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Research Note

Genetic variability in segregating generations of greengram (*Vigna radiata L.*Wilczek) for quantitative traits.

I.Mariyammal[1], M. Pandiyan[2], C. Vanniarajan[1], J. S. Kennedy [4] and N. Senthil[3]

[1]Department of Plant Breeding and Genetics, Agricultural College and Research Institute, Tamil Nadu Agricultural University, Madurai, Tamil Nadu, India
[2]Agricultural College and Research Institute, Tamil Nadu Agricultural University, Eachangkottai, Tamil Nadu, India
[3]Department of Plant Molecular Biology and Bioinformatics, Center for Plant Molecular Biology and Biotechnology, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu, India
[4]Horticulture Research Station, Tamil Nadu Agricultural University, Yercaud, Salem, Tamil Nadu. India
E-Mail: mpandiyan8@yahoo.co.in

Abstract
Variability studies were carried out in the present study for eight quantitative traits such as days to first flowering, plant height, number of clusters per plant, number of pods per cluster, total number of pods per plant, number of seeds per pod, 100 seed weight and single plant yield. Significant variability did exist among F_2 of two crosses for all the eight quantitative characters recorded. The variation was recorded to be the highest for plant height followed by number of pods per plant. Highest GCV and PCV estimates were observed for number of pods per plant in all the three crosses. Hence direct selection based on these traits would be effective. Based on heritability and genetic advance, most of the traits except plant height and single plant yield recorded high heritability coupled with low genetic advance in all these crosses. These findings revealed presence of dominance and epitasis gene effect and the selection based on these traits may not be rewarding.

Pulses play a vital role to meet the protein requirement of human diet. They are considered as poor people's meat as it is the cheapest source of protein. It constitutes the main source of essential amino acids for vegetarian population of India. In developing countries, pulses serve as a major source of protein when compared to greater dependence of animal protein (56%) in developed countries. People in developing countries get only 12 per cent protein from animal source, whereas, 80 per cent protein requirement is met from plant sources, mainly pulses. However, in India, the net availability of pulses has started improving and presently reached 47.2 g/day/capita (GoI, 2016) as compared to 60 g/day/person in 1951. Indian Council of Medical Research recommends the intake of protein per person must be 65 gm/day.

Greengram [*Vigna radiata* (L.).Wilczek] is one of the important pulse crops grown in India. It contains about 23.4 per cent protein, 57.3 per cent carbohydrate, 3.8 per cent fibres, 4.5 per cent ash, 1per cent fat and 9.7 per cent water (Anonymous. 2011). In the rice rotation system, greengram has diversified and strengthened the cropping system, alleviated the disadvantages of the cereal-cereal cropping system, and improved the productivity of the soil. In India, the major production of greengram is from the following states *viz.,* Madhya Pradesh, Maharashtra, Uttar Pradesh,

Andhra Pradesh, Karnataka and Rajasthan with larger area (43.05 lakh ha), production (20.07 lakh tonnes) and productivity (481 kg/ha). In Tamil Nadu the production (1.21 lakh tones) and productivity (642 kg/ha) of mungbean was obtained from an area of 1.89 lakh ha (Tiwari *et al*., 2017).The major constraints in achieving higher yield of this crop are lack of genetic variability, absence of suitable ideotypes for different cropping systems, poor harvest index and susceptibility to diseases. Therefore, improvement of this crop is needed through utilization of available genetic diversity. The success of hybridization programme depends upon selection of suitable parents which are genetically diverse from existing germplasm. The primary aim of the breeder is to improve the available genotypes by evolving superior varieties. Genetic variability studies provide basic information regarding the genetic properties of the population based on which breeding methods are formulated for further improvement of the crop. In the present study, the main objective is to assess genetic variability in F_2 populations of two greengram crosses among yield contributing traits.

The material chosen for increasing yield and its attributes in greengram consisted of three greengram genotypes *viz.,*VBN2, RIL 165and RIL 169. The seed materials were obtained from National Pulses Research Centre (NPRC), Vamban

and Agriculture Research Station (ARS), Virinjipuram. The details of the seed materials selected are given in the table 1.Two crosses namely VBN2 x RIL 165 and VBN 2 x RIL 169 were effected during January, 2018. F_2 populations of these hybrids along with their parents were sown during June, 2018 at Agriculture College and Research Institute, Thanjavur. Each F_2 generation was sown in row of 4m. Length with a spacing of 30 x 10 cm. A total of 40 plants per row were uniformly maintained. Each F_2 population consisted of more than 160 plants. The recommended packages of agronomic practices were followed throughout the crop period. Observations were taken on every F_2 populations for days to first flowering, plant height(cm.), number of clusters per plant, number of pods per plant, number of pod per plants, number of seeds per pod, 100seed weight (g.) and single plant yield (g.). Data on these eight biometrical traits were utilised for statistical analysis, to study the variability (PCV and GCV), heritability and genetic advance as percentage of mean. Variability analysis was performed using TNAUSTAT (Manivannan, 2014).

The genotypic and phenotypic coefficient of variation, heritability (broad sense), genetic advance as percentage of mean for each character of two crosses are presented in table 2. In the present study, significant variability did exist among the two F_2 populations for eight quantitative characters recorded. The estimates of variability parameters were worked out according to the method suggested by Burton, 1952. The genotypic and phenotypic variations were recorded to be the highest for number of pods per plant followed by single plant yield. High GCV and PCV estimates were recorded for number of pods per plant in both crosses. This indicated the presence of variation in greengram for yield attributing traits. Hence, direct selection based on these traits would be effective. Similar findings had been reported by Borah and Hazarika (1996) and Reddy *et al*., (2004).

In the cross VBN 2 x RIL 165, high general mean was recorded for plant height followed by days to first flowering, number of pods per plant, number of seeds per pod, single plant yield, number of cluster per plant, 100 seed weight and number of pods per cluster (Table 2). High phenotypic variance (PV) and genotypic variance (GV) were registered by the plant height and number of pods per plant. The traits,100 seed weight showed low phenotypic variance and genotypic variance. Based on PCV was higher than GCV in all the traits, which indicated that these traits are influenced by environment. All the traits registered high heritability (>60%) except number of pods per

cluster. Highest heritability was observed for 100 seed weight (97.91 %) followed plant height (94.72 %), number of cluster per plant (92.23%), single plant yield (87.83 %), number of seeds per pod (87.54 %), number of pods per plant (87.46 %) and days to first flowering (74.28 %). The highest GAM (> 20%) was observed for plant height (52.28 %), number of cluster per plant (25.00 %), number of pods per cluster (30.61) and single plant yield (25.17) (Table2.). With respect to heritability estimates, all the traits except number of pods per cluster recorded high heritability, indicating predominance of additive gene action for expression of these traits. High heritability and high genetic advance as percentage of mean were recorded for the traits, plant height, number of cluster per plant and single plant yield. We can go for improvement of these characters through direct selection in this cross. High heritability with moderate genetic advance as percentage of mean was recorded for number of pods per plant, number of seeds per plant and 100 seed weight and moderate genetic advance and high genetic advance recorded for number of pods per cluster. Whereas days to first flowering recorded high heritability with low genetic advance as percentage of mean which indicated these traits are highly influenced by environment and direct selection for improvement of these traits would not be rewarding. Similar finding was reported by Reddy *et al*., (2011), Pinchhyo *et al*., (2016) and Keerthiga *et al*., (2018).

In F_2 population of cross VBN 2 x RIL 169, highest mean values recorded for plant height followed by number of pods per plant, days to first flowering, number of seeds per pod, single plant yield, number of cluster per plant, number of pods per cluster and 100 seed weight (Table 2 .). High phenotypic variance and genotypic variance observed in number of pods per plant and plant height and all other traits recorded low values except single plant yield. The traits number of pods per plant, single plant yield, number of cluster per plant, number of pods per cluster and plant height recorded high magnitude of PCV and GCV which indicates that these traits are influenced by environment. Heritability varied from 46.39 % in days to first flowering to96.30 % in plant height (Table 2). High heritability coupled with high genetic advance as per mean was recorded for plant height, number of clusters per plant, number of pods per cluster, which indicates that these traits can be improved by effective simple selection as additive gene effect plays a major role. High heritability with moderate genetic advance as percentage of mean was recorded in number of pods per plant, number of seeds per pod, 100 seed weight and single plant yield and moderate

heritability with low genetic advance as percentage of mean was recorded for days to first flowering. Hence, we cannot go for simple selection for improvement of these traits. Similar findings had been reported by Tabasum *et al*., (2010), Narasimhulu *et al*., (2013) and Divya *et al*., (2018).

Based on this study, magnitude of all the phenotypic variance was higher to genotypic variance exhibited the pronounced effects of environment. Both the crosses had high heritability for single plant yield and indicated the presence of additive effect and more gain of selection in next generation. Improvement in single plant yield of greengram could be brought through simple selection programme. The traits number of pods per cluster in VBN2 x RIL 165 and days to first flowering in VBN 2 x RIL 169 recorded medium heritability. It needs to be studied further as traits. Selection process can be delayed to later generation for improvement of these traits in these crosses.

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Table 1. Details of the parent materials

S.No	Greengram genotypes (parents)	Parentage
1.	VBN 2	Cross derivative of VGG 4 x MH 309
2.	RIL 165	F9 RILs developed from VRM(Gg)1 X TNAU RED crosses.
3.	RIL 169	

Table 2. Estimates of genetic variance in F_2 population of two crosses

Characters / crosses	VBN 2 x RIL 165								VBN 2 x RIL 169							
	Mean	PV	GV	PCV	GCV	h^2 (%)	GA	GAM (%)	Mean	PV	GV	PCV	GCV	h^2 (%)	GA	GAM (%)
Days to first flowering	23.70	17.49	12.99	17.65	15.21	74.28	2.23	9.40	19.79	3.73	1.73	9.76	6.65	46.39	1.14	5.74
Plant height (cm)	34.44	85.15	80.65	26.80	26.08	94.72	18.00	52.28	33.07	84.38	81.25	27.78	27.26	96.30	18.22	55.10
No. of clusters per plant	6.39	6.44	5.94	39.70	38.12	92.23	1.60	25.00	7.11	6.93	5.80	37.00	33.86	83.76	1.78	24.98
No. of pods per cluster	2.81	0.99	0.49	35.44	24.99	49.74	0.86	30.61	3.70	1.11	0.98	28.48	26.83	88.73	1.09	29.39
No. of pods per plant	17.76	99.70	87.20	56.22	52.58	87.46	3.39	19.07	25.78	103.86	99.36	39.52	38.66	95.67	2.87	11.13
No. of seeds per pod	9.71	4.01	3.51	20.63	19.31	87.54	1.52	15.62	10.27	2.74	2.24	16.10	14.55	81.72	1.42	13.78
100 seed weight (g)	3.21	0.19	0.19	13.74	13.60	97.91	0.51	15.88	3.43	0.15	0.13	11.17	10.38	86.40	0.67	19.50
Single plant yield(g)	7.81	11.46	10.07	43.34	40.62	87.83	1.97	25.17	8.76	11.73	11.24	39.09	38.26	95.82	1.65	18.85

GCV – Genetic Coefficient of Variance ; PCV – Phenotypic Coefficient of Variance.
GCV, PCV and Genetic advance as percent of mean: Low – Less than 10% ; Moderate – 10-20% ; High – More than 20%
Heritability: Low – Less than 30% ; Moderate – 30-60% ; High – More than 60%