RESEARCH ARTICLE Legume Research- An International Journal, Volume 45 Issue 3: 292-298 (March 2022)

Studies on Combining Ability for Seed Yield and Its Related Traits in Blackgram [*Vigna mungo* (L.) Hepper]

Ranjana Patial, R.K. Mittal, V.K. Sood, Shahnawaz Ahmed

10.18805/LR-4187

ABSTRACT

An experiment was carried out in blackgram using line × tester mating design to estimate the GCA effect of parents and SCA effect of 54 hybrids for yield and its traits using 27 lines and two testers. The relative estimates of variance due to specific combining ability (SCA) were higher than general combining ability (GCA) variances for all twelve traits, indicating predominance of non-additive gene action. Combining ability estimates showed significant genetic variance in lines for all traits whereas testers had significant genetic variance for nine traits. On the basis of GCA effects, among the lines and testers IC-436910, IC-413306, IC-398973, IC-343885 and HPBU-111 respectively, were good combiners for most of the traits and can be used in future breeding programme. Specific combining ability studies indicated cross IC-436910 × HPBU-111 as best specific combiner for the economically important traits *viz*., plant height, branches per plant, seed yield per plant and days to 75% maturity. Such crosses could be further exploited to obtain transgressive segregants in future breeding programme.

Key words: Blackgram, General combining ability, Line × tester analysis, Specific combining ability.

INTRODUCTION

Blackgram [*Vigna mungo* (L.) Hepper], 2n=2x=22 popularly known as urdbean, black lentil, mungobean, matpe bean or mash, belonging to the sub-genus *Ceratotropis*, is a grain legume, originated from central Asia and India with *Vigna mungo* var. *silvestris* as its progenitor which is found wild in India (Lukoki *et al.* 1980). It is one of the nutritious pulse crops, extensively cultivated in the Indian sub-continent and to a lesser extent in Thailand, Australia and other Asian and South Pacific countries (Poehlman 1991). It is an important short duration self pollinated pulse crop grown in many parts of India. It forms a significant component of dietary carbohydrates (60%), fat (1.5%), minerals, amino acids and vitamins. Compared to other legume requirement in Indian sub continent and is highly nutritious with protein (25-26%), crops, urdbean is known for its synchronous maturity, non-shattering pods, more clusters and pods with large seeds. However, its yield is low in contrast to other grain legumes. Low productivity in this crop is attributable to its narrow genetic base due to common ancestry of various superior genotypes, poor plant type, cultivation under marginal and harsh environmental conditions and vulnerability to abiotic and biotic stresses. Hence, there is a strong need to improve the productivity of blackgram. This could be achieved by studying the genetic architecture of this crop. However, success depends primarily upon identification of best parental lines which may produce desirable gene combinations. Selection of parental lines on the basis of their genetic value is key requirement for any successful crop improvement programme.

Combining ability is the relative ability of a genotype to transmit its desirable performance to its crosses. It is one of the powerful tools available to estimate the combining ability effects and it aids in selecting the desirable parents and crosses for the exploitation of heterosis (Sarker *et al.* 2002; Muhammad *et al.* 2007). The knowledge of the type of gene action involved in the expression of yield and component traits is essential to choose an appropriate breeding strategy to isolate desirable segregations in later generation. The present investigation was undertaken to generate information on the nature of gene action and combining ability in line × tester biometrical technique to identify elite parents and superior hybrid combination in blackgram.

Department of Crop Improvement, CSK Himachal Pradesh Krishi Vishvavidyalaya, Palampur-176 062, Himachal Predesh, India.

Corresponding Author: Ranjana Patial, Department of Crop Improvement, CSK Himachal Pradesh Krishi Vishvavidyalaya, Palampur-176 062, Himachal Predesh, India.
Email: ranjanapatial.agric@gmail.com

How to cite this article: Patial, R., Mittal, R.K., Sood, V.K. and Ahmed, S. (2022). Studies on Combining Ability for Seed Yield and Its Related Traits in Blackgram [*Vigna mungo* (L.) Hepper]. Legume Research. 45(3): 292-298. DOI: 10.18805/LR-4187.

Submitted: 02-07-2019 **Accepted:** 13-02-2020 **Online:** 18-06-2020

MATERIALS AND METHODS

Twenty-nine genetically diverse genotypes of blackgram (*Vigna mungo* L.) obtained as Indigenous collection from IIPR, Kanpur were crossed in line × tester mating design. Twenty-seven (Lines) genotypes were used as a female (IC-281980, IC-282007, IC-282008, IC-436910, IC-281989, IC-398973, IC-281982, IC-282001, IC-398956, IC-413306, IC-413307, IC-281993, IC-343962, IC-413305, IC-398998, IC-281992, IC-413304, IC-436852, IC-282002, IC-281990, IC-281995, IC-343885, IC-343947, IC-282004, IC-413309, IC-343943 and IC-281984) and two (Testers) as male parents (HPBU-111 and Him Mash-1) to produce 54 hybrid combinations during *Kharif* 2016. These F_1 hybrids along with their parents were evaluated in randomized block design (RBD) with three replicates during *Kharif* 2017 at the Experimental Farm, Department of Crop Improvement, CSK HPKV, Palampur (HP).

The data were recorded on ten random competitive plants in each replication for the traits *viz.*, plant height (cm), branches per plant, pods per plant, pod length (cm), seeds per pod, 100-seed weight (g), biological yield per plant (g), seed yield per plant (g) and harvest index (%). The protein content (%) was determined by using macro-Kjeldhal method Jackson (1976). For, days to 50% flowering and days to 75% maturity observations were recorded on plot basis. Recommended package of practices were followed for raising the crop. The data so generated were analyzed as per Panse and Sukhatme (1984). Combining ability analysis was carried out following the method of Kempthorne (1957). Estimates of additive and dominance variance, average degree of dominance and narrow sense heritability were calculated as per line × tester analysis.

RESULTS AND DISCUSSION

Analysis of variance for parents (27 lines and two testers) and their hybrids revealed highly significant genotypic differences for all the traits namely days to 50% flowering, days to 75% maturity, plant height (cm), branches per plant, pod length (cm), pods per plant, seeds per pod, seed yield per plant (g), biological yield per plant (g), 100-seed weight, harvest index (%) and protein content (%) indicating substantial amount of genetic variability in the material under study (Table 1). Hence, it offers a better scope for further improvement of breeding material by the selection of promising genotypes in blackgram breeding programme. The significant variation for all the traits was also observed by earlier workers *viz.*, Kumar *et al.* (2017) for seed yield, number of branches, pods, clusters, 100-seed weight, fodder biomass and harvest index; Chauhan *et al.* (2018) for all studied traits; Bandi *et al.* (2018) for days to 50% flowering, days to maturity, plant height (cm), number of branches per plant, number of clusters per plant, number of pods per plant, pod length (cm), number of seeds per pod, 100-seed weight (g) and grain yield per plant (g) in blackgram.

Analysis of variance for combining ability

Analysis of variance for combining ability (Table 2) revealed that mean squares due to crosses were highly significant ($P \leq 0.01$) for all the traits under study. Similar results were observed by Patial *et al.* (2018). One should proceed for line × tester analysis only if the crosses mean squares are significant. The further partitioning of mean squares into lines, testers and line × tester interactions revealed that mean squares due to lines were highly significant ($P \leq 0.01$) for all the traits *viz.*, days to 50% flowering, days to 75% maturity, plant height (cm), branches per plant, pod length (cm), pods per plant, seeds per pod, seed yield per plant (g), biological yield per plant (g), 100-seed weight, harvest index (%) and

Table 1: Analysis of variance for different traits in urdbean.

		Mean sum of squares		
Source of variation→		Replication	Treatment	Error
Traits ↓	df→	2	110	220
Days to 50% flowering		1.90	31.84**	3.86
Days to 75% maturity		0.47	34.53**	4.97
Plant height (cm)		0.83	91.19**	4.76
Branches per plant		0.38	7.03**	0.17
Pod length (cm)		0.56	1.60**	0.11
Pods per plant		2.37	367.86**	5.58
Seeds per pod		0.14	1.11*	0.07
Biological yield per plant (g)		0.74	196.49**	2.31
Seed yield per plant (g)		0.05	4.59**	0.03
Harvest index (%)		0.62	93.52**	2.85
100 seed weight (g)		0.01	1.14*	0.07
Protein content (%)		2.55	7.32**	1.73

*Significance at $P \leq 0.05$; **Significance at $P \leq 0.01$.

Table 2: Analysis of variance for combining ability for different traits in urdbean.

Source of variation →		Replication	Crosses	Lines	Testers	Lines × Testers	Error
Traits ↓	df →	2	53	26	1	26	106
Days to 50% flowering		2.52	26.48**	18.52**	114.17**	31.07**	4.63
Days to 75% maturity		2.00	28.32**	20.47**	144.50**	31.71**	5.18
Plant height (cm)		0.91	73.72**	97.04**	4.48	53.07**	4.81
Branches per plant		0.30	6.73**	8.48**	1.07*	5.20**	0.18
Pod length (cm)		0.17	1.55**	1.27**	2.27**	1.81**	0.1
Pods per plant		3.95	125.78**	153.00**	63.92**	100.93**	7.63
Seeds per pod		0.07	0.85**	1.06**	0.46*	0.66**	0.08
Biological yield per plant(g)		0.06	55.35**	65.96**	31.42**	45.65**	2.44
Seed yield per plant (g)		0.06	2.94**	4.60**	2.52**	1.30**	0.03
Harvest index (%)		1.94	36.22**	62.41**	36.13**	10.03**	1.4
100 seed weight (g)		0.01	1.17**	0.84**	0.06	1.53**	0.07
Protein content (%)		2.11	8.12**	10.47**	6.39	5.84**	1.66

*Significance at $P \leq 0.05$; **Significance at $P \leq 0.01$.

protein content (%). The mean squares due to testers were significant for days to 50% flowering, days to 75% maturity, branches per plant, pod length (cm), pods per plant, seeds per pod, seeds yield per plant (g), biological yield per plant (g) and harvest index (%). Highly significant mean squares for lines and testers indicated existence of additive variance. The lines exhibited greater magnitude of mean squares as compared to testers for all the traits except, for three traits *viz*., days to 50% flowering, days to 75% maturity and pod length. This indicated a wider genetic diversity of lines as compared to the testers for these traits. This observation was in agreement with the findings of Chakraborty *et al.* (2010) and Surashe *et al.* (2017).

Genetic parameters and proportional contribution of lines, testers and their interactions

In a breeding programme, once the appropriate parents and potential crosses are identified, the next important step is to adopt a suitable breeding strategy for the management of generated variability which largely depends upon type of gene action in the population for the traits under genetic improvement (Cockerham 1961; Sprauge 1966). The estimates of additive variances (σ^2A), dominance variances (σ^2D) and proportional contribution of lines, testers and their interactions to the total variances are presented in Table 3. Magnitude of dominance variance (σ^2D) was found to be higher than additive variance (σ^2A) for all the traits, which indicated the preponderance of non-additive gene action for these traits. Gill *et al.* (2014) found that the relative estimates of dominance variance were higher than additive variance for days to 50% flowering, days to maturity, plant height and number of pods per plant. The average degree of dominance more than unity reveal over dominance confirming the above findings. Hence, non-additive genetic variance was important in controlling these traits. Similar results were reported by Govindaraj and Subramanian (2001), Manivannan (2002), Selvam and Elangaimannan (2010), Chakraborty *et al.* (2010) and Thamodharan *et al.* (2017) for plant height, branches per plant, days to 50% flowering, days to maturity, cluster per plant, pods per cluster, 100-seed weight and pod length. Narrow sense heritability is the proportion of additive genetic variance to total phenotypic variance. The narrow sense heritability (h^2ns) estimates were classified as high (>50%), medium (30-50%) and low (<30%). All the traits showed low narrow-sense heritability, indicating that non-fixable component of variation is governing by these traits (Table 3).

The proportional contribution of lines ranged from 34.31% (days to 50% flowering) to 74.34% (seed yield per plant). The proportional contribution of testers ranged from 0.33% (biological yield per plant) to 9.63% (days to 75% maturity) (Table 3). The proportional contribution of line × tester interactions ranged from 22.31% (seed yield per plant) to 62.65% (100 seed weight). The contribution of lines was found to be higher than individual contribution of testers for all the traits studied. This indicated the presence of wide genetic diversity among the lines as compared to the testers. The contribution of line × tester interaction was found to be higher than the individual contribution of testers for all the traits studied, indicating the higher estimates of variances due to specific combining ability which further confirmed the active involvement of non-additive gene action in the inheritance of different traits studied. The per cent contributions of lines, testers and their interactions to the total variance of various quantitative traits in the blackgram crosses were estimated by Chakraborty *et al.* (2010).

General combining ability (GCA) and specific combining ability (SCA)

The GCA and SCA effects of lines and testers are presented in Table 4 and 5. The GCA effects is a good estimates of additive gene action (Sprague and Tatum, 1942) reflecting the performance of parental lines in combination with all other lines. Estimates of the general combining ability (GCA)

Table 3: Estimation of genetic components of variances and proportional (%) contribution of lines, testers and their interactions in urdbean.

Traits ↓	Additive Variance (σ^2A)	Dominance Variance (σ^2D)	Average degree of dominance (σ^2D / σ^2A)$^{1/2}$	Heritability (h^2ns %)	Contribution (%)		
					Lines	Testers	Interaction
Days to 50% flowering	0.07	8.86	11.25	0.74	34.31	8.13	57.55
Days to 75% maturity	0.06	8.82	12.12	0.53	35.46	9.63	54.91
Plant height (cm)	0.34	15.99	6.86	2.09	65.25	0.43	34.31
Branches per plant	0.03	1.68	7.48	1.10	59.19	0.75	40.06
Pod length (cm)	0.01	0.57	7.55	0.71	40.05	2.75	57.20
Pods per plant	0.41	31.81	8.81	2.23	64.95	1.41	33.64
Seeds per pod	0.01	0.20	4.47	0.66	52.29	4.46	43.25
Biological yield per plant(g)	0.03	0.42	3.74	3.92	72.72	0.33	26.95
Seed yield per plant (g)	0.16	14.28	9.45	5.62	74.34	3.35	22.31
Harvest index (%)	0.01	0.48	6.93	0.66	37.42	6.11	56.46
100 seed weight (g)	0.43	2.85	2.57	1.09	36.70	0.65	62.65
Protein content (%)	0.07	8.86	11.25	1.91	63.25	1.48	35.27

Table 4: Estimates of general combining ability (GCA) effects of lines (females) and testers (males) for different traits.

	Days to 50% flowering	Days to 75% maturity	Plant height (cm)	Branches per plant	Pod length (cm)	Pods per plant	Seeds per pod	Biological yield per plant (g)	Seed yield per plant (g)	Harvest index (%)	100 seed weight (g)	Protein content (%)
Lines												
IC-281980	0.72	0.11	3.76**	0.66**	0.22	-19.47**	0.50**	11.36**	-3.67**	-8.04**	-0.57**	0.27
IC-282007	-0.28	-0.22	-2.19*	-0.63**	-0.60**	0.78	-0.56**	-8.31**	-1.05**	2.75**	-0.07	-0.51
IC-282008	-3.12**	-3.22**	-1.59	0.30	-0.23	6.53**	-0.23*	-4.21**	0.08	1.24	-0.05	-1.25*
IC-436910	-1.45	-2.22*	10.79**	5.91**	0.63**	31.00**	0.99**	52.46**	11.55**	-0.70	0.01	2.30**
IC-281989	2.05*	2.78**	14.94**	2.54**	0.01	25.07**	-0.51**	39.07**	7.71**	-2.15*	0.68**	-0.11
IC-398973	-1.12	-1.89*	8.54**	1.61**	0.03	15.06**	-0.39**	30.88**	4.86**	-3.12**	0.67**	2.24**
IC-281982	1.72	2.11*	-1.47	0.06	-0.16	-11.26**	-0.67**	3.26**	-2.48**	-12.99**	-0.64**	-0.88
IC-282001	0.38	0.44	0.02	0.65**	-0.65**	-5.36**	0.30**	-0.28	-1.26**	-8.82**	0.08	0.84
IC-398956	0.22	1.28	-0.54	0.78**	0.53**	0.54	0.65**	-2.49**	-0.37**	-0.05	-0.44**	0.07
IC-413306	-0.62	-1.22	2.40*	1.09**	0.11	12.40**	0.13	-2.42**	1.44**	6.38**	0.34**	1.99**
IC-413307	-0.62	-0.06	2.54**	-0.05	-0.21	11.28**	-1.05**	9.29**	2.11**	-5.12**	0.08	-1.22*
IC-281993	0.38	1.11	2.47**	0.77**	-0.06	-4.24**	0.31**	-6.22**	-1.17**	-0.38	-0.24*	-0.09
IC-343962	0.05	-0.39	-1.13	-2.56**	0.15	-8.40**	0.27*	-10.77**	-1.98**	-0.07	-0.45**	-0.74
IC-413305	3.05**	1.94*	5.58**	-0.46**	-0.07	6.08**	0.43**	3.78**	0.88**	5.11**	-0.01	0.05
IC-398998	1.55	1.61	-6.87**	-2.71**	-0.46**	-5.88**	0.24*	-10.92**	-2.08**	-0.87	0.32**	0.33
IC-281992	3.38**	3.61**	-7.50**	-2.69**	-0.45**	-11.47**	-0.84**	-13.08**	-2.56**	0.31	-0.26*	-1.43**
IC-413304	3.38**	3.28**	-7.30**	-2.51**	-0.61**	-11.08**	-0.63**	-14.97**	-2.45**	5.21**	0.03	-0.61
IC-436852	-3.45**	-3.06**	-2.52**	-0.54**	-0.48**	4.53**	-0.46**	-5.52**	0.93**	5.40**	0.57**	-0.79
IC-282002	-0.62	0.28	-5.92**	0.85**	0.57**	-9.52**	1.21**	-14.58**	-2.07**	8.75**	0.44**	0.49
IC-281990	0.55	0.28	3.09**	-1.88**	-0.43**	-3.44**	-0.48**	-9.80**	-1.39**	3.75**	-0.46**	0.35
IC-281995	-0.12	0.61	-4.50**	-0.48**	0.94**	-1.85	0.19	-4.47**	-0.72**	-1.65	0.46**	1.05*
IC-343885	-0.45	-0.39	-1.14	0.41**	0.46**	3.01**	0.14	6.13**	1.34**	-1.09	0.39**	2.11**
IC-343947	-2.62**	-2.72**	-4.39**	-0.44**	0.12	-5.59**	0.17	-11.49**	-1.75**	3.65**	0.23*	-1.46**
IC-282004	-1.45	-1.56	-6.59**	-1.26**	0.31*	-11.65**	0.25*	-13.38**	-2.68**	-1.05	-0.55**	-1.94**
IC-413309	0.38	-0.39	-1.10	0.42**	-0.21	-7.95**	-0.28*	-9.84**	-2.34**	-4.12**	0.14	-1.57**
IC-343943	-1.12	-1.56	-0.69	0.79**	0.93**	2.79**	0.57**	-8.58**	-0.47**	6.34**	-0.57**	2.27**
IC-281984	-0.78	-0.56	1.31	-0.63**	-0.39**	-1.90	-0.22*	-4.90**	-0.43**	1.33	-0.10	-1.76**
SE(g_i)±	0.87	0.93	0.94	0.16	0.13	0.97	0.11	0.50	0.13	0.99	0.10	0.52
SE(g_i- g_j)±	1.22	1.32	1.33	0.22	0.19	1.37	0.15	0.70	0.19	1.40	0.14	0.73
Testers												
HPBU-111	0.84**	0.94**	0.44	0.20**	0.12**	1.67**	0.16**	1.10**	0.70**	1.99**	-0.05	0.20
HM-1	-0.84**	-0.94**	-0.44	-0.20**	-0.12**	-1.67**	-0.16**	-1.10**	-0.70**	-1.99**	0.05	-0.20
SE ± (gi)	0.24	0.25	0.26	0.04	0.04	0.26	0.03	0.14	0.04	0.27	0.03	0.14
SE ± (gi-gj)	0.33	0.36	0.36	0.06	0.05	0.37	0.04	0.19	0.05	0.38	0.04	0.20

*Significance at $P \leq 0.05$; **Significance at $P \leq 0.01$.

Table 5: Estimates of specific combining ability (SCA) effects of promising crosses along with GCA status of their parents for different traits in urdbean.

Trait	Crosses	SCA effects	*Per se* performance	GCA status of parents
Days to 50% flowering	IC-281995 × Him Mash-1	-4.66**	42.33	L × H
	IC-281989 × HPBU-111	-4.17**	46.67	M × L
Days to 75% maturity	IC-436910 × HPBU-111	-5.11**	66.33	H × L
	IC-281995 × HPBU-111	-4.39**	68.00	L × H
Plant height (cm)	IC-281980 × Him Mash-1	9.23**	25.16	H × L
	IC-436910 × HPBU-111	6.79**	21.63	H × L
Branches per plant	IC-281980 × Him Mash-1	3.36**	3.87	M × L
	IC-436910 × HPBU-111	3.22**	4.50	H × H
Pod length (cm)	IC-282002 × HPBU-111	1.25**	4.29	H × H
	IC-343947 × Him Mash-1	1.09**	6.17	L × M
Pods per plant	IC-413307 × HPBU-111	21.32**	26.96	H × L
	IC-436852 × HPBU-111	14.09**	20.32	H × L
Seeds per pod	IC-343947 × Him Mash-1	1.16**	5.23	L × M
	IC-281993 × Him Mash-1	0.93**	5.48	H × M
Biological yield per plant(g)	IC-281980 × Him Mash-1	32.18**	13.42	H × H
	IC-282007 × Him Mash-1	2.94**	20.74	L × H
Seed yield per plant(g)	IC-413307 × HPBU-111	4.43**	2.64	H × L
	IC-436910 × HPBU-111	3.64**	3.22	H × L
Harvest index (%)	IC-281980 × HPBU-111	10.55**	5.35	M × H
	IC-282008 × HPBU-111	10.52**	12.47	L × H
100-seed weight (g)	IC-413306 × Him Mash-1	0.94**	5.58	H × L
	IC-413304 × HPBU-111	0.91**	10.46	L × L
Protein content (%)	IC-398956 × HPBU-111	1.94**	24.40	L × L
	IC-398998 × HPBU-111	1.81**	24.52	L × L

M- Medium, L- Low, H- High.

effect (Table 4) for the lines and testers for the traits indicated that no single parent was a good general combiner for all traits under study. However, line IC-436910 (11.55**), IC-281989 (7.71**), IC-398973 (4.86**), IC-413307 (2.11**), IC-413306 (1.44**), IC-343885 (1.34**), IC-436852 (0.93**) and IC-413305 (0.88**) were found to be good general combiners for seed yield per plant. The parental lines IC-436910 (2.30**), IC-343943 (2.27**), IC-398973 (2.24**), IC-343885 (2.11**), IC-413306 (1.99**) and IC-281995 (1.05*) were best general combiners for protein content.

Earliness is an important breeding objective. Because negative heterosis is required to achieve earliness, lines IC-436852 (-3.45**, -3.06**), IC-343947 (-2.62**, -2.72**), IC-282008 (-3.12**, -3.22*) exhibited significant GCA values for days to 50% flowering and days to 75% maturity respectively. Among testers, Him Mash-1 was good general combiner for earliness whereas, HPBU-111 was good general combiner for branches per plant, pod length (cm), pods per plant, seeds per pod, biological yield per plant (g), seed yield per plant (g) and harvest index (%). Overall, IC-436910, IC-413306, IC-398973 and IC-343885 lines were good general combiners for seed yield and other quantitative traits and among these lines, IC-436910 was the best general combiner for maximum number of traits *i.e.* days to 75% maturity, plant height, branches per plant, pod length, pods per plant, seeds per pod, biological yield per plant, seed yield per plant and protein content. The GCA effect revealed that in order to synthesize a dynamic population with most of the favorable genes, it will be pertinent to make use of these parents, which are good general combiner for several traits, in a multiple crossing program to obtain desirable transgressive segregants for higher seed yield.

Another important aspect from practical point of view, which needs consideration, is the identification of potential cross combinations for obtaining desirable transgressive segregants with a higher degree of probability. The specific combining ability is the deviation from the performance predicted on the basis of general combining ability (Allard, 1960). The cross combinations with highest SCA effects along with mean performances and GCA effects of parents are listed in Table 5.

The cross combination IC-436910 × HPBU-111 recorded significant positive SCA effects and high *per se* performance for days to 75% maturity, plant height, branches per plant and seed yield per plant. The cross IC-281980 × Him Mash-1 recorded significant positive SCA effects for plant height, branches per plant and biological yield per plant. IC-343947 × Him Mash-1 showed significant positive SCA effects for pod length and seeds per pod. For days to 50% flowering and 75% maturity, IC-281995 × Him Mash-1 was found to be highly significant negative SCA effects as well as low mean values indicating early maturity. It was observed that the desirable cross combination included high × high, medium x high, high × low, medium x medium and low × low type of general combiner (Table 5). The high × medium or vice-versa combination could be due to additive and additive × additive types of gene action which are fixable in nature. The desirable performance of cross combination like low × medium, medium × medium general combiners may be ascribed to complimentary gene effects.

Various workers have recorded good general combiners and specific combiners for various traits in blackgram with different genetic material Gill *et al.* (2014), Kumar *et al.* (2014), Gill *et al.* (2015), Sanjeev *et al.* (2015), Balouria *et al.* (2016) and Thamodharan *et al.* (2017). Similarly, Barad *et al.* (2008), Patil *et al.* (2011), Nath *et al.* (2018) reported in mungbean. Hence, the lines and cross-combinations with significant and positive GCA, SCA effects could be utilized for selection of superior segregants for developing improved cultivars in future.

CONCLUSION

Estimate of genetic parameters in the present study described that the magnitude of dominant variance (σ^2D) was found to be higher than additive variance (σ^2A) for all the traits, which indicated the preponderance of non-additive gene action. Combining ability results showed that, the relative size of GCA variances was higher than SCA variances for most of the traits. Hence, is clear that quantitative traits governs yield were under the control of both additive and non-additive gene action. It is concluded that breeding methods such as recurrent selection or biparental mating followed by selection would be ideal to exploit both non--additive and additive gene action.

REFERENCES

Allard, R.W. (1960). Principles of Plant Breeding. John Wiley and Sons. Inc., New York and London.

Balouria, S., Mittal, R.K., Sood, V.K. and Bindra, S. (2016). Combining ability studies for seed yield and its component traits in urdbean [*Vigna mungo* (L.) Hepper]. Research on Crops. 17: 729-734.

Bandi, H.R.K., Rao, N.R., Krishna, K.V. and Srinivasulu, K. (2018). Variability, heritability and genetic advance for quantitative characters in rice fallow blackgram [*Vigna mungo* (L.) Hepper]. International Journal of Current Microbiology and Applied Sciences. 7: 171-176.

Barad, H.R., Pithia, M.S. and Vachhani, J.H. (2008). Heterosis and combining ability studies for economic traits in genetically diverse lines of mungbean [*Vigna radiata* (L.) Wilczek]. Legume Research. 31: 68-71.

Chakraborty, S., Kumar, H.B., Kumar, B.B., Pathak, D, Kalita, H. and Barman, B. (2010). Genetic parameters and combining ability effects of parents for seed yield and other quantitative traits in Blackgram [*Vigna mungo* (L.) Hepper]. Notulae Scientia Biologicae. 2: 121-126.

Chauhan, S., Mittal, R.K., Sood, V.K. and Patial, R. (2018). Evaluation of genetic variability, heritability and genetic advance in blackgram [*Vigna mungo* (L.) Hepper].). Legume Research. 1-6.

Cockerham, C. (1961). Implications of genetic variances in a hybrid breeding programme. Crop Science. 1: 47–52.

Gill, R.K., Singh, I., Kumar, A. and Singh, S. (2015). Assessment of combining ability for various quantitative traits in summer urdbean. Electronic Journal of Plant Breeding. 6: 412-416.

Gill, R.K., Singh, I., Singh, S. and Singh, P. (2014). Studies on combining ability for grain yield and component traits in *kharif* urdbean. Legume Research. 37: 575-579.

Govindaraj, P. and Subramanian, M. (2001). Combining ability analysis in blackgram. Legume Research. 15: 59-64.

Grakh, S.S. and Chaudhary, M.S. (1985). Heterosis for early maturing and high yield in *Gossypium arboreum*. Indian Journal of Agricultural Sciences. 55:10-13.

Kempthorne, O. (1957). An introduction to Genetic Statistics. John Wiley and Sons Inc, New York, pp 458–471.

Kumar, G.V., Vanaja, M., Premkumar, B.A., Lakshmi,N.J. and Sarkar, B. (2017). Heterosis and combining ability studies in blackgram (*Vigna mungo* L. Hepper) under alfisols of SAT region, India. Electronic Journal of Plant Breeding. 8: 541-547.

Kumar, G.V., Vanaja, M., Reddy, P.R.R., Salini, K., Abraham, B. and Lakshmi, N.J. (2014). Studies on combining ability and genetic advance in blackgram [*Vigna mungo* (L.) Hepper] under Rainfed Condition. Journal of Agriculture and Allied Sciences. 3(3): 14-24.

Lukoki, L., Marechal, R., Otoul, E. (1980). Les ancetressauvages des haricots cultives: *Vigna radiata* (L.) Wilczek et *V. mungo* (L.) Hepper. Bulletin du Jardin Botanique National de Belgique. 50: 385-391.

Manivannan, N. (2002). Genetic diversity in cross derivatives of greengram [*Vigna radiata* (L.) Wilczek]. Legume Research. 25: 50-52.

Muhammad, R., Cheema, A.A. and Muhammad, A. (2007). Line × tester analysis in Basmati rice. Pakistan Journal of Botany. 39: 2035-2042.

Nath, Anamika, Maloo, S.R., Bharti Baudh., Dubey, R.B. and Verma, Rajani (2018). Combining ability analysis in mungbean [*Vigna radiate* (L.) Wilczek]. Legume Research-An International Journal. 41: 519-525.

Panse, V.G. and Sukhatme, P.V. (1984). Statistical Methods for Agricultural Workers. ICAR Publication, New Delhi pp: 145-152.

Patial, R., Mittal, R.K. and Sood, V.K. (2018). Estimation of heterosis for seed yield and yield contributing traits in urdbean [*Vigna mungo* (L.) Hepper]. International Journal of Chemical Studies. 6: 2385-2390.

Patil, A.B., Desai, N.C., Mule, P.N. and Khandelwal, V. (2011). Combining ability for yield and component characters in mungbean. Legume Research. 34: 190-195.

Poehlman, J.M. (1991). History, Description, Classification and Origin. In: The mungbean (JM Poehlman) West View, Boulder. PP 6-21.

Sanjeev, B.G., Krishnappa, M.R., Shekara, B.G. and Rudraswamy, P. (2015). Gene action and combining ability for fodder yield and its contributing traits in fodder cowpea [*Vigna unguiculata* (L.) Walp.]. Forage Research. 40: 218-221.

Sarker, U., Biswas, P.S., Prasad, B. and Mian, M.A.K. (2002). Heterosis and genetic analysis in rice hybrids. Pakistan Journal of Biological Sciences. 5: 1-5.

Selvam, Y.A. and Elangaimannan, R. (2010). Combining ability analysis for yield and its component traits in Blackgram [*Vigna mungo* (L.) Hepper]. Electronic Journal of Plant Breeding. 1: 1386-1391.

Sprague, G.F. (1966). Quantitative Genetics in Plant Improvement. In: Plant Breeding. A symposium on Plant Breed. [(Ed.) Kenneth, J Frey]. Iowa State Univ Press Ames, Iowa, pp 315-354.

Sprague, G.F. and Tatum, L.A. (1942). General versus specific combining ability in single crosses of corn. Journal of American Society of Agronomy. 34: 923-932.

Surashe, S.M., Patil, D.K. and Gite, V.K. (2017). Combining ability for yield and yield attributes characters in greengram [*Vigna radiata* (L.) Wilczek]. International Journal of Current Microbiology and Applied Sciences. 6: 3552-3558.

Thamodharan, G., Ramalingam, A. and Geetha, S. (2017). Estimation of genetic parameters and combining ability analysis in blackgram [*Vigna mungo* (L.) Hepper]. Legume Research. 4: 401-408.