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Heterosis and combining ability studies for yield and yield components in blackgram (*Vigna Mungo* L. Hepper) under different environmental conditions of Prayagraj region, India

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Abstract
Twenty one crosses of blackgram were produced in line x tester fashion, the F_1 crosses along with the parents were grown during *kharif* (timely sown, late sown) and *zaid* (timely sown, late sown) to assess heterosis and combining ability for yield and yield components over different environments. The pooled analysis of variance revealed significant variability for crosses, environments, environment x crosses and environments x line x tester effect for all characters. Two lines UTTARA and KU 96-3 were identified as good general combiners for seed yield which can serve as parental lines in crop improvement programme. Among 21 crosses, three crosses *viz.*, MASH 338 × PU 31, UH 82-23 × M 1-1 and UTTARA × PU 31 exhibited positive significant relative heterosis and heterobeltiosis, as well as significant specific combining ability for seed yield. Hence, these crosses can be utilized for seed yield improvement through recurrent selection.

Keywords: Blackgram, line x tester, heterosis, gca, sca and seed yield

Introduction

Pulses occupy a unique position in the world of agriculture by virtue of its high protein content, which is almost double of cereals (Gowda *et al*., 2014) [5], and the demand of vegetarian population can be fulfilled hence also considered as "A poor man's meat". Besides, nutritive value food legumes tend to fix atmospheric nitrogen to N-compounds upto 72—350 kg per hectare per year and provide soil cover that helps to sustain soil health. Considering blackgram, a self-pollinated pulse crop contains 24% protein, 60% carbohydrates, 1.3% fat and is the richest source of phosphoric acid among pulses (5-6% richer than others). In India, blackgram accounts for 13% total pulses area and 10% total pulses production. In order to meet the domestic consumption requirement, 2-3 million tonnes of pulses are imported annually (Sakila and Pandiyan, 2018) [11]. Thus, there is a need to increase production and productivity of pulses in order to provide adequate food to burgeoning population to combat hunger and malnutrition in the years to come.

The lower productivity in blackgram is one of the constraints for large scale production. To increase the production and productivity of blackgram it is essential to develop a high yielding pureline variety by selection from segretating generations of superior crosses involving superior parents. (Vijay Kumar *et al.,* 2017) [18]. The success of breeding procedure is determined by useful gene combinations, gca and sca would provide very useful information of gene action and helps in deciding the breeding procedure for genetic improvement of such traits (Kachave *et al.,* 2015) [15]. Exploitation of hybrid vigour of F_1's helps in production of superior crosses, presented in terms of heterosis (superiority of F1 over its mid-parent) and heterobeltiosis (superiority over its better parent) (Soehend and Srinivas, 2005) [13]. Keeping in view the necessity in finding out superior heterotic crosses, this study is conducted with the objective to identify superior cross combinations through line x tester fashion and estimating the extent of heterosis.

Materials and Methods

Ten blackgram genotypes containing seven lines *viz.*, UTTARA, DPU 88-31, MASH 338, AZAD-1, VALLABH URD, KU 96-3 and UH 82-23, three testers *viz.*, M 1-1, PU 19 and PU 31 were used as parents in the crossing programme (line x tester design as per Kempthrone, 1957) [7]. The total entries 21 F_1's and 10 parents planted in Randomized Block Design (RBD) comprising of three replications were sown during *Kharif* (Timely, Late) comprising of three replications were sown during *Kharif* (Timely, Late) and *Zaid* (Timely, Late) 2016-2017 at

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Field Experimentation Centre of Department of Genetics and Plant Breeding, Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj, Uttar Pradesh. Each row of 1m length consisting of 10 plants with spacing 30cm row to row and 10cm plant to plant was maintained. Recommended package of practices were followed to raise a healthy crop.

Data were recorded on days to 50% flowering, branches/plant, clusters/plant, 100 seed weight, harvest index, seed yield/plant and protein content (Lowry et al., 1951) [8]. The seed yield and yield attributes data over environments were analysed for line × tester analysis as proposed by Kempthrone (1957) [7], relative heterosis (Turner, 1953) [16] and heterobeltiosis.

Results and discussions
The analysis of variance mean sum of squares due to crosses, environments, environments × crosses and environments × lines × testers exhibited significance for all the characters. Line × tester effect was also significant for all the characters, indicating the presence of sufficient genetic diversity among the genotypes, presented in Table 1.

The range of relative heterosis varied from -26.89** to 49.03** and heterobeltiosis from -33.61** to 44.86** for seed yield/plant (Table 3). Six crosses among twenty one crosses exhibited positive significance for both relative heterosis and heterobeltiosis. Among these six crosses, the top crosses exhibiting high positive significance for both relative heterosis and heterobeltiosis were UTTARA × PU 31, UH 82-23 × M 1-1, UTTARA × M 1-1, KU 96-3 × PU 19 and MASH 338 × PU 31. These results are in accordance with the results of Beena Thomas et al. (2008) [1] and Bhagirath Ram et al. (2013) [2] observing high heterosis for seed yield. The cross UTTARA × PU 31 also observed positive significant relative heterosis and heterobeltiosis for yield attributes clusters/plant (29.97**, 16.94*), 100 seed weight (20.36**, 20.31**) (Table 2), harvest index (14.02**, 7.15*), earliness in flowering (-13.85**, -20.45 **) along with significant protein content (7.71**, 5.38**). Similar findings are also carried out by Beena Thomas et al. (2008) [1], Rama Kant and Srivastava, (2012) [10], Srivastava and Singh, (2013) [14] and Suguna et al. (2017) [15].

Table 1: Analysis of variance for seed yield and components pooled over environments in blackgram

Source of variation	df	Days to 50% flowering	Branches/ plant	Clusters/ plant	100 seed weight	Harvest index	Seed yield/ plant	Protein content
Replication	2	4.20	0.08	6.06*	0.003	1.50	2.26	0.05
Environments	3	412.55**	3.51**	294.05**	13.18**	190.27**	243.58**	49.73**
Crosses	20	22.85**	0.81**	18.10**	0.85**	66.41**	12.15**	8.53**
Line effect	6	41.24*	0.68	29.02	1.26*	134.33*	18.00	13.60
Tester effect	2	43.00*	0.87	5.32	2.26*	0.97	3.51	7.95
Line × tester effect	12	10.30**	0.86**	14.78**	0.41**	43.36**	10.67**	6.10**
Env × crosses	60	4.97**	1.13**	7.82**	0.51**	32.11**	7.61**	5.62**
Env × L × T effect	36	5.51**	0.84**	7.71**	0.32**	34.92**	7.31**	6.13**
Error	240	2.40	0.03	1.43	0.07	2.47	1.18	0.16

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

Table 2: Estimates of relative heterosis% (Ha) and Heterobeltiosis% (Hb) pooled over environments for days to 50% flowering, branches/plant, clusters/plant and 100 seed weight

Crosses	Days to 50% flowering		Branches/plant		Clusters/plant		100 seed weight	
	Ha	Hb	Ha	Hb	Ha	Hb	Ha	Hb
UTTARA × M 1-1	-9.42**	-10.70 **	11.98 **	-1.81	8.75	-9.86	19.73**	17.58**
UTTARA × PU 19	-9.73**	-15.33**	16.55 **	15.71 **	29.51**	25.14**	15.28**	12.96**
UTTARA × PU 31	-13.85**	-20.45 **	-10.29 **	-10.29 **	29.97**	16.94*	20.36**	20.31**
DPU 88-31 × M 1-1	-3.67	-6.42*	14.40 **	9.39 *	23.65**	4.28	34.46**	30.89**
DPU 88-31 × PU 19	-2.77	-7.51 *	7.87 **	-2.14	7.32	5.90	26.65**	25.20**
DPU 88-31 × PU 31	-0.40	-6.76 *	-22.62 **	-29.35 **	-14.30*	-21.39**	34.43**	33.18**
MASH 338 × M 1-1	-20.00**	-22.30 **	2.04	-11.35 **	21.62**	0.26	9.74**	5.39
MASH 338 × PU 19	-11.57**	-15.27**	-3.20	-3.55	-18.53**	-21.80**	15.24**	14.96**
MASH 338 × PU 31	-9.33**	-14.52**	12.54 **	11.35 **	39.96**	25.16**	27.33**	24.42**
AZAD-1 × M 1-1	-4.07	-6.47 *	40.16 **	22.14 **	85.92**	63.68**	14.93**	4.19
AZAD-1 × PU 19	4.76	0.00	-5.00	-5.00	-3.87	-7.36	30.98**	23.04**
AZAD-1 × PU 31	-0.82	-6.82 *	12.95 **	12.14 **	17.38*	12.96	29.24**	19.07**
VALLABHURD × M 1-1	6.51*	0.01	-9.66 **	-18.12 **	17.11*	7.48	13.81**	9.72**
VALLABHURD × PU 19	-6.62*	-7.38*	-2.09	-6.29 *	3.04	-4.99	14.21**	14.02**
VALLABHURD × PU 31	2.52	0.00	-18.80 **	-21.74 **	-11.78	-12.47	23.59**	21.24**
KU 96-3 × M 1-1	2.63	-2.15	24.30 **	20.91 **	36.94**	16.55*	21.98**	19.75**
KU 96-3 × PU 19	2.44	0.00	30.16 **	16.21 **	9.72	9.46	13.74**	11.49**
KU 96-3 × PU 31	1.64	-2.38	27.42 **	14.49 **	11.73	3.55	21.18**	21.09**
UH 82-23 × M 1-1	-1.09	-1.43	16.19 **	3.86	52.07**	49.35**	38.12**	29.54**
UH 82-23 × PU 19	1.55	-5.07	13.31 **	10.07 **	8.37	-6.18	34.55**	30.96**
UH 82-23 × PU 31	3.92	-4.35	4.07	1.81	17.49*	8.86	18.00**	12.56**

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

Table 3: Estimates of relative heterosis% (Ha) and Heterobeltiosis% (Hb) pooled over environments for harvest index, seed yield/plant and protein content

Crosses	Harvest index		Seed yield/pant		Protein content	
	Ha	Hb	Ha	Hb	Ha	Hb
UTTARA × M 1-1	-0.37	-1.06	35.73**	27.53**	-3.02*	-7.25**
UTTARA × PU 19	5.79*	-2.82	16.12*	15.97*	2.44	1.53
UTTARA × PU 31	14.02**	7.15*	49.03**	44.86**	7.71**	5.38**
DPU 88-31 × M 1-1	10.02**	9.44**	27.83**	12.52	6.94**	3.21*
DPU 88-31 × PU 19	-3.10	-10.85**	17.42*	9.40	-3.65*	-3.65*
DPU 88-31 × PU 31	-8.56**	-13.93**	-26.89**	-33.61**	22.35**	18.61**
MASH 338 × M 1-1	6.73**	1.64	19.21**	3.23	-3.22*	-6.20**
MASH 338 × PU 19	-7.29**	-10.14**	-9.95	-17.56*	3.59*	3.13*
MASH 338 × PU 31	10.36**	9.59**	27.61**	22.46**	-7.20**	-10.42**
AZAD-1 × M 1-1	1.30	-5.14	-4.04	-17.86*	5.60**	2.98
AZAD-1 × PU 19	-3.57	-4.88	13.06	2.22	-2.59	-3.62*
AZAD-1 × PU 31	-1.03	-2.09	6.44	-6.12	3.52*	-0.68
VALLABHURD × M 1-1	15.59**	12.00**	-2.67	-5.77	10.15**	2.57
VALLABHURD × PU 19	-8.83**	-18.11**	5.66	2.53	11.22**	7.16**
VALLABHURD × PU 31	-27.26**	-33.20**	2.64	2.39	18.94**	18.19**
KU 96-3 × M 1-1	-3.62	-8.28**	23.45**	11.23	6.15**	4.64**
KU 96-3 × PU 19	12.05**	8.68**	31.36**	25.48**	-6.33**	-8.32**
KU 96-3 × PU 31	-10.94**	-11.50**	12.44	4.61	2.29	-2.88
UH 82-23 × M 1-1	6.14	3.90	33.44**	32.98**	4.07**	-2.66
UH 82-23 × PU 19	-7.52**	-12.77**	11.20	4.92	14.53**	10.86**
UH 82-23 × PU 31	-15.22**	-18.13**	2.70	-0.48	13.01**	12.83**

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

The significant gca for seed yield was observed in two lines *viz.*, UTTARA and KU 96-3 whereas no testers observed significant gca effects (Table 4)**.** The line UTTARA also exhibited positive significant gca for clusters/plant, 100 seed weight, harvest index and protein content, whereas line KU 96-3 showed positive significance for clusters/plant. Similar findings were observed by Vijay Kumar *et al.* (2017) [18]. Line MASH 338 and tester PU 31 observed negative significant gca effect for days to 50% flowering. Among ten parental lines, four lines *viz.*, UTTARA, DPU 88-31, VALLABH

URD and UH 82-23 and two testers *viz.*, M 1-1, PU 31 showed significant positive gca for protein content, whereas one line MASH 338 and one tester M 1-1 for branches/plant, three lines *viz.*, UTTARA, AZAD-1 and KU 96-3 for clusters/plant, three lines *viz.*, UTTARA, DPU 88-31 and MASH 338 and two testers *viz.*, M 1-1 and PU 31 for 100 seed weight and three lines *viz.*, UTTARA, MASH 338 and AZAD-1 for harvest index exhibited positive significant gca effects. Similar results were reported by Narsimhulu *et al.* (2014) [9].

Table 4: General combining ability for seed yield and components in blackgram - pooled over environments

Lines	Days to 50% flowering	Branches/ plant	Clusters/ plant	100 seed weight	Harvest index	Seed yield/ plant	Protein content
UTTARA	-0.35	0.03	0.60*	0.13*	1.74**	0.87**	0.34**
DPU 88-31	-0.08	-0.24**	-0.66*	0.25**	-0.92*	-0.51*	0.39**
MASH 338	-1.66**	0.22**	0.31	0.12*	2.14**	0.19	-1.01**
AZAD-1	0.54*	0.03	1.05**	0.04	1.94**	0.35	-0.48**
VALLABH URD	-0.33	0.02	-1.47**	-0.25**	-2.80**	-1.09**	0.76**
KU 96-3	-0.02	-0.06*	0.67*	-0.05	-0.79*	0.65**	-0.30**
UH 82-23	1.90**	-0.003	-0.50*	-0.23**	-1.31**	-0.45*	0.29**
M 1-1	0.81**	0.09**	0.24	0.12**	-0.05	0.05	0.17**
PU 19	-0.28	0.02	0.01	-0.19**	0.12	0.17	-0.36**
PU 31	-0.53*	-0.11**	-0.26	0.07*	-0.08	-0.23	0.18**
CD 95% GCA (testers)	0.34	0.04	0.27	0.07	0.36	0.24	0.09
CD 95% GCA (lines)	0.52	0.05	0.42	0.10	0.54	0.36	0.14

Positive and significant sca for seed yield was exhibited by five crosses *viz.*, UTTARA × PU 31, DPU 88-31 × PU 19, MASH 338 × PU 31, AZAD-1 × PU 19 and UH 82-23 × M 1-1, significant sca for branches/plant was observed in eight crosses *viz.*, UTTARA × PU 19, DPU 88-31 × M 1-1, MASH 338 × PU 31, AZAD-1 × M 1-1, VALLABHURD × M 1-1, VALLABHURD × PU 19, KU 96-3 × PU 31 and UH 82-23 × M 1-1, for clusters/plant in five crosses *viz.*, UTTARA × PU 31, DPU 88-31 × PU 19, MASH 338 × PU 31, AZAD-1 × M 1-1 and UH 82-23 × M 1-1, for 100 seed weight in two crosses *viz.*, DPU 88-31 × PU 31 and KU 96-3 × M 1-1, for harvest index in seven crosses *viz.*, UTTARA × PU 31, DPU

88-31 × PU 19, MASH 338 × PU 31, AZAD-1 × PU 19, VALLABHURD × M 1-1, KU 96-3 × PU 19 and UH 82-23 × M 1-1, for protein content in nine crosses *viz.*, UTTARA × PU 19, UTTARA × PU 31, DPU 88-31 × M 1-1, DPU 88-31 × PU 31, MASH 338 × M 1-1, AZAD-1 × M 1-1, VALLABHURD × PU 31, UH 82-23 × PU 19 and UH 82-23 × PU 31 presented in Table 5.

In the present study high significant sca for seed yield was observed in UTTARA × PU 31 and also exhibited best *per se* performance due to significant gca of the parent UTTARA. It indicates that additive gene action was predominant in the genetic control of seed yield/plant. Similar results were

reported by Das and Das Gupta, (1999) [4] in sesame and Chakraborty *et al*. (2010) [3] in blackgram. While the other crosses MASH 338 × PU 31 and AZAD-1 × PU 19 showed significant sca for seed yield but the parents of these crosses had non-significant gca effect. It indicates that in these crosses, non-additive gene action was predominant for seed yield. Ushakumari *et al*. (2010) [17], Sathya and Jayamani, (2011) [12], Vijay Kumar *et al*. (2014) [19] and Kachave *et al*. (2015) [6] reported similar findings in blackgram.

Conclusion
From the present study it is concluded that crosses UTTARA × PU 31, MASH 338 × PU 31 and UH 82-23 × M 1-1 were considered promising for yield improvement programme as they excelled in significant heterosis along with significant sca for seed yield and yield attributes. Two lines *viz.*, UTTARA and KU 96-3 were identified as good general combiners and can be used in future hybridization programme.

Table 5: Specific combining ability estimates for seed yield and components in blackgram - pooled over environments

Crosses	Days to 50% flowering	Branches /plant	Clusters/ plant	100 seed weight	Harvest index	Seed yield/ plant	Protein content
UTTARA × M 1-1	-0.31	-0.21**	-1.55**	0.07	-1.25*	-0.73*	-0.78**
UTTARA × PU 19	0.20	0.17**	0.59	0.02	0.001	-0.18	0.47**
UTTARA × PU 31	0.12	0.04	0.96*	-0.09	1.25*	0.91*	0.32*
DPU 88-31 × M 1-1	-0.17	0.39**	0.02	-0.07	-0.52	0.54	0.29*
DPU 88-31 × PU 19	0.003	-0.11*	0.77*	-0.12	1.69**	0.68*	-0.65**
DPU 88-31 × PU 31	0.17	-0.28**	-0.79*	0.19*	-1.17*	-1.22**	0.36*
MASH 338 × M 1-1	-0.67	-0.26**	-0.45	-0.27*	-0.30	-0.13	0.87**
MASH 338 × PU 19	0.92*	-0.07	-1.09*	0.16	-2.41**	-1.22**	-0.08
MASH 338 × PU 31	-0.25	0.33**	1.54**	0.11	2.71**	1.36**	-0.79**
AZAD-1 × M 1-1	-0.87	0.11*	1.47**	-0.11	-1.92**	-0.95*	0.76**
AZAD-1 × PU 19	1.14*	-0.14*	-0.45	0.06	1.06*	0.81*	0.13
AZAD-1 × PU 31	-0.27	0.02	-1.02*	0.05	0.85	0.14	-0.89**
VALLABHURD × M 1-1	1.91**	0.13*	-0.18	-0.03	1.90**	0.22	-0.36*
VALLABHURD × PU 19	-1.41*	0.14*	0.71	0.04	-1.47*	-0.22	-0.13
VALLABHURD × PU 31	-0.50	-0.27**	-0.54	-0.01	-0.43	0.004	0.50**
KU 96-3 × M 1-1	0.19	-0.31**	-0.30	0.30*	0.04	0.05	0.15
KU 96-3 × PU 19	-0.55	0.01	-0.18	-0.24*	1.00*	0.25	-0.17
KU 96-3 × PU 31	0.37	0.30**	0.48	-0.06	-1.04*	-0.31	0.02
UH 82-23 × M 1-1	-0.06	0.13*	0.99*	0.12	2.04**	1.01*	-0.93**
UH 82-23 × PU 19	-0.30	-0.01	-0.36	0.08	0.13	-0.12	0.43**
UH 82-23 × PU 31	0.37	-0.13*	-0.64	-0.20*	-2.17**	-0.89*	0.49**
CD 95% SCA	0.90	0.09	0.73	0.18	0.94	0.63	0.24

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