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Genetic Variability for Yield and Its Related Traits in Green gram [*Vigna radiata* (L.) Wilczek]

Mohd Abdus Subhan Salman[1], Ch. Anuradha[1], V. Sridhar[2], E. Ram Babu[1], SNCVL. Pushpavalli[1]

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ABSTRACT

Background: Green gram [*Vigna radiata* (L.) Wilczek] is an ancient and well known pulse crop of Asian countries. Specific traits should be considered for high yield in green gram as selection criteria in future breeding program.

Methods: The investigation material comprised of 128 F_6 RIL (Recombinant Inbred LINE) population sown at College Farm, Professor Jayashankar Telangana State Agricultural University during *Rabi*-2019-20. The yield and yield attributes were recorded to conduct genetic variability, heritability broad sense (h^2), genetic advance (GA) and genetic advance as % of mean (GAM).

Result: Analysis of variance revealed significant differences among the RILs, indicating the presence of genetic variability for almost all the traits studied. High PCV and GCV estimates was noticed for number of pods per plant, seed yield per plant, number of cluster per plant and number of pods per cluster. High heritability along with high genetic advance as per cent of mean was observed for number of pods per plant, seed yield per plant, number of cluster per plant, number of pods per cluster, number of branches per plant, number of seeds per pod and plant height indicating the role of additive genes in governing the inheritance of these traits and could be improved through selection. The traits *viz*. seed yield per plant, number of pods per plant, number of clusters per plant and number of pods per cluster had recorded high PCV, GCV, high heritability along with high genetic advance as per cent of mean indicated these traits were less influenced by environment and possess high genetic variability. Hence these RILs would be suitable for green gram breeding programmes to develop improved varieties. The present findings of the RIL population will be useful for development of high seed yielding variety in green gram.

Key words: GCV, Genetic advance, Heritability broad sense (h^2), PCV, RILs, Variability studies.

INTRODUCTION

Green gram [*Vigna radiata* (L.) R. Wilczek var. *radiate*], also known as Mung bean or moong, is an important legume crop in countries of Asia, Africa and latin America, belonging to the papilionoid subfamily of genus Vigna, sub genus Ceratotrophis and family Fabaceae. Green gram [*Vigna radiata* (L.) R. Wilczek] has been cultivated in India since prehistoric times and is considered to be a native crop of India (Vavilov, 1926). Green gram protein is easily digested without flatulence. The protein is comparatively rich in lysine, an amino acid that is deficient in cereal grains but cereals are rich in methionine, cystine and cysteine, the sulphur bearing amino acid. Green gram is accentuated due to its nutritional value. Hundred gram of green gram seeds contains energy (234 cal), protein (24.6%), fat (1.0%), fiber (2.2 g), carbohydrates (57.5%), calcium (0.08 g), phosphorus (0.045 g) and iron (5.7 mg), vitamin B (300 mg) and thiamin (0.525 mg) (Srivastava and Ali, 2004). Green gram is a self-pollinated diploid grain legume (2n=2x=22) crop with a small genome size of 579 Mb/1C (Arumuganathan *et al.,* 1991). This crop play an important role in crop rotation due to their ability to fix atmospheric nitrogen, thus growing green gram helps to improve soil fertility and benefit subsequent crops.

Selection of superior parents exhibiting better heritability and genetic advance for various characters is an essential prerequisite for any yield improvement programme. Genetic variability with the help of suitable parameters such as genotypic and phenotypic coefficient of variation, heritability and genetic advance are absolutely necessary to start an efficient breeding program. Studies on genetic diversity are of considerable importance to classify the available genotypes into discrete classes, so that the parents belonging to diverse groups can be selected. The present study is formulated to study the genetic variability, heritability and genetic advance in green gram Recombinant Inbred LINEs (RILs).

[1]Institute of Biotechnology, Professor Jayashankar Telangana State Agricultural University, Rajendranagar, Hyderabad-500 030, Telangana, India.
[2]Agricultural Research Station (ARS), Madhira, Khammam-507 203, Telangana, India.

Corresponding Author: Ch. Anuradha, Institute of Biotechnology, Professor Jayashankar Telangana State Agricultural University, Rajendranagar, Hyderabad-500 030, Telangana, India.
Email: anu.gene@gmail.com

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MATERIALS AND METHODS

The Experimental material comprised of 128 F_6 RIL (Recombinant Inbred LINE) population derived from a cross of MGG-295 and WGG-42. The experiment was laid out in a randomised completely block design (RBD) consisting of 128 RILs of green gram in two replications, sown at college farm, Professor Jayashankar Telangana State Agricultural University during *Rabi*-2019-20. Each RIL lines were grown in 2 rows of 4 m length with row to row spacing of 30 cm and plant to plant spacing of 10 cm. Observations for all the yield and yield contributing traits were recorded on five plants in each RIL.

The data was recorded for twelve yield related traits *viz*., days to initial flowering, days to 50% flowering, days to maturity, number of branches per plant, number of clusters per plant, number of pods per clusters, number of pods per plant, number of seeds per pod, plant height (cm), pod length (cm), seed yield per plant (g) and hundred seed weight (g). The data recorded on the above characters were subjected to statistical analysis such as analysis of variance (Fisher, 1936), coefficient of variation (Burton and Devane, 1953) and genetic advance (Johnson *et al*., 1955).

RESULTS AND DISCUSSION

Analysis of variance

The mean values of quantitative traits of five randomly selected plants in each of the RIL and check entries were used for statistical analysis. Mean data for twelve characters were subjected to analysis of variance for experimental design. The mean sum of squares with respect to various morphological traits has been given in Table 1. The analysis of variance as a measure of variability revealed significant differences amongst the RILs for all the characters. Rao *et al*. (2006), Singh *et al*. (2009), Reddy *et al*. (2011), Hemavathy *et al*. (2015) and Dhoot *et al*. (2017) also reported significant differences for all the characters studied. The existence of satisfactory variability indicated that the RIL population of green gram under research was good enough for further study (Table 1).

GCV and PCV estimates

Phenotypic coefficient of variation (PCV) was found higher than that of genotypic coefficient of variation (GCV) for all the traits, suggesting the role of environmental factors on various characters, also suggested by Khajudparn and Tantasawat (2011). The genotypes showed significant differences in respect of all the characters studied (Table 2).

Genotypic coefficient of variation (GCV)

GCV ranged from 4.201 per cent (days to 50% flowering) to 46.172 per cent (number of pods per plant). High GCV was observed for number of pods per plant (46.172), seed yield per plant (38.104), number of pods per clusters (32.539), number of cluster per plant (28.514). Number of seeds per pod (12.05), Number of branches per plant (14.925) and plant height (12.563) exhibited moderate GCV. Low GCV

Table 1: Analysis of variance for various traits in green gram.

Source of variation	df	DFF (Days)	DF50 (Days)	DM (Days)	NBP (nos.)	NPC (nos.)	NCP (cm)	NPP (nos.)	NSP (g)	PH (cm)	PL (cm)	SYP	SW (g)
Replication	1	8.952^{NS}	9.855^{NS}	0.418^{NS}	0.002^{NS}	0.071^{NS}	0.056^{NS}	0.380^{NS}	0.279^{NS}	4.181^{NS}	0.359^{NS}	0.001^{NS}	0.028^{NS}
Treatments	129	14.947***	14.972 ***	53.79 **	0.55***	5.03***	6.31***	120.58***	6.300***	25.08***	0.63***	2.67***	0.317***
Error	129	6.25	7.123	33.651	0.040	0.083	0.103	0.214	0.349	1.629	0.172	0.034	0.112

***: Significance at 0.01 probability levels; ** and * :Significance at 0.05 and 0.1 probability levels; NS: Non significant; DFF: Days to initial flowering, DF50: Days to 50% flowering, DM: Days to maturity, NBP: Number of branches per plant, NPC: Number of pods per cluster, NCP: Number of cluster per plant, NPP: Number of pods per plant, NSP: Number of seeds per pod, PH: Plant height, PL: Pod length, SYP: Seed yield per plant and SW: 100 seed weight.

was exhibited by 100 seed weight (9.537), days to initial flowering (4.722), days to maturity (4.291), days to 50% flowering (4.201) (Table 2).

Phenotypic coefficient of variation (PCV)

The PCV ranged from 7.049 per cent (days to 50% flowering) to 46.254 per cent (number of pods per plant). High PCV was observed for number of pods per plant (46.254), seed yield per plant (38.587), number of pods per cluster (33.078) and number of clusters per plant (28.984). Moderate PCV was noticed in number of seeds per pod (17.716), number of branches per plant (15.617), hundred seed weight (13.77) and plant height (13.408). Days to maturity (8.941), Pod length (8.64) and days to initial flowering (7.375), days to 50% flowering (7.049) exhibited low PCV (Table 2).

High PCV and GCV estimates for pods per plant, seed yield per plant were reported by Rao *et al.* (2006); Raturi *et al.* (2015); Anand *et al.* (2016); Garg *et al.* (2017) and Parimala *et al*. (2020). High PCV and GCV estimates for pods per plant was observed by Talukdar *et al*. (2020). Moderate PCV and GCV were found for plant height, number of branches per plant, number of seeds per pod and 100 seed weight. Similar results were also observed by Pandey *et al.* (2007) and Nand and Anuradha (2013) for branches per plant, Rao *et al.* (2006); Makeen *et al.* (2007) and Kumhar and Choudhary (2007) for 100 seed weight. Mehta *et al*. (2019) for number of branches per plant. Lowest PCV and GCV estimates were obtained for days to 50% flowering, pod length and days to maturity. These results are in correspondence with Rao *et al.* (2006); Makeen *et al.* (2007), Kumhar and Choudhary (2007); Nand and Anuradha (2013), Zuge *et al*. (2019) and Asari *et al*. (2019) for days to 50% flowering and days to maturity. Perera *et al*. (2017) for days to maturity. The results obtained for PCV and GCV showed that there is considerable possibility of further improvement and by appropriate selection for these characters and development of high yielding variety can take place. Low values of genotypic and phenotypic coefficient of variation were noted for pod yield, days to maturity and days to 50% flowering which indicated low range of variation for these characters in the genotypes, thus offering little scope for further improvement of these characters through simple selection.

Heritability broad sense (h^2)

The heritability broad sense (h^2) ranged from 23.00 per cent (days to maturity) to 99.60 per cent (number of pods per plant). High heritability was observed in number of pods per plant (99.6), seed yield per plant (97.5), number of clusters per plant (96.8), number of pods per cluster (96.80), number of seeds per pod (89.50), plant height (87.8), number of branches per plant (86.5). Moderate heritability was observed in pod length (57.2), hundred seed weight (47.9), days to initial flowering (41.07), days to 50% flowering (35.5). Low heritability was observed for days to maturity (23.0) (Table 2).

Similar results were reported by Natarajan *et al.* (1988), Saxena and Singh (2007). Hemavathy *et al.* (2015), Garg *et al.* (2017) for plant height, seed yield per plant and number of pods per plant. Mehendi *et al*. (2018) for number of pods per cluster, seed yield per plant. Zuge *et al*. (2019) reported high heritability for plant height, number of pods per plant and similarly moderate values were recorded for pod length. Asari *et al*. (2019) reported high heritability for plant height, number of pods per plant, number of branches per plant, number of pods per cluster, number of cluster per plant, number of pods per plant, number of seeds per pod and seed yield per plant. These results are in correspondence with the findings of Reddy *et al.* (2003) and Makeen *et al.* (2007). For reliable selection high heritability of a character needs to be accompanied by high genetic advance (Johnson *et al.,* 1955) because such

Table 2: Magnitude of variability and estimates of heritability and genetic advance for various characters in RILs of green gram.

Trait	Coefficient of variation			h^2 (%)	GA	GAM	Mean	CV
	PCV%	GCV%	ECV%					
DFF	7.375	4.722	5.662	41.07	2.751	6.229	44.159	5.662
DF50	7.049	4.201	5.660	35.5	2.432	5.158	47.154	5.660
DM	8.941	4.291	7.843	23	3.138	4.243	73.961	7.843
NBP (nos)	15.617	14.925	5.739	86.5	0.973	27.828	3.498	5.739
NPC (nos)	33.078	32.539	5.945	96.8	3.187	65.939	4.834	5.945
NCP (nos)	28.984	28.514	5.199	96.8	3.572	57.786	6.182	5.199
NPP (nos)	46.254	46.172	2.792	99.6	15.953	94.946	16.802	2.752
NSP (nos)	17.716	16.759	5.744	89.5	3.361	32.659	10.292	5.744
PH (cm)	13.408	12.563	4.684	87.8	6.609	24.250	27.256	4.684
PL (cm)	8.640	6.537	5.651	57.2	0.748	10.187	7.339	5.651
SYP (g)	38.587	38.104	6.084	97.5	2.338	77.513	3.016	6.084
SW (g)	13.773	9.537	9.937	47.9	0.456	13.604	3.361	9.937

DFF: Days to initial flowering, DF50: Days to 50% flowering, DM: Days to maturity, NBP: Number of branches per plant, NPC: Number of pods per cluster, NCP: Number of cluster per plant, NPP: Number of pods per plant, NSP: Number of seeds per pod, PH: Plant height, PL: Pod length, SYP: Seed yield per plant and SW: 100 seed weight.

characters are mostly controlled by additive gene action. Similar results were obtained by the presence of high heritability indicates preponderance of additive gene action in expression of these traits and they can be improved through individual plant selection.

Genetic advance

A perusal of genetic advance for all the quantitative traits under study ranged from 0.45 per cent (hundred seed weight) to 15.95 per cent (number of pods per plant). Moderate genetic advance was expressed by number of pods per plant (15.95) and remaining parameters observed low genetic advance that is plant height (6.60), number of cluster per plant (3.57), number of seed per plant (3.36), number of pods per cluster (3.18), days to maturity (3.13), days to first flowering (2.75), days to 50% flowering (2.43), seed yield per plant (2.33), number of branches per plant (0.97), pod length (0.74) and hundred seed weight (0.45). (Table 2). Similar results were observed by Nand and Anuradha (2013) and Malli *et al.* (2018) for days to initial flowering, days to 50% flowering, days to full maturity, 100 seed weight and pod length. Raturi *et al.* (2015) for plant height and number of branches per plant.

Genetic advance as percent of mean (GAM)

A perusal of genetic advance for all the quantitative traits under study ranged from 4.24 per cent (days to maturity) to 94.94 per cent (number of pods per plant). High genetic advance was observed for the traits *i.e*. number of pods per plant (94.94 per cent), seed yield per plant (77.51), number of pods per cluster (65.93), number of clusters per plant (57.78), number of seeds per pod (32.65), number of branches per plant (27.82) and plant height (24.25). Moderate GAM was observed in hundred seed weight (13.60), pod length (10.18). Days to initial flowering (6.22), days to 50% flowering (5.15) and days to maturity (4.24) expressed low GAM (Table 2).

Similar results were observed by Manivannan *et al*. (1996), Pandiyan *et al.* (2006). Nand and Anuradha (2013) for number of pods per plant, number of seeds per pod, seed yield per plant. Hemavathy *et al*. (2015) for plant height, days to 50% flowering, days to maturity, number of cluster per plant, number of pods per cluster, number of pods per plant, hundred seed weight and seed yield per plant. Asari *et al.* (2019) for seed yield per plant, number of pods per plant, number of clusters per plant, number of branches per plant and plant height.

High heritability estimates coupled with high or moderate genetic advance was observed for number of branches per plant, number of pods per cluster, number of cluster per plant, number of pods per plant, number of seeds per pod, plant height and seed yield per plant. Similar results were reported by Baisakh *et al*. (2016) for plant height and pods per plant. Muthuswamy *et al*. (2019) for plant height, number of branches per plant, number of pod per plant, and seed yield per plant. Pavan *et al*. (2019) for pods per plant, seed yield per plant, plant height and number of branches per plant. Asari *et al*. (2019) for plant height, number of branches per plant, number of cluster per plant, number of pods per plant and seed yield per plant.

CONCLUSION

The results from the present investigation concludes that significant differences recorded for all the characters among the RIL population included in the study, indicating presence of sufficient variation among them. On the basis of obtained results from this experiment it can be concluded that on the basis of high PCV, GCV, high heritability along with high genetic advance as per cent of mean for the traits *i.e*. single plant yield, number of pods per plant, number of clusters per plant and number of pods per cluster can be used as selection criteria in future breeding program. Hence these RILs can be used for crop improvement. The present findings will contribute to future breeding strategies aimed to incorporate resistance and high yield in green gram.

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