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Combining ability analysis for seed yield and its component characters in greengram (*Vigna radiata* (L.) Wilczek.)

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Abstract
Combining ability analysis was carried out in 36 F_1's derived out of half diallel using nine parents in Greengram. Significant differences were observed for GCA and SCA among parents and hybrids for all the traits under study. Analysis of combining ability revealed that mean squares due to general and specific combining ability were highly significant for all the characters indicating importance of both additive as well as non-additive gene effects involved in the expression of all the characters. However, higher magnitude of specific combining ability variances for almost all the traits pointed out that the preponderance of non additive component of the genetic variance was involved in the expression of the characters. For the improvement of seed yield, the crosses involving the parents, MGG-347, WGG-42, LGG-543, RM 12-13 and KM 11-564, need special consideration. The cross combination, MGG-347 X KM 11-564, was the best for high seed yield on the basis of SCA. The specific crosses, WGG-42 X RM 12-13, LGG-543 X KM 11-564 and MGG-347 X RM 12-13, revealed high number of pods coupled with high seed yield.

Keywords: greengram, combining ability analysis, *Gca*, *Sca*, yield components

Introduction
Proper choice of parents to get desirable recombinants through hybridization is very crucial in a crop improvement programme. The dilemma of utilization of parents to cross has now become more puzzling because of available genetic variability in a crop like Greengram is limited. Therefore, future Greengram breeding may endeavour on sound basis to achieve further increase in present stagnant yields. Combining ability analysis is a useful technique that provides information on breeding values of the parental material and nature of genetic variability in F_1 generation. Equipped with this information, a breeder can better select parents for hybridization and adopt appropriate breeding scheme to handle elite crosses. The diallel analysis approach (Griffing, 1956) [1] is a precise test to ascertain relative contribution of general combining abilities (GCA), specific combining abilities (SCA) and reciprocal effects for quantitative traits among cross variations. Most investigations on gene action and combining ability studies in Greengram by diallel analysis have attributed preponderance of variability due to GCA (Kumar *et al*. (2010) [2] and Narsimhulu *et al.* (2014) [3]. Some studies have also concluded predominance of SCA variance for most of the characters related to yield (Anbuselvan (2012) [4] and Manoj and Amit (2015) [5]. Present study was undertaken to evaluate nine Greengram varieties with regard to genetic mechanism involved in controlling yield and its components in terms of combining ability which will be used for setting suitable selection criteria.

Materials and Methods
The experimental material consisted of nine Greengram genotypes/varieties (MGG-371, MGG-347, MGG-351, WGG-42, LGG-543, K-851, RM-12-11, RM-12-13and KM-11-564) which were phenotypically different and of diverse nature. These 9 parents were crossed to generate 36 F_1's using diallel mating design (excluding reciprocals) at College Farm, College of Agriculture, PJTSAU, Rajendranagar, Hyderabad. The parents along with hybrids were grown during *Kharif* 2015 in Randomized Complete Block Design with three replications to study the inheritance and combining abilities for yield and its attributing traits. One row of each genotype was dibbled keeping 30 and 10 cm spacing

between and within rows, respectively. Basal fertilizer dose @ 25 kg N + 60 kg P_2O_5 per hectare was applied and during crop growth period agronomic practices were used as recommended for Greengram crop. The data for days to maturity were recorded when about 90% pods turned brown/black. Other quantitative data i.e., plant height (cm), number of branches per plant, number of cluster per plant, number of pods per plant, 100 seed weight (g), seed yield per plant and harvest index were recorded on 10 guarded plants selected randomly and then averaged to per plant basis. Pod length (cm) and seeds per pod were taken on 10 pods selected at random within each genotype. The seed weight was recorded for each genotype after counting 100 seeds by seed counter and weighed in grams. The protein was estimated according to the modified Kjeldhal's method of Piper (1966) [6]. The estimates of variance for both the general and specific combining abilities and their effects were computed according to Model I (fixed effect model) and Method II (parents and crosses, excluding reciprocals) as given by Griffing (1956) [1].

Results

The combining ability analysis partitions the genotypic variability into variances due to general combining ability (GCA) and specific combining ability (SCA) which represent additive and dominance effects, respectively. The combining ability analysis also helps in identifying desirable parents to be used for a given trait in a breeding programme. Similarly superior cross combinations can also be detected through this analysis. In the present study, the analysis of variance for nine parents in half diallel fashion revealed significant differences among parents and hybrids for all the characters studied hence there is enough scope for selection among the varieties.

Analysis of variance revealed significant differences among the genotypes, parents and hybrids for all characters except number of seeds per pod and protein content in parents (Table 1). This may obviously be attributed to the existence of sufficient variation among the parents and hybrids. Average performance of hybrids was different from that of the parents for all characters except protein content, as evident from the significant parent's vs crosses source of variation for the characters studied. These results were in consonance with that of Patil *et al*. (2011) [7] and Anbu Selvam (2012) [4] for seed yield per plant and other related traits.

Analysis for combining ability of variances due to general and specific combining ability was significant for all the characters studied (Table 2) indicating the presence of adequate amount of variability and there is possibility of selection of desirable plants for trait of interest. A wide range of variation was observed σ2gca for most of the characters studied. Variances due to general combining ability were higher as compared to specific combining ability for all the characters. The maximum GCA was recorded for plant height at maturity and number of pods per plant while minimum for 100 seed weight. The ratios of general combining ability variances were high for the characters days to maturity, number of primary branches per plant and protein content (Table 3). Further, it revealed that both the additive and non-additive gene effects are important in inheritance all characters. The comparison of magnitude of general combining ability and specific combining ability variance indicated that the non- additive genetic effects were predominant in the characters, days to 50 % flowering, plant height, number of pods per plant, pod length, number of seeds per pod, 100 seed weight, seed yield per plant and harvest index which suggested prime role of non-additive gene action. These results are in accordance with Narsimhulu *et al.* (2014) [3] and Manoj and Amit (2015) [5] revealed that magnitude of general combining ability (*gca*) variances were smaller than the specific combining ability (*sca*) variances for number of clusters per plant, seeds per pod and 100 seed weight. The additive genetic effects were predominant for control of the characters, days to maturity, number of primary branches per plant and protein content suggesting influenced by additive gene action, also confirmed by σ2gca / σ2sca ratio which was more than unity. The present results are in corroboration with the findings of Vijay Kumar *et al.* (2017) [8]. The predominant role of additive gene action in the inheritance of protein content was also reported by Elizebeth *et al.* (2016) [9].Under the circumstances, where both additive and non-additive gene actions were in operation, the most appropriate and effective breeding approach would be to mop up the additive genes and simultaneously maintaining degree of heterozygosity for exploiting dominance component by adopting biparental mating and *inter se* crossing between suitable lines followed by recurrent selection.

Discussion

Potentiality of parent to be used in hybridization or of cross used for commercial hybrid may be determined by comparing the *per se* performance of the parent, the F_1 value and the combining ability effects. The parents showed significant high general combining ability for twelve characters presented in Table 4. From which it can concluded that none of the parent reported uniformity in high general combining ability for all the characters. The parent MGG-347 exhibited highly significant *gca* for characters, seed yield per plant, number of branches per plant, plant height, number of clusters per plant and number of pods per plant and KM 11-564 and RM 12-13 for seed yield per plant, number of branches per plant, number of pods per plant, number of seeds per plant, 100 seed weight and harvest index. RM 12-11 for three characters number of seeds per pod, protein content and harvest index. While, WGG-42 for days to 50% flowering and days to maturity and LGG-543 for primary branches per plant and number of pods per plant. Considering the *gca* performance it could be concluded that the parent showing significant high or average *gca* effects were also having higher or average mean value for respective characters. For instance parent MGG-347 exhibited positive and significant *gca* effect and have high mean value for seed yield per plant, number of branches per plant, number of clusters per plant, number of pods per plant and 100 seed weight. Similarly, superior parent KM 11-564 was good general combiner for seed yield per plant have higher *per se* performance for number of branches per plant, plant height, number of clusters per plant, number of pods per plant, pod length and harvest index. The present investigation also confirmed that some of the parents having significant positive *gca* effects for seed yield per plant also showed positive gca effects for one or more of yield contributing traits and can also be concluded that parents, who exhibited high *per se* performance, also displayed good general combining ability effects. Hence, *per se* performance may be used effectively for the selection of parents. Similar results of positive association of *per se* performance and general combining ability and it's usefulness in selection of the parents were also reported by Vijay Kumar *et al.* (2017) [8]. The parents showing high general combining ability with *gca* effects and the hybrids showing best specific combinations with *sca* effects for different characters were presented in Table 5.

The hybrids, MGG-347 X KM 11-564, LGG-543 X KM 11-564 and WGG-42 X RM 12-13 showed the significant positive *sca* effect for seed yield per plant. The hybrids, MGG-347 X RM 12-13 and LGG-543 X KM 11-564 exhibited highest significant positive *sca* effect for number of seeds per pod. While hybrids MGG-347 X RM 12-13 and LGG-543 X KM 11-564 revealed significant positive *sca* effect for 100 seed weight and hybrids WGG-42 X KM 11-564,MGG-371 X RM 12-13 and K-851 X RM 12-13 recorded maximum significant positive *sca* effect for the character protein content. The best combinations for seed yield per plant viz., MGG-347 X KM 11-564, LGG-543 X KM 11-564 and WGG-42 X RM 12-13 involved one or both the parents having either good or average or poor general combiner for seed yield, and possessed high *gca* effects (parent) and also exhibited significant *sca* effects (crosses) in desirable directions for one or more yield contributing attributes. To cite an example, the hybrids viz., MGG-347 X KM 11-564, WGG-42 X RM 12-13 and LGG-543 X KM 11-564 displayed significant *sca* effects for six, three and six characters, respectively in desirable direction including seed yield per plant (Table 5).

The relationship between *gca* and *sca* effects confirmed that significant and desirable *sca* effects can occur in any group of *gca* of parents indicating the presence of higher order interactions in the expression of these traits and in addition to this, *sca* effects occurred because it all depends upon how well genes from two parents interact. The occurrence of high *sca* effects in good x good group might be due to cumulative effect of high combining loci and no mutual cancelation of gene effects between high general combining loci. On the other hand high *sca* effects in good x average or average x good, average x poor or poor x average group might be due to complementation of low, good and poor or average combining loci. Therefore, based on outstanding performance of selective parents and crosses in present study, can be concluded that desirable parents could be used as donors to get high yield and the selective crosses were identified as outstanding for seed yield and its components traits due to possessing high *sca* effect for seed yield may further be utilized in future under breeding programme.

The overall ranking of genotypes studied revealed that genotypes like “MGG-347”, “WGG-42”, “LGG-543” and “KM 11-564” could be a useful source of elite allelic resources based on their general combining ability effects, specific combining ability effects and *per se* performance of both the parents and crosses. These parents are expected to give heterotic combinations resulting from the non-additive gene action and also results in the evolution of transgressive segregants for high yielding genotypes ensuing from complementary epitasis, additive type of gene action and recombination of latent genetic variability hidden in the heterogenetic blocks of such crosses. Normally, *sca* alone would not contribute tangibly in the improvement of self pollinated crops, except where commercial heterosis is feasible. However, *sca* resulting from the heterozygosity of polygenes governing yield and yield components may result in the evolution of recombinants possessing desirable gene aggregates in a homozygous line.

Table 1: Analysis of variance (mean squares) for twelve characters in Greengram by diallel design.

Source of variation	df	Days to flowering	Days to maturity	Primary branches	Plant height	No. of clusters/ plant	No. of pods/plant	Pod length	No. of seeds/pod	100 seed wt	Seed yield /plant (g)	Protein content (%)	Harvest index (%)
Replications	2	3.89	0.63	0.309	11.247	3.355	4.765	0.507 **	0.454	0.038	3.288	0.799	6.399
Treatments	44	2.67**	2.77**	0.610 **	28.431 **	3.662 **	101.399 **	0.486 **	1.352 **	0.276 **	23.026 **	1.205 *	28.481 **
Parents	8	3.46**	2.75**	0.435 **	14.853 *	0.762	97.130 **	0.293 **	0.19	0.076 **	19.725 **	1.21	14.230 **
Crosses	35	2.03**	2.86**	0.606 **	31.687 **	3.026 **	105.171 **	0.531 **	1.605 **	0.279 **	38.954 **	1.204	25.427 **
Parents Vs Crosses	1	2.28	0.6	2.141 **	23.105	49.142 **	3.536	0.445 *	1.78	1.791 **	11.123 **	1.209	249.397 **
Error	88	2.00	2.14	0.127	6.465	1.182	6.42	0.09	0.591	0.025	1.465	0.791	3.629

Table 2: Estimation of general combining ability effects of parents for yield contributing characters in Greengram

	Days to flowering	Days to maturity	Primary branches	Plant height	No. of clusters/plant	No. of pods/ plant	Pod length	No. of seeds/ pod	100 seed wt	Seed yield /plant (g)	Protein content (%)	Harvest index (%)
MGG-351	0.80*	0.43	-0.19*	1.13	-3.05**	-0.07	-0.20**	-0.28	-0.24*	-0.81 *	0.32*	1.25*
MGG-347	-0.04	0.13	0.26**	2.45*	0.94**	3.12**	0.06	0.13	0.21*	1.29 **	0.16	0.34
WGG-42	-2.33**	-2.58**	0.12	-0.69	-0.02	-0.89	-0.01	0.02	0.05	0.51	-0.01	-0.94*
MGG-371	2.17**	1.92**	-0.38**	-0.91	0.59**	2.12	-0.03	-0.20	0.03	-0.69 *	-0.03	0.05
LGG-543	-1.08	-0.45	0.20*	1.07	0.15	2.58**	0.07	0.17	0.01	-0.06	-0.20	0.58
K-851	-0.08	1.02**	0.14	-1.08	-1.08**	2.15	-0.12*	0.14	0.04	0.16	0.48**	-2.55**
RM 12-11	1.45**	0.68*	0.17	-5.13**	0.29	2.30	0.06	0.39*	-0.08	-1.04 **	0.44 **	1.12**
RM12-13	-0.70	0.98**	0.18*	4.84**	1.05**	5.12**	0.16 *	0.21	0.21*	1.58 **	0.08	0.18
KM11-564	-0.10	0.22	0.82**	2.68**	1.20**	4.57**	0.28**	0.34*	0.25 **	3.31**	0.15	2.19**
S.E (gi) +	0.38	0.30	0.09	0.97	0.23	0.96	0.05	0.15	0.10	0.34	0.14	0.46
S.E (gi-gj) +	0.34	0.27	0.06	0.87	0.20	0.87	0.07	0.12	0.09	0.30	0.12	0.41

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

Table 3: Analysis of variance for combining ability for twelve characters in Greengram

Source of varaiation	df	Days to flowering	Days to maturity	Primary branches	Plant height	No. of clusters/ plant	No. of pods/ plant	Pod length	No. of seeds/ pod	100 seed wt	Seed yield /plant (g)	Protein content (%)	Harvest index (%)
GCA	8	32.68 **	25.96**	1.13 **	94.09 **	0.53**	27.87**	5.52**	10.62**	3.10 **	3.72 **	4.68 *	4.93**
SCA	36	12.45**	12.47**	0.62 **	8.90	0.39**	2.46 **	1.00 **	1.52 **	0.43 **	0.70 **	0.82**	2.30**
Error	88	1.85	3.13	0.09	3.30	0.03	0.31	0.11	0.13	0.01	0.07	0.17	0.55

Components of variance

Source of varaiation	Days to flowering	Days to maturity	Primary branches	Plant height	No. of clusters/ plant	No. of pods/ plant	Pod length	No. of seeds/ pod	100 seed wt	Seed yield /plant (g)	Protein content (%)	Harvest index (%)
σ^2 *gca*	3.08	9.14	1.53	7.45	0.05	2.15	0.54	1.04	0.30	0.36	9.07	0.49
σ^2 *sca*	10.60	5.82	1.10	8.65	0.36	3.75	0.89	1.39	0.42	0.63	5.60	1.75
σ^2 error	1.85	3.13	0.09	3.30	0.03	0.31	0.11	0.13	0.01	0.07	0.17	0.55
σ^2 g /σ^2 s Ratio	0.29	1.57	1.39	0.86	0.13	0.57	0.61	0.75	0.73	0.58	1.62	0.28

Table 4: Parents showing significant and high general combining ability for seed yield and its components traits in Greengram

Parent	No. of characters	Per se performance	Characters
MGG-351	2	22.57 31.17	Protein content Harvest index
MGG-347	4	3.01 9.13 26.40 10.40	Primary branches No of clusters / plant No of pods / plant No.of seeds/pod
WGG-42	4	33.19 64.82 3.17 8.63	Days to 50 % flowering Days to maturity 100 seed wt Seed yield /plant (g)
MGG-371	2	8.43 25.01	No of clusters / plant No of pods / plant
LGG-543	4	2.96 25.57 3.23 9.43	Primary branches No of pods / plant 100 seed wt Seed yield /plant (g)
K-851	3	2.81 24.95 23.45	Primary branches No of pods / plant Protein content
RM 12-11	3	27.00 8.67 11.00	No of pods / plant No of clusters / plant No.of seeds/pod
RM12-13	5	3.00 9.38 7.38 3.60 30.02 28.47	Primary branches No of clusters / plant Pod length 100 seed wt Harvest index No of pods / plant
KM11-564	6	3.23 9.90 27.87 7.72 10.80 31.68	Primary branches No of clusters / plant No of pods / plant Pod length No.of seeds/pod Harvest index

Table 5: Top ranking parents with respect to *per se* performance and gca effects and the three top ranking hybrids with respect to *per se* performance and their sca effects

Character	Best general combiners	*gca* effects	Best performing hybrids (*per se* performance)	Status of the parents	No. of crosses with significant *sca* effects	*sca* effects
Days to 50% flowering	WGG-42 MGG-347	- 2.33** 0.04	MGG-347 X WGG-42 WGG-42 X RM 12-13 WGG-42 X LGG-543	poor x good good x average good x average	3	-2.53** -1.92** -1.54*
Days to maturity	WGG-42 MGG-347	- 2.58** 0.13	MGG-347 X WGG-42 MGG-347 X KM11-564 WGG-42 X LGG-543	poor x good poor x poor good x average	3	-1.93** -1.53** -1.29*
No. of primary branches per plant	KM 11-564 RM 12-13 MGG-347	0.82** 0.26** 0.18*	LGG-543 X KM11-564 MGG-347X KM11-564 WGG-42 X RM 12-13	good x good good x good average x good	8	1.09** 1.08** 1.02**
Plant height (cm)	RM 12-13 KM 11-564 MGG-347	4.84** 2.68** 2.45*	WGG-42 X KM 11-564 MGG-347 X KM 11-564 LGG-543X KM 11-564	poor x good good x good average x good	11	5.04** 3.95* 3.54*
No. of clusters per plant	KM 11-564 RM 12-13, MGG-347	1.20** 1.05** 0.94**	MGG-347 X KM11-564 WGG-42 X RM12-13 LGG-543 X KM 11-564	good x good poor x good average x good	7	2.02* 1.67** 1.38**
No. of pods per plant	RM 12-13 KM 11-564 MGG-347	5.12** 4.57** 3.12**	MGG-347 X KM 11-564 LGG-543 X KM 11-564	good x good good x good	12	9.24** 7.55**
Pod length (cm)	KM 11-564 MGG-347	0.28** 0.06	MGG-347 X KM 11-564 WGG-42X KM 11-564 LGG-543 X KM 11-564	average x good poor x good average x good	8	0.69** 0.67** 0.58**
No. of seeds per pod	RM 12-11 MGG-347 KM 11-564	0.34** 0.15 0.13	MGG-347 X RM 12-13 MGG-347 X KM 11-564 MGG-371 X KM11-564	poor x average poor x good poor x good	8	1.27** 1.16** 0.95*
100 seed weight (g)	KM 11-564 MGG-347 RM 12-13	0.25** 0.21* 0.21*	MGG-347 X RM12-13 LGG-543 X KM 11-564 MGG-347 X KM 11-564	good x good average x good good x good	9	0.42** 0.41** 0.40**

Protein content (%)	K-851 RM 12-13	0.48** 0.08	WGG-42 X KM 11-564 MGG-371 X RM12-13 K-851 X RM12-13	poor x average poor x average good x average	6	1.28** 1.01** 0.98**
Harvest index (%)	KM 11-564 MGG-351	2.19** 1.25**	MGG-351 X RM12-13 RM 12-11 X KM11-564 MGG-371 X KM11-564	good x average good x good poor x good	9	11.17** 9.08** 6.77**
Seed yield per plant (g)	KM 11-564 MGG-347 RM 12-13	3.31** 1.58** 1.29**	MGG-347 X KM 11-564 LGG-543 X KM11-564 WGG-42 X RM12-13	good x good poor x good average x good	10	3.36** 3.22** 3.14**

Conclusion

Breeding by pedigree method would result in partial exploitation of additive and additive x additive types of gene action. Under such situation any suitable method of recurrent selection programme should be adopted. It is also proposed to utilize diallel selective mating system to capitalize on additive genetic variance and enhance genetic recombinants. Therefore, for the improvement of grain yield in greengram, other breeding methods including biparental mating among selected F2 segregants from crosses involving the parents “MGG-347”, “WGG-42”, “LGG-543” and “KM 11-564” need special considerations. From the further segregating generation of these biparental populations, the desirable plants can be selected and used in other conventional breeding programme. By this technique the improvement in the population can be effectively made and at the same time superior segregants selected and carried further for the development of high yielding pure lines of mungbean. *gca* and *sca* information shows the kind of progeny which must be evaluated for the relevant traits. If *sca* effects are significant, specific hybrid combinations must be evaluated. Alternatively, if *gca* is significant and *sca* not, then the performance of a single cross progeny can adequately be predicted on the basis of *gca*. In the present experiment, *gca* mean squares was high for plant height, days to maturity, pod length and seed weight and thus the performance of a particular single cross for these characters could successfully be predicted on the basis of *gca*.

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