among the green gram germplasm for the characters studied. The Tocher's method of cluster analysis grouped fifty green gram genotypes into ten clusters and is presented in Table 2. Among the 10 clusters, clusters I and II were the largest clusters with 17 genotypes each, followed by cluster V (6 genotypes), cluster IV (3 genotypes) and cluster III with 2 green gram genotypes. The remaining clusters were solitary. The genotypes, OBGG 52, Ambagaon local, EC 693356, EC 693367 and BKG formed solitary clusters.

Table 2: Composition of clusters in 50 green gram genotypes

Cluster number	No. of accessions	Constituent genotypes
I	17	PDM 139, ML 1299, OUM 11-5, V2 -11, NM 92, VC 6368, KPS 1, PAU 911, Tarm 1, IPM 99-125, Pusa 9072, V2-22, V1-19, OGG 12, Makarjhola local, Bhawanipatna local, Kendrapara local
II	17	OUM 62, Kalahandi local, Keonjhar local A,T 43-1-3, VC6372, LGG 460, ML 1666, VC 6173, KPS 2, IPM 02-03, LGG-407, Pusa 9531, PDM 54, OBGG 177, Jharsuguda local, Sujatha, EC 693376
III	2	EC 693363, IPM 02-14
IV	3	EC 693358, EC 693369, NM 94
V	6	Pusa Vishal, HUM 12, ML 818, Dhauli, T 32-2-3, IPM 02-17
VI	1	OBGG-52
VII	1	Ambagaon local
VIII	1	EC 693356
IX	1	EC 693367
X	1	BKG

Inter and intra cluster distances

The cluster distances (inter and intra) of 10 clusters were calculated and presented in Table 3. Inter and intra cluster distances were categorized as less, medium and high according to Rao (1952). The moderate intra cluster distance was observed for cluster V (27.35), cluster IV (24.67) and cluster III (21.53). This implies that the genetic divergence among the genotypes within the clusters is medium and exchange of genes can happen between the genotypes of these clusters. Cluster I (19.11), and cluster II (18.61) recorded low intra cluster distance, which indicates that the genotypes have a common ancestor in their pedigree. The remaining clusters were solitary with intra cluster distance of zero.

Inter cluster distances were found highest between cluster X & V (95.16) followed by cluster X &IV (79.29), cluster IX & V (75.37), cluster VII & V (72.98), cluster X & VIII (70.65), cluster X & VI (67.74), cluster IX & IV (66.92), cluster III & IV (63.03), cluster IV & V (60.84), cluster II & V (60.14), cluster X & I (58.45), cluster VIII & IV (55.54), cluster IV & VII (53.15), cluster X & II (52.72), cluster X & III (52.27), cluster III & V (51.72), cluster IX & VIII (49.19), cluster IX & VI (48.43), cluster VIII & VII (47.48), cluster I & IV (44.59), cluster I & V (43.96), cluster V & VI (42.76), cluster VIII & II (42.00), cluster II & III (41.79), cluster VI & VII (41.10), cluster VIII & V (40.94), cluster IX & I (40.5), cluster IX & II (39.49), cluster IV & VI (37.81), cluster III & VI (37.23), cluster III & VII (37.82), cluster I &VII (36.58), cluster II & IV (34.54), cluster IX & III (32.93), cluster VIII & III (32.79), cluster I & II (30.27) and cluster VIII & I (30.2). Thus these cluster pairs are highly divergent and the genotypes from these cluster pairs can be selected as parents for hybridisaton programme to yield high heterotic responses and better segregants.

Table 3: Average inter and intra cluster (diagonal) D values of ten clusters

Clusters	I	II	III	IV	V	VI	VII	VIII	1X	X
I	**19.11**	30.27	28.71	44.59	43.96	24.19	36.58	30.12	40.50	58.45
II		**18.61**	41.79	34.54	60.14	28.02	27.47	42.00	39.49	52.72
III			**21.53**	63.03	51.72	37.23	37.82	32.79	32.93	52.27
IV				**24.67**	60.84	37.81	53.15	55.54	66.92	79.29
V					**27.35**	42.76	72.98	40.94	75.37	95.16
VI						**0.00**	41.10	20.15	48.43	67.74
VII							**0.00**	47.48	17.74	29.98
VIII								**0.00**	49.19	70.65
IX									**0.00**	23.17
X										**0.00**

Cluster mean value

The cluster mean values of 10 clusters for each character were calculated and presented in Table 4. The number of pods per plant, plant height, flowering time and maturity duration recorded maximum variability between the clusters. Cluster I recorded the highest cluster mean value for seed yield per plant (4.68). Cluster IV recorded the lowest cluster mean for days to 50 per cent flowering (32) and days to maturity (63). Cluster VI recorded maximum cluster mean for number of primary branches per plant (2.94). Cluster IX recorded highest mean for plant height (45.37), number of clusters per plant (6.10), number of pods per plant (24.60) and number of seeds per pod (12.30). Cluster X with single genotype, BKG had maximum cluster mean for pod length (12.44) and 100 seed weight (7.38).

Table 4: Cluster means for 10 characters in 50 green gram genotypes

Clusters	DF	DM	PH	NB	NC	NP	PL	NS	HS	SY
I	34.15	65.18	42.09	1.50	4.79	16.99	6.31	10.73	3.26	4.68
II	36.18	67.18	37.93	1.52	4.13	13.65	6.68	10.59	3.22	3.78
III	35.25	66.25	37.34	1.27	4.30	16.25	6.45	9.95	3.18	4.07
IV	32.00	63.00	36.08	0.25	4.03	13.27	8.34	11.23	4.48	4.50
V	34.75	65.75	40.45	1.81	4.18	15.04	6.78	9.85	3.92	4.23
VI	33.00	64.00	30.00	2.94	4.26	12.13	6.17	6.93	3.21	3.34
VII	39.50	70.50	32.67	1.55	3.50	7.90	6.04	9.60	2.39	1.91
VIII	36.00	67.00	41.50	1.54	4.40	19.40	8.83	11.00	2.62	3.63
IX	38.50	69.50	45.37	1.62	6.10	24.60	6.55	12.30	2.49	3.44
X	40.00	70.00	41.93	2.20	1.50	4.50	12.44	11.90	7.38	3.45

DF: Days to 50% flowering, DM: Days to maturity, PH: Plant height, NB: No of primary branches, NC: No of clusters per plant, NP: No of pods per plant, PL: Pod length, NS: No of seeds per pod, HS: 100 seed weight, SY: Seed yield per plant

Contribution of different characters towards genetic divergence

The contribution of characters towards genetic divergence is calculated and presented in Table 5. The 100 seed weight (54.86%) recorded maximum contribution towards total diversity followed by number of primary branches per plant (13.55%), number of clusters per plant (8.82%), pod length (5.63%), plant height (4.98%), number of pods per plant (4.08%), number of seeds per pod (3.92%), days to 50 per cent flowering (3.27%) and seed yield per plant (0.90%). Days to maturity had no contribution for genetic diversity within the germplasm studied. High contribution of 100 seed weight on genetic divergence was reported earlier in green gram by Mishra *et al.* (1995), Sinha *et al.* (1999), RangaRao *et al.* (2005), Haritha and Reddy, (2003), Prasanna *et al.* (2013) and Vajjaramatti (2017). Thus 100 seed weight, number of primary branches per plant, number of clusters per plant, pod length, plant height and number of pods per plant should be considered while selection of parents for hybridization.

Table 5: Contribution of 10 characters towards genetic divergence in 50 green gram genotypes

Characters	Number of times ranked first	Contribution (%)
100 seed weight (g)	672	54.86
Number of primary branches per plant	166	13.55
Number of clusters per plant	108	8.82
Pod length (cm)	69	5.63
Plant height (cm)	61	4.98
Number of pods per plant	50	4.08
Number of seeds per pod	48	3.92
Days to 50% flowering	40	3.27
Seed yield per plant (g)	11	0.9
Days to maturity	0	0

Conclusion

Germplasm collections conserve the genetic diversity of crop species and their wild relatives. The selection of genetic divergent parents among a set of germplasm is very important as hybridization between diverse parents yield transgressive segregants. The present study was done to study the variability and genetic diversity within 50 green gram genotypes. The high genetic variability was observed among the 50 green gram genotypes for 10 characters studied. High PCV and GCV was observed for number of primary branches per plant, seed yield per plant, number of pods per plant and 100 seed weight. High heritability coupled with high genetic advance as per cent of mean was recorded for all the characters except days to maturity and days to 50% flowering. The genetic diversity analysis using D^2 statistics grouped 50 genotypes into 10 clusters. Cluster I and cluster II were the largest clusters having 17 genotypes each. Low to high inter cluster distances and low to medium intra cluster distances were observed among different clusters. Clusters IV and V were observed as the highly divergent clusters. Cluster I recorded highest mean for seed yield per plant and cluster V recorded highest mean value for number of clusters per plant, number of pods per plant and number of seeds per pod. High mean value of pod length and 100 seed weight was observed in cluster X. The 100 seed weight contributed maximum towards genetic divergence followed by number of primary branches per plant and number of clusters per plant.

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