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Studies on Combining Ability and Heterosis for Seed Yield and Yield Components in Blackgram (*Vigna mungo* L. Hepper)

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ABSTRACT

The study was conducted during *kharif* (June–September, 2022) and *rabi* (October–December, 2022–23) at Agriculture Research Station, Madhira, Telangana, India to study on the combining ability analysis in blackgram for yield and its component traits through Line×Tester design. Twenty four crosses derived after crossing six lines and four testers were evaluated in line×tester analysis. Predominance of non-additive gene action was observed for most of the yield components except harvest index, which was under the control of additive gene action. Among the lines TU-94-2, MBG-207 and GBG-1 and testers IC-436638 and ABFBG-23RS were identified as good general combiners for days to 50% flowering, plant height, number of pods plant^{-1}, pod length, number of seeds pod^{-1} and 100 seed weight. The crosses TBG-104×IC-436638, MBG-1070×LBG-20, TU-94-2×ABFBG-26RD and TU-94-2×LBG-20 have shown significantly favorable specific combining ability effects for seed yield plant^{-1} as well as yield attributes. Most of the crosses exhibiting high specific combining effects involved high×low combinations indicating additive×dominance, dominance×dominance type of gene interactions. Studies on heterosis indicated that majority of crosses showing high specific combining ability effects also exhibited high heterosis. The cross TBG-104×IC-436638 recorded high estimates of heterosis for seed yield plant^{-1} and also for number of clusters plant^{-1}, pod length and biological yield plant^{-1}. The superior crosses identified were TBG-104×IC-436638, TU-94-2×ABFBG-26RD and GBG-1×LBG-20 could be exploited for recombination breeding for development of varieties.

KEYWORDS: Blackgram, line×tester, SCA, heterosis, seed yield

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1. INTRODUCTION

Blackgram [*Vigna mungo* (L.) Hepper], also known as "urdbean", "black matpe bean" and "mash" etc., is amongst the most important *kharif* and *rabi* pulse crops grown in India belonging to the family: Fabaceae. The pulse crop has chromosome number 2n=2x=22 (Dana, 1980). India is the primary centre of origin of blackgram and Central Asia is believed to be the secondary centre of origin (De Candolle, 1882; Vavilov, 1926; Zukovskij, 1962) with *Vigna mungo* var. silvestris as its progenitor which is found wild in India Lukoki et al. (1980). It is a great source of quickly and easily digestible high quality protein used in the preparation of dal, curries, soups, desserts and snacks. High values of lysine make urdbean a perfect complement to rice in terms of balanced human nutrition and rich source of phosphoric acid, protein (24%), minerals (3.2%), fat (1.4%), carbohydrates (57.3%) and moisture (9.7%). It is an important short duration self pollinated pulse crop grown in many parts of India (Priyanka et al., 2022). Urdbean is known for its synchronous maturity, non shattering pods, more clusters and pods with large seeds. India is the largest producer and consumer of blackgram in the world. It is suitable for growing in all the three seasons in India and produces 2.34 mt annually from a 4.67 m ha area with average productivity of 501 kg ha^{-1} (Anonymous, 2021). It is also grown in rice fallow conditions with minimum management practices. The yield of this crop is stagnated over two decades and significant seasonal as well as year to year variation in yield was recorded due to non-availability of high yielding and stable performing cultivars (Kumar et al., 2017). 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 (Patial et al., 2022). Productivity can be improved by developing suitable varieties with high yield potential. Combining ability analysis is an important tool to select the best parents for hybridization to get the novel segregants in the recombination breeding and understanding the magnitude of gene action involved in the inheritance of quantitative traits of economic importance. The magnitude of heterosis enable to select the desirable parents for developing superior F_1 hybrids that may be exploited for hybrid vigour and for building better gene pool to be employed in population improvement. (Yashpal et al., 2015; Fasahat et al., 2016). Line×Tester (Kempthrone, 1957) analysis which is one of the breeding strategies used to predict general combining ability (GCA) to select suitable lines, testers and crosses that have good specific combining ability (SCA). Heterosis has important implications for both in F_1 and for adopting transgressive segregants in F_2 generation (Bhagirath et al., 2013; Thamodharan et al., 2016). The presence of heterosis and its exploitation in blackgram has not been commercialized due to limited extent of out crossing (Singh, 2000). However, highly heterotic crosses can be used for development of high yielding varieties in self-pollinated crops. With this idea, combining ability analysis was performed in blackgram for yield and its component traits through line×tester design to select the good parental lines and crosses for further improvement of blackgram.

2. MATERIALS AND METHODS

The study was conducted during *kharif* (June–September, 2022) and *rabi* (October–December, 2022–23) at Agricultural Research Station Madhira, Telangana, India with Latitude 17°58' N and Longitude: 79°40' E. The material comprised of high yielding, photo insensitive and diversified six lines, GBG-1, MBG-1070, TBG-104, TU94-2, MBG-207 and LBG-752 and four testers IC-436638, ABFBG-23RS, ABFBG-26RD and LBG-20 were crossed in line×tester design. The six lines, four testers and 24 crosses were grown in a randomized block design with three replications and each entry was sown in two rows of 4 m length with a spacing of 30×10 cm^2. All the recommended cultural practices were followed to obtain healthy crop.

Observations were recorded on five randomly selected plants without border effect for eleven yield and its attributes except for days to 50% flowering and days to maturity on plot basis, plant height (cm), number of clusters plant^{-1}, number of pods plant^{-1}, pod length (cm), number of seeds pod^{-1}, 100 seed weight (g), biological yield (kg), harvest index (%) and seed yield plant^{-1} (g). The mean values of all the quantitative characters were worked out and the analysis of variance for combining ability through line×tester was carried out following the technique given by Kempthorne, (1957). The degree of dominance was calculated by using the formula $(\sigma^2D/\sigma^2A)1/2$ where σ^2D dominance or specific combining ability variance (SCA) and σ^2A was additive or general combining ability variance (GCA) along with heterosis estimates (Hays et al., 1955). The statistical analysis was carried out using AGRISTAT software.

3. RESULTS AND DISCUSSION

3.1. *Analysis of variance*

The analysis of variance of line×tester analysis for eleven yield and its attributing traits were presented in Table 1.

The Anova revealed that the mean squares due to parents were shown significant for yield and yield attributes except for three traits number of seeds pod^{-1}, harvest index and seed yield plant^{-1}. Lines were recorded significance for all traits except number of clusters plant^{-1}, number of pods plant^{-1}, number of seeds pod^{-1}, harvest index and seed yield plant^{-1}. Testers shown significance for most of the traits except for number of seeds pod^{-1}, biological yield, harvest index and seed yield plant^{-1}. The mean squares due to line×tester interaction showed significance for important yield attributing traits such as number of pods plant^{-1}, pod length and 100 seed weight. This revealed that except for harvest index, all the traits shown significant variation and was controlled by both additive and non additive type of gene action while harvest index governed by additive type of gene action. Hence, any approach that facilitated simultaneous exploitation of both additive and non-additive gene effects would be more desirable for the improvement of the trait. The greater magnitude of SCA variance than GCA variance indicated the role of non-additive gene action for all the eleven characters. The additive (σ^2A) and dominance variance (σ^2D) revealed that dominance variance (σ^2D) was greater than the additive variance (σ^2A) for all the characters. The ratio of (σ^2A)/(σ^2D) ranged from 0.07 (number of seeds pod^{-1}) to 0.81 (number of pods plant^{-1}). Similar results were reported by Govindaraj and Subramanian, (2001), Manivannan, (2002), Selvam and Elangaimannan, (2010), Chakraborty et al. (2010), Yashpal et al. (2015), Thamodharan et al. (2017), Kumar et al. (2017), Patial et al. (2022) and Surendhar et al. (2023) for plant height, days to 50% flowering, days to maturity, cluster plant^{-1}, number of clusters plant^{-1}, 100-seed weight, pod length and seed yield plant^{-1}.

3.2. *General combining ability*

The GCA effects of the lines and testers presented in Table 2 depicted that among the six lines and four testers taken for this study neither the lines nor the testers recorded significant positive GCA for all the quantitative traits. Similar results were reported by Yashpal et al. (2015) and Debbarma et al. (2022). Based on the combining ability effects, the lines and testers values were categorized in three groups as good (G), average (A) and poor (P) general combiners. The parents with significant GCA effects towards desirable direction were considered as good general

Table 1: Analysis of variance for combining ability in line×tester design for seed yield and yield components in blackgram (*Vigna mungo* L.)

Source of variation	Degrees of freedom	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of clusters plant^{-1}	No. of pods plant^{-1}
Replications	2	10.97**	0.35	1.96	1.39	37.50*
Treatments	33	4.79**	6.29**	33.75**	5.40**	86.86**
Parents	9	5.72**	5.68**	26.19**	3.90**	69.27**
Parents (Line)	5	3.82*	4.98*	35.38**	2.32	21.22
Parents (Testers)	3	9.63**	8.08**	17.63**	7.78**	136.51**
Parents (L vs T)	1	3.47	2.00	5.97	0.16	107.80**
Parents vs crosses	1	2.97	0.66	22.75**	35.63**	0.58
Crosses	23	4.51**	6.77**	37.19**	4.67**	97.49**
Line effect	5	2.99	7.98	26.18	3.57	81.22
Tester effect	3	3.38	10.62	49.16	3.02	130.67
Line×tester effect	15	5.25**	5.59**	38.47**	5.37**	96.28**
Error	66	1.30	1.92	2.51	1.05	9.83
Total	101	2.63	3.32	12.71	2.48	35.55
GCA		1.07	1.66	12.54	0.06	0.96
SCA		6.27	6.43	32.36	0.52	2.37
σ^2A (F=1)		2.14	3.32	25.09	0.13	1.92
σ^2D (F=1)		6.27	6.43	32.36	0.52	2.37
σ^2A/σ^2D		0.34	0.11	0.77	0.24	0.81
GCA/SCA		0.17	0.25	0.38	0.12	0.40
Degree of dominance		1.71	2.93	1.13	2.0	1.11

Table 1: Continue...

Source of variation	Pod length (cm)	No. of seeds pod^{-1}	100 Seed weight (g)	Biological yield (kg)	Harvest index (%)	Seed yield plant^{-1}
Replications	0.40**	0.90	0.06	0.49	53.86	0.52
Treatments	0.61**	1.22**	0.55**	1.57**	15.40	0.78**
Parents	1.16**	0.32	0.35**	1.07*	5.28	0.39
Parents (Line)	0.44**	0.15	0.36**	1.31*	6.81	0.53
Parents (Testers)	2.50**	0.59	0.36**	0.98	3.23	0.29
Parents (L vs T)	0.68**	0.32	0.31*	0.12	3.81	0.01
Parents vs Crosses	0.01**	3.90**	2.35**	0.89	0.19	0.32
Crosses	0.43	1.46**	0.55**	1.80**	20.02	0.95**
Line effect	0.57**	2.27	0.55	2.78	10.06	0.54
Tester effect	0.36	0.47	0.46	1.86	23.84	0.84
Line×Tester effect	0.40**	1.38**	0.56**	1.46**	22.58	1.11**
Error	0.07	0.43	0.05	0.53	18.17	0.37
Total	0.25	0.70	0.21	0.87	17.97	0.51
GCA	0.01	0.01	0.08	0.61	29.96	0.82
SCA	0.04	0.18	0.25	3.07	146.0	2.43
σ^2A (F=1)	0.02	0.01	0.16	1.23	59.93	1.65
σ^2D (F=1)	0.05	1.08	0.25	3.07	146.0	2.43
σ^2A/σ^2D	0.39	0.07	0.64	0.4	0.41	0.68
GCA/SCA	0.25	0.05	0.32	0.2	0.2	0.34
Degree of dominance	1.58	3.69	1.24	1.21	1.57	1.56

*: Significant at (p=0.05) level; **: Significant at (p=0.01) level

combiners, with positive GCA effects were considered as average general combiners and the parents with negative GCA effects were designated as poor general combiners. The line TU-94-2 was found to be good general combiner for important yield components like number of pods plant^{-1}, pod length and 100 seed weight where as negative significant for plant height, therefore the line can be used for developing the dwarf stature plant with high yield. Similar results were also recorded by Patel et al. (2010). The line MBG-207 had shown positive significant GCA effects for number of seeds pod^{-1} followed by biological yield and highest positive seed yield plant^{-1}. The results obtained were in accordance with the results of Panigrahi et al. (2015). Another line GBG-1 had shown positive GCA effect for seed yield plant^{-1} and recorded positive significant GCA effect for number of clusters plant^{-1}, number of seeds pod^{-1} and results of present investigation was also reported by Panigrahi et al. (2015) and Thamodharan et al. (2016). Line TBG-104 had recorded significant and found to be good combiner for plant height and number of pods plant^{-1}. MBG-1070 had the negative significant general combining ability effect for days of maturity, hence desirable for development of early maturity plant types. The results obtained were similar with the results of Patel et al. (2010), Chakraborty et al. (2010) and Haque et al. (2013). Similarly, the tester IC-436638 was a good general combiner showing positive significant GCA effects for plant height, number of clusters plant^{-1}, number of pods plant^{-1}, pod length and 100 seed weight. The negative estimates of GCA for the tester LBG-20 for days to maturity and plant height were effective for developing early and short stature plant types in desirable direction.

3.3. Specific combining ability

SCA was the deviation from the performance predicted on the basis of general combining ability and is due to non additive gene effect. The usefulness of a particular cross in exploiting heterosis was judged by SCA effects depicted in Table 3. Significant positive SCA effect for seed yield plant-1was recorded by four hybrids GBG-1×LBG-20(0.929), TBG-104×IC-436638(0.854), MBG-207×ABFBG-23RS(0.774) and MBG-1070×ABFBG-23RS(0.765) and almost all the crosses have at least one parent with positive GCA effect. In addition, the cross TBG-104×IC-436638 was a good specific combiner for number of clusters plant^{-1}, pod length and biological yield while negative significant for days to maturity. Hence, the cross could be used as specific combiner to develop earliness with high seed yield. Among crosses GBG-1×IC-436638 recorded significant

Table 2: Estimation of general combining ability (gca) effects in parents for seed yield and yield components in blackgram (*Vigna mungo* L.)

Parents	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of clusters plant^{-1}	No. of pods plant^{-1}	Pod length (cm)	No. of seeds pod^{-1}	100 Seed weight (g)	Biological yield (kg)	Harvest index (%)	Seed yield plant^{-1}
Lines											
GBG 1	-0.208	0.139	-0.583	0.631*	-3.654***	-0.103	0.403*	-0.208**	0.269	-0.085	0.154
MBG-1070	0.458	-1.611***	0.250	-0.528	-1.646	0.022	-0.322	-0.025	-0.747***	1.665	-0.221
TBG-104	-0.042	0.722	2.492***	-0.169	1.88^{8*}	-0.178*	-0.231	-0.117	-0.331	0.082	-0.171
TU-94-2	-0.875*	0.306	-2.050***	-0.486	3.471***	0.222**	-0.139	0.408***	0.111	-0.526	0.004
MBG-207	0.292	0.222	0.158	-0.169	1.013	-0.253**	0.678***	0.017	0.636**	-0.076	0.338
LBG-752	0.375	0.222	-0.267	0.722*	-1.071	0.289***	-0.389*	-0.075	0.061	-1.060	-0.104
SE	0.32	0.40	0.45	0.29	0.90	0.07	0.19	0.06	0.21	1.23	0.17
(gi-gj)	0.46	0.56	0.64	0.42	1.28	0.10	0.27	0.09	0.29	1.74	0.25
Testers											
IC-436638	-0.042	0.556	1.072**	0.519*	3.488***	0.203**	0.219	0.172**	0.175	0.626	0.188
ABFBG-23RS	0.514	0.722*	1.467***	-0.353	0.438	-0.036	-0.164	0.022	0.019	-1.685	-0.207
ABFBG-26RD	0.069	-0.389	-0.356	-0.303	-1.035	-0.036	-0.058	-0.217***	-0.458*	0.832	-0.168
LBG-20	-0.542	-0.889**	-2.183***	0.136	-2.890***	-0.131*	0.003	0.022	0.264	0.226	0.188
SE	0.26	0.32	0.37	0.24	0.73	0.06	0.15	0.05	0.17	1.00	0.14
(gi-gj)	0.38	0.46	0.52	0.34	1.04	0.08	0.22	0.07	0.24	1.42	0.20

SCA effect for plant height, number of pods plant^{-1} and 100 seed weight, GBG-1×ABFBG-23RS for plant height, pod length and number of clusters plant^{-1}, MBG-1070×LBG-20 for number of pods plant^{-1}, pod length and days to 50% flowering, TU94-2×ABFBG 26RD for plant height, number of pods plant^{-1} and 100 seed weight, TU 94-2×LBG-20 for plant height, number of seeds pod^{-1} and 100 seed weight and MBG-207×IC-436638 for number of pods plant^{-1}, pod length and plant height in desired direction for three characters each. However no cross combined all the values in a desirable direction indicating the necessity of previous breeding value of the parents to combine desirable SCA effects in a single cross. Majority of the crosses with high SCA effects are involved with high×low combinations indicating additive×dominance, dominance×dominance type of gene interactions. The results obtained were in similar with the findings of Singh et al. (2022). The cross MBG-1070×LBG-20 for days to 50% flowering and TBG-104×IC-436638 and TU 94-2×ABFBG-23RS for days to maturity were found negative significant SCA effects and could be driven in a desirable direction. The results obtained were in accordance with results of Reddy et al. (2021) and Surendhar et al. (2023). Significant positive estimates of SCA effects for the trait plant height were recorded for GBG-1×IC-436638, GBG-1×ABFBG-23RS, TBG-104×LBG-20, TU-94-2×ABFBG 26 RD, TU-94-2×LBG-20, MBG-207×ABFBG-23RS and LBG-752×IC-436638. Similar findings were recorded by Nandini et al. (2022) and Singh et al. (2022). Good specific combiners for number of clusters plant^{-1} were GBG-1×ABFBG-23RS and TBG-104×IC-436638, for number of pods plant^{-1} GBG-1×IC-436638 followed by MBG-1070×LBG-20, TU 94-2×ABFBG-26 RD, MBG-207×IC-436638 and LBG-752×ABFBG-23RS and results obtained were similar with findings of Ragul et al. (2021). The crosses GBG-1×ABFBG-23RS followed by MBG-1070×LBG-20, TBG-104×IC-436638 and MBG-207×IC-436638 found significant positive for pod length and obtained results were in accordance with Prasad and Murugan, 2015. For the trait number of seeds pod^{-1}, the best specific combiners were TU 94-2×LBG-20 followed by LBG-752×ABFBG-26 RD, for the trait 100 seed weight GBG-1×IC-43368 followed by MBG-1070×IC-436638, TBG-104×ABFBG-23RS, TU-94-2×ABFBG-26RD, TU 94-2×LBG-20 and MBG-207×LBG-20 whereas, for biological yield, the crosses GBG-1×LBG-20 and TBG-104×IC-436638 recorded positive significant SCA estimates in desirable direction. The estimated results were similar with Panigrahi et al. (2015) and Boraiah et al. (2019). In these crosses all kinds of parental combinations like high×high, high×low, medium×medium and medium×low gene interactions were found. In contrast to the GCA effects, the SCA effects represented dominance and epistatic component of variation and that was not fixable in nature. This suggested that either additive×additive or additive×dominance genetic interaction were predominant and reported by Abinaya et al. (2020). The crosses showing high SCA effects involved either both or one good general combining parents and they could be successfully exploited for varietal improvement and expected to produce transgressive segregants carrying fixable gene effects. In crosses with medium×low GCA effects, the high positive SCA effect might be due to the dominant×recessive interaction expected to produce desirable segregants in subsequent generation. In many crosses however, high×high GCA lead to inferior hybrids for many studied traits i.e., MBG-207×IC-436638, MBG-207×LBG-20, GBG-1×IC-436638 and GBG-1×LBG-20 for seed yield plant^{-1}, TU 94-2×IC-436638 for 100 seed weight; TBG-104×ABFBG-23RS for plant height and also many studied traits indicating epistatic gene action controlling for the studied traits. Few crosses exhibited medium×low general combiners showed high SCA effects i.e., TBG-104×IC-436638, TU 94-2×ABFBG-26RD and GBG-1×ABFBG-26RD for seed yield plant^{-1},

Table 3: Estimation of specific combining ability (sca) effects in crosses for seed yield and yield components in blackgram (*Vigna mungo* L.)

Crosses	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of clusters plant^{-1}	No. of pods plant^{-1}
GBG-1×IC-436638	-0.292	-1.139	3.144**	-1.103	7.388***
GBG-1×ABFBG-23RS	0.819	0.361	3.117**	1.503*	-5.229**
GBG-1×ABFBG-26RD	0.264	2.139*	-1.861*	0.053	-3.257
GBG-1×LBG-20	-0.792	-1.361	-4.400***	-0.453	1.099
MBG-1070×IC-436638	1.708*	-0.722	0.378	0.856	0.612
MBG-1070×ABFBG-23RS	0.486	0.111	1.617	0.794	-8.104***
MBG1070×ABFBG-26RD	-0.736	-0.111	-2.361*	-0.689	1.401
MBG-1070×LBG-20	-1.458*	0.722	0.367	-0.961	6.090**
TBG-104×IC-436638	-0.458	-1.722*	-0.031	2.631***	-5.321**
TBG-104×ABFBG-23RS	-0.347	1.444	-2.258*	-1.497*	3.063
TBG-104×ABFBG-26RD	1.764*	0.222	-0.269	-1.214*	2.535
TBG-104×LBG-20	-0.958	0.056	2.558**	0.081	-0.276
TU-94-2×IC-436638	-0.958	2.361**	-4.822***	-1.053	-1.738
TU-94-2×ABFBG-23RS	-1.181	-1.806*	-3.717***	0.819	2.146
TU-94-2×ABFBG26RD	-0.736	-1.028	4.606***	0.903	6.785***
TU-94-2×LBG-20	2.875***	0.472	3.933***	-0.669	-7.193***
MBG-207×IC436638	-0.792	1.444	-3.364***	-1.369*	3.754*
MBG-207×ABFBG-23RS	0.653	-0.056	3.575***	-0.964	0.271
MBG-207×ABFBG-26RD	0.431	-1.278	0.231	1.186	-2.624
MBG-207×LBG-20	-0.292	-0.111	-0.442	1.147	-1.401
LBG-752×IC-436638	0.792	-0.222	4.694***	0.039	-4.696*
LBG-752×ABFBG-23RS	-0.431	-0.056	-2.333*	-0.656	7.854***
LBG-752×ABFBG-26RD	-0.986	0.056	-0.344	-0.239	-4.840*
LBG-752×LBG-20	0.625	0.222	-2.017*	0.856	1.682
CD 95% SCA	1.327	1.614	1.845	1.196	3.645
SE	0.65	0.80	0.91	0.59	1.81
Sij-skl	0.93	1.13	1.29	0.84	2.56
Sij-sik	1.23	1.50	1.71	1.11	3.38

Table 3: Continue...

Crosses	Pod length (cm)	No. of seeds pod^{-1}	100 Seed weight (g)	Biological yield (kg)	Harvest index (%)	Seed yield plant^{-1}
GBG-1×IC-436638	-0.436**	0.564	0.303*	-0.325	-3.726	-0.671
GBG-1×ABFBG-23RS	0.569***	0.114	0.153	-0.903*	-0.749	-0.643
GBG-1×ABFBG-26RD	0.136	-0.592	-0.175	0.308	1.435	0.385
GBG-1×LBG-20	-0.269	-0.086	-0.281*	0.919*	3.040	0.929*
MBG-1070×IC-436638	-0.294	0.156	0.319*	0.292	0.057	0.171
MBG-1070×ABFBG-23RS	-0.022	-0.261	-0.164	0.581	3.301	0.765*
MBG1070×ABFBG-26RD	-0.122	0.200	0.142	-0.142	-1.215	-0.240
MBG-1070×LBG-20	0.439**	-0.094	-0.297*	-0.731	-2.143	-0.696
TBG-104×IC-436638	0.439**	0.597	0.011	1.042*	1.940	0.854*
TBG-104×ABFBG-23RS	-0.089	-0.019	0.561***	-0.336	-2.015	-0.418
TBG-104×ABFBG-26RD	0.178	-0.058	-0.367*	-0.692	1.401	-0.257
TBG-104×LBG-20	-0.528**	-0.519	-0.206	-0.014	-1.326	-0.179
TU-94-2×IC-436638	0.039	-0.594	-0.814***	-0.633	-0.151	-0.388
TU-94-2×ABFBG-23RS	0.178	0.089	-0.164	-0.311	-0.140	-0.193
TU-94-2×ABFBG26RD	-0.022	-0.550	0.508***	0.467	-0.357	0.235
TU-94-2×LBG-20	-0.194	1.056**	0.469**	0.478	0.649	0.346
MBG-207×IC436638	0.314*	0.022	-0.056	-0.792	3.332	-0.021
MBG-207×ABFBG-23RS	-0.481**	0.739	-0.139	0.831	2.410	0.774*
MBG-207×ABFBG-26RD	-0.081	-0.367	-0.367*	0.275	-1.974	-0.099
MBG-207×LBG-20	0.247	-0.394	0.561***	-0.314	-3.768	-0.654
LBG-752×IC-436638	-0.061	-0.744	0.236	0.417	-1.451	0.054
LBG-752×ABFBG-23RS	-0.156	-0.661	-0.247	0.139	-2.807	-0.285
LBG-752×ABFBG-26RD	-0.089	1.367***	0.258	-0.217	0.710	-0.024
LBG-752×LBG-20	0.306	0.039	-0.247	-0.339	3.549	0.254
CD 95% SCA	0.311	0.770	0.275	0.846	4.955	0.716
SE	0.15	0.38	0.13	0.42	2.46	0.35
Sij-skl	0.21	0.54	0.19	0.59	3.48	0.50
Sij-sik	0.28	0.71	0.25	0.78	4.60	0.66

number of clusters plant^{-1}, pod length and biological yield suggesting the dominance×recessive interaction might be due to genetic diversity in the form of heterozygous loci. Therefore, the crosses were expected to produce desirable segregants and could be exploited successfully in varietal improvement programmes. Whereas, in some crosses TU 94-2×ABFBG-26RD for plant height, GBG-1×LBG-20 for pod length showed low×low general combining ability but high SCA effects suggesting predominant epistatic gene action. It was also revealed that the poor×good general combiners exhibited high SCA have to be improved through population improvement programme, where as in crosses having high SCA due to poor×poor general combiners might be exploited for heterosis breeding. The obtained results were in accordance with the Balouria et al. (2016) and Kumar et al. (2017).

3.4. Heterosis

The estimates of mid-parental heterosis, heterobeltiosis and standard heterosis for yield and its attributes were depicted in Table 4. In the present study, considerable heterosis existed both in positive and negative direction. In general positive heterosis was desirable for yield and most traits, where as negative heterosis was desirable for earliness. Out of 24 crosses, two crosses GBG-1×LBG-20 followed by MBG-1070×LBG-20 exhibited significant negative average heterosis, heterobeltiosis and standard heterosis for days to 50% flowering, the cross MBG-1070×ABFBG-23RS for days to maturity, GBG-1×LBG-20, MBG-1070 ×ABFBG-26RD, TV-94-2×IC-436638, TU-94-2×ABFBG-23RS, TU-94-2×LBG-20, MBG-207×LBG-20, LBG-

752×ABFBG -23RS, LBG-752×ABFBG-26RD and LBG-752×LBG-20 for plant height. The negative heterosis for days to 50% flowering and days to maturity was desirable for development of earliness and short stature plant type. The cross TBG-104×IC-436638 had recorded significant positive standard heterosis and average heterosis. Number

Table 4: Heterosis over mid parent (MP), better parent (BP) and standard check (SC) for seed yield and yield components in blackgram (*Vigna mungo* L.)

Crosses	Days to 50% flowering			Days to maturity			Plant Height (cm)			Number of clusters plant^{-1}		
	MP	BP	SC	MP	BP	SC	MP	BP	SC	MP	BP	SC
GBG-1×IC-436638	1.53	0.00	-4.32*	0.24	-0.47	-1.85	20.58**	15.12**	-5.87	-0.48	-0.96	-14.17
GBG-1×ABFBG-23RS	3.37	2.99	-0.72	2.36	1.40	0.46	10.71**	-2.41	-4.87	-1.15	-18.35*	7.50
GBG-1×ABFBG-26RD	1.12	0.75	-2.88	1.86	-0.45	1.39	-5.76	-13.27**	-23.29**	1.17	-2.26	-10.00
GBG-1×LBG-20	-5.45**	-8.45**	-6.47**	-0.96	-1.43	-4.17*	-19.39**	-25.10**	-35.11**	-4.04	-10.83	-10.83
MBG-1070×IC-436638	8.88**	8.46**	1.44	-2.35	-2.35	-3.70*	9.87*	8.72*	-11.10**	-2.13	-12.21	-4.17
MBG-1070×ABFBG-23RS	5.30**	3.73	0.00	-1.17	-1.40	-2.31	5.13	-4.26	-6.68	-30.10**	-36.08**	-15.83
MBG1070×ABFBG-26RD	1.52	0.00	-3.60	-4.39**	-5.91**	-4.17*	-7.87*	-12.24**	-22.38**	-34.16**	-39.31**	-33.75**
MBG-1070×LBG-20	-4.41*	-8.45**	-6.47**	-1.19	-2.35	-3.70*	-3.95	-7.60	-19.95**	-34.66**	-37.40**	-31.67**
TBG-104×IC-436638	2.31	1.53	-4.32*	-1.40	-2.30	-1.85	14.66**	14.54**	-6.14	23.53*	9.70	22.50*
TBG-104×ABFBG-23RS	1.89	0.75	-2.88	3.02*	2.30	2.78	-0.91	-8.80*	-11.10**	-50.68**	-54.43**	-40.00**
TBG-104×ABFBG-26RD	5.66**	4.48*	0.72	-1.60	-2.27	-0.46	4.87	1.02	-10.65**	-37.01**	-42.54**	-35.83**
TBG-104×LBG-20	-4.76*	-8.45**	-6.47**	0.24	-1.84	-1.39	9.21*	6.25	-7.94*	-18.90*	-23.13*	-14.17
TU-94-2×IC-436638	-1.53	-3.01	-7.19**	5.44**	4.69**	3.24*	-21.45**	-26.14**	-31.41**	-17.54	-18.69	-27.50*
TU-94-2×ABFBG-23RS	-2.62	-2.99	-6.47**	0.47	-1.40	-2.31	-23.66**	-25.46**	-27.35**	-23.02**	-35.44**	-15.00
TU-94-2×ABFBG 26RD	-2.62	-2.99	-6.47**	-2.33	-4.55**	-2.78	-0.45	-2.82	-9.75**	-4.37	-5.88	-13.33
TU-94-2×LBG-20	1.09	-2.11	0.00	1.91	1.43	-1.39	-6.99*	-10.11*	-16.52**	-23.35*	-27.50*	-27.50*
MBG-207×IC436638	2.70	2.31	-4.32*	4.76**	3.29*	1.85	-7.20	-10.22*	-21.48**	-25.64**	-33.08**	-27.50*
MBG-207×ABFBG -23RS	5.30**	3.73	0.00	2.61	0.93	0.00	6.39	0.93	-1.62	-44.44**	-49.37**	-33.33**
MBG-207×ABFBG-26RD	3.79*	2.24	-1.44	-2.11	-5.00**	-3.24*	-4.05	-4.59	-15.61**	-6.03	-13.08	-5.83
MBG-207×LBG-20	-2.21	-6.34**	-4.32*	1.69	1.44	-2.31	-10.83**	-11.25**	-22.38**	-4.80	-8.46	-0.83
LBG-752×IC-436638	2.99	-0.72	-0.72	0.23	-0.46	-0.46	9.14**	-0.81	-0.81	8.48	1.25	1.25
LBG-752×ABFBG-23RS	-0.37	-2.16	-2.16	0.47	0.00	0.00	-17.73**	-18.77**	-18.77**	-29.50**	-37.97**	-18.33
LBG-752×ABFBG-26RD	-2.56	-4.32*	-4.32*	-2.29	-3.18*	-1.39	-13.31**	-18.32**	-18.32**	-8.89	-12.50	-12.50
LBG-752×LBG-20	-3.20	-4.23*	-2.16	0.00	-1.85	-1.85	-22.63**	-27.80**	-27.80**	6.67	6.67	6.67

Table 4: Continue...

Crosses	Number of pods plant^{-1}			Pod length (cm)			Number of seeds pod^{-1}			100 seed weight (g)		
	MP	BP	SC	MP	BP	SC	MP	BP	SC	MP	BP	SC
GBG-1×IC-436638	42.62**	23.79**	19.72**	-9.09	-11.29*	-1.79	21.64*	16.85	6.12	-10.69**	-15.22**	14.71*
GBG-1× ABFBG-23RS	-22.07**	-22.30**	-24.41**	-7.96*	-19.39**	18.75**	-1.08	-4.69	-6.63	-11.84**	-12.90**	5.88
GBG-1× ABFBG-26RD	-15.29*	-20.39**	-23.00**	6.67	-3.23	7.14	-7.30	-7.30	-15.82	-24.48**	-26.61**	-10.78
GBG-1×LBG-20	-20.97**	-27.53**	-15.96*	-13.58**	-15.32**	-6.25	-1.62	-5.21	-7.14	-20.50**	-23.39**	-6.86
MBG-1070× IC-436638	17.43*	-3.25	6.29	-0.42	-0.84	5.36	-1.69	-8.42	-11.22	-8.89*	-10.87*	20.59**
MBG-1070× ABFBG-23RS	-29.37**	-33.42**	-26.85**	-16.20**	-27.88**	6.25	-21.47**	-21.88*	-23.47**	-17.79**	-21.21**	1.96
MBG1070× ABFBG-26RD	-1.73	-12.82	-4.23	5.45	-2.52	3.57	-9.24	-12.11	-14.80	-14.86**	-19.70**	3.92
MBG-1070×LBG-20	-8.11	-10.53	3.76	9.24	9.24	16.07**	-16.23*	-16.67	-18.37*	-19.03**	-24.24**	-1.96
TBG-104× IC-436638	7.72	-12.40	-0.47	25.82**	13.56*	19.64**	6.44	-1.55	-3.06	-10.84*	-19.57**	8.82
TBG-104× ABFBG-23RS	8.64	0.83	14.55*	-14.62**	-32.73**	-0.89	-16.88*	-17.10*	-18.37*	6.03	1.65	20.59**
TBG-104× ABFBG-26RD	9.64	-4.13	8.92	21.43**	17.82**	6.25	-12.67	-16.06	-17.35*	-22.81**	-24.79**	-13.73*
TBG-104×LBG-20	-16.56**	-17.41**	-4.23	-11.21*	-20.17**	-15.18*	-22.08**	-22.28*	-23.47**	-11.50*	-13.04*	-1.96
TU-94-2×IC-436638	37.60**	20.54**	14.08	10.29*	7.20	19.64**	-9.25	-13.74	-19.90*	-19.69**	-26.09**	0.00
TU-94 2×AB FBG-23RS	21.3^{3}**	19.69*	16.43*	-9.66*	-20.61**	16.96**	-11.23	-13.54	-15.31	-1.27	-3.31	14.71*
TU-94-2×ABF BG26RD	39.50**	32.44**	25.35**	10.62*	0.00	11.61	-16.67*	-17.58	-23.47**	11.59*	11.11*	27.45**
TU-94-2×LBG-20	-23.32**	-30.36**	-19.25*	-4.10	-6.40	4.46	6.95	4.17	2.04	17.75**	17.24**	33.33**
MBG-207×IC436 638	39.38**	17.03*	22.63**	5.79	3.23	14.29*	13.64	6.38	2.04	-10.32*	-18.12**	10.78
MBG-207×ABF BG-23RS	3.16	-0.54	4.23	-32.87**	-41.21**	-13.39*	10.53	9.37	7.14	-9.79*	-12.40*	3.92
MBG-207×ABF BG-26RD	-3.17	-12.28	-8.08	-3.11	-12.10*	-2.68	-1.64	-4.26	-8.16	-20.35**	-21.37**	-9.80
MBG-207×LBG-20	-18.33**	-22.27**	-9.86	-4.53	-6.45	3.57	-4.74	-5.73	-7.65	10.92*	10.43*	24.51**
LBG-752×IC-436638	8.61	-7.04	-7.04	15.65**	12.71*	18.75**	-19.44*	-26.02**	-26.02**	-0.83	-13.77**	16.67**
LBG-752×ABF BG-23RS	21.37**	19.72**	19.72**	-11.19**	-25.45**	9.82	-29.90**	-30.61**	-30.61**	-10.31*	-17.36**	-1.96

Table 4: Continue...

Crosses	Number of pods plant^{-1}			Pod length (cm)			Number of seeds pod^{-1}			100 seed weight (g)		
	MP	BP	SC	MP	BP	SC	MP	BP	SC	MP	BP	SC
LBG-752×ABFBG-26RD	-13.75*	-20.19**	-20.19**	17.37**	11.61	11.61	6.95	2.04	2.04	-1.37	-7.69	5.88
LBG-752×LBG-20	-13.91*	-19.84**	-7.04	16.02**	12.61*	19.64**	-16.49*	-17.35*	-17.35*	-7.83	-13.04*	-1.96

of pods plant^{-1} had shown significant positive standard heterosis, heterobeltiosis and average heterosis for crosses GBG-1×IC-436638, TU-94-2×ABFBG-23RS, TU-94-2×ABFBG-26RD,MBG-207×IC-436638 and LBG-752×ABFBG-23RS. The crosses TBG-104×IC-436638, TBG-104×ABFBG-26RD, LBG-752×IC436638 and LBG752×LBG-20 had shown significant for average heterosis, heterobeltiosis and standard heterosis. The cross GBG-1×IC-436638 had recorded significant positive for average heterosis while none of the crosses recorded significant for heterobeltiosis and standard heterosis. For 100 seed weight, the crosses TU-94-2×ABFBG-26RD, TU-94-2×LBG-20 and MBG-207×LBG-20 were found significant positive for average heterosis, heterobeltiosis and standard heterosis, whereas the GBG-1×IC-436638, MBG-1070×IC-436638, TBG-104×ABFBG-23RS. TU-34-2×ABFBG-23RS and LBG-752×IC-436638 has recorded significant for only standard heterosis. None of the crosses have recorded significant positive average heterosis, heterobeltiosis and standard heterosis for harvest index. For the trait seed yield plant^{-1}, crosses GBG-1×LBG-20 (26.11**),TBG-104×IC-436638 (20.20**), TU94-2×LBG-20 (15.27**) and MBG-207×ABFBG-23RS (20.69**) recorded significant positive standard heterosis. The similar results were recorded by Bhagirath et al. (2013), Kumar et al. (2017) and Debbarma et al. (2022). Results of heterosis indicated that majority of the crosses having high SCA effects also exhibited high heterosis. The cross TBG-104×IC-436638 recorded high estimates of heterosis for plant height, number of clusters plant^{-1}, pod length, biological yield and seed yield plant^{-1}. The crosses showing significant SCA effects had also better chances for producing transgressive segregates. The heterosis for seed yield plant^{-1} could be attributed mainly to the manifestation of heterosis in the component characters like plant height, days to 50% flowering, number of pods plant^{-1}, pod length and 100 seed weight. Similar results were also recorded by Ramakant et al. (2012), Yashpal et al. (2015), Thamodharan et al. (2016) and Kumar et al. (2017). All the crosses with high heterosis involved either one high GCA and low GCA line or tester. Based on the mean performance, combining ability and heterosis, the superior crosses identified were TBG-104×IC-436638, TU-94-2×ABFBG-26RD and GBG-1×LBG-20 and these crosses could be utilized in future breeding programmes.

4. CONCLUSION

The variance due to SCA was higher than variance due to GCA in most of the traits indicated predominance of non-additive gene effect. The lines TU-94-2, MBG-207, GBG-1 and in testers IC-436638 and ABFBG-23RS could be utilized to develop pure line varieties. The crosses viz., TBG-104×IC-436638, MBG-1070×LBG-20, TU-94-2×ABFBG-26RD and TU-94-2×LBG-20 have shown significant SCA effect for seed yield plant^{-1} and these crosses could be used in future breeding programs. The hybrid TBG-104×IC-436638 recorded high estimates of heterosis for seed yield plant^{-1} and also for most of the important characters and could be used for heterosis breeding more effective than FYM most characteristics, particularly in berry-related traits.

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