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Elucidation of Nature of Gene Action and Combining Ability Associated with Economic Traits in Greengram [*Vigna radiata* (L.) Wilczek]

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ABSTRACT

Background: Narrow genetic base and lack of exploitable variation have become a major constraint for yield improvement in greengram. Identifying genetically superior parents and breeding scheme to be adopted become a pre-requisite for the development of elite cultivars. Thereby, blending the knowledge on gene action and combining ability plays a key role.

Materials: Combining ability analysis was carried out in twenty-five crosses derived out of Line × Tester mating design using 5 lines and 5 testers. The hybrids, parents and the check variety were evaluated in a RBD with two replications and ten quantitative characters were recorded.

Result: Non-additive gene action was found to be prevalent for the quantitative traits observed. Exploring the *per se* and *gca* effects, COGG13-39 and VGG18-002 were adjudged as the best parents and the crosses involving above parents will be productive for synthesizing a dynamic population with superior recombinants. Meanwhile, exploring the *per se, sca* and heterosis, the best specific crosses identified for seed yield/plant and pods per plant were, V2709 × GAM5 and COGG13-39 × VGG16-058. They can be further exploited to obtain transgressive segregants for higher yield, bold seeds and bruchid resistance through appropriate breeding strategy.

Key words: Combining ability and gene action, Greengram, Line × tester analysis.

INTRODUCTION

In India, Greengram [*Vigna radiata* (L.) Wilczek] is the third most important short duration leguminous crop and it is well suited to a large number of cropping systems. Greengram is the supreme and affordable source of high quality and easily digestible protein. It occupies a significant position in Indian food shelves as sprouts in their diet. Despite, India being a largest producer and accounting for 45% of world production (Kakde *et al.,* 2019), the productivity (601 kg/ha) still remains low (Indiastat, 2021). To ensure that the rising population meets out food demand and cheaper protein source, a potential breakthrough in breeding by increasing production and productivity in greengram is essential. However, for developing high yielding cultivar the most important criteria to be considered are the selection of appropriate parents and breeding strategy to be employed in the breeding programme. This in turn, relies on the knowledge of genetics of traits of economic interest. With this backdrop, a systematic approach of combining ability analysis was carried out to gather a better information on gene action and to identify superior parents and crosses for further exploitation.

MATERIALS AND METHODS

The present study was carried out at an experimental farm of Department of Pulses, Tamil Nadu Agricultural University, Coimbatore. Five morphologically diverse high yielding lines, *viz.,* IPM409-4, V2802, V2709, COGG13-39 and VBN5 were crossed with five bold seeded donors (test weight >5g) *viz*., VGG16-058, VGG18-002, WGG42, BGS9 and GAM5 in a Line × Tester mating design during *summer*, 2022 to synthesise 25 crosses. Among the selected lines, V2802 and V2709 are the donors for bruchid resistance. In addition, testers VGG18-002, WGG42 and BGS9 are with long pods (>10 cm). During *kharif*, 2022, all crosses along with parents and check variety, CO8 were raised in a single row of 4 metres with spacing of 30 × 10 cm in a RBD with two

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replications. All recommended agronomic and plant protection practices were adopted to raise a healthy crop. True hybrids were identified based on contrasting traits in the respective parents.

Observations for number of days to 50% flowering were computed on plot basis. In contrast, observations for plant height (cm), branches per plant, clusters per plant, pods per cluster, pods per plant, pod length (cm), seeds per pod, hundred seed weight (g) and seed yield/plant (g) were recorded on five randomly chosen plants from each entry. All the traits observed were subjected to analysis of variance and the analysis of variance for combining ability in Line × Tester design was based on Kempthorne (1957). Magnitude of additive and dominance variance were computed based on Line x Tester analysis using TNAUSTAT-statistical package (2014). The degree of dominance was derived based on the square root of, ratio of dominance variance (SCA) to additive variance (GCA). For each attribute, standard heterosis was computed. The correlation coefficients of seed yield/plant with other quantitative traits were calculated based on formula given by Goulden (1952) by using statistical package STAR version 2.0.1.

RESULTS AND DISCUSSION

Analysis of variance for combining ability

Analysis of variance for combining ability (Table 1) revealed significant differences among the crosses for all the measured traits. On partitioning the variance into lines, testers and their interaction, the variance due to lines showed highly significant differences for all the traits except for seeds per pod. The variance due to testers and interaction effects (Line × Tester) showed significant differences for days to 50 per cent flowering, plant height, pods per plant, hundred seed weight and seed yield/plant. In addition, pods per cluster were significantly varied among testers and clusters per plant and seeds per pod in interaction. Significant mean squares of lines and testers indicated the presence of additive variance. In agreement with this finding, significant mean squares in lines, testers and their interaction for yield and its related attributes were documented by Mohan *et al.* (2019) and Muthuswamy (2022) in greengram.

Nature of gene action

An insight into the nature of gene action, permits the plant breeders to determine the breeding strategy to be adopted for the successful crop improvement programme. The magnitude

Table 1: Analysis of variance for combining ability for ten quantitative traits.

Traits	Mean sum of squares					
	Replications	Crosses	Lines	Testers	L × T	Error
	df 1	24	4	4	16	24
Days to 50% flowering	0.32	25.29**	92.30**	40.65**	4.70**	0.53
Plant height	6.28	92.49**	316.31**	37.60*	50.26**	9.52
Branches per plant	0.01	0.55**	1.89**	0.43	0.24	0.19
Clusters per plant	5.35	12.70**	42.38**	2.21	7.91**	1.90
Pods per cluster	0.47	0.88*	2.27**	1.44*	0.39	0.40
Pods per plant	7.30	136.84**	280.25**	169.82**	92.74**	3.28
Pod length	0.19	1.16**	4.68**	0.33	0.48	0.36
Seeds per pod	0.01	0.53*	0.59	0.41	0.54*	0.26
Hundred seed weight	0.19	0.78**	2.61**	0.67**	0.36*	0.15
Seed yield/plant	7.37	60.53**	68.28**	96.91**	49.49**	4.17

*Significance at P≤0.05; **Significance at P≤0.01.

Table 2: Magnitude of GCA and SCA variances and proportional contributions of lines, testers and their interactions.

Traits	GCA	SCA	SCA/GCA	Degree of dominance	Proportional contribution (%)		
					Lines	Testers	L × T
Days to 50% flowering	0.77	2.09	2.71	1.65	60.82	26.79	12.39
Plant height	1.58	20.37	12.89	3.59	57.00	6.78	36.23
Branches per plant	0.01	0.03	3.00	1.73	57.18	13.13	29.69
Clusters per plant	0.18	3.01	16.72	4.09	55.60	2.90	41.50
Pods per cluster	0.02	0.01	0.50	0.71	43.21	27.44	29.35
Pods per plant	1.65	44.73	27.11	5.21	34.13	20.68	45.18
Pod length	0.03	0.06	2.00	1.41	67.36	4.79	27.85
Seeds per pod	0.01	0.14	14.00	3.74	18.69	12.98	68.33
Hundred seed weight	0.02	0.10	5.00	2.24	55.40	14.15	30.45
Seed yield/plant	0.41	22.66	55.27	7.43	18.80	26.69	54.51

of SCA variance for all the assessed traits except for pods per cluster were higher than the corresponding GCA variance, as revealed by their ratio greater than unity, propounding the preponderance of non-additive genetic effects (Table 2). Meanwhile, the degree of dominance was also greater than unity for all the observed traits except for pods per cluster indicating over dominance. These results pointed out that selection should be practiced at the later generations. Similar findings of the relative estimates of dominance variance higher than the additive variance for all the yield and its associated traits in greengram was reported by Singh *et al.* (2016) and Viraj *et al.* (2020). On contrary, Latha *et al.* (2018) reported comparatively higher additive variance for branches per plant and Nath *et al.* (2018) for days to 50% flowering, primary branches, clusters per plant and seed yield/plant in greengram.

Contribution of lines and testers to total variance ranged from 18.80 (seed yield/plant) to 60.82 per cent (days to 50% flowering) and from 2.90 (clusters per plant) to 26.79 per cent (days to 50% flowering), respectively. The contribution of interaction ranged from 12.39 (days to 50% flowering) to 68.33 per cent (seeds per pod). Among the three components, the relative contribution of lines was higher for all the traits except for seeds per pod and seed yield/plant. This specified that the lines were genetically diverse. Besides, the higher contribution of interaction component to variance for seeds per pod and seed yield/plant, it also imparted higher variance than the testers for most of the traits. Moreover, it reiterated the role of non-additive gene action in inheritance of these traits. Conventionally, employing heterosis breeding in greengram is impractical, thereby, hybridization followed by selection will be productive. The results of higher contribution of interaction to the total variance was in congruent with reports of Muthuswamy (2022) in greengram and Patial *et al.* (2022) in blackgram.

General combining ability

The *gca* effect, a good estimate of additive gene action, can be used to determine the potential parent and its ability to transfer desired traits to their progenies. In the present study, the estimates of *gca* effects of all the five lines and five testers revealed that none of them were a good general combiner for all the characters observed. However, lines *viz.,* COGG13-39, VBN5 and testers *viz.,* VGG16-058, VGG18-002 and GAM5 were good general combiners for seed yield/plant (Fig 1). In addition, COGG13-39 recorded significant positive *gca* for the traits *viz.,* plant height, pods per cluster, pods per plant, pod length and hundred seed weight. Similarly, VBN5 recorded significant positive *gca* for plant height, branches per plant clusters per plant, pods per plant and pod length. Likewise, the tester, VGG16-058 was identified as a good general combiner for pods per cluster and hundred seed weight and VGG18-002 for pods per plant in addition to yield. The findings also indicated that the line, IPM409-4 and two testers *viz.,* VGG16-058 and VGG18-002 were with significant negative *gca* for days to 50% flowering and can be exploited for earliness (Fig 1). Significant *gca* effects are due to additive gene action and it is fixable in the segregating generations. Significant *gca* effects for all the yield related variables were also documented by Nath *et al.* (2018), Samantaray *et al.* (2018), Mohan *et al.* (2019) and Muthuswamy (2022) in greengram.

Specific combining ability

Higher probability of desirable segregants can be obtained only from the potential cross combinations. Specific combining ability effects helps in identifying such potential crosses. It is the result of non-additive gene action. Based on *sca* effect, the best specific combiners for seed yield/plant identified were V2709 ×GAM5, COGG13-39 ×VGG16-058 and VBN5×VGG16-058 (Fig 2). At least, one of the parents involved in the above crosses recorded high *gca*. All the above crosses, also recorded significant *sca* for pods per plant. Besides these traits, COGG13-39×VGG16-058 and VBN5×VGG16-058 recorded significant negative *sca* for days to 50 per cent flowering. The cross V2709×GAM 5 had desirable *sca* effect for clusters per plant. Seven promising crosses *viz.,* IPM409-4×WGG42, IPM409-4× BGS9, V2709×VGG16-058, COGG13-39×VGG16-058, COGG13-39×VGG18-002, VBN5×WGG42 and VBN5× GAM5 recorded significant *sca* in desirable direction for days to 50% flowering (Fig 2). Early maturing segregants that escapes the terminal drought stress can be isolated by exploiting the above crosses. Cross combinations *viz.*, COGG13-39×VGG 18-002, VBN5×VGG18-002 and VBN5×GAM5 involving high *gca* parents with non-significant *sca* effects for single plant yield can be selected for recombination breeding. These crosses are more likely to throw desirable segregants with bold seed and increased yield. The research findings of Muthuswamy (2022) also reported such specific combiners with non-significant *sca* involving significant *gca* parents for pods per cluster, seeds per pod, pod length and hundred seed weight in greengram.

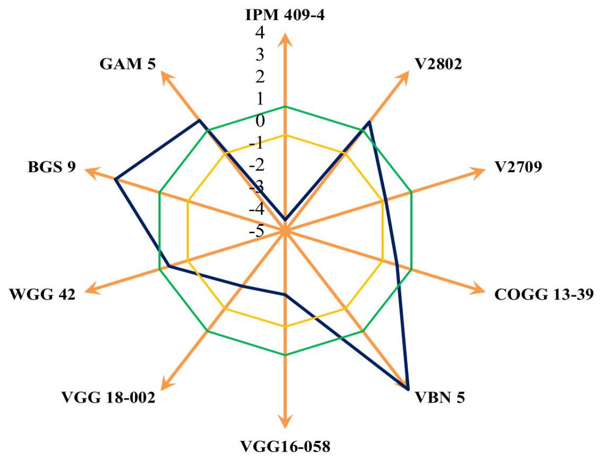
Selection of best parents based on *per se* and *gca* effect and best crosses based on *per se, sca* effect and standard heterosis for yield correlated traits

Selection was carried out based on the performance of parents and crosses for yield correlated traits. The traits plant height (0.37), clusters per plant (0.51), pods per cluster (0.56), pods per plant (0.69), pod length (0.58), hundred seed weight (0.29) reported positive and significant correlations with seed yield/plant.

In any crossing programme, phenotypically superior parents does not always yield good recombinants in segregating generations. Genetic worth of the parents should be considered for selection. Therefore, combination of *per se* performance and *gca* effects helps to select parents with reservoir of desirable genes to obtain superior segregants. The parents that excelled in *per se* and *gca* for yield correlated traits were tabulated in Table 3. VBN5 was found to be the promising line, to improve plant height, clusters per plant and pods per plant as it recorded significant mean and *gca* for the above traits. Whereas, the line, COGG13-39 and tester, VGG18-002 were excelling with higher mean and also good general combiners for seed yield/ plant. Both the parents also recorded superior performance for pods per plant. Based on the correlation analysis, the correlation coefficient of pods per plant (0.69) with seed yield/ plant was higher. Therefore, crossing program involving the best parents for seed yield/plant and pods per plant *viz.,* COGG13-39 and VGG18-002 will be productive for synthesizing a segregating population with superior recombinants. In addition, VGG18-002 is a bold seeded type and more likely to throw a desirable segregant for higher seed weight when it is used in the crossing programme.

Comparative evaluation of crosses based on *per se*, *sca* and standard heterosis revealed that the good specific combiners for seed yield/plant *viz.,* V2709×GAM5, COGG13-39×VGG16-058 and VBN5×VGG16-058 were identified as outstanding with significant mean (25.75, 29.13, 25.01 g, respectively) and standard heterosis over CO8 (33.42, 50.96, 29.56%, respectively) (Table 3). Out of which, two crosses (V2709×GAM 5 and COGG13-39×VGG 16-058) were remarkable for pods per plant. In all the specific combiners identified above, at least one of the parents was a good general combiner. Furthermore, for the traits correlated with yield, the excelling crosses with high mean, *sca* and standard heterosis were V2802×WGG42 and V2802×GAM5 for clusters per plant and IPM409-4×VGG18-002, V2802× GAM5, V2709×GAM5, COGG13-39×BGS9, VBN5×BGS9 and VBN5×GAM5 for pods per plant. Collectively, out of three, two specific combiners that excelled in seed yield and pods per plant, V2709×GAM5 and COGG 13-39×VGG 16-058 can be utilized to develop high yielding

1a. Days to 50% flowering



1b. Seed yield/plant

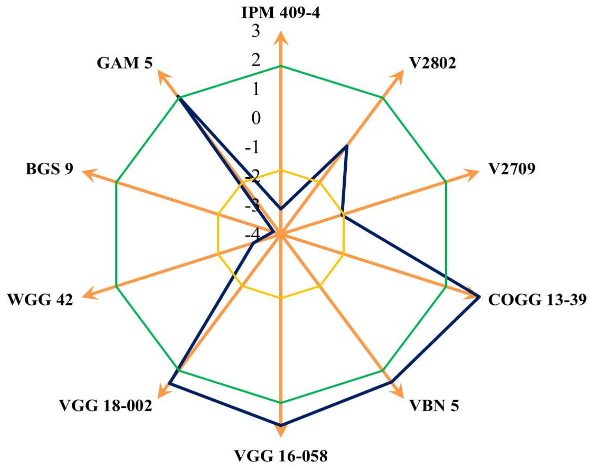


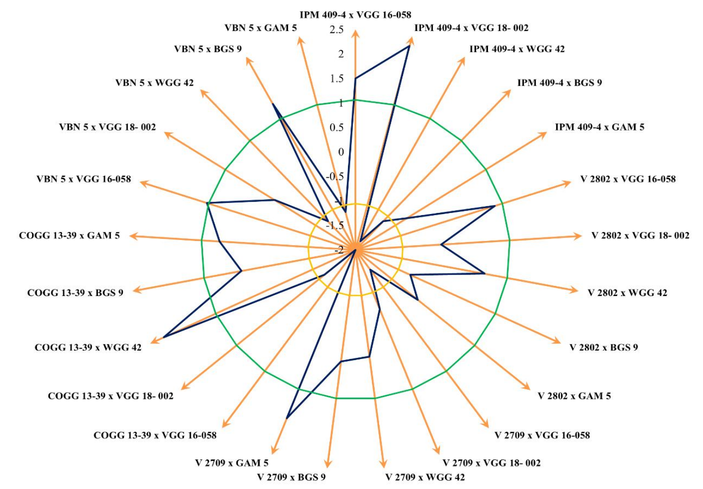
Fig 1: Estimates of general combining ability effects (genotypes lying outside green and inside yellow polygon recorded significant positive and negative *gca* effects respectively).

Table 3: Best parents based on *gca* effect and *per se* performance and best crosses based on *sca* effect, *per se* performance and standard heterosis for yield correlated traits.

Traits	Correlation coefficient with seed yield/plant	Parents with significant positive *gca* effect		*Per se* performance	Significant *gca* and *Per se*	Crosses with significant positive *sca* effect		*Per se* performance	Standard heterosis over CO8 (%)	*gca* status of parents	Significant *sca*, *Per se* and standard heterosis
		Parents	Values			Crosses	values				
Plant height	0.37**	COGG 13-39^L	-6.69**	52.27**	COGG 13-39	V 2802×WGG 42	10.65**	49.73**	-1.05	M × M	-
(cm)		VBN5 ^{L}	7.28**	52.95**	VBN 5	V 2709×BGS 9	6.76**	40.03	-20.35**	L × L	
Clusters	0.51**	VBN5 ^{L}	3.14**	16.34**	VBN 5	V 2802×WGG 42	3.01**	12.78*	30.16*	M × M	V 2802xWGG 42
per plant						V 2802×GAM 5	2.35*	12.66*	29.04*	M × M	V 2802xGAM 5
						V 2709×GAM 5	2.43*	11.59	18.03	L × M	
Pods per	0.56**	COGG 13-39 ^{L}	0.52*	6.34	-	-	-			-	-
cluster		VGG16-058 ^{T}	0.47*	5.16							
Pods per	0.69**	COGG 13-39 ^{L}	4.22**	59.17**	COGG 13-39VBN	IPM 409-4×VGG 18-002	4.92**	54.17*	15.24**	L × H	IPM 409-4×VGG
plant		VBN5 ^{L}VGG 18-002 ^{T}	6.60**	68.83**	5VGG 18-002	IPM 409-4×WGG 42	2.92*	42.67	-9.22	L × L	18-002
			6.76**	48.00**		V 2802×WGG 42	7.43**	50.67	7.80	L × L	V 2802×GAM 5
						V 2802×GAM 5	7.58**	53.50*	13.83**	L × M	V 2709×GAM 5
						V 2709×GAM 5	6.09**	53.17*	13.12**	L × M	COGG 13-39×VGG
						COGG13-39×VGG 16-058	5.05**	57.93**	23.27**	H × M	16-058COGG 13-
						COGG 13-39×BGS 9	4.84**	62.01**	14.97**	H × L	39×BGS 9VBN
						VBN 5×VGG 16-058	2.74*	41.67	23.40**	H × M	5×BGS 9VBN
						VBN 5×BGS 9	9.43**	61.00**	29.79**	H × L	5×GAM 5
						VBN 5×GAM 5	2.99*	58.33**	24.12 **	H × M	
Pod length	0.58**	COGG 13-39 ^{L}	1.01**	7.83	-	-	-	-	-	-	-
(cm)		VBN 5 ^{L}	0.40*	7.14							
Hundred	0.29*	COGG 13-39 ^{L}	0.86**	3.11	-	-	-		8.70**	-	-
seed	-	VGG16-058 ^{T}	0.41**	5.00					6.55**		
weight (g)									3.10*		
Seed	1.00**	COGG 13-39 ^{L}	2.96**	19.80**	COGG 13-39	V 2709×GAM 5	8.70**	25.75**	33.42**	L × H	V 2709xGAM 5
yield/		VBN 5 ^{L}	2.28**	10.63	VGG 18-002	COGG 13-39×VGG	6.55**	29.13**	50.96**	H × H	COGG 13-39×VGG
plant (g)		VGG16-058 ^{T}	2.57**	15.57		16-058	3.10*	25.01**	29.56*	H × H	16-058
		VGG 18-002 ^{T}	2.35**	21.98**		VBN 5xVGG 16-058					VBN 5×VGG 16-058
		GAM 5 ^{T}	1.86**	11.97							

^{L} Lines ^{T} Testers L (Low)- Significant negative *gca*; M (Medium)- Non-significant *gca*; H (High)- Significant positive *gca*; *Significance at P≤0.05 **Significance at P≤0.01.

2a. Days to 50% flowering



2b. Seed yield/plant

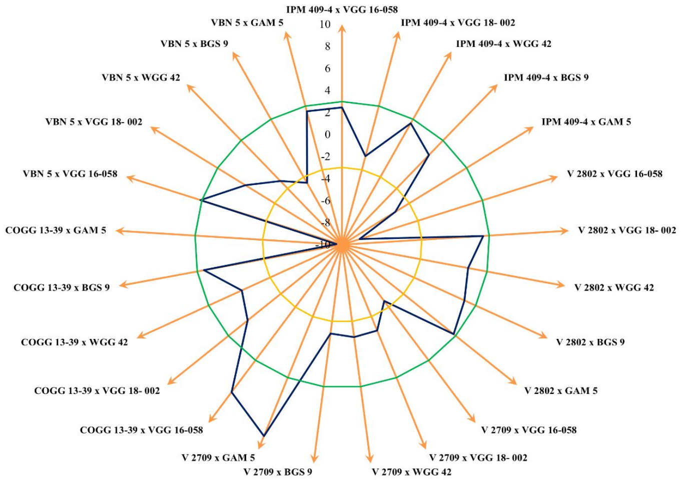


Fig 2: Estimates of specific combining ability effects (genotypes lying outside green and inside yellow polygon recorded significant positive and negative *sca* effects respectively).

varieties with desirable traits. In particular, the cross, V2709×GAM5 could be exploited to derive the segregants with resistance to bruchid infestation and higher seed weight, since the parents involved are potential donors for bruchid resistance (V2709) with bold seeds (GAM5). In the same way, exploiting the cross, COGG13-39×VGG16-058 is more likely to yield desirable segregants with increased yield and higher seed weight, since it utilizes the high yielding line and a bold seeded tester. In greengram, pedigree method of breeding can be employed to get desirable segregants from such crosses. The best specific combiners identified, V2709×GAM 5 and COGG13-39×VGG16-058 involved low × high and high × high *gca* parents indicating additive × dominance and additive gene action, respectively. Nath *et al.* (2018) also identified good specific combiners with high × high and low × high *gca* effects in greengram.

CONCLUSION

Significant SCA and GCA variance implied the role of both additive and non-additive genetic effects. Therefore, breeding strategy that exploits both these effects simultaneously should be employed. Though magnitude of SCA/GCA ratio was higher, exploiting non-additive gene action through heterosis breeding is impractical. Pedigree breeding *i.e.* hybridization followed by selection can be employed. From this approach, high yielding superior segregants with bruchid resistance and higher seed weight can also be selected from the crosses, V2709×GAM5 and COGG13-39×VGG16-058.

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Conflict of interest: None.

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