

## Estimation of genetic parameters and combining ability analysis in blackgram [*Vigna mungo* (L.) Hepper]

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Received: 12-09-2015

Accepted: 23-12-2015

DOI:10.18805/lr.v0iOF.9598

### ABSTRACT

An experiment was carried out in blackgram using line x tester mating design to estimate the *gca* effect of parents (six lines and five testers) and *sca* effect of 30 hybrids for yield and its traits. Estimates of *gca* and *sca* variances, degree of dominance, predictability ratio and narrow sense heritability revealed that only three traits *viz.*, pods per plant, seeds per pod and single plant yield were controlled by additive gene action and hence showed high narrow sense heritability. Magnitude of non-additive gene action was higher than the additive gene action for traits like plant height, days to 50% flowering, cluster per plant, 100 seed weight, days to maturity, branches per plant and pod length. Three parents 'MDU1, ADT3 and LBG-752 were the best combiners and three crosses 'MDU1 x VBN (Bg) 6, LBG-752 x VBN (Bg) 6, LBG-752 x Mash-114 showed high *per se* performance and significant positive *sca* for yield. For exploiting both additive and non-additive gene action recurrent selection to be followed to improve yield in blackgram.

**Key words:** Additive, Narrow sense heritability, Non-additive, Predictability ratio, *sca* and *gca* effect.

### INTRODUCTION

Blackgram [*Vigna mungo* (L.) Hepper] is a self-pollinating diploid ( $2n=2x=22$ ) annual crop with a small genome size of 574Mbp (Kachave *et al.*, 2015). It is also known as urdbean and is considered as third important pulse crop after chickpea and pigeonpea, which is grown in various agro ecological conditions and season under diverse cropping system. It is grown over an area of around 3.26 million ha with annual production of 1.76 million tones (Soren *et al.*, 2012). Major blackgram cultivating states are Tamil Nadu, Andhra Pradesh, Karnataka, Maharashtra, Rajasthan and Uttar Pradesh (Bhagirath Ram *et al.*, 2010). The under production of blackgram in the country posed the situation of importing blackgram from other countries like Srilanka, Malaysia and Thailand to fulfill the dietary requirement of our present population (Girish *et al.*, 2012). To fulfill the national demands there is a need to adapt a comprehensive crop improvement programmes to develop a variety which is adapted to various agro climatic conditions. Choice of better parents for crop improvement programme and selecting of suitable hybrids of our choice is based mainly on test for their combining ability effects, general combining ability (*gca*) of parents and specific combining ability (*sca*) of hybrids. The present study was aimed to estimate the gene action and to select suitable parent and breeding procedure for effective crop improvement programme.

### MATERIALS AND METHODS

This study was conducted at Agricultural College and Research Institute, Madurai during *kharif*-2014 and *rabi*-

2015. Seeds of eleven black gram parental materials adapted to diverse agro climatic conditions, which comprises six lines, *viz.*, ADT3, MDU1, CO6, LBG-752, ADT5, and KUG-688 and five testers, *viz.*, VBN (Bg) 4, VBN (Bg) 6, Mash-114, Ultra and PU-31 were collected from National Pulses Research Station, Vamban and Pulses Department, Tamil Nadu Agricultural University, Coimbatore. Crosses were effected during *kharif*-2014 by hand emasculation and pollination method in LXT mating design (Kempthorne, 1957). The  $F_1$ s and their parents were studied during, *rabi*-2015 to analyse their performance for yield and its traits. Seeds of 30  $F_1$ s and 11 parents (in adjacent rows) were sown at a spacing of 30x10 cm in 2 x 2m plot in randomized complete block design (RBD) with two replications. Observations on twelve yield and its traits were recorded on both  $F_1$ s and parents. The mean values of all the quantitative traits were worked out and analysed using TNAU STAT, LXT software package to get the information on relative contributions of genetic components determined to obtain estimates of *gca* variance ( $\sigma_{gca}^2$ ) and *sca* variance ( $\sigma_{sca}^2$ ) for each character. Additive variance ( $\sigma_A^2$ ) and dominance variance ( $\sigma_D^2$ ) were estimated as  $\sigma_A^2 = 2(\sigma_{gca}^2)$  and  $\sigma_D^2 = (\sigma_{sca}^2)$ . Genotypic variance ( $\sigma_g^2$ ) and phenotypic variance ( $\sigma_p^2$ ) were also calculated as  $\sigma_g^2 = \sigma_A^2 + \sigma_D^2$ , and  $\sigma_p^2 = \sigma_g^2 + \sigma_e^2$ . Heritability in the narrow ( $h^2_{ns}$ ) sense was calculated from the estimated components of variances as;  $h^2_{ns} = \sigma_a^2 / \sigma_p^2$ . The relative size of variances due to *gca* and *sca* on progeny performance were estimated following Baker's predictability ratio (PR) as  $PR = 2 \sigma_{gca}^2 / 2(\sigma_{gca}^2 + \sigma_{sca}^2)$

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(Baker, 1978). The average degree of dominance was estimated as  $\sqrt{H/D} = \sqrt{\sigma_{sca}^2 / \sigma_{gca}^2}$  (Singh and Chaudhary, 1979).

## RESULTS AND DISCUSSIONS

**Analysis of variance:** The analysis of variance of line x tester analysis for eleven yield and its attributing traits were presented in Table 1. The ANOVA revealed that the mean squares due to genotypes and parents were differed among themselves at  $p=0.01$  or  $0.05$  for yield and yield attributes including single plant yield, except for four traits *viz.*, plant height, clusters per plant, pods per plant and seeds per pod the parents were not signified. Lines were differed among themselves at  $0.05$  probabilities for branches per plant, days to 50 per cent flowering, seeds per pod and pod length and at  $0.01$  propability level significant for 100 grain weight and single plant yield. Whereas, testers were differed for days to 50 per cent flowering, days to maturity and seeds per pod at  $0.05$  per cent significant level and for pod length, 100 grain weight and single plant yield attributing traits signified at  $0.01$  per cent probability level. The mean squares due line x tester interaction signified for important yield attributing traits such as was similar to that of lines and testers for six traits. This revealed that excerpt seeds per pod, all the traits show significant variation was controlled by both additive and non-additive type of genetic component but former one was may governs by additive type of gene action (Cheralu *et al.*, 1999). The significant differences among different genotypes of urdbean and their F1 hybrids for grain yield and other component traits in different sets of material were also reported by Singh Mohar (2008) and Baradhan and Thangavel, 2011, Govindaraj and Subramanian, 2001, Manivannan, 2002 and Panigrahi *et al.*, 2015. The analysis of variance suggested that significant differences were existed for genotypes, parents, lines, testers and their interaction (lxt) for various quantitative traits promoting yield. The presence of variability among parents and genotypes justified the use of these genotypes as parents in the present line x tester analysis.

**Per se performance:** Mean performance all the parents and their hybrids were presented in Table 2 and 3. Neither the lines nor the testers showed the best *per se* performance for all the quantitative traits. This could be due to differential internal ad-justments between seed yield/plant and its components in different parents (Chakraborty *et al.*, 2010). Although line "MDU1" recorded highest single plant yield (5.15 gm) followed CO6, LBG-752 and ADT3 with mean single plant yield of 4.75, 4.60 and 4.60 gm respectively. Among the thirty cross combination evaluated for mean performance on yield the F<sup>1</sup> derived from 'MDU1xVBN (Bg) 6' cross said to have recorded highest mean yield of 5.37 gm followed by 'MDU1 x Mash-114, MDU1 x Uttra, CO6 x VBN (Bg) 4 and LBG-752 x VBN (Bg) 4 with mean single plant yield of 5.19, 4.93, 4.85 and 4.70 gm respectively. From

**Table 1:** ANOVA for line x tester analysis in black gram

Source	df	Mean Squares										
		Plant height (cm)	Branches per plant	Days to 50% flowering	Days to maturity	Clusters per plant	Pods per cluster	Pods per plant	Seeds per pod	Pod length (cm)	100 weight (g)	seed yield / plant(g)
Replications	1	1.07	0.32	3.12	5.38	0.04	0.01	1.48	0.01	0.05	0.01	0.02
Genotypes	40	12.45**	0.38**	4.29**	21.55**	1.85**	0.33**	21.37**	0.85**	0.27**	0.31**	0.33**
Parents	10	2.64	0.10*	3.95**	12.13**	0.27	0.14*	4.25	0.64	0.24**	0.20**	0.21**
Parents vs. Crosses	1	88.58**	1.23**	1.92	3.00	8.09**	1.17*	207.2**	1.85*	0.35*	0.58**	0.72**
Line (c)**	5	27.56**	1.45**	4.08**	33.71**	6.02**	1.09**	61.07**	1.99**	0.71**	0.62**	0.69**
Test (c)	4	11.82*	0.15*	12.48**	61.58**	1.35*	0.12	15.40*	1.23*	0.25**	0.33**	0.33**
LxT (c)	20	9.91**	0.26**	3.01**	16.14**	1.37**	0.24**	11.90	0.55	0.18**	0.27**	0.28**
Crosses	29	13.21**	0.45**	4.50**	25.44**	2.17**	0.37**	20.86**	0.89**	0.28**	0.34**	0.35*
Lines (P)**	5	3.27	0.13*	3.08*	4.13	0.47	0.08	3.88	0.85*	0.14*	0.17**	0.16**
Testers (P)	4	2.26	0.04	3.40*	7.15*	0.08	0.17	3.85	0.75*	0.36**	0.09**	0.08**
Lines x Testers (P)	20	0.98	0.28*	10.44**	72.01**	0.05	0.60**	207.22	0.136	0.25*	0.81**	0.85**
<b>Error</b>	40	3.51	0.04	1.05	2.75	0.39	0.06	6.51	0.36	0.06	0.02	0.02

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

\*\*Lines in crosses

\*\*\*Lines as parents

**Table 2:** *Per se* performance of lines and testers for different quantitative traits in black gram

Parents	Plant height (cm)	Branches per plant	Days to 50% flowering	Days to maturity	Clusters per plant	Pods per cluster	Pods per plant	Seeds per pod	Pod length (cm)	100 seed weight (g)	Seed yield/plant (g)
<b>Lines</b>											
ADT3	25.00	2.15	35.00	71.00	5.95	2.50	27.00	6.50	4.40	4.20	4.40
MDU1	28.35	2.65	37.50	73.50	5.55	2.60	28.50	7.00	4.80	4.95	5.15
CO6	24.20	2.55	34.50	70.00	6.05	2.85	26.00	5.50	3.75	4.35	4.75
LBG-752	24.40	2.10	34.00	69.50	7.00	3.00	24.50	6.50	4.45	4.20	4.60
ADT5	22.25	2.10	34.50	70.00	5.95	2.90	25.00	6.50	4.00	4.56	3.95
KUG-688	21.90	2.10	35.00	71.00	6.00	2.90	23.00	5.50	4.10	4.40	4.40
mean	23.68	2.28	35.08	70.83	6.08	2.79	24.58	6.25	4.12	4.18	4.38
SE	0.835 <sup>t</sup>	0.10	0.48	0.78	0.31	0.10	1.23	0.28	0.12	0.06	0.06
CD(P=0.05)	1.71	0.21	0.98	1.60	0.63	0.20	2.53	0.57	0.22	0.12	0.12
CD(P=0.01)	2.31	0.28	1.32	2.15	0.85	0.26	3.40	0.76	0.30	0.16	0.16
<b>Testers</b>											
VBN(BG)4	23.00	2.10	34.50	69.00	5.65	2.35	23.00	6.50	4.45	3.95	4.15
VBN(BG)6	24.90	2.05	33.50	67.50	6.10	2.65	22.00	6.00	4.25	3.85	4.00
Mash-114	23.60	1.90	32.50	65.50	6.15	2.40	24.00	6.00	3.90	3.65	3.85
Uttra	22.10	1.95	35.50	69.00	6.10	2.15	22.50	5.50	4.05	3.50	3.70
PU-31	22.70	2.10	32.50	65.00	5.95	2.75	25.50	5.60	4.25	4.00	4.20
mean	23.26	2.05	33.70	67.20	5.99	2.46	23.40	6.20	4.33	3.79	3.98
SE	0.76	0.09	0.44	0.72	0.29	0.09	1.13	0.25	0.10	0.05	0.05
CD(P=0.05)	1.56	0.19	0.90	1.46	0.58	0.18	2.31	0.51	0.20	0.11	0.11
CD(P=0.01)	2.11	0.26	1.21	1.97	0.79	0.24	3.11	0.70	0.27	0.14	0.14

these mean performance study it was envisaged that the highest mean performance recorded parents *viz.*, MDU1, CO6 and LBG-752 said have transmit their best performance to their progeny for traits in question. The crosses are likely to produce transgressive segregants for single plant yield in succeeding generations (Chakraborty *et al.*, 2010; Geleta and Labuschagne, 2006; Vijay Kumar, 2014).

**gca effects:** Experimental results pertaining to *gca* effects of parents *i.e.*, lines and testers were presented in Table 4. The *gca* effect is a good estimate of additive gene action (Sprague and Tatum, 1942). Among the six lines and 5 testers taken for these study neither the lines nor the tester recorded highly significant positive *gca* and best general combiner for all the quantitative traits. Among six lines 'MDU1' recorded positive significant *gca* for eight quantitative traits *viz.*, plant height, branches per plant, cluster per plant, pods per cluster, pods per plant, seeds per pod, pod length and single plant yield followed by LBG-752 and ADT3 for seven and six yield attributes respectively. So it is referred that the line 'MDU1' was taken as the best general combiner in this study. Similarly, among three testers 'VBN (Bg) 6 and Mash-114' recorded each with positive *gca* effects for four traits were the best general combiner for days to 50 per cent flowering, days to maturity, 100 grain weight; single plant yield, and plant height, pods per cluster, pods per plant and pod length respectively. Results on *gca* suggested that the line 'MDU1' and testers 'VBN (Bg) 6 and Mash-114' found to have the best general combiner for yield and its attributes. It may have transfer superior performance (additive gene)

to their progeny. So, these could be used as parents hybridization programme in future to get desirable transgressive segregants to increase the yield (Das and Das Gupta, 1999).

**sca effects:** Results on *sca* effects of thirty cross combination for eleven quantitative traits were depicted in Table 5. The estimation of *sca* effect is an indicative of presence non-additive type of gene action. Preponderance of dominance (non-additive) gene action is importance for production of transgressive segregants, which out performs both the parents and falls outside the range of both the parents for traits in question (Rojas and Sprague, 1952). Among thirty F<sub>1</sub>s studied for their performance none of the cross recorded significant positive *sca* effects for all the traits, but cross combination 'MDU1x VBN (Bg) 6 (branches per plant, seeds per pod, 100 grain weight and single plant yield) and 'LBG-752 x VBN (Bg) 6' (branches per plant, pods per cluster, 100 grain weight and single plant yield) each with four traits showed positive *sca* for effects. This was closely followed by, LBG-752 x Mash-114, LBG-752 x Uttra and LBG-752 x PU 31, each with positive significant effect for three traits. But the cross derivatives of MDU1 and LBG-752 along with all the testers recorded significant *sca* effect on an average for two important traits like 100 grain weight and single plant yield revealed that there might be of non additive type of gene action either form lines or tester predominant in the increasing yield. Above mentioned top ranking crosses could have the potential to produce transgressive segregants for yield and it attributes.

**Table 3.** *Per se* performance of thirty L X T crosses of black gram in F<sub>1</sub> generation for different quantitative traits

Cross	Plant height (cm)	Branches per plant	Days to 50% flowering	Days to maturity	Clusters per plant	Pods per cluster	Pods per plant	Seeds per pod	Pod length (cm)	100 seed weight (g)	Seed yield/plant (g)
ADT3/VBN(BG)4	28.00	3.25	35.50	71.00	5.50	3.15	26.50	6.50	4.55	4.45	4.35
ADT3/VBN(BG)6	28.95	2.85	37.50	73.50	6.50	3.40	27.00	7.50	5.15	4.65	4.20
ADT3/MASH-114	26.40	2.65	36.50	73.50	6.50	3.30	29.50	6.50	4.35	3.45	3.65
ADT3/Ultra	24.35	2.75	35.00	70.00	7.50	3.00	28.00	7.00	4.80	3.85	4.15
ADT3/PU31	26.65	2.80	33.50	63.50	6.50	3.25	29.50	7.00	4.70	4.10	4.35
MDU1/VBN(BG)4	24.20	2.35	32.50	63.00	5.50	2.40	22.50	5.50	4.25	4.15	4.35
MDU1/VBN(BG)6	24.75	2.20	37.00	76.00	6.00	2.55	29.50	5.50	4.20	4.55	5.37
MDU1/MASH-114	26.55	2.45	36.00	66.00	6.50	2.85	34.50	6.00	4.25	4.35	5.19
MDU1/Ultra	24.80	2.30	33.00	63.50	5.50	2.25	27.00	6.50	4.05	4.00	4.93
MDU1/PU31	24.50	1.95	33.50	65.50	5.00	2.20	25.50	6.00	4.00	3.50	4.70
CO6/VBN(BG)4	24.30	2.15	34.50	70.00	5.50	2.70	25.50	5.50	4.00	4.78	4.90
CO6/VBN(BG)6	24.750	2.32	34.50	70.00	5.95	2.80	28.50	6.50	4.10	4.75	4.85
CO6/MASH-114	24.65	2.00	35.50	71.50	5.90	2.40	25.00	7.00	4.65	3.55	3.75
CO6/Ultra	21.40	2.15	34.00	70.00	6.40	2.90	24.50	6.50	4.10	4.00	4.15
CO6/PU31	21.10	2.10	37.00	72.50	6.40	2.35	23.50	6.00	3.35	3.50	3.70
LBG-752/VBN(BG)4	22.45	2.25	35.50	69.00	5.95	3.50	26.00	6.50	4.10	4.90	4.70
LBG-752/VBN(BG)6	25.60	2.95	34.50	68.00	7.50	3.95	28.00	6.00	4.15	4.25	4.45
LBG-752/MASH-114	29.75	2.80	33.50	66.00	8.25	3.75	29.00	7.50	4.25	4.45	4.65
LBG-752/Ultra	29.55	2.05	32.50	63.50	8.25	3.70	26.00	7.50	4.35	4.70	4.20
LBG-752/PU31	29.65	2.45	34.50	68.00	8.10	3.60	33.50	7.50	4.35	4.20	4.50
ADT5/VBN(BG)4	29.40	2.25	36.50	71.00	7.25	3.55	29.50	6.00	4.25	4.45	4.75
ADT5/VBN(BG)6	24.95	2.05	36.50	72.00	6.35	3.00	26.00	6.50	4.65	4.90	4.55
ADT5/MASH-114	29.25	2.55	34.50	68.50	8.00	3.10	29.00	7.50	5.15	4.65	4.25
ADT5/Ultra	24.85	2.45	32.50	63.50	6.00	2.40	22.50	7.50	4.55	4.90	4.10
ADT5/PU31	22.90	2.20	34.50	69.00	6.10	2.90	23.00	7.00	4.20	4.20	4.40
KUG-688/VBN(BG)4	24.30	2.30	36.00	70.50	6.25	2.85	28.00	7.50	4.80	4.05	4.25
KUG-688/VBN(BG)6	28.95	3.45	34.50	69.50	8.25	3.05	30.50	6.00	4.10	4.00	4.20
KUG-688/MASH-114	28.05	3.80	33.50	67.50	7.25	3.00	30.50	6.50	4.45	4.15	4.35
KUG-688/Ultra	27.65	3.30	32.50	63.50	7.90	2.80	28.50	6.50	4.85	4.30	4.50
KUG-688/PU31	24.20	2.15	35.00	70.50	5.95	2.65	26.50	6.00	4.25	4.15	4.35
General mean	25.84	2.45	34.80	68.75	6.75	2.91	27.63	6.57	4.36	4.19	4.41
SE	1.32	0.14	0.72	1.17	0.44	0.17	1.81	0.41	0.17	0.10	0.10
SED	1.87	0.21	1.02	1.66	0.63	0.24	2.55	0.60	0.24	0.13	0.13
CD(P=.05)	3.76	0.42	2.06	3.34	1.26	0.49	5.12	1.21	0.48	0.26	0.26
CD(P=.01)	5.02	0.56	2.74	4.45	1.68	0.65	6.83	0.64	0.64	0.35	0.35

**Genetic parameters:** The *gca* and *sca* variances and heritability parameters were computed in Table 6 and 7. The general combining ability variances ( $\sigma^2_{gca}$ ) was lower than specific combining ability variances ( $\sigma^2_{sca}$ ) for most of the traits but was higher for pods per plant and seeds per pod. The estimate of predictability ratio of quantitative traits was revealed that the predominance of non-additive gene action except for pods per plant, seeds per pod and single plant yield was thought to have controlled by additive gene. The degree of dominance effect was higher than unity (1.00) except for pods per plant (0.70), seeds per pod (0.86) and single plant yield (0.95). Estimate of heritability was lower for all the traits it was ranged between 3.29 – 63.26 per cent. The highest narrow sense heritability was recorded for single plant yield with 63.26 per cent followed by closely followed closely by pods per plant with 43.88 per cent, seeds per pod with 32.96 per cent and 100 grain weight with 18.18 per

cent. The higher heritability is due to predominance of additive gene action and less influenced by environmental variances and effects. Other traits were recorded lower level of heritability revealed that traits could have under the control of environmental variances and effects. Similar results were reported by Singh and Singh (1971), Das Gupta and Das (1987), Chakraborty and Borua (1998), Dana and Das Gupta (2001).

## CONCLUSIONS

From the estimate of combining ability variances, *per se* performance and heritability the present study described that the relative size of *sca* variances was higher than *gca* variances for most of the traits except few which are recorded high *gca*, heritability and partial dominance effect. Hence, is clear that quantitative characters governs yield were under the control of both additive and non-additive gene action. It is suggest that breeding methods

**Table 4:** Estimates of *gca* effects of lines and testers in black gram

Parents	Plant height (cm)	Branches per plant	Days to 50% flowering	Days to maturity	Clusters per plant	Pods per cluster	Pods per plant	Seeds per pod	Pod length (cm)	100 seed weight (g)	Seed yield/plant (g)
ADT3	1.03	0.41 **	0.80 *	1.55 **	0.55 *	0.31 **	1.47	0.33	0.35 **	-0.09 *	-0.06
MDU1	3.88 **	0.20 *	-0.40	-1.95 **	1.25 **	4.46 **	2.23 *	0.67 **	2.21 **	0.08	0.11 *
CO6	-2.95 **	-0.31 **	0.70 *	2.65 **	-0.52 *	-0.28 **	-2.43 **	-0.37	-0.34 **	-0.31 **	-0.34 **
LBG-752	1.56 *	-0.31 **	-0.70 *	-1.85 **	0.86 **	0.39 **	3.67 **	0.43 *	-0.12	0.11 *	0.13 **
ADT5	0.43	-0.15	0.10	0.05	-0.01	0.08	-1.63	0.33	0.20 *	0.43 **	0.44 **
KUG-688	0.79	0.55 **	-0.50	-0.45	0.37	-0.04	1.17	-0.07	0.13	-0.06	-0.08
SE(for lines)	0.59	0.07	0.34	0.55	0.22	0.06	0.87	0.19	0.07	0.04	0.04
<b>Testers</b>											
VBN(BG)4	-0.39	-0.02	0.28	0.33	-0.26	-0.05	-0.97	-0.23	-0.04	0.09 *	0.10 *
VBN(BG)6	0.20	0.02	1.28 **	3.25 **	0.34	0.05	0.45	-0.40 *	0.01	0.14 **	0.14 **
Mash-114	1.61 **	0.13	0.12	0.08	0.32	0.16 *	1.78 *	0.27	0.16 *	-0.09 *	-0.11 **
Uttra	-0.40	0.05	-1.55	-3.08 **	0.01	-0.07	-0.55	0.35	0.09	0.10 **	0.10 *
PU-31	-1.00	-0.17 *	-0.13	-0.58	-0.41	-0.09	-0.72	0.02	-0.22 **	-0.25 **	-0.24 **
SE(for testers)	0.55	0.06	0.31	0.50	0.19	0.06	0.79	0.18	0.07	0.04	0.04

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

Table 5: Estimates of *sca* effects of 9 crosses for various quantitative traits in black gram crosses

Cross	Plant height (cm)	Branches per plant	Days to 50% flowering	Days to maturity	Clusters per plant	Pods per cluster	Pods per plant	Seeds per pod	Pod length (cm)	100 seed weight (g)	Seed yield/plant (g)
ADT3/VBN(BG)4	1.52	0.41 *	-0.38	0.37	0.46	-0.02	-0.63	-0.17	-0.12	0.26 **	0.25 *
ADT3/VBN(BG)6	1.88	-0.03	0.62	-0.05	0.86	0.13	1.45	-0.23	0.43 *	0.41 **	0.41 **
ADT3/MASH-114	-2.08	-0.34 *	0.78	3.12 *	-1.12 *	-0.08	-1.38	-0.67	-0.51 **	-0.56 **	-0.59 **
ADT3/Ultra	-2.12	-0.16	0.95	2.78 *	0.19	-0.15	-0.55	-0.25	0.00	-0.35 **	-0.30 **
ADT3/PU31	0.78	0.11	-1.97 *	-6.22 **	-0.39	0.12	1.12	0.08	0.21	0.25 **	0.24 *
MDU1/VBN(BG)4	-0.36	0.12	-2.18 **	-4.13 **	0.26	0.00	-1.93	-0.17	0.14	-0.05	-0.05
MDU1/VBN(BG)6	-0.41	0.47 *	1.32	-5.95 **	0.16	0.05	-0.35	1.00 *	0.04	0.41 **	0.43 **
MDU1/MASH-114	-0.01	0.07	1.48	-0.88	0.68	0.24	1.32	-0.17	-0.06	0.33 **	0.36 **
MDU1/Ultra	0.24	-0.00	0.15	-0.22	-1.01 *	-0.13	0.15	0.25	-0.19	0.21 *	0.25 **
MDU1/PU31	0.54	-0.13	-0.77	-0.72	-0.09	-0.17	0.82	0.08	0.07	0.36 **	0.36 **
CO6/VBN(BG)4	1.80	0.03	-1.28	-1.73	0.53	0.12	3.27	0.03	0.02	0.73 **	0.73 **
CO6/VBN(BG)6	-0.09	0.15	-0.28	-1.65	-0.62	0.12	-0.15	-0.30	-0.03	-0.37 **	-0.36 **
CO6/MASH-114	0.16	-0.27	-0.12	0.02	-0.65	-0.39 *	-1.98	0.53	0.48 **	-0.24 *	-0.21 *
CO6/Ultra	-1.09	-0.04	0.05	1.68	0.16	0.34 *	-0.15	-0.05	-0.01	0.02	-0.02
LBG-752/PU31	-0.79	0.13	1.63 *	1.68	0.58	-0.19	-0.98	-0.22	-0.45 *	-0.13	-0.13
LBG-752/VBN(BG)4	-4.56 **	0.13	1.12	1.77	-1.40 **	0.75 **	-5.33 *	-0.27	-0.10	0.49 **	0.54 **
LBG-752/VBN(BG)6	-0.25	0.48 **	-0.88	-2.15	-0.45	0.40 *	-1.75	-0.60	-0.10	0.39 *	0.33 *
LBG-752/MASH-114	3.75 **	-0.27	-0.72	-0.98	0.32	0.29	0.92	0.23	-0.14	0.24 *	0.22 *
LBG-752/Ultra	2.55	-0.14	-0.05	-0.32	0.63	0.47 **	3.25	0.15	0.02	0.30 **	0.36 **
LBG-752/PU31	3.25 *	-0.21	0.53	1.68	0.90	0.39 *	2.92	0.48	0.33	0.15	0.20 *
ADT5/VBN(BG)4	3.53 *	-0.03	1.32	1.87	0.77	0.61 **	4.47 *	-0.67	-0.27	-0.26 **	-0.20 *
ADT5/VBN(BG)6	-1.52	-0.27	0.32	-0.05	-0.73	-0.04	-0.45	-0.00	0.08	0.14	0.16
ADT5/MASH-114	1.37	0.12	-0.52	-0.38	0.94	-0.05	1.22	0.33	0.43 *	0.12	0.11
ADT5/Ultra	-1.02	0.10	-0.85	-2.22	-0.75	-0.52 **	-2.95	0.25	-0.10	0.18	0.15
ADT5/PU31	-2.37	0.07	-0.27	0.78	-0.23	-0.01	-2.28	0.08	-0.14	-0.17	-0.21 *
KUG-688/VBN(BG)4	-1.94	-0.68 **	1.42	1.87	-0.61	0.03	0.17	1.23 **	0.35 *	-0.17	-0.18
KUG-688/VBN(BG)6	2.12	0.43 *	-1.08	-2.05	0.79	0.13	1.25	-0.10	-0.40 *	-0.27 **	-0.27 **
KUG-688/MASH-114	-0.18	0.67 **	-0.92	-0.88	-0.19	-0.03	-0.08	-0.27	-0.20	0.11	0.13
KUG-688/Ultra	1.42	0.25	-0.25	-1.72	0.77	-0.00	0.25	-0.35	0.27	0.07	0.07
KUG-688/PU31	-1.43	-0.68 **	0.83	2.78 *	-0.76	-0.14	-1.58	-0.52	-0.02	0.27 **	0.26 **
<b>S E (SCA effects)</b>	1.32	0.16	0.76	1.23	0.49	0.15	1.95	0.43	0.17	0.09	0.09

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



such as recurrent selection or biparental mating followed by selection would be ideal to exploit both non-additive and additive gene action. Since, most of traits were under the control of dominance gene in present study heterosis breeding could be applied to exploit hybrid vigour for yield and yield attributes.

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