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Genetic Variability for Yield and Yield Attributing Traits in F_3 Generation of Green Gram

S. Sindhu[1*], M. Shanthi Priya[1], L. Prashanthi[2] and P. Sudhakar[3]

[1]*Department of Genetics and Plant Breeding, S.V. Agricultural College, Tirupati, India*
[2]*Department of Genetics and Plant Breeding, RARS, Tirupati, India*
[3]*Department of Crop Physiology, S.V. Agricultural College, Tirupati, India*

**Corresponding author*

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A B S T R A C T

The present investigation was carried out in the F_3 population of three green gram crosses *viz.*, MGG-347 x MGG-351, MGG-351 x LGG-460 and LGG-460 x LGG-528. High PCV and high GCV was recorded for clusters per plant, pods per plant, pod yield and seed yield per plant for the two crosses, MGG-351 x LGG-460 and LGG-460 x LGG-528 indicating the existence of wide variability for these traits in the progenies of these crosses. High heritability coupled with high genetic advance as per cent of mean were recorded for clusters per plant, pods per plant, pod yield and seed yield in cross MGG-351 x LGG-460 and for clusters per plant and pods per plant in cross LGG-460 x LGG-528. This indicates scope of selection for these traits in particular population, since there is a wide range of variation and additive gene action.

Introduction

Green gram (*Vigna radiata* (L). Wilczek) popularly known as mung bean is the third important legume after chickpea and pigeon pea. It is a self-pollinating, short duration legume that belongs to family *Fabaceae* with a chromosome number of 2n=22. It is mainly grown for its seeds which are used as whole or splits (dhal). The major constraints of green gram production are cultivation under low rainfall condition, low fertile lands, frequent dry spells, poor availability of quality seeds, lack of improved varieties and narrow genetic base. There is an urgent need to enhance the genetic potential of green gram for yield.

In order to improve the yield through selection, it is essential to have a thorough knowledge on genetic variability available in the germplasm and the extent to which the desirable traits are heritable, which requires a letter insight of the ancillary characters for better selection. Therefore, the present study was aimed at finding out nature and

magnitude of genetic variability studies in segregating population of the green gram for grain yield and other yield component traits for further breeding programme.

Genetic parameters such as genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) are useful in detecting the amount of variability present in germplasm. Burton (1952) suggested that the GCV along with heritability estimate could provide better picture of the advance to be expected by phenotypic selection. Heritability values along with genetic advance would be more reliable and helpful in predicting the gain under selection than heritability estimate alone. With these parameters, the present investigation was undertaken for the genetic improvement of green gram.

Materials and Methods

The present investigation was carried out at dry land farm of Sri Venkateswara Agricultural College, Tirupati. The experimental material consisted of four parents *viz*., MGG-347, MGG-351, LGG-460 and LGG-528 and three F_3 populations of the crosses, MGG-347 x MGG-351, MGG-351 x LGG-460 and LGG-460 x LGG-528. The experiment was laid out in a compact family block design with three replications during *kharif*, 2016. Each cross along with its parents constitutes a family.

The F_3 populations were grown in 25 rows of 2.5m length and parents in single rows of 2.5m length. The parents and the F_3 populations were sown following a spacing of 30cm between the rows and 10cm between the plants within a row. Fifteen plants in each rows were tagged randomly for recording the observations. Data were recorded for yield and yield attributing traits *viz.*, plant height, primary branches per plant, clusters per plant, pods per cluster, pods per plant, pod length, seeds per pod, hundred seed weight, harvest index, pod yield and seed yield per plant. The data thus generated were subjected to statistical analysis.

The mean values obtained for each character were subjected to analysis of variance using Compact Family Block Design according to the following model as described by Chandel, 2015. The analysis was carried out in two stages by taking crosses as families. The structure of analysis of variance when crosses (families) were raised in Compact Family Block Design with r replication is as shown in table 1.

The analysis for the progenies under each family was done separately for each character. The form of analysis of variance for progenies was conducted as shown in table 2.

Before making comparison, a test of homogeneity of error variance for progenies was carried out for each character by applying Bartlett's test of homogeneity as described by Panse and Sukhatme (1985).

From table 2, the following statistics were computed

(1) Standard error of mean (S.Em) $= \sqrt{M6}/r$

(2) Critical difference (C.D.) =

S.Em x $\sqrt{2}$ x t $_{(0.05) \text{ at error degree of freedom}}$

(3) Coefficient of variation (C.V.) % =

$$\frac{\sqrt{M6}}{\text{Mean of progenies}} \times 100$$

Phenotypic and genotypic coefficients of variation (PCV and GCV) were computed according to Burton (1952). Heritability in broad sense [h^2 (bs)] was calculated by the

formula given by Lush (1940). From the heritability estimates, the genetic advance was estimated by the formula given by Johnson *et al.,* (1955a).

Results and Discussion

Analysis of variance (ANOVA) was done to know the variations among the progenies based on the 11 morphological traits. The analysis of variance for all the characters studied in three crosses of green gram was presented in Table 3. The analysis of variance between families revealed that the mean squares due to crosses were significant for pods per plant. The Bartlett's test for homogeneity of error variances for three crosses indicated that the error variances were homogeneous for all the characters except for plant height, primary branches per plant and pod length.

The analysis of variance among progenies within each family indicated significant differences among progeny means for all the characters studied in all the crosses except pods per plant, pods per cluster and seeds per pod in MGG-347 x MGG-351 and hundred seed weight in the crosses MGG-347 x MGG-351, MGG-351 x LGG-460 and LGG-460 x LGG-528.

The Bartlett's test for homogeneity of error variances for the progenies within each crosses indicated that the error variances were homogeneous for plant height, primary branches per plant, pods per cluster, pod length, seeds per pod, hundred seed weight and harvest index in cross MGG-347 x MGG-351, plant height, primary branches per plant, clusters per plant, pods per cluster, seeds per pod, hundred seed weight and harvest index in cross MGG-351 x LGG-460 and plant height, primary branches per plant, pods per cluster, pod length, seeds per pod, hundred seed weight and harvest index in cross LGG-460 x LGG-528.

Genetic parameters

Segregation, by allowing allelic recombination, increases the variability among population. The estimates of genetic parameters *viz.*, phenotypic and genotypic coefficient of variation (PCV and GCV), heritability in broad sense, genetic advance and genetic advance as per cent of mean were computed for eleven characters in three crosses of mung bean and were presented in Table 4.

The analysis revealed that for all the characters phenotypic coefficient of variation (PCV) was slightly higher than the genotypic coefficient of variation (GCV), so it is evident that expression of the characters is mainly governed by the genotypes itself along with meagre effect of environment. This finding also get corroborated with Venkateswarlu (2001a), Dikshit *et al.,* (2002), Reddy *et al.,* (2003) and Tejbir *et al.,* (2009).

In the present study, high PCV and high GCV was recorded for clusters per plant, pods per plant, pod yield and seed yield per plant in the crosses, MGG-351 x LGG-460 and LGG-460 x LGG-528. This indicates the existence of wide variability for these traits in the progenies of these crosses. Muralidhara *et al.,* (2016) reported the same results for these traits in both F_2 and F_3 generations of the cross LM 192 x MDU 3465. Saxena and Singh (2001) also got the same result with respect to the clusters per plant and pods per plant.

Low variability was recorded for plant height, pod length, seeds per pod and hundred seed weight in all the three crosses. Varma and Garg (2003) also got the same results for these traits. Iranna and Kajjidoni (2008) reported same results for pod length, seeds per pod and hundred seed weight.

In the cross MGG-351 x LGG-460, high heritability and high genetic advance was observed for clusters per plant, pods per plant, pod yield and seed yield. In the cross LGG-460 x LGG-528, high heritability coupled with high genetic advance was observed for clusters per plant and pods per plant. This suggests that the high heritability most likely due to additive gene effect. Hence, these traits may be subjected to any selection scheme to develop the stable genotypes in particular crosses. Similar results were observed for all these traits by Muralidhara *et al.*, (2016) in both F_2 and F_3 generations of the cross LM 192 x MDU 3465. Rahim *et al.*, (2010) observed high heritability and genetic advance for plant height, pods per plant, seeds per pod and seed yield per plant. Shrivastava and Singh (2012) study revealed high heritability and genetic advance for seed yield per plant and number of pods per plant. Rohman *et al.*, (2003), Gupta *et al.*, (2004) and Kapoor *et al.*, (2005) also found similar result. In the cross MGG-347 x MGG-351 low heritability and low genetic advance was shown by plant height, primary branches per plant, pods per plant, pods per cluster, seeds per pod, hundred seed weight and harvest index. In the cross LGG-460 x LGG-528, low heritability and low genetic advance was observed for primary branches per plant, hundred seed weight and harvest index. It indicates that these characters were highly influenced by environmental effects and selection for such traits would be ineffective in these crosses.

In the crosses MGG-351 x LGG-460 and LGG-460 x LGG-528, high heritability coupled with moderate genetic advance was observed for pod length indicating the presence of additive as well as non-additive gene action (Parameswarappa, 2005; Kodanda *et al.*, 2011).

Table.1 Analysis of variance in Compact Family Block Design with r replication

Source	Df	MS	Expected mean squares
Replications	(r-1)	M_1	$\sigma^2_{e1} + \sigma^2_r$
Families	(f-1)	M_2	$\sigma^2_{e1} + \sigma^2_f$
Error	(r-1) (f-1)	M_3	σ^2_{e1}

Table.2 Analysis of variance for progenies

Source	df	MS	Expected mean squares
Replications	(r-1)	M_4	$\sigma^2_{e2} + p\ \sigma^2_r$
Progenies within families	(p-1)	M_5	$\sigma^2_{e2} + r\ \sigma^2_p$
Error	(r-1) (p-1)	M_6	σ^2_{e2}

Where,

r = number of replication

f = number of families

p = number of progenies within each family

σ^2_p= progeny variance within family

σ^2_r= replication variance

σ^2_{e1} = error variance for families

σ^2_{e2} = error variance for progenies

Table.3 Analysis of variance (mean squares) between families and between progenies within families of three crosses for different characters in green gram

Sources of variation	df	PH	NPB	NCP	NPP	NPC	PL	NSP	HSW	HI	PY	SY
Analysis of Variances between Families												
Replications	2	2897.91*	0.80	17.34	3235.21**	11.24*	2.14	5.96	0.69	288.39	404.35*	146.92*
Crosses	2	302.62	0.19	52.55	1240.99*	1.76	3.41	2.65	0.35	115.84	243.67	98.00
Error	4	220.60	3.02	14.13	177.21	1.43	0.71	6.28	0.19	270.06	41.29	16.94
Bartlett's test		S	S	NS	NS	NS	S	NS	NS	NS	NS	NS
Analysis of Variances between progenies within families												
		MGG-347 x MGG-351										
Replications	2	2118.42**	5.82**	0.62	1073.04**	7.94**	3.15**	17.96**	0.07	88.23**	278.00**	98.74**
Progenies	26	21.06*	0.24	2.33**	59.92	0.17	0.21**	0.56	0.03	19.07	6.76*	2.65*
Error	52	12.22	0.21	0.96	41.15	0.13	0.07	0.37	0.02	16.60	3.90	1.54
Bartlett's test		NS	NS	S	S	NS	NS	NS	NS	NS	S	S
		MGG-351 x LGG-460										
Replications	2	648.26**	0.70**	44.96**	1931.17**	3.91**	0.10	0.06	0.94**	501.82**	163.07**	63.76**
Progenies	26	56.27**	0.16**	30.43**	824.24**	0.39**	0.40**	1.04**	0.05	34.83**	23.34**	8.02**
Error	52	25.94	0.07	1.54	36.03	0.13	0.03	0.27	0.03	9.46	3.78	1.44
Bartlett's test		NS	NS	NS	S	NS	S	NS	NS	NS	S	S
		LGG-460 x LGG-528										
Replications	2	572.41**	0.32	0.03	585.41**	2.25**	0.31**	0.51	0.08*	238.46**	45.87**	18.31**
Progenies	26	35.44**	0.17	13.91**	366.64**	0.33**	0.40**	0.77**	0.01	22.38	33.00**	12.83**
Error	52	14.24	0.12	1.63	59.44	0.11	0.03	0.25	0.01	17.84	6.13	2.57
Bartlett's test		NS	NS	S	S	NS	NS	NS	NS	NS	S	S

*-Significant at 5 % level; **-Significant at 1% level S- significant; NS- non significant
PH - Plant height, NPB -No. of primary branches, NCP - No. of clusters per plant, NPP -Number of pods per plant,
NPC-No. pods per cluster, PL -Pod length, NSP -No. seeds per pod, HSW - Hundred seed weight,
HI -Harvest index PY -Pod yield, SY - Seed yield

Table.4 Parameters of genetic variability for three crosses in green gram

Characters	Crosses	Mean	C. V.	E. V.	G. V.	P.V.	GCV	PCV	H^2 (bs)	GA	GAM
Plant Height	MGG-347 x MGG-351	59.58	5.87	12.22	2.95	15.17	2.88	6.54	19.43	1.56	2.62
	MGG-351 x LGG-460	62.48	8.15	25.94	10.11	36.05	5.09	9.61	28.04	3.47	5.55
	LGG-460 x LGG-528	63.24	5.97	14.24	7.07	21.31	4.20	7.30	33.16	3.15	4.99
Primary Branches/ Plant	MGG-347 x MGG-351	2.01	22.78	0.21	0.01	0.22	0.45	23.27	4.15	0.04	1.99
	MGG-351 x LGG-460	2.01	13.06	0.07	0.03	0.10	8.61	15.64	30.27	0.20	9.75
	LGG-460 x LGG-528	2.09	16.62	0.12	0.02	0.14	6.36	17.80	12.78	0.10	4.68
Clusters/ Plant	MGG-347 x MGG-351	5.43	18.08	0.96	0.45	1.42	12.43	21.94	32.09	0.79	14.50
	MGG-351 x LGG-460	6.74	18.43	1.54	9.63	11.17	46.07	49.62	86.20	5.94	88.10
	LGG-460 x LGG-528	6.89	18.50	1.63	4.09	5.72	29.35	34.69	71.57	3.53	51.15
Pods/ Plant	MGG-347 x MGG-351	27.13	23.64	41.15	6.26	47.41	9.22	25.38	13.20	1.87	6.90
	MGG-351 x LGG-460	34.25	17.52	36.03	262.74	298.76	47.33	50.47	87.94	31.31	91.43
	LGG-460 x LGG-528	34.91	22.08	59.44	102.40	161.84	28.99	36.44	63.27	16.58	47.50
Pods/ Cluster	MGG-347 x MGG-351	3.12	11.73	0.13	0.01	0.15	0.40	12.26	8.56	0.07	2.16
	MGG-351 x LGG-460	2.96	12.03	0.13	0.09	0.21	9.99	15.64	40.82	0.39	13.15
	LGG-460 x LGG-528	3.25	10.40	0.11	0.07	0.19	8.22	13.26	38.43	0.34	10.50
Pod Length cm	MGG-347 x MGG-351	6.10	4.37	0.07	0.05	0.12	3.48	5.58	38.79	0.27	4.46
	MGG-351 x LGG-460	5.85	3.09	0.03	0.12	0.15	5.96	6.72	78.78	0.64	10.90
	LGG-460 x LGG-528	6.26	2.77	0.03	0.12	0.15	5.64	6.28	80.52	0.65	10.42
Seeds/ Pod	MGG-347 x MGG-351	7.39	8.24	0.37	0.06	0.44	3.42	8.92	14.64	0.20	2.69
	MGG-351 x LGG-460	7.43	6.96	0.27	0.26	0.53	6.84	9.76	49.16	0.73	9.88

	LGG-460 x LGG-528	7.72	6.51	0.25	0.17	0.43	5.38	8.45	40.54	0.54	7.06
Characters	**Crosses**	**Mean**	**C. V.**	**E. V.**	**G. V.**	**P.V.**	**GCV**	**PCV**	**H^2 (bs)**	**GA**	**GAM**
100 Seed Weight	MGG-347 x MGG-351	3.54	4.31	0.02	0.00	0.03	1.47	4.56	10.47	0.03	0.98
	MGG-351 x LGG-460	3.41	5.26	0.03	0.01	0.04	2.26	5.72	15.55	0.06	1.83
	LGG-460 x LGG-528	3.50	2.54	0.01	0.00	0.01	0.02	2.68	9.70	0.02	0.53
Harvest Index	MGG-347 x MGG-351	31.92	12.77	16.60	0.82	17.42	2.84	13.08	4.73	0.41	1.27
	MGG-351 x LGG-460	29.53	10.42	9.46	8.45	17.92	9.85	14.33	47.19	4.11	13.93
	LGG-460 x LGG-528	30.84	13.70	17.84	1.51	19.35	3.99	14.27	7.82	0.71	2.30
Pod Yield	MGG-347 x MGG-351	8.37	23.60	3.90	0.96	4.85	11.68	26.33	19.68	0.89	10.67
	MGG-351 x LGG-460	8.30	23.42	3.78	6.52	10.30	30.76	38.66	63.32	4.19	50.43
	LGG-460 x LGG-528	11.34	21.83	6.13	8.96	15.09	26.40	34.26	59.38	4.75	41.91
Seed Yield	MGG-347 x MGG-351	5.28	23.51	1.54	0.37	1.91	11.50	26.17	19.31	0.55	10.41
	MGG-351 x LGG-460	5.10	23.57	1.44	2.19	3.64	29.04	37.40	60.28	2.37	46.45
	LGG-460 x LGG-528	7.09	22.60	2.57	3.42	5.99	26.09	34.52	57.13	2.88	40.62

For this trait improvement can be made opting the two to three cycles of recurrent selection followed by pedigree or single seed descent methods of breeding (Dadepeer *et al.,* 2009; Dhananjay *et al.,* 2009 and Rahim *et al.,* 2010).

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