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D Bharathi
Department of Genetics and Plant Breeding, SV Agricultural College, Tirupati Acharya NG Ranga Agricultural University, Lam, Guntur, Andhra Pradesh, India

K Hariprasad Reddy
Department of Genetics and Plant Breeding, SV Agricultural College, Tirupati Acharya NG Ranga Agricultural University, Lam, Guntur, Andhra Pradesh, India

D Mohan Reddy
Department of Genetics and Plant Breeding, SV Agricultural College, Tirupati Acharya NG Ranga Agricultural University, Lam, Guntur, Andhra Pradesh, India

P Lata
Department of Genetics and Plant Breeding, SV Agricultural College, Tirupati Acharya NG Ranga Agricultural University, Lam, Guntur, Andhra Pradesh, India

B Ravindra Reddy
Department of Genetics and Plant Breeding, SV Agricultural College, Tirupati Acharya NG Ranga Agricultural University, Lam, Guntur, Andhra Pradesh, India

Combining ability studies for various quantitative traits in blackgram [*Vigna mungo* (l.) hepper]

D Bharathi, K Hariprasad Reddy, D Mohan Reddy, P Lata and B Ravindra Reddy

Abstract
A diallel set of six parents and their 21 F_1 were studied for 13 quantitative traits to determine the nature of gene action in parents and hybrid population. The analysis of variance revealed significant differences for general combining ability (GCA) and specific combining ability (SCA) indicating the presence of additive as well as non-additive gene effects for genetic factors controlling the traits. The components due to *sca* variances ($\sigma^2 sca$) were higher than *g ca* variances ($\sigma^2 gca$) for most of the traits except for days to maturity and number of pods per plant indicating the preponderance of non-additive gene action in the inheritance of these traits. Based on mean performance and *g ca* effects the genotypes *viz*., LBG 752, TU 94-2, LBG 787 were adjudged as the best parents as for yield and yield components. The crosses *viz*., TU 94-2 × LBG 752, LBG 787 × LBG 752 and TBG 104 × LBG 752 were identified as best specific cross combinations as they exhibited high mean and *sca* effects for most of the yield and yield attributes. Hence, these crosses could be exploited in further breeding programmes to isolate desirable segregants with high yield and yield attributes.

Keywords: Black gram, combining ability, gca, sca

Introduction

Black gram [*Vigna mungo* (L.) Hepper], popularly known as urdbean is one of the important short duration nutritious pulse crops grown in a wide range of agro climatic conditions in all the three seasons. It is a cheap source of dietary protein (25-26%), which also contains 67 per cent carbohydrates, 3-5 percent fibre and 1.74 percent fat. It is also an excellent source of essential amino acids, fatty acids, mineral and vitamins and which makes important in human food from the point of view of nutrition. It ranks third among the major pulses after chickpea and pigeon pea. In Andhra Pradesh, it is grown in an area about 3.81 lakh hectares with a production of 3.13 lakh tones and a productivity of 902 kg ha-[1] (Ministry of Agriculture, Govt. of India, 2018).

Despite having superior nutritional quality over the cereals and being well adapted under local conditions, the production and productivity of pulse crops including balck gram have been slowing down lessening food and nutrition security of millions of smallholder and other farming communities. The low production might be attributed to several constraints such as non-availability of location specific varieties suitable for round the year cultivation, besides susceptibility to various biotic and abiotic stresses. Hence, there is a strong need to improve the productivity of black gram. This could be achieved by studying the genetic architecture of this crop. Genetic information on major yield attributes is a pre-requisite for any crop improvement programme. However, success depends primarily upon identification of best parental lines which may produce desirable gene combinations. Diallel mating design suggested by Griffing (1956) [2] is one of the important and commonly used method for evaluating the varieties/ lines for their combining ability and genetic architecture. This method not only aids in estimating the general combining ability effects of the parents and specific combining ability effects of crosses in a fixed set of parental lines. The knowledge of the type of gene action involved in the expression of yield and component traits is essential to choose an appropriate breeding strategy to isolate desirable segregants in later generations.

The present study was therefore, carried out to know the type of gene action governing yield and yield component traits to identify the parents and crosses which could be exploited for future breeding programme.

Correspondence
D Bharathi
Department of Genetics and Plant Breeding, SV Agricultural College, Tirupati Acharya NG Ranga Agricultural University, Lam, Guntur, Andhra Pradesh, India

Materials and Methods

The material for study consisted of six parents and 15 F_1 s which were sown in Randomized Block Design (RBD) with three replications at dry land farm of Sri Venkateswara Agricultural College, Tirupati during *Rabi* 2016-17. Each genotype was raised in 3m length with spacing of 30×10cm. Recommended agronomic practices were followed to raise a good crop. Observations were recorded for days to 50 % flowering, days to maturity, SPAD chlorophyll meter reading, specific leaf area, 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, 100 seed weight, harvest index and seed yield per plant. The data for yield and yield components were recorded on five randomly selected plants in each entry in each replication except days to 50% flowering and days to maturity which were taken on plot basis. Analysis of data for general and specific combining ability was carried out following Griffing (1956) [2] method II, Model I (fixed effect model) from 6×6 half diallel mating design.

Results and discussion

In the present study the analysis of variance revealed that mean squares due to genotypes were significant for all the 13 quantitative traits indicating presence of sufficient amount of variability among the parents and crosses (Table 1). The relative estimates of variance due to specific combining ability (sca) were higher than variance due to general combining ability (gca) for most of the traits except for days to maturity and number of pods per plant indicating the predominance of non-additive gene action for these traits and suggesting that selection in early segregating generations will be desirable for exploiting non-additive gene action. These results are in accordance with Baradhan and Thangavel (2011) [10], Panigrahi *et al.* (2015) [5] and Kachave *et al.* (2015) [4]. Additive gene action for days to maturity was reported by Suguna *et al.* (2017) [8] similarly Sharma and Pandey (1996) [7] and Thamodharan *et al.* (2016) [9] for reported additive gene action for number of pods per plant. However, non-additive gene action for days to maturity and number of pods per plant was reported by Isha parveen *et al.* (2012) [3] and Panigrahi *et al.* (2015) [5] in black gram.

Table 1: ANOVA for combining ability for yield and yield components in black gram.

S. No	Character	Mean sum of squares			$\sigma^2 gca$	$\sigma^2 sca$	$\sigma^2 gca / \sigma^2 sca$
		G c a (DF=5)	*S c a* (DF=15)	Error (DF=40)			
1	Days to 50% flowering (days)	18.55*	4.43**	0.25	2.29	4.18	0.55
2	Days to maturity (days)	24.77**	2.68**	0.22	3.07	2.46	1.25
3	SCMR	59.13**	31.88**	3.89	6.90	27.99	0.25
4	Specific leaf area ($cm^2 g^{-1}$)	443.26**	152.98**	35.40	50.98	117.58	0.43
5	Plant height (cm)	110.62**	15.97**	1.91	13.59	14.07	0.97
6	No. of primary branches per plant	1.28**	0.25**	0.01	0.16	0.24	0.66
7	No. of clusters per plant	7.96**	3.96**	0.09	0.98	3.87	0.25
8	No. of pods per plant	244.67**	29.24**	1.74	30.37	27.50	1.10
9	Pod length (cm)	0.09**	0.21**	0.01	0.01	0.20	0.05
10	No. of seeds per pod	0.45**	0.50**	0.02	0.05	0.49	0.11
11	100 seed weight (g)	0.17**	0.16**	0.01	0.02	0.16	0.13
12	Harvest index (%)	89.66**	28.53**	2.97	10.84	25.56	0.42
13	Seed yield per plant (g)	21.27**	2.87**	0.13	2.64	2.75	0.96

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

In any plant breeding programme for developing high yielding hybrids or varieties the basic need is the choice of parents with high mean values as they are expected to produce desirable segregants upon crossing (Gilbert, 1958) [1]. Based on the overall mean performance of parents and crosses revealed that neither the parents nor the crosses showed the best *per se* performance for all the quantitative traits (Table 2).Based on *per se* performance the parents *viz.,* KU 1006 and TBG 104 were earlier to flower, while KU 1006 and LBG 787 were earliest to mature. Hence, these parents could be exploited to evolve short duration varieties. Considering yield and yield attributes the genotype LBG 752 and LBG 787 were found to be the best parents as they registered significantly high *per se* performance for 10 yield and yield attributing traits. The next best parent TU94-2 registered significantly high *per se* values for eight yield attribute. Therefore, it could be suggested that selection of these parents in hybridization

programme would be effective for improvement of yield and yield attributes.

Among the 15 cross combinations, the crosses *viz.*, TBG 104 × KU 1006 followed by TU 94-2 × KU 1006 and TBG 104 × LBG 752 were earliest to flower, while, the crosses *viz.*, TU 94-2 × KU 1006, LBG 787 × KU 1006 and TBG 104 × KU 1006 were earliest to mature. Hence these crosses could be exploited to evolve early maturing varieties. The perusal of mean performance of the crosses for yield and yield contributing traits revealed that, the cross LBG 787 × LBG 752 recorded high *per se* performance for eleven yield and yield contributing traits followed by the crosses viz., TU 94-2 × LBG 752 and LBG 787× TBG 104 for 10 traits. The next best crosses manifested high *per se* performance for seven yield and yield attributing traits were MBG 1045× KU 1006 and LBG 787× TBG 104. Hence, the crosses with high *per se* could be successfully utilized in breeding programme for the development of high yielding varieties in black gram.

Table 2: Mean performance of six parents and 15 crosses for yield and yield components in black gram.

S. No	Genotype	DFF	DM	SCMR	SLA (cm² g⁻¹)	PH (cm)	NPB	NCP	NPP	PL (cm)	NSP	100 SW (g)	HI (%)	SYP (g)
1	LBG 787	41.33	76.33	47.80	162.47	36.67	3.00	10.87	37.93	5.08	5.67	4.69	33.74	9.77
2	TU 94-2	42.67	79.67	52.75	181.46	42.74	3.27	13.27	40.60	4.97	5.53	5.20	38.45	11.99
3	MBG-1045	41.67	81.00	40.90	198.77	34.80	2.93	10.53	24.20	5.01	5.87	4.87	30.67	6.42
4	TBG 104	38.67	78.67	43.87	158.53	30.77	3.00	10.87	30.00	4.87	5.73	4.99	32.54	8.94
5	LBG 752	40.00	78.00	48.42	164.80	35.87	3.20	12.20	38.73	5.04	5.60	5.04	36.72	10.71
6	KU 1006	36.00	71.33	40.82	169.43	29.60	2.20	9.13	23.47	4.73	5.47	4.74	27.67	5.96
	Mean of parents	40.06	77.50	45.76	172.58	35.08	2.93	11.15	32.49	4.95	5.65	4.92	33.30	8.97
	Crosses													
7	LBG 787 × TU 94-2	41.67	80.33	50.67	192.21	41.91	3.73	11.60	41.27	5.09	5.73	4.55	37.33	10.58
8	LBG 787 × MBG 1045	42.00	79.00	42.90	167.11	40.28	3.53	13.87	27.80	5.24	6.13	3.87	34.93	8.56
9	LBG 787 × TBG 104	42.33	80.67	45.60	172.03	37.67	3.13	12.27	36.40	4.98	6.67	5.08	35.74	10.82
10	LBG 787 × LBG 752	41.67	78.33	53.26	177.31	38.50	4.13	15.47	48.13	5.75	6.8	5.44	47.88	14.98
11	LBG 787 × KU 1006	38.67	74.00	48.67	176.91	31.48	2.80	11.20	34.93	4.78	5.07	4.76	25.67	9.16
12	TU 94-2 × MBG 1045	43.00	78.33	35.56	188.22	43.83	3.27	10.73	23.53	4.82	4.93	5.32	35.21	8.88
13	TU 94-2 × TBG 104	43.33	82.00	49.87	199.97	40.08	3.53	9.40	37.67	5.44	6.67	5.23	39.96	11.62
14	TU 94-2 × LBG 752	41.33	80.33	60.73	198.51	44.66	4.2	16.20	47.00	5.31	6.93	5.51	46.25	14.12
15	TU 94-2 × KU 1006	35.67	72.00	46.77	181.28	40.28	2.87	9.87	25.67	4.64	5.20	4.99	26.87	7.74
16	MBG 1045× TBG 104	39.00	79.67	41.17	203.44	32.37	2.27	11.13	25.67	4.94	5.93	5.16	21.93	6.19
17	MBG 1045 × LBG 752	43.67	80.00	38.17	202.21	32.48	2.80	14.40	24.87	5.36	5.73	5.19	38.94	11.95
18	MBG 1045 × KU 1006	43.33	76.33	51.32	190.85	26.96	1.87	14.40	16.47	6.23	6.20	5.31	36.44	6.40
19	TBG 104 × LBG 752	35.67	77.00	55.71	163.62	39.75	4.27	13.20	32.00	5.34	5.47	5.16	34.56	9.88
20	TBG 104 × KU 1006	35.33	75.67	45.83	159.98	18.83	1.73	7.87	20.13	4.85	5.00	5.07	25.81	7.45
21	LBG 752× KU 1006	37.33	76.67	40.30	176.66	33.25	2.33	9.20	43.80	4.12	4.00	4.12	27.90	6.87
	Mean of crosses	40.27	78.02	47.10	183.35	36.16	3.10	12.05	32.36	5.13	5.76	4.98	34.36	9.67
	General mean	40.20	77.86	46.68	179.92	35.81	3.05	11.76	32.40	5.03	5.73	4.97	34.06	9.46
	SE	0.50	0.47	1.97	5.95	1.38	0.12	0.30	1.32	0.08	0.13	0.08	1.72	0.32
	CV	2.15	1.04	7.31	5.72	6.67	6.63	4.43	7.05	2.89	4.04	2.67	8.76	5.79
	CD.5%	1.43	1.35	5.61	16.91	3.93	0.33	0.86	3.75	0.24	0.38	0.22	4.94	0.90

DFF: Days to 50% flowering, DM: Days to maturity, SCMR: SPAD chlorophyll meter reading, SLA: Specific leaf area, PH: Plant height, NPB: No. of primary branches per plant, NCP: No. of clusters per plant, NPP: No. of pods per plant, PL: Pod length, NSP: No. of seeds per pod, 100SW:100 seed weight, HW: Harvest index, SYP: Seed yield per plant

The *gca* effects reflect performance of parents in combination with all other parents, so the parents with highest *gca* effects should have greater impact on the trait improvement. The general combining ability effects of parents for different traits are presented in Table 3. The overall estimates of *g ca* effects revealed that none of the parents was all round good general combiner for all the 13 characters studied. The parent LBG 787 was identified as the best combiner as it expressed good *g ca* effects for nine traits followed by TU 94-2 for eight characters and LBG 752 for seven characters in desirable direction. Hence, these genotypes could be considered as good donor source for improving seed yield in future breeding programmes.

The *sca* effect is an important criterion for the evaluation of hybrids. Results on *sca* effects of 15 cross combinations for 13 traits were depicted in Table 3.Based on *sca* effects none of the cross recorded significant positive *sca* effects for all the traits. The crosses TU 94-2 × LBG 752 was identified as the best specific combiner as it exhibited good *sca* effects and high *per se* for nine traits followed by the cross LBG 787 × LBG 752 for eight traits. Similarly, the next best cross was TBG 104 × LBG 752 showed good *sca* effects for the seven traits followed by LBG 787 × TBG 104 and LBG 787 × MBG 1045 for six traits each. Hence, these crosses could be exploited to isolate transgresive segregants in subsequent generations in black gram. The results are in akin with findings of Bhardhan and Thangavelu (2011) [10], Isha parveen *et al.* (2012) [3], Panigrahi *et al.* (2015) [5] and Thamodharan *et al.* (2016) [9].

Table 3: Estimates of general combining ability (*gca*) effects of parents and specific combining ability (*sca*) effects of crosses.

S. No.	Parents	DFF	DM	SCMR	SLA (cm² g⁻¹)	PH (cm)	NPB	NCP	NPP	PL (cm)	NSP	100-SW (g)	HI (%)	SYP (g)
1	LBG 787	0.94**	-0.01	1.21	-6.43**	1.53**	0.25**	0.45**	4.71**	0.06*	0.20**	-0.21**	1.33**	0.91**
2	TU 94-2	1.11**	0.90**	2.76**	7.65**	5.66**	0.35**	0.22*	3.70**	-0.04	0.05	0.15**	3.01**	1.32**
3	MBG-1045	1.61**	1.28**	-4.51**	10.93**	-0.68	-0.22**	0.38**	-7.50**	0.13**	0.07	-0.02	-1.20*	-1.44**
4	TBG 104	-1.06**	0.90**	-0.14	-5.73**	-2.59**	-0.05	-0.87**	-1.86**	-0.03	0.14**	0.11**	-1.92**	-0.31**
5	LBG 752	-0.22	0.40*	2.25**	-1.75	1.18*	0.35**	1.29**	5.81**	0.05	0.00	0.09**	3.82**	1.61**
6	KU 1006	-2.39**	-3.47**	-1.56*	-4.67**	-5.11**	-0.67**	-1.47**	-4.85**	-0.18**	-0.46**	-0.13**	-5.05**	-2.08**
	S.E. *g(j)*	0.16	0.15	0.64	1.92	0.45	0.04	0.10	0.43	0.03	0.04	0.02	0.56	0.10
	Crosses													
1	LBG 787 × TU 94-2	-0.60**	1.57**	-0.02	10.71**	-1.14	0.09	-0.86**	0.47	-0.01	-0.25**	-0.36**	-1.07	-1.13**
2	LBG 787 × MBG 1045	-0.76**	-0.14	-0.51	-17.67**	3.58**	0.45**	1.24**	-1.80**	-0.03	0.13*	-0.86**	0.75	-0.38**
3	LBG 787 × TBG 104	2.24**	1.90**	-2.19*	3.91	2.87**	-0.11**	0.89**	1.16**	-0.12**	0.60**	0.21**	2.27**	0.75**
4	LBG 787 × LBG 752	0.74**	0.07	3.08**	5.22*	-0.06	0.49**	1.94**	5.22**	0.56**	0.86**	0.60**	8.68**	2.98**
5	LBG 787 × KU 1006	-0.10	-0.39	2.30**	7.73**	-0.78	0.17**	0.43**	2.69**	-0.18**	-0.40**	0.13**	-4.67**	0.86**

6	TU 94-2 × MBG 1045	0.07	-1.72**	-9.40**	-10.63**	3.00**	0.09	-1.66**	-5.05**	-0.36**	-0.92**	0.22**	-0.66	-0.48**
7	TU 94-2 × TBG 104	3.07**	2.32**	0.53	17.77**	1.16	0.19**	-1.75**	3.44**	0.43**	0.75**	0.00	4.80**	1.14**
8	TU 94-2 × LBG 752	0.24	1.15**	9.01**	12.34**	1.97**	0.45**	2.90**	5.10**	0.22**	1.15**	0.29**	5.35**	1.71**
9	TU 94-2 × KU 1006	-3.26**	-3.30**	-1.15	-1.97	3.89**	0.14**	-0.68**	-5.57**	-0.22**	-0.12	0.00	-5.16**	-0.97**
10	MBG 1045× TBG 104	-1.76**	-0.39	-0.90	17.96**	-0.22	-0.51**	-0.17	2.64**	-0.24**	0.00	0.10**	-9.01**	-1.54**
11	MBG 1045 × LBG 752	2.07**	0.45*	-6.28**	12.76**	-3.87**	-0.38**	0.94**	-5.84**	0.10**	-0.07	0.15**	2.27**	2.31**
12	MBG 1045 × KU 1006	3.90**	0.65**	10.68**	4.31	-3.09**	-0.30**	3.70**	-3.57**	1.20**	0.86**	0.49**	8.63**	0.45**
13	TBG 104 × LBG 752	-3.26**	-2.18**	6.88**	-9.17**	5.31**	0.92**	0.99**	-4.35**	0.24**	-0.40**	-0.01	-1.40	-0.89**
14	TBG 104 × KU 1006	-1.43**	0.36	0.82	-9.90**	-9.31**	-0.60**	-1.59**	-5.55**	-0.02	-0.40**	0.11**	-1.28	0.36**
15	LBG 752× KU 1006	-0.26	1.86**	-7.10**	2.81	1.34*	-0.40**	-2.41**	10.45**	-0.83**	-1.27**	-0.81**	-4.93**	-2.13**
	S.E. $s_{(ii)}$	0.44	0.42	1.75	5.27	1.22	0.10	0.27	1.17	0.08	0.12	0.07	1.53	0.28
	S.E. $s_{(ij)}$	0.21	0.20	0.83	2.51	0.58	0.05	0.13	0.56	0.04	0.06	0.03	0.73	0.13

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

DFF: Days to 50% flowering, DM: Days to maturity, SCMR: SPAD chlorophyll meter reading, SLA: Specific leaf area, PH: Plant height, NPB: No. of primary branches per plant, NCP: No. of clusters per plant, NPP: No. of pods per plant, PL: Pod length, NSP: No. of seeds per pod, 100SW:100 seed weight, HW: Harvest index, SYP: Seed yield per plant

Conclusion

Based on *per se* and *gca* effects it could be concluded that the parents *viz.,* LBG 752, TU 94-2 and LBG 787 were considered as good donor parents for yield and yield components while the crosses viz., TU 94-2 × LBG 752, LBG 787 × LBG 752 and TBG 104 × LBG 752 were identified as superior cross combinations based on mean performance and *sca* effects. Hence, these crosses could be exploited in further breeding programmes to isolate desirable segregants with high seed yield in black gram.

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