

Original Research Article

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## Analysis of Transgressive Segregation in Three Crosses of Green Gram [*Vigna radiata* (L.) Wilczek]

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### ABSTRACT

#### Keywords

Self-pollinated crops, Transgressive segregation, F<sub>3</sub> populations

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The success of selection in self-pollinated crops depends on the extent to which breeders can fix transgressive segregation in early generations. The objectives of this research were to detect the multiple traits transgressive segregant families of the early generation of mungbean. The present investigation involves three F<sub>3</sub> populations of MGG-347 x MGG-351, MGG-351 x LGG-460 and LGG-460 x LGG-528. Good number of transgressive segregants was observed over better parent for number of clusters per plant, pod length, SLA at 50 DAS, SCMR at 50 DAS, harvest index, pod yield and seed yield per plant in the cross LGG-460 x LGG-528 compared to other two crosses.

### Introduction

Green gram [*Vigna radiata* (L.) Wilczek] is 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). In India, green gram is cultivated in an area of 30.19 lakh hectares with a production of 15.03 lakh tonnes and average productivity of 498 kg ha<sup>-1</sup> (India stat, 2014-2015). Selection plays an important role in the plant breeding program, specifically in

producing new superior genotypes. Transgressive segregation analysis can identify desirable breeding lines at the F<sub>3</sub> generation in self-pollinated crops. Early generation selection can save considerable resources required for breeding. With these objectives, 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<sub>3</sub> 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 *kharrif*, 2016. Each cross along with its parents constitutes a family. The F<sub>3</sub> populations were grown in 25 rows of 2.5m length and parents in single rows of 2.5m length. The parents and the F<sub>3</sub> populations were sown following a spacing of 30cm between the rows and 10cm between the plants within a row. Fifteen plants in each row were tagged randomly for recording the observations. Data were recorded for yield, harvest index and water use efficiency related 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, SLA after 35 DAS and 50 DAS, SPAD chlorophyll meter reading (SCMR) after 35 DAS and 50 DAS, harvest index, pod yield and seed yield per plant.

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 under:

In the present study, transgressive segregants were identified by finding the number of plants exceeding mean value of the higher parent or lagging behind the mean value of the lower parent by critical difference at 5 per cent level. The data recorded on 1125 individual plants for each cross was used for calculating the transgressive segregants.

## Results and Discussion

The analysis of variance for all the fifteen characters studied in three crosses of green gram was presented in Table 1. The analysis of variance between families revealed that the mean squares due to crosses were significant for the characters *viz.*, number of pods per plant, specific leaf area after 35 DAS, specific leaf area at 50 DAS and SCMR at 50 DAS.

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 number of primary branches per plant, number of pods per plant, number of pods per cluster, harvest index and number of seeds per pod in cross MGG-347 x MGG-351; number of primary branches per plant and harvest index in the cross LGG-460 x LGG-528 and hundred seed weight in all the three crosses *viz.*, MGG-347 x MGG-351, MGG-351 x LGG-460 and LGG-460 x LGG-528.

Transgressive individuals with values exceeding the better parent were observed for all the characters in all the crosses. The number of such plants that fitted this definition among all the three crosses is presented in Table 2 and percentage of the transgressive segregants in each cross for fifteen characters were represented in the Fig. 1.

A good number of transgressive segregants were observed for number of primary branches per plant, number of pods per plant and SCMR at 35 DAS in the cross MGG-347 x MGG-351; plant height, number of pods per cluster, number of seeds per pod, hundred seed weight and SLA at 35 DAS in the cross MGG-351 x LGG-460; number of clusters per plant, pod length, SLA at 50 DAS, SCMR at 50 DAS, harvest index, pod yield and seed yield in the cross LGG-460 x LGG-528.

**Table.1** 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	SLA (35 DAS)	SLA (50 DAS)	SCMR (35 DAS)	SCMR (50 DAS)	HI	PY	SY
<b>Analysis of Variances between Families</b>																
Replications	2	2897.91*	0.80	17.34	3235.21**	11.24*	2.14	5.96	0.69	14407.59**	13347.84*	128.59	641.20**	288.39	404.35*	146.92*
Crosses	2	302.62	0.19	52.55	1240.99*	1.76	3.41	2.65	0.35	29488.72**	41180.93**	172.05	197.84*	115.84	243.67	98.00
Error	4	220.60	3.02	14.13	177.21	1.43	0.71	6.28	0.19	199.43	1647.78	35.80	11.03	270.06	41.29	16.94
Bartlett's test		S	S	NS	NS	NS	S	NS	NS	NS	S	NS	S	NS	NS	NS
<b>Analysis of Variances between progenies within families</b>																
MGG-347 x MGG-351																
Replications	2	2118.42*	5.82*	0.62	1073.04**	7.94*	3.15*	17.96*	0.07	3287.67**	11295.69**	30.12**	261.30**	88.23**	278.00**	98.74**
Progenies	26	21.06*	0.24	2.33**	59.92	0.17	0.21*	0.56	0.03	6119.29**	3964.86**	25.16**	3.88**	19.07	6.76*	2.65*
Error	52	12.22	0.21	0.96	41.15	0.13	0.07	0.37	0.02	186.65	225.73	2.14	1.38	16.60	3.90	1.54
Bartlett's test		NS	NS	S	S	NS	NS	NS	NS	S	S	S	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*	4704.13**	2439.71**	61.50**	131.85**	501.82**	163.07**	63.76**
Progenies	26	56.27**	0.16*	30.43*	824.24**	0.39*	0.40*	1.04**	0.05	4036.60**	3070.36**	27.57**	5.50**	34.83**	23.34**	8.02**
Error	52	25.94	0.07	1.54	36.03	0.13	0.03	0.27	0.03	143.54	109.23	1.69	1.31	9.46	3.78	1.44
Bartlett's test		NS	NS	NS	S	NS	S	NS	NS	S	S	NS	S	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*	6814.65**	2908.10**	108.58**	270.11**	238.46**	45.87**	18.31**
Progenies	26	35.44**	0.17	13.91*	366.64**	0.33*	0.40*	0.77**	0.01	7601.30**	2971.38**	17.33**	6.59**	22.38	33.00**	12.83**
Error	52	14.24	0.12	1.63	59.44	0.11	0.03	0.25	0.01	209.04	68.03	2.41	0.69	17.84	6.13	2.57
Bartlett's test		NS	NS	S	S	NS	NS	NS	NS	S	S	S	S	NS	S	S

\*-Significant at 5 % level; \*\*-Significant at 1% level

PH - Plant height,  
 NPB -No. of primary branches,  
 NPC- No. pods per cluster,  
 PL -Pod length,  
 HI -Harvest index  
 PY -Pod yield,  
 SLA (35 DAS) - Specific leaf area after 35 DAS,  
 SCMR (35 DAS) - SPAD chlorophyll meter reading after 35 DAS,

S- significant; NS- non significant  
 NCP - No. of clusters per plant,  
 NPP - Number of pods per plant,  
 NSP -No. seeds per pod,  
 HSW - Hundred seed weight,  
 SY - Seed yield  
 SLA (50 DAS) - Specific leaf area after 50 DAS,  
 SCMR (50 DAS)-SPAD chlorophyll meter reading after 50 DAS

**Table.2** Transgressive segregants for fifteen characters in F<sub>3</sub> population of three green gram crosses

Trait/Cross	F <sub>3</sub> generation		Parents		No. of transgressive segregants	
	Highest plant value	Lowest plant value	Higher Parent value	Lower Parent value	Higher than highest parent	Lower than lowest parent
<b>Plant height</b>						
<b>MGG-347 x MGG-351</b>	93	23	55.11 (MGG-347)	54.67 (MGG-351)	414 (36.8%)	135 (12%)
<b>MGG-351 x LGG-460</b>	92	22	51.27 (MGG-351)	49.89 (LGG-460)	807 (71.33%)	35 (3.11%)
<b>LGG-460 x LGG-528</b>	97	26	60.64 (LGG-460)	58.76 (LGG-528)	315 (28%)	78 (6.93%)
<b>Number of primary branches</b>						
<b>MGG-347 x MGG-351</b>	5	-	2.22 (MGG-351)	1.98 (MGG-347)	100 (8.89%)	347 (30.84%)
<b>MGG-351 x LGG-460</b>	5	-	2.69 (MGG-351)	2.09 (LGG-460)	31 (2.75%)	307 (27.28%)
<b>LGG-460 x LGG-528</b>	5	-	2.24 (LGG-460)	2 (LGG-528)	55 (4.88%)	279 (24.8%)
<b>Clusters per plant</b>						
<b>MGG-347 x MGG-351</b>	24	1	5.67 (MGG-347)	5.36 (MGG-351)	160 (14.22%)	222 (197.33%)
<b>MGG-351 x LGG-460</b>	55	2	18.69 (MGG-351)	13.78 (LGG-460)	16 (1.42%)	1040 (92.44%)
<b>LGG-460 x LGG-528</b>	51	1	6.93 (LGG-460)	5.36 (LGG-528)	200 (17.78%)	135 (12%)
<b>Pods per plant</b>						
<b>MGG-347 x MGG-351</b>	288	4	29.47 (MGG-347)	26.98 (MGG-351)	168 (14.93%)	271 (24.08%)
<b>MGG-351 x LGG-460</b>	225	1	105.4 (MGG-351)	30.93 (LGG-460)	125 (11.11%)	480 (42.67%)
<b>LGG-460 x LGG-528</b>	247	3	45.78 (LGG-460)	25.18 (LGG-528)	151 (13.42%)	147 (13.06%)
<b>Pods per cluster</b>						
<b>MGG-347 x MGG-351</b>	7.2	1	3.54 (MGG-347)	2.87 (MGG-351)	160 (14.22%)	200 (17.78%)
<b>MGG-351 x LGG-460</b>	7.4	1	2.99 (MGG-351)	2.91 (LGG-460)	251 (22.31%)	298 (26.48%)
<b>LGG-460 x LGG-528</b>	9	1	3.83 (LGG-460)	3.12 (LGG-528)	122 (10.84%)	274 (24.35%)
<b>Pod length</b>						
<b>MGG-347 x MGG-351</b>	10.22	3	6.53 (MGG-351)	5.71 (MGG-347)	102 (9.06%)	101 (8.98%)
<b>MGG-351 x LGG-460</b>	14.36	3.58	6.6 (MGG-351)	5.51 (LGG-460)	35 (3.11%)	83 (7.38%)
<b>LGG-460 x LGG-528</b>	9.2	4.14	6.05 (LGG-460)	5.02 (LGG-528)	406 (36.08%)	68 (6.04%)

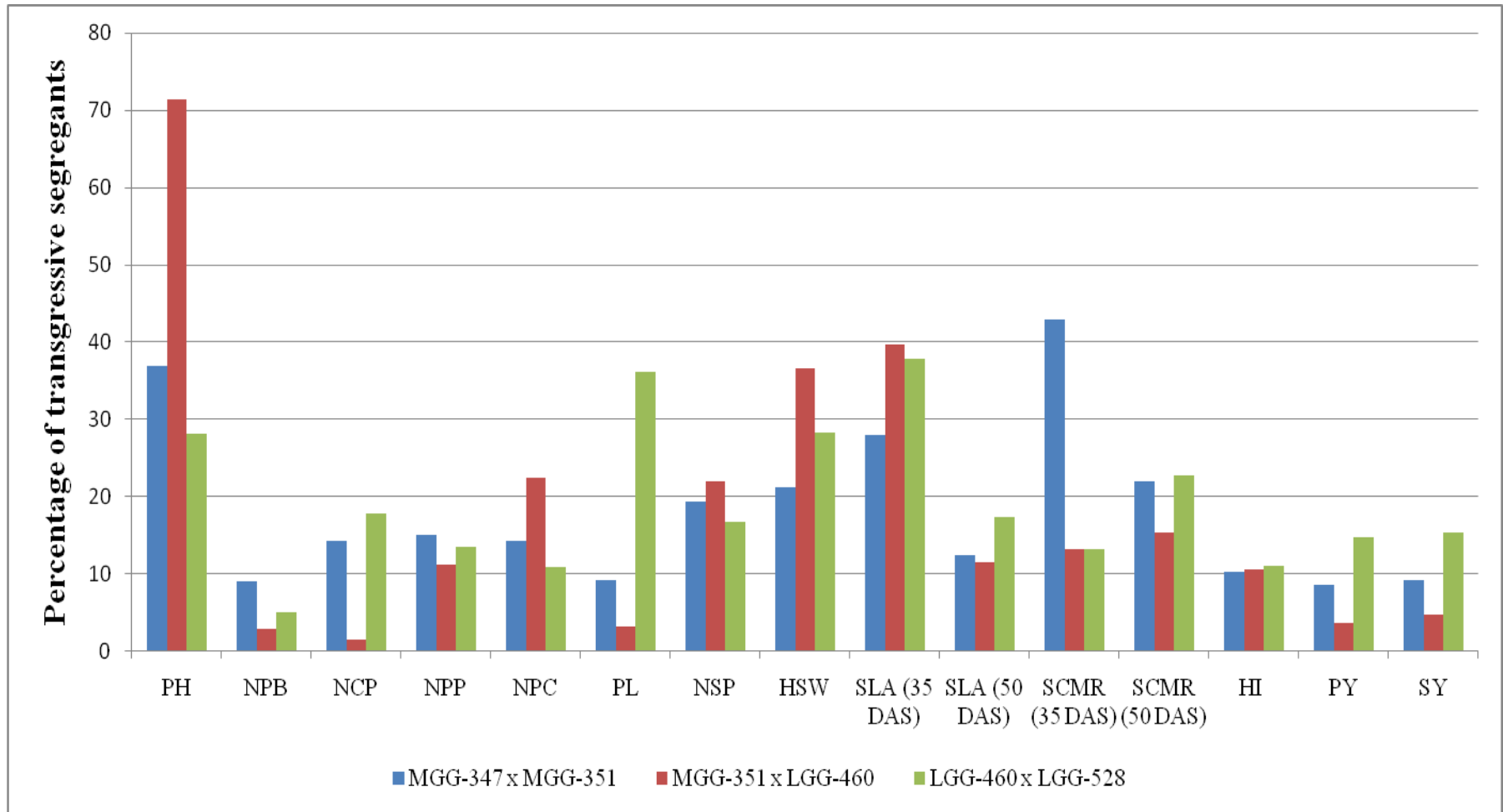
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Trait/Cross	F <sub>3</sub> generation		Parents		No. of transgressive segregants	
	Highest plant value	Lowest plant value	Higher parent value	Lower parent value	Higher than highest parent	Lower than lowest parent
<b>Seeds per pod</b>						
<b>MGG-347 x MGG-351</b>	12.6	1.2	7.76 (MGG-351)	6.92 (MGG-347)	216 (19.2%)	187 (16.62%)
<b>MGG-351 x LGG-460</b>	12.6	2.2	7.6 (MGG-351)	7.32 (LGG-460)	246 (21.87%)	232 (20.62%)
<b>LGG-460 x LGG-528</b>	13.6	1.8	8.09 (LGG-460)	7.21 (LGG-528)	187 (16.62%)	185 (16.44%)
<b>100 seed weight</b>						
<b>MGG-347 x MGG-351</b>	4.68	1.5	3.52 (MGG-351)	3.41 (MGG-347)	238 (21.16%)	117 (10.4%)
<b>MGG-351 x LGG-460</b>	4.89	1.36	3.4 (MGG-351)	3.24 (LGG-460)	411 (36.53%)	187 (16.62%)
<b>LGG-460 x LGG-528</b>	4.63	1.54	3.46 (LGG-460)	3.46 (LGG-528)	318 (28.27%)	157 (13.96%)
<b>Specific leaf area (35 DAS)</b>						
<b>MGG-347 x MGG-351</b>	531.03	16.59	190.94 (MGG-351)	157.38 (MGG-347)	326 (28.96%)	314 (27.91%)
<b>MGG-351 x LGG-460</b>	543.83	46.44	208.02 (MGG-351)	187.3 (LGG-460)	338 (30.04%)	446 (39.64%)
<b>LGG-460 x LGG-528</b>	548.8	25.56	209.46 (LGG-460)	191.52 (LGG-528)	434 (38.58%)	424 (37.69%)
<b>Specific leaf area (50 DAS)</b>						
<b>MGG-347 x MGG-351</b>	598.41	29.46	272.78 (MGG-351)	159.6 (MGG-347)	258 (22.93%)	138 (12.27%)
<b>MGG-351 x LGG-460</b>	564.33	33.92	262.3 (MGG-351)	198.74 (LGG-460)	428 (38.04%)	128 (11.37%)
<b>LGG-460 x LGG-528</b>	561.32	85.12	207.06 (LGG-460)	196.66 (LGG-528)	510 (45.33%)	194 (17.24%)
<b>SPAD chlorophyll meter reading (35 DAS)</b>						
<b>MGG-347 x MGG-351</b>	63.1	30.4	47.36 (MGG-347)	46.02 (MGG-351)	482 (42.84%)	21 (1.87%)
<b>MGG-351 x LGG-460</b>	58.7	29.5	50.46 (LGG-460)	44.84 (MGG-351)	148 (13.16%)	223 (19.82%)
<b>LGG-460 x LGG-528</b>	62.5	29.6	49.97 (LGG-528)	46.99 (LGG-460)	147 (13.06%)	437 (38.84%)
<b>SPAD chlorophyll meter reading (50 DAS)</b>						
<b>MGG-347 x MGG-351</b>	54.5	24.6	37.38 (MGG-347)	35.21 (MGG-351)	246 (21.87%)	379 (33.69%)
<b>MGG-351 x LGG-460</b>	55.6	20.4	35.15 (MGG-351)	32.03 (LGG-460)	171 (15.20%)	240 (21.33%)
<b>LGG-460 x LGG-528</b>	57.3	20	35.87 (LGG-528)	32.53 (LGG-460)	255 (22.66%)	272 (24.18%)

Cont...

Trait/Cross	F <sub>3</sub> generation		Parents		No. of transgressive segregants	
	Highest plant value	Lowest plant value	Higher parent value	Lower parent value	Higher than highest parent	Lower than lowest parent
<b>Harvest index</b>						
<b>MGG-347 x MGG-351</b>	86.2	5.03	34.56 (MGG-347)	30.57 (MGG-351)	115 (10.22%)	158 (14.04%)
<b>MGG-351 x LGG-460</b>	92.2	2.44	34.02 (MGG-351)	33.35 (LGG-460)	118 (10.48%)	358 (31.82%)
<b>LGG-460 x LGG-528</b>	80.38	2.56	34.36 (LGG-460)	31.91 (LGG-528)	124 (11.02%)	252 (22.40%)
<b>Pod yield</b>						
<b>MGG-347 x MGG-351</b>	43.99	0.18	12.29 (MGG-347)	8.46 (MGG-351)	96 (8.53%)	332 (29.50%)
<b>MGG-351 x LGG-460</b>	55.76	0.11	17.49 (MGG-351)	11.49 (LGG-460)	40 (3.55%)	660 (58.67%)
<b>LGG-460 x LGG-528</b>	60.61	0.16	14.89 (LGG-460)	11.46 (LGG-528)	167 (14.71%)	466 (41.42%)
<b>Seed yield</b>						
<b>MGG-347 x MGG-351</b>	28.61	0.02	7.6 (MGG-347)	5.23 (MGG-351)	102 (9.06%)	295 (26.22%)
<b>MGG-351 x LGG-460</b>	33.1	0.03	10.11 (MGG-351)	6.06 (LGG-460)	52 (4.62%)	507 (45.06%)
<b>LGG-460 x LGG-528</b>	37.87	0.02	9.32 (LGG-460)	6.55 (LGG-528)	171 (15.20%)	382 (33.96%)

**Fig.1** Bar chart representing percentage of transgressive segregants for fifteen characters in three crosses of green gram



PH - Plant height,  
 NPC- No. pods per cluster,  
 HI -Harvest index  
 SLA (35 DAS) - Specific leaf area after 35 DAS,  
 SCMR (35 DAS) - SPAD chlorophyll meter reading after 35 DAS,

NPB -No. of primary branches,  
 PL -Pod length,  
 PY -Pod yield,

NCP - No. of clusters per plant,  
 NSP -No. seeds per pod,  
 HSW - Hundred seed weight,  
 SY - Seed yield  
 SLA (50 DAS) - Specific leaf area after 50 DAS  
 SCMR (50 DAS)-SPAD chlorophyll meter reading after 50 DAS

**The structure of analysis of variance when crosses (families) were raised in Compact Family Block Design with r replication is as under**

Source	Df	MS	Expected mean squares
Replications	(r-1)	M <sub>1</sub>	$\sigma_{e1}^2 + \sigma_r^2$
Families	(f-1)	M <sub>2</sub>	$\sigma_{e1}^2 + \sigma_f^2$
Error	(r-1) (f-1)	M <sub>3</sub>	$\sigma_{e1}^2$

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 following table

Source	df	MS	Expected mean squares
Replications	(r-1)	M <sub>4</sub>	$\sigma_{e2}^2 + p \sigma_r^2$
Progenies within families	(p-1)	M <sub>5</sub>	$\sigma_{e2}^2 + r \sigma_p^2$
Error	(r-1) (p-1)	M <sub>6</sub>	$\sigma_{e2}^2$

Where,

r = number of replication

f = number of families

p = number of progenies within each family

$\sigma_p^2$  = progeny variance within family

$\sigma_r^2$  = replication variance

$\sigma_{e1}^2$  = error variance for families

$\sigma_{e2}^2$  = error variance for progenies

Dhole and Reddy (2011) reported fifteen (4.79%) transgressive segregants for hundred seed weight in the cross Rsel-246 x JL-781 and one (0.0027%) transgressive segregants for seed yield per plant in the cross Rsel-246 x JL-781, in F<sub>2</sub> populations of respective crosses in green gram. Shivakumar *et al.*, (2013) found more number of transgressive segregants for number of seeds per plant followed by number of pods per plant and yield per plant in F<sub>2</sub> populations and F<sub>2</sub> derived F<sub>3</sub> progenies from the cross between ICC 13124 and WR315 in chickpea. Kerem *et al.*, (2017) reported highest transgressive segregants in seeds per plant (270%), number of pods per plant (193%), biological yield (86%) and seed yield (60%) in F<sub>2</sub> and F<sub>3</sub> populations derived from cross between *C. arietinum* (CA 2969) and *C. reticulatum* (AWC 613) of chickpea.

Transgressive segregants were attributed to constellation of completely or incompletely

dominant genes that are dispersed between their parents. A track on these transgressive segregants should be maintained and forwarded to further generation till they reach nearly homozygous condition. Then most promising one can be used for the development of better genotype.

All the three crosses had thrown a good number of transgressive segregants over better parent for seed yield per plant. More number of transgressive segregants for number of clusters per plant, pod length, SLA at 50 DAS, SCMR at 50 DAS, harvest index, pod yield and seed yield per plant were recorded in the cross LGG-460 x LGG-528 compared to other two crosses *viz.*, MGG-347 x MGG-351 and MGG-351 x LGG-460. Hence, forwarding these transgressive segregants to further generation, contributes to the development of most promising genotype which is better than both the parents. This suggested that it is possible to



develop and identify purelines that outperform the parental limits in these crosses.

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