

## Genetic Analysis of Diverse Greengram (*Vigna radiata* L.) Genotypes for Combining Ability and Gene Action for Yield and its Associated Traits

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**ABSTRACT:** The studies on combining ability and its interrelationships in cultivated greengram (*Vigna radiata* L.) can help in improving the decade old yield stagnation. The present investigation was undertaken in 18 F<sub>1</sub>'s derived out of line × tester mating design using six lines and three testers. Analysis of variance for combining ability revealed significant differences due to genotypes, parents and crosses indicating the existence of wider variability in the material. The results revealed that *sca* variance was relatively greater in magnitude than *gca* variance for the traits, days to 50% flowering, number of branches plant<sup>-1</sup>, number of clusters plant<sup>-1</sup>, number of pods plant<sup>-1</sup> and harvest index indicating that these traits were predominantly governed by non-additive gene action. The characters *viz.*, days to maturity, plant height, number of pods cluster<sup>-1</sup>, pod length, number of seeds pod<sup>-1</sup>, 100-seed weight and seed yield plant<sup>-1</sup> exhibited greater *gca* variance than *sca* variance which indicated that additive gene action was involved in the expression of these characters. Among the parents, LGG-460, IPM-409-4, VBN(Gg)2, IPM-205-7, IPM-410-3 and IC-251786 were found to be good general combiners for seed yield and some of its component traits. These parents could be utilized in future breeding programme for development of high yielding genotypes. On the basis of *sca* effects, the cross combinations, MGG-347×IC-251786, VBN(Gg)2×IPM-2-14, IPM-205-7×IPM-2-14, IPM-409-4×IC-251786 and VBN(Gg)2×IPM-410-3 were considered as best specific combiners for seed yield and most of the yield attributes. Further these crosses could be advanced for selection of superior transgressive segregants.

**Keywords:** Greengram, Combining ability, Line × Tester analysis, Gene action, *gca*, *sca* and Yield components.

### INTRODUCTION

Greengram is one of the major short duration pulse crops with wider adaptability. India is the leading producer of the crop globally and is grown in almost all parts of the country. In India, greengram is cultivated in an area of 51.30 lakh ha with total production and productivity of 30.85 lakh tonne and 601 kg ha<sup>-1</sup> respectively (INDIASTAT, 2020-21). The major greengram growing states are Rajasthan, Karnataka, Maharashtra, Madhya Pradesh and Odisha. The present production of greengram is not sufficient to meet the requirements, the lower productivity is mainly attributed to low genetic yield potentiality, indeterminate growth habit, canopy architecture, cultivation in marginal land and biotic stresses. Thus, there is an immediate need to increase production and productivity for food and nutritional security and to

combat protein energy malnutrition, which requires efforts to enhance the genetic yield potential of the existing varieties by restructuring their plant type. In order to accomplish this, combining ability analysis will provide the information to identify desirable parents and the genetic construction of the crosses. It also offers information about the nature of gene action and the relative magnitude of fixable and non-fixable genetic variances, which can be used to select superior parents for crossing programmes and to develop superior varieties with desirable characters (Kohakade *et al.* 2021). Keeping in view of the above the present study was undertaken to evaluate nine parents and eighteen hybrids through line × tester analysis with regard to the nature of gene action controlling various quantitative traits in terms of combining ability which will be used for setting suitable selection criteria.

## MATERIAL AND METHODS

The experimental material consists of six genotypes of greengram as lines (MGG-295, MGG-347, LGG-460, IPM-409-4, VBN(Gg)2 and IPM-205-7) and three genotypes as testers (IPM-2-14, IPM-410-3, IC-251786). Each entry was sown in five rows of 4m length with two staggered sowings during *kharif*, 2021. Crosses were effected in line  $\times$  tester mating design and the seed of 18 hybrids was obtained.

The parents along with hybrids were evaluated during *rabi*, 2021-22 in Randomized Block Design with three replications to study the gene action and combining ability for yield and its attributing traits. Each entry was sown in 3 rows of 3m length in each replication, seeds were dibbled with a spacing of 30 cm between rows and 10 cm between plants. The recommended package of practices and need based plant protection measures were taken up.

Observations were recorded in ten randomly selected plants both in parents and hybrids on days to 50% flowering, days to maturity, plant height, number of branches plant<sup>-1</sup>, number of clusters plant<sup>-1</sup>, number of pods cluster<sup>-1</sup>, number of pods plant<sup>-1</sup>, pod length, number of seeds pod<sup>-1</sup>, 100-seed weight, seed yield plant<sup>-1</sup> and harvest index. The data was subjected to the analysis of variance as per the method suggested by Panse and Sukhatme (1985) to test the differences between the genotypes for all the characters and combining ability analysis was carried out according to the method given by Kempthorne (1957).

## RESULTS AND DISCUSSION

The analysis of variance revealed the existence of significant differences among the genotypes for the characters studied, which indicates the presence of considerable amount of variation in the material under study. Analysis of variance for combining ability revealed that, there was significant difference among the genotypes studied (Table 1). Parents exhibited significant differences for all the traits, indicating the presence of greater diversity among the parents under study, except for the trait number of pods cluster<sup>-1</sup>. Crosses showed significant differences for all the traits studied, indicating the varying performance of cross combinations. Parents *vs.* crosses registered significant differences for the traits, days to maturity, plant height, number of branches plant<sup>-1</sup>, number of clusters plant<sup>-1</sup>, number of pods cluster<sup>-1</sup>, number of pods plant<sup>-1</sup>, 100-seed weight, seed yield plant<sup>-1</sup> and harvest index, indicating the presence of considerable amount of average heterosis in the hybrids for these traits. The line  $\times$  tester effects were significant for all the traits except for days to maturity and pod length, which indicated that hybrids differed significantly in their *sca* effects.

The ratio of *GCA/SCA* variances revealed that, both additive and non-additive genetic components of variation played important role in expression of the characters studied (Table 2). The *sca* variances were higher than *gca* variances for five traits studied *viz.*, days to 50% flowering, number of branches plant<sup>-1</sup>,

number of clusters plant<sup>-1</sup>, number of pods plant<sup>-1</sup> and harvest index which indicated the predominance of non-additive gene action, therefore the hybrid breeding programme is more appropriate for the improvement of these traits. The earlier researchers, Prasad *et al.* (2015), Bhavani *et al.* (2016); Singh *et al.* (2016); Vaidya *et al.* (2016); Kumar *et al.* (2017); Latha *et al.* (2018); Kohakade *et al.* (2021) also reported non-additive gene action for those characters. Whereas the traits such as days to maturity, plant height, number of pods cluster<sup>-1</sup>, pod length, number of seeds pod<sup>-1</sup>, 100-seed weight and seed yield plant<sup>-1</sup> were governed by additive gene action which is evident from greater magnitude of *gca* variance than *sca* variance. Additive gene action for these traits were also reported by Khaimiccho *et al.* (2016); Vaidya *et al.* (2016); Eswaran *et al.* (2017); Latha *et al.* (2018); Nath *et al.* (2018); Abinaya *et al.* (2020).

Based on the *gca* effects, the lines LGG-460, IPM-409-4, VBN(Gg)2, IPM-205-7 and the testers IPM-410-3, IC-251786 showed significant superiority and these were identified as good general combiners for yield and its attributing traits (Table 3). Among the six lines studied, the line LGG-460 was found to be most promising and it showed desirable *gca* effect for seed yield plant<sup>-1</sup> and its yield components such as plant height, number of branches plant<sup>-1</sup>, number of clusters plant<sup>-1</sup>, number of pods cluster<sup>-1</sup>, number of pods plant<sup>-1</sup>, pod length and number of seeds pod<sup>-1</sup>. The next best line was IPM-409-4 which registered good *gca* effect for seed yield and some of its component traits. The lines VBN(Gg)2 and IPM-205-7 exhibited positive *gca* effect for one or more yield components. The tester IC-251786 was found to be promising for plant height (1.546), 100-seed weight (0.395) and harvest index (0.615). The trait number of clusters plant<sup>-1</sup> was recorded high in IPM-410-3 (0.267). These parents could be utilized in future breeding programme for development of high yielding genotypes.

With regard to specific combining ability the crosses *viz.*, IPM-205-7 $\times$ IPM-2-14, VBN(Gg)2 $\times$ IPM-2-14, MGG-347 $\times$ IC-251786, MGG-347 $\times$ IPM-410-3, MGG-295 $\times$ IPM-2-14, IPM-409-4 $\times$ IC-251786, VBN(Gg)2  $\times$  IPM-410-3, LGG-460 $\times$ IC-251786, MGG-347 $\times$ IPM-2-14, IPM-409-4 $\times$ IPM-2-14, IPM-205-7 $\times$ IC-251786, MGG-295 $\times$ IPM-410-3 and VBN(Gg)2 $\times$ IC-251786 were considered as good specific combiners for yield and some of its component characters (Table 4). The crosses *viz.*, IPM-205-7  $\times$  IPM-2-14 (0.792), MGG-347  $\times$  IC-251786 (0.709) and IPM-409-4 $\times$ IC-251786 (0.438) were considered as potential cross combinations for seed yield. In addition to seed yield these crosses showed superior positive *sca* effect for number of branches plant<sup>-1</sup>, number of clusters plant<sup>-1</sup>, number of pods plant<sup>-1</sup>, harvest index. These cross combinations could be further exploited through heterosis breeding or selection of superior transgressive segregants through recombination breeding.

The present study also confirmed that some of the parents having significant positive *gca* effects for seed yield plant<sup>-1</sup> also exhibited positive *gca* effects for one

or more of yield contributing traits. Based on *per se* performance, *sca* effects and *gca* status, five crosses viz., IPM-205-7×IPM-2-14, MGG-347×IC-251786, IPM-409-4×IC-251786, VBN(Gg)2×IPM-410-3 and VBN(Gg)2×IPM-2-14 were considered as promising for

seed yield plant<sup>-1</sup>. Similar results of significant association of mean performance and general combining ability and its importance in selection of the parents were also reported by Kumar *et al.* (2017).

**Table 1: Analysis of variance for combining ability for yield and yield attributing traits in greengram.**

Source of variation	df	Mean sum of squares for											
		Days to 50% flowering	Days to maturity	Plant height	Number of branches plant <sup>-1</sup>	Number of clusters plant <sup>-1</sup>	Number of pods cluster <sup>-1</sup>	Number of pods plant <sup>-1</sup>	Pod length	Number of seeds pod <sup>-1</sup>	100-seed weight	Seed yield plant <sup>-1</sup>	Harvest index
Replications	2	0.83	0.78	0.05	0.01	0.02	0.03	1.33	0.13	0.33	0.00	0.02	0.01
Treatments	26	15.18**	20.91**	80.80**	1.11**	1.82**	0.41**	31.92**	0.39**	1.90**	1.59**	2.23**	5.66**
Parents	8	43.25**	44.75**	66.49**	0.28*	1.22**	0.09	14.96*	0.36*	0.96**	3.77**	1.15**	2.34**
Parents (Line)	5	49.69**	69.57*	93.28**	0.25*	1.69**	0.12	20.02**	0.38	1.09**	0.18**	1.44**	2.08**
Parents (Testers)	2	40.44**	3.00	31.93**	0.03	0.27	0.08	3.54	0.27	0.73	9.00**	0.55**	0.29**
Parents (L vs T)	1	16.67**	4.17	1.69*	0.96**	0.76	0.03	12.52	0.45	0.74	11.22**	0.92**	7.77**
Parents vs Crosses	1	0.01	26.89**	2.51*	1.16**	10.48**	1.96**	94.30**	0.49	0.59	0.86**	9.98**	2.61**
Crosses	17	2.87**	9.33**	92.14**	1.49**	1.59**	0.46**	36.23**	0.39**	2.42**	0.61**	2.29**	7.39**
Line Effect	5	3.93	27.96**	226.84**	1.69	1.70	0.99*	53.39	0.81*	5.63*	0.23	5.58*	6.88
Tester Effect	2	0.24	3.72	116.59*	0.37	0.98	0.16	14.32	0.23	0.43	2.20*	0.27	7.01
Line * Tester Eff.	10	2.86**	1.14	19.90**	1.61**	1.66**	0.25*	32.03**	0.23	1.21**	0.47**	1.04**	7.73**
Error	52	0.85	1.28	0.02	0.10	0.19	0.11	5.73	0.16	0.32	0.00	0.05	0.00
Total	80	5.51	7.64	26.28	0.42	0.72	0.20	14.13	0.24	0.83	0.52	0.76	1.84

\*, \*\* Significant at 5 and 1 % levels, respectively.

**Table 2: Estimates of GCA and SCA variances and gene action for yield and yield attributing traits in greengram.**

Source of variation	Days to 50% flowering	Days to maturity	Plant height	Number of branches plant <sup>-1</sup>	Number of clusters plant <sup>-1</sup>	Number of pods cluster <sup>-1</sup>	Number of pods plant <sup>-1</sup>	Pod length	Number of seeds pod <sup>-1</sup>	100-seed weight	Seed yield Plant <sup>-1</sup>	Harvest index
<sup>2</sup> <i>gca</i>	0.18	2.16	25.44	0.14	0.17	0.07	4.17	0.05	0.40	0.18	0.43	1.03
<sup>2</sup> <i>sca</i>	0.67	-0.04	6.63	0.50	0.49	0.05	8.77	0.02	0.29	0.16	0.33	2.58
<sup>2</sup> <i>gca</i> / <sup>2</sup> <i>sca</i>	0.27	-48.54	3.84	0.27	0.35	1.47	0.47	2.52	1.34	1.14	1.29	0.39
Degree of dominance	1.92	0.14	0.51	1.91	1.69	0.82	1.45	0.63	0.86	0.93	0.88	1.58
Gene action	Non-Additive	Additive	Additive	Non-Additive	Non-Additive	Additive	Non-Additive	Additive	Additive	Additive	Additive	Non-Additive

GCA – General combining ability, SCA – Specific combining ability, <sup>2</sup> *gca* – Variance due to general combining ability, <sup>2</sup> *sca* - Variance due to specific combining ability.

**Table 3: Estimates of general combining ability effects for yield and yield attributing traits in greengram.**

Characters	Days to 50% flowering	Days to maturity	Plant height	Number of branches plant <sup>-1</sup>	Number of clusters plant <sup>-1</sup>	Number of pods cluster <sup>-1</sup>	Number of pods plant <sup>-1</sup>	Pod length	Number of seeds pod <sup>-1</sup>	100-seed weight	Seed yield plant <sup>-1</sup>	Harvest index
Parents												
LINES												
MGG-295	-0.204	1.333 **	-4.314 **	0.102	-0.056	-0.131	0.815	-0.521 **	-1.522 **	-0.069 **	-0.087	-1.739 **
MGG-347	0.463	-1.556 **	3.134 **	0.169	-0.044	-0.131	-0.585	-0.008	-0.164	-0.202 **	-0.455**	0.123 **
LGG-460	-0.537	1.889 **	5.273 **	0.680 **	0.789 **	0.573 **	3.770 **	0.386 **	0.441 *	-0.001	1.309**	0.666 **

IPM-409-4	-0.870 **	-1.333 **	0.479 **	-0.331 **	-0.078	0.166	0.504	-0.061	0.452 *	-0.024 **	0.475**	0.322 **
VBN(Gg)2	0.907 **	-1.889 **	3.150 **	-0.043	-0.056	-0.083	-0.830	0.060	0.582 **	0.005	0.322**	0.449 **
IPM-205-7	0.241	1.556 **	-7.722 **	-0.576 **	-0.556 **	-0.394 **	-3.674 **	0.144	0.212	0.291 **	-0.920**	0.179 **
<b>S.E. (for line)</b>	0.308	0.377	0.050	0.105	0.145	0.111	0.798	0.135	0.188	0.006	0.078	0.021
<b>TESTERS</b>												
IPM-2-14	-0.093	-0.389	1.391 **	-0.165 *	-0.100	-0.107	-0.702	0.075	0.068	-0.271 **	-0.132*	0.018
IPM-410-3	-0.037	-0.111	-2.937 **	0.074	0.267 *	0.078	1.004	-0.129	-0.177	-0.124 **	0.109	-0.633**
IC-251786	0.130	0.500	1.546 **	0.091	-0.167	0.029	-0.302	0.054	0.109	0.395 **	0.023	0.615**
<b>S.E. (for tester)</b>	0.218	0.266	0.035	0.075	0.103	0.078	0.564	0.095	0.133	0.004	0.055	0.015

\*, \*\* Significant at 5 and 1 % levels, respectively.

**Table 4: Estimates of specific combining ability effects for yield and yield attributing traits in crosses of greengram.**

Characters Crosses	Days to 50% flowering	Days to maturity	Plant height	Number of branches plant <sup>-1</sup>	Number of clusters plant <sup>-1</sup>	Number of pods cluster <sup>-1</sup>	Number of pods plant <sup>-1</sup>	Pod length	Number of seeds pod <sup>-1</sup>	100-seed weight	Seed yield plant <sup>-1</sup>	Harvest index
MGG-295 × IPM-2-14	0.759	-0.278	-2.497 **	0.509 **	0.511	0.163	1.424	0.226	0.912 **	0.333 **	0.186	1.275 **
MGG-295 × IPM-410-3	0.370	0.111	-1.751 **	-0.396 *	-0.156	-0.034	-2.481	-0.007	-0.729 *	0.059 **	-0.115	-2.677 **
MGG-295 × IC-251786	-1.130 *	0.167	4.249 **	-0.113	-0.356	-0.129	1.057	-0.219	-0.183	-0.393 **	-0.070	1.402 **
MGG-347 × IPM-2-14	0.759	0.611	0.289 **	-1.324 **	-1.100 **	-0.126	-4.709 **	-0.191	-0.292	0.246 **	-0.634 **	-1.687 **
MGG-347 × IPM-410-3	-0.963	-0.333	1.584 **	0.570 **	0.333	-0.201	0.619	-0.072	0.683 *	0.202 **	-0.075	0.144 **
MGG-347 × IC-251786	0.204	-0.278	-1.873 **	0.754 **	0.767 **	0.327	4.091 **	0.263	-0.391	-0.447 **	0.709 **	1.543 **
LGG-460 × IPM-2-14	-0.241	0.167	3.360 **	0.031	-0.433	-0.008	-0.998	-0.376	-0.624	-0.496 **	-0.334 *	-0.540 **
LGG-460 × IPM-410-3	0.037	0.222	-2.821 **	-0.541 **	0.067	-0.204	1.130	0.353	-0.005	-0.076 **	0.225	0.354 **
LGG-460 × IC-251786	0.204	-0.389	-0.538 **	0.509 **	0.367	0.212	-0.131	0.023	0.628	0.572 **	0.109	0.186 **
IPM-409-4 × IPM-2-14	0.093	-0.611	0.577 **	-0.324	-0.433	-0.212	-2.365	0.029	-0.005	0.341 **	-0.409 **	-0.793 **
IPM-409-4 × IPM-410-3	1.037	0.778	0.290 **	0.170	0.067	0.014	0.796	0.072	0.521	-0.113 **	-0.029	0.879 **
IPM-409-4 × IC-251786	-1.130 *	-0.167	-0.867 **	0.154	0.367	0.198	1.569	-0.102	-0.516	-0.228 **	0.438 **	-0.086 *
VBN(Gg)2 × IPM-2-14	-0.352	0.611	-0.727 **	0.454 *	0.811 **	0.148	2.902 *	-0.063	-0.077	-0.144 **	0.400 **	0.927 **
VBN(Gg)2 × IPM-410-3	-0.741	-1.000	2.559 **	0.281	0.244	0.384	1.030	-0.011	0.116	0.002	0.433 **	1.095 **
VBN(Gg)2 × IC-251786	1.093 *	0.389	-1.831 **	-0.735 **	-1.056 **	-0.532 **	-3.931 **	0.074	-0.039	0.143 **	-0.832 **	-2.023 **
IPM-205-7 × IPM-2-14	-1.019	-0.500	-1.001 **	0.654 **	0.644 *	0.036	3.746 *	0.374	0.085	-0.280 **	0.792 **	0.817 **
IPM-205-7 × IPM-410-3	0.259	0.222	0.141	-0.085	-0.556 *	0.040	-1.093	-0.334	-0.587	-0.074 **	-0.439 **	0.205 **
IPM-205-7 × IC-251786	0.759	0.278	0.861 **	-0.569 **	-0.089	-0.076	-2.654	-0.040	0.502	0.354 **	-0.353 *	-1.023 **
<b>SE (Sij - Skl)</b>	0.754	0.923	0.123	0.258	0.356	0.271	1.955	0.331	0.459	0.015	0.192	0.051
<b>SE (Sij - Sik)</b>	1.152	1.409	0.188	0.395	0.544	0.414	2.986	0.505	0.702	0.022	0.293	0.078

\*, \*\* Significant at 5 and 1 % levels, respectively.

## CONCLUSION

From the study it can be inferred that, LGG-460 and IPM-409-4 were found to be the best general combiners for yield and other yield attributing traits. These parental lines could be used in future breeding programmes to realize high yielding crosses as well as for development of transgressive segregants. The crosses IPM-205-7×IPM-2-14, MGG-347×IC-251786 and IPM-409-4×IC-251786 were identified as superior for seed yield and yield components. Hence desirable segregants from these crosses can be exploited to develop high yielding greengram cultivars for different agro ecologies.

## FUTURE SCOPE

Pulses particularly greengram is an excellent option for sustainable agri food systems of rainfed farming. The current yield is very low and stagnant around 601 kg/ha in this crop. To combat the protein energy mal nutrition there is a need to enhance the productivity of this pulse. In this context the present study will aid the crop improvement researchers across the globe in selection of parents and to develop a strong breeding pipeline of greengram crop.

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**Conflict of Interest.** None.

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