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Heterosis for yield and quality traits in blackgram [*Vigna mungo* (L.)]

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Abstract

Fifteen hybrids of blackgram were developed by crossing six distinct blackgram genotypes *viz.,* LBG 787, LBG 752, TU94-2, TBG 104, MBG 1045 and KU 1006 in half diallel mating design without reciprocals and evaluated for estimation of heterosis for sixteen traits including yield, its components and quality traits. Based on estimates of heterosis, the crosses *viz.,* TU 94-2 × LBG 752, LBG 787 × LBG 752 exhibited significant mid parent, better parent and standard heterosis in desirable direction for majority of the yield, yield attributes and few quality traits while the crosses *viz.,* TU 94-2 × KU 1006 and MBG 1045 × KU 1006 exhibited significant heterosis for most of the quality traits along with early maturity. Hence, these crosses could be successfully exploited for development of high yielding varieties with improved quality in future breeding programmes.

Keywords: Blackgram, half diallel, heterosis, yield, quality traits

Introduction

Blackgram [*Vigna mungo* (L.) Hepper], a diploid (2n=2x=22), self-pollinated grain legume belongs to the family Fabaceae. It is one of the important short duration pulse crops grown in a wide range of agro-climatic conditions. It is grown in cropping systems as a mixed crop, catch crop, sequential crop besides being grown as a sole crop under residual soil moisture conditions. It is nutritionally important crop with about 25% protein nearly three times that of cereals, 60% carbohydrates, 1.3% fat as well as important vitamins and minerals (Ghafoor *et al.*, 2001) [4], making it a balanced diet when supplemented with cereals. Though, legumes are considered as the major source of dietary proteins but its protein quality however does not reach the dietary level by in animal products. This may be due to unbalanced amino acid composition in the protein (Norton *et al.*, 1985) [11].

In India the per capita daily availability of pulses has come down significantly from 51.1 grams per day in 1971 to about 42.00 grams in 2015-2016 as against WHO recommendation of 80 grams per day per capita. This is mainly due to stagnation in the production of pulses over the last three decades. The low production might be attributed due to several constraints such as non-availability of location specific varieties suitable for cultivation round the year, poor harvest index and susceptibility to various biotic and abiotic stresses. Heterosis is a valuable tool in determining superior parents and specific cross combinations, for the development of pure line varieties in a self-pollinated crop like blackgram. The information on magnitude of heterosis provides the basis for selection of diverse segregants in subsequent generations (Arunachalam *et al.*, 1984) [1]. Hence, the present study was undertaken to untangle the genetic information on heterosis and extent of heterosis for yield, its components and quality traits in blackgram crosses for selection of promising cultures in segregating generation to improve yield and nutritional quality.

Materials and Methods

Six genotypes *viz.,* LBG 787, LBG 752, TU94-2, TBG 104, MBG 1045 and KU 1006 were chosen as parental materials and mated in diallel fashion omitting reciprocals during kharif 2016. The resulting 15 F_1 hybrids and parents were evaluated during rabi 2016-17 at S.V Agricultural college, Tirupati in Randomized Block Design (RBD) with three replications by following the recommended package and practices appropriately throughout the cropping season. The observations for eleven yield, yield attributes *viz.*, plant height, number of primary branches per plant, number of clusters per plant, number of pods per plant, pod length, number of seeds per pod, seed yield per plant, 100 seed weight and harvest index, were recorded from 5 randomly selected plants for each genotype per replication except for days to 50 per cent flowering and maturity for which the observations were recorded on plot basis. The five quality traits *viz.,* protein content was estimated by using the method of Lowry *et al.* (1951) [9], whereas carbohydrate, lysine, tryptophan and methionine contents were estimated by the method proposed by Sadasivam and Manickam (1996) [14].

The mean of the five plants were used to compute relative heterosis (MH), heterobeltiosis (BH) and standard heterosis (SH). The superiority of F_1 over the mid-parent, better parent and standard parent was estimated as per the formula given by Shull (1908), respectively. The significance of heterosis was tested by using 't' test as suggested by Snedecor and Cochran (1967) [18] and Paschal and Wilcox (1975) [12].

Result and Discussion

The scope of exploitation of hybrid vigour depends on directions and magnitude of heterosis and type of gene action involved. Heterosis is measured as per cent increase or decrease over mid parent (relative heterosis), over better parent (heterobeltiosis) and over best parent (economic heterosis). The estimates of heterosis among 15 crosses over mid parent, better parent and standard parent were presented in Table 1 to 5 and the relative merit of superiority is discussed character wise. The standard variety is LBG-752.

The magnitude of heterosis varies widely for different traits as well as for different crosses. Usually, negative heterosis has been considered desirable for the traits like days to 50% flowering and days to maturity. For days to 50% flowering and days to maturity, among fifteen crosses evaluated, three crosses *viz.*, TU 94-2 × KU 1006, and TBG 104 × KU1006 exhibited significant negative negative mid, better and standard parent heterosis. Hence, these crosses could be exploited in the future breeding programme for selecting elite transgressive segregants for earlier maturity. The results were in agreement with the findings of Ramakant and Srivastava (2012) [13], Thamodharan *et al.* (2016) [20] and Suguna *et al.* (2017) [19].

A perusal of results of plant height revealed that the crosses TU 94-2 × LBG 752 and LBG 787 × TU 94-2 exhibited significant positive relative and standard heterosis. For number of primary branches per plant the crosses *viz.,* TBG 104 × LBG 752, LBG 787 × LBG 752 and TU 94-2 × LBG 752 exhibited highly significant positive heterosis over mid parent, better parent and standard check. Results of heterosis for number of clusters per plant revealed that the crosses *viz.,* MBG 1045 × KU 1006 and LBG 787 × LBG 752 exhibited significant positive heterosis over mid, better parent and standard parent (LBG 752). Significant positive heterosis for number of plant height, primary branches per plant and number of clusters per plant were earlier reported by Thamodharan *et al.* (2016) [20].

Number of pods per plant known to contribute directly towards seed yield and identification of superior crosses for this trait is most worthy. The crosses *viz.,* LBG 752 × KU 1006, LBG 787 × LBG 752 and TU 94-2 × LBG 752 were considered as a best crosses since they exhibited significant positive relative heterosis, heterobeltiosis and standard heterosis. Out of 15 F_1 s, four crosses over midparent, three crosses each over mid and better parent recorded significant positive heterosis. Similar observation was made by, Elangaimannan *et al.* (2008b) [2] and Karande *et al.* (2013) [8]. The crosses *viz.,* MBG 1045 × KU 1006 and LBG 787 × LBG 752 exhibited significant positive heterosis over mid parent, better parent and standard parent for pod length. For number of seeds per pod,high per cent of significant positive heterosis over mid parent, better parent and standard parents was recorded by the crosses *viz.,* TU 94-2 × LBG 752, LBG 787 × LBG 752 and TU 94-2 × TBG 104. Similarly, the highest estimates of significant positive relative heterosis, heterobeltiosis and standard heterosis for 100-seed weight registered by the crosses *viz.*LBG 787 × LBG 752, TU 94-2 × LBG 752 and MBG 1045 × KU 1006 and were considered as superior crosses. The expression of positive heterosis for pod length, number of seeds per pod and 100- seed weight were reported by Elangaimannan *et al.* (2008b) [2] and Thamodharan *et al.* (2016) [20].

Harvest index is a reliable measure of relative translocation of assimilates in the plant system and is a better index of the seed yield potential of the genotype. In the present investigation results of heterosis for harvest index revealed that the crosses *viz.*, LBG 787 × LBG 752 and TU 94-2 × LBG 752 exhibited high per cent of relative heterosis, heterobeltiosis and standard heterosis. A similar finding of positive heterosis for harvest index was reported by Singh and Srivastava (1981) [17].

Improvement in seed yield has been the ultimate goal of any breeding programme, so, existence of considerable heterosis is always desirable for the improvement of the trait. Six out of fifteen crosses, four crosses for each heterobeltiosis and standard heterosis of showed highly positive and significant heterosis in desirable direction. High magnitude of significant positive relative, better parent and economic heterosis was recorded in the cross LBG 787 × LBG 752 followed by TU 94-2 × LBG 752 and MBG 1045 × LBG 752 and these crosses could be utilized in the future breeding programmes The results are in parallel with the findings of Karande *et al.* (2013) [8] and Thamodharan *et al.* (2016) [20] for seed yield per plant in blackgram.

Results of heterosis for protein content revealed that, out of 15 crosses, the crosses MBG 1045 × TBG 104 and TU 94-2 × KU 1006 exhibited high per cent of heterosis over mid parent, better parent and standard parents. Since the protein content is one of the important characters for deciding the quality of the variety, it would be worthwhile to use the above crosses for enhancement of protein content in future breeding programmes. Similar results were reported by Waldia *et al.* (1981) [21]. The crosses TU 94-2 × LBG 752 and LBG 787 × TU 94-2 for lysine content and only one cross TU 94-2 × LBG 752 for tryptophan content exhibited significant positive relative heterosis, hererobeltiosis and economic heterosis. Hence,it was suggested that these crosses could be utilized in the future breeding programmes for improvement of these traits in blackgram. The findings are conformity with the Waldia *et al.* (1981) [21] who reported significant positive heterosis for tryptophan content in blackgram.

Methionine is one of the important limited sulphur containing essential amino acid in pulses. The relative heterosis varied from 33.18% and -57.72%, heterobeltiosis varied from -66.95 % to 10.73 % and standard heterosis from -47.27 % to 27.93 %. Among fifteen crosses, the cross LBG 787 × TU 94-2 registered highest significant mid parent heterosis while, LBG 787 × TBG 104 heterobeltosis and TU 94-2 × KU 1006 standard heterosis. Hence, these crosses could be exploited in future breeding programme to improve high methionine content in blackgram varieties.

Table 1: Percentage of mid parent heterosis (MH), better parent heterosis (BH) and standard parent heterosis (SH) for days to 50% flowering, days to maturity and plant height (cm)

S. No.	Crosses	Days to 50% flowering			Days to maturity			Plant height (cm)		
		MH	BH	SH	MH	BH	SH	MH	BH	SH
1	LBG 787 × TU 94-2	-0.79	-2.34	4.17*	2.99**	0.84	2.99**	5.54	-1.95	16.84**
2	LBG 787 × MBG 1045	1.20	0.80	5.00**	0.42	-2.47**	1.28	12.71**	9.83	12.30*
3	LBG 787 × TBG 104	5.83**	2.42	5.83**	4.09**	2.54**	3.42**	11.70*	2.71	5.02
4	LBG 787 × LBG 752	2.46	0.81	4.17*	1.51*	0.43	0.43	6.15	4.98	7.34
5	LBG 787 × KU 1006	0.00	-6.45**	-3.33	0.23	-3.06**	-5.13**	-4.99	-14.15*	-12.22*
6	TU 94-2 × MBG 1045	1.98	0.78	7.50**	-2.49**	-3.29**	0.43	13.06**	2.56	22.21**
7	TU 94-2 × TBG 104	6.56**	1.56	8.33**	3.58**	2.93**	5.13**	9.06	-6.22	11.76*
8	TU 94-2 × LBG 752	0.00	-3.13	3.33	1.90*	0.84	2.99**	13.64**	4.50	24.53**
9	TU 94-2 × KU 1006	-9.32**	-16.41**	-10.83**	-4.64**	-9.62**	-7.69**	11.37*	-5.75	12.31*
10	MBG 1045× TBG 104	-2.90	-6.40**	-2.50	-0.21	-1.65	2.14*	-1.28	-6.99	-9.76
11	MBG 1045 × LBG 752	6.94**	4.80**	9.17**	0.63	-1.23	2.56**	-8.07	-9.43	-9.43
12	MBG 1045 × KU 1006	11.59**	4.00	8.33**	0.22	-5.76**	-2.14*	-16.26**	-22.52**	-24.82**
13	TBG 104 × LBG 752	-9.32**	-10.83**	-10.83**	-1.70*	-2.12*	-1.28	19.30**	10.83	10.83
14	TBG 104 × KU 1006	-5.36**	-8.62**	-11.67**	0.89	-3.81**	-2.99**	-37.61**	-38.79**	-47.49**
15	LBG 752× KU 1006	-1.75	-6.67**	-6.67**	2.68**	-1.71	-1.71	1.58	-7.30	-7.30
	S.E.	0.61	0.70		0.58	0.66		1.69	1.95	

* : Significant at 5% level; ** : Significant at 1% level; Standard variety: LBG 752

Table 2: Percentage of mid parent heterosis (MH), better parent heterosis (BH) and standard parent heterosis (SH) for no. of primary branches per plant, no of clusters per plant and No of pods per plant

S. No.	Crosses	No. of primary branches per plant			No. of clusters per plant			No. of pods per plant		
		MH	BH	SH	MH	BH	SH	MH	BH	SH
1	LBG 787 × TU 94-2	19.15**	14.29**	16.67**	-3.89	-12.56**	-4.92	5.09	1.64	6.54
2	LBG 787 × MBG 1045	19.10**	17.78**	10.42*	29.55**	27.53**	13.66**	-10.52*	-26.71**	-28.23**
3	LBG 787 × TBG 104	4.44	4.44	-2.08	12.85**	12.81**	0.55	7.16	-4.04	-31.84
4	LBG 787 × LBG 752	33.33**	29.17**	29.17**	34.07**	26.78**	26.78**	25.57**	24.27**	24.27**
5	LBG 787 × KU 1006	7.69	-6.67	-12.50*	11.96**	3.00	-8.20*	13.79*	-7.91	-9.81
6	TU 94-2 × MBG 1045	5.38	0.00	2.08	-9.80**	-19.10**	-12.02**	-27.37**	-42.04**	-39.24**
7	TU 94-2 × TBG 104	12.77**	8.16	10.42*	-22.10**	-29.15**	-22.95**	6.70	-7.22	-2.75
8	TU 94-2 × LBG 752	29.90**	28.57**	31.25**	27.23**	22.11**	32.79**	18.49**	15.76**	26.68**
9	TU 94-2 × KU 1006	4.88	-12.24*	-10.42*	-11.90**	-25.63**	-19.13**	-19.88**	-36.78**	-33.73**
10	MBG 1045× TBG 104	-23.60**	-24.44**	-29.17**	4.05	2.45	-8.74*	-5.29	-14.44*	-33.73*
11	MBG 1045 × LBG 752	-8.70	-12.50*	-12.50*	26.69**	18.03**	18.03**	-20.97**	-35.80**	-1.38
12	MBG 1045 × KU 1006	-27.27**	-36.36**	-41.67**	46.44**	36.71**	18.03**	-30.91**	-31.96**	-57.49**
13	TBG 104 × LBG 752	37.63**	33.33**	33.33**	14.45**	8.20*	8.20*	-6.89	-17.38**	-8.43
14	TBG 104 × KU 1006	-33.33**	-42.22**	-45.83**	-21.33**	-27.61**	-35.52**	-24.69**	-32.89**	-32.89**
15	LBG 752× KU 1006	-13.58*	-27.08**	-27.08**	-13.75**	-24.59**	-24.59**	40.84**	13.08**	13.08**
	S.E.	0.14	0.17		0.37	0.43		1.61	1.86	

* : Significant at 5% level; ** : Significant at 1% level; Standard variety: LBG 752

Table 3: Percentage of mid parent heterosis (MH), better parent heterosis (BH) and standard parent heterosis (SH) for pod length(cm), no of seeds per pod and 100-seed weight(g)

S. No.	Crosses	Pod length (cm)			No of seeds per pod			100-seed weight (g)		
		MH	BH	SH	MH	BH	SH	MH	BH	SH
1	LBG 787 × TU 94-2	1.39	0.33	1.06	2.38	1.18	2.38	-8.02**	-12.56**	-9.79**
2	LBG 787 × MBG 1045	3.93	3.22	3.97	6.36*	4.55	9.52**	-19.04**	-20.59**	-23.21**
3	LBG 787 × TBG 104	0.20	-1.84	-1.12	16.96**	16.28**	19.05**	4.99*	1.80	0.79
4	LBG 787 × LBG 752	13.74**	13.33**	14.15**	20.71**	20.00**	21.43**	11.93**	8.00**	8.00**
5	LBG 787 × KU 1006	-2.62	-5.91*	-5.22*	-8.98**	-10.59**	-9.52**	0.88	0.28	-5.62*
6	TU 94-2 × MBG 1045	-3.44	-3.79	-4.43	-13.45**	-15.91**	-11.90**	5.56**	2.24	5.49*
7	TU 94-2 × TBG 104	10.57**	9.46**	7.94**	18.34**	16.28**	19.05**	2.72	0.64	3.84
8	TU 94-2 × LBG 752	6.09**	5.36*	5.36*	24.55**	23.81**	23.81**	7.55**	5.90**	9.26**
9	TU 94-2 × KU 1006	-4.29	-6.57**	-7.87**	-5.45	-6.02	-7.14*	0.44	-3.97	-0.93
10	MBG 1045× TBG 104	0.10	-1.26	-1.92	2.30	1.14	5.95	4.63*	3.41	2.38
11	MBG 1045 × LBG 752	6.70**	6.35*	6.35*	0.00	-2.27	2.38	4.71*	2.98	2.98
12	MBG 1045 × KU 1006	27.86**	24.37**	23.54**	9.41**	5.68	10.71**	10.43**	8.96**	5.36*
13	TBG 104 × LBG 752	7.70**	5.89*	5.89*	-3.53	-4.65	-2.38	2.89	2.38	2.38
14	TBG 104 × KU 1006	1.01	-0.41	-3.77	-10.71**	-12.79**	-10.71**	4.11*	1.54	0.53
15	LBG 752× KU 1006	-15.62**	-18.19**	-18.19**	-27.71**	-28.57**	-28.57**	-15.78**	-18.25**	-18.25**
	S.E.	0.10	0.12		0.16	0.19		0.09	0.11	

* : Significant at 5% level; ** : Significant at 1% level; Standard variety: LBG 752

Table 4: Percentage of mid parent heterosis (MH), better parent heterosis (BH) and standard parent heterosis (SH) for harvest index (%), seed yield per plant (g) and protein content (mg/g)

S. No.	Crosses	Harvest index (%)			Seed yield per plant(g)			Protein content (mg/g)		
		MH	BH	SH	MH	BH	SH	MH	BH	SH
1	LBG 787 × TU 94-2	3.41	-2.93	1.66	-2.70	-11.79**	-1.18	-13.57**	-15.42**	-16.85**
2	LBG 787 × MBG 1045	8.47	3.55	-4.86	5.89	-12.17*	-19.99**	-6.14**	-10.87**	-6.74**
3	LBG 787 × TBG 104	7.84	5.93	-2.67	15.75**	10.94*	1.06	10.26**	9.28**	4.69**
4	LBG 787 × LBG 752	35.93**	30.41**	30.41**	46.45**	39.93**	39.93**	-0.48	-3.41*	-3.41*
5	LBG 787 × KU 1006	-16.39*	-23.91**	-30.09**	16.19**	-6.02	-14.39**	0.39	-5.78**	1.07
6	TU 94-2 × MBG 1045	1.86	-8.44	-4.11	-3.58	-25.97**	-17.07**	6.07**	2.87	7.63**
7	TU 94-2 × TBG 104	12.57*	3.92	8.83	11.07**	-3.06	8.60*	-7.25**	-8.44**	-9.98**
8	TU 94-2 × LBG 752	23.05**	20.27**	25.96**	24.41**	17.74**	31.89**	-3.15*	-3.97*	-3.97*
9	TU 94-2 × KU 1006	-18.73**	-30.13**	-26.83**	-14.03**	-35.42**	-27.65**	12.47**	7.77**	15.60**
10	MBG 1045× TBG 104	-30.63**	-32.62**	-40.28**	-19.42**	-30.76**	-42.17**	12.79**	8.02**	13.03**
11	MBG 1045 × LBG 752	15.58*	6.06	6.06	39.67**	11.74**	11.74**	-7.20**	-9.26**	-5.05**
12	MBG 1045 × KU 1006	24.92**	18.80*	-0.75	2.84	-0.36	-40.21**	3.89**	2.61	10.07**
13	TBG 104 × LBG 752	-0.20	-5.87	-5.87	0.59	-7.69	-7.69	-14.44**	-16.23**	-16.23**
14	TBG 104 × KU 1006	-14.26*	-20.68**	-29.70**	-0.51	-16.74**	-30.46**	4.48**	-1.11	6.08**
15	LBG 752× KU 1006	-13.34*	-24.02**	-24.02**	-17.82**	-35.78**	-35.78**	11.44**	7.66**	15.49**
	S.E.	2.11	2.14		0.43	0.50		3.27	3.77	

* : Significant at 5% level; ** : Significant at 1% level; Standard variety: LBG 752

Table 5: Percentage of mid parent heterosis (MH), better parent heterosis (BH) and standard parent heterosis (SH) for lysine content (mg/g), tryptophan content (mg/g) and methionine content (mg/g)

S. No.	Crosses	Lysine content (mg/g)			Tryptophan content (mg/g)			Methionine content (mg/g)		
		MH	BH	SH	MH	BH	SH	MH	BH	SH
1	LBG 787 × TU 94-2	25.48**	20.01**	10.51**	54.19**	27.01**	83.66**	33.18**	7.34*	11.33**
2	LBG 787 × MBG 1045	-40.33**	-57.98**	-13.51**	-44.77**	-63.87**	9.70	-57.72**	-65.12**	-44.34**
3	LBG 787 × TBG 104	12.60**	-9.09**	24.31**	18.62**	-9.61**	61.50**	19.15**	10.73**	14.84**
4	LBG 787 × LBG 752	3.32	-4.92*	-4.92*	16.17**	12.47*	12.47*	-25.98**	-27.31**	-24.61**
5	LBG 787 × KU 1006	-45.72**	-61.71**	-21.65**	-46.92**	-65.00**	2.77	-55.20**	-63.51**	-39.84**
6	TU 94-2 × MBG 1045	-30.55**	-49.74**	3.45	-29.17**	-47.72**	58.73**	-17.51**	-42.35**	-8.01*
7	TU 94-2 × TBG 104	7.07**	-10.42**	22.50**	-9.00**	-17.67**	47.09**	-5.25	-18.86**	-27.73**
8	TU 94-2 × LBG 752	80.28**	73.15**	73.15**	84.37**	55.94**	125.48**	11.59**	-8.79*	-8.79*
9	TU 94-2 × KU 1006	4.44**	-24.28**	54.95**	17.32**	-12.45**	157.06**	12.06**	-22.39**	27.93**
10	MBG 1045× TBG 104	-30.07**	-41.8**	19.79**	-27.74**	-42.61**	74.24**	-57.58**	-66.95**	-47.27**
11	MBG 1045 × LBG 752	5.47**	-21.64**	61.28**	-14.76**	-43.34**	72.02**	-52.45**	-61.32**	-38.28**
12	MBG 1045 × KU 1006	-38.05**	-38.23**	27.13**	-39.15**	-40.15**	81.72**	-24.86**	-26.07**	21.88**
13	TBG 104 × LBG 752	-36.25**	-44.81**	-24.53**	-45.53**	-57.52**	-24.10**	-24.17**	-28.32**	-28.32**
14	TBG 104 × KU 1006	-37.61**	-47.96**	6.50**	-32.32**	-45.57**	59.83**	-41.08**	-54.62**	-25.20**
15	LBG 752× KU 1006	-17.09**	-38.29**	26.29**	19.21**	-20.09**	134.63**	-9.14**	-27.01**	20.31**
	S.E.	0.10	0.12		0.06	0.07		0.05	0.06	

* : Significant at 5% level; ** : Significant at 1% level; Standard variety: LBG 752

Conclusion

In conclusion, the magnitude of heterosis exhibited in the present investigation indicated that the crosses *viz.*, TU 94-2 × LBG 752, LBG 787 × LBG 752 exhibited significant mid parent, better parent and standard heterosis in desirable direction for majority of the yield, yield attributes and few quality traits while the crosses *viz.*, TU 94-2 × KU 1006 and MBG 1045 × KU 1006 exhibited significant heterosis for most of the quality traits along with early maturity. Hence, these crosses could be successfully exploited for development of high yielding varieties along with the better quality in blackgram.

References

1. Arunachalam V, Bandopadhyay A, Nigam SN, Gibbons RW. Heterosis in relation to genetic divergence and specific combining ability in groundnut (*Arachis hypogaea* L.). Euphytica. 1984;33(1):33-39.
2. Elangaimannan R, Anbuselvam Y, Venkatesan M, Karthikeyan P. Heterosis and inbreeding depression for yield and yield attributes in urdbean. Madras Agricultural Journal. 2008b;95(7/12):453-457.
3. Fonseca S, Patterson FL. Yield Component Heritabilities and Interrelationships in Winter Wheat (*Triticum aestivum* L.) 1. Crop Science. 1968;8(5):614-617.
4. Ghafoor A, Ahmad Z, Afzal M, Qureshi AS. Influence of genetic diversity and combining ability in determining hybrid vigour in black gram. Journal of Genetics and Plant Breeding. 2001;54:125-131.
5. Gopi KA, Reddisekhar M, Raja Reddy K, Subramanyam Reddy K. Heterosis and combining ability studies in urdbean (*Vigna mungo* L. Hepper). Legume Research. 2003;26(4):280-283.
6. Govardhan G. Genetic analysis of yield, yield attributes and drought tolerant traits in mungbean [*Vigna radiata* (L.) Wilczek] Ph.D, Thesis, Acharya N.G. Ranga Agricultural University, Lam, Guntur; c2015.
7. Jansman AJM. Bioavailability of proteins in legume seeds. Grain Legumes (AEP). 1996;11:19.
8. Karande SP, Rewale AP, Nilakh SB. Heterosis for yield and yield attributing traits in black gram (*Vigna mungo* (L) Hepper.). Bioinfolet. 2013;10(2):679-684.

9. Lowry OH, Rosebrough NJ, Farr AL, Randall RJ. Protein measurement with the Folin phenol reagent. The Journal of Biological Chemistry. 1951;193:265-275.
10. Natarajan C, Rathinaswamy R. Heterosis and inbreeding depression in black gram. Madras Agricultural Journal. 1999;86(7-9):447-450.
11. Norton G, Bliss FA, Bressani R. Biochemical and nutritional attributes of grain legumes. In Summer field RJ., Roberts EH. Grain legume crops. London: Collins. 1985, 73-114.
12. Paschal EH, Wilcox JR. Heterosis and combining ability in exotic soybean germplasm. Crop Science. 1975;15:344-349.
13. Ramakant, Srivastava RK. Inheritance of some quantitative characters in urdbean [*Vigna mungo* (L.) Hepper]. Journal of Food Legumes. 2012;25(1):1-8.
14. Sadasivam S, Manickam A. Biochemical methods. New age International (P) Ltd., New Delhi. 1996, 8-9.
15. Saravanan K, Sabesan T, Thangavel P, Siddesh Kumar J, Ganesan J. Heterosis for yield and yield components in black gram (*Vigna mungo* L. Hepper). Legume Research. 2004;27(3):209-212.
16. Shull GH. Methods of Plant Breeding by Hayes, H.K., Immer, F.R and Smith, D.C. 1955. McGraw Hill Company, New York. 53, 1914.
17. Singh P, Srivastava AN. Heterosis in blackgram. Current Science. 1981;50:683-684.
18. Snedecor GW, Cochran WG. Statistical methods. 6th Edition. Iowa State University Press, Ames, Iowa, 1967.
19. Suguna R, Savitha P, Ananda Kumar CR. Inheritance of genetic variability, combining ability and heterosis for yellow mosaic virus disease resistance and yield improvement in Blackgram [Vigna mungo (L.) Hepper]. International Journal of Current Microbiology and Applied Sciences. 2017;6(11):2416-2442
20. Thamodharan G, Geetha S, Ramalingam A, Ushakumari R. Studies on heterosis in blackgram (*Vigna mungo* (L.) Hepper). Electronic Journal of Plant Breeding. 2016;7(3):670-676.
21. Waldia RS, Popli S, Dhindsa KS, Popli S. Heterosis for protein and tryptophan contents in urdbean (*Vigna mungo* (L.) Hepper). Haryana Agricultural University Journal Research. 1981;11:27-30.