



Research Article

COMBINING ABILITY ANALYSIS IN BLACKGRAM (*Vigna mungo* (L.) Hepper)

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Abstract: Combining ability studies were carried out through line x tester analysis involving four lines and five testers for nine quantitative traits in blackgram. The relative estimates of variance due to specific combining ability (sca) were higher than variance due to general combining ability (gca) for plant height and number of pods per plant indicating the pre-dominance of non-additive gene action for these traits. The parents ACM-16-017, VBN (Bg)8, KKM1 and ACM-16-014 were good general combiners for number of clusters per plant, number of pods per plant and days to 50% flowering. The cross 'ACM-16-017xVBN8' exhibited significant positive sca effects for number of clusters per plant, number of pods per plant, number of seeds per pod, 100 seed yield and single plant yield along with high per se performance. The crosses; ACM-16-017xVBN8, ACM-16-017xKKM1, ACM-16-014xVBN8 and ACM-16-014xKKM1 recorded highly significant sca effects as well as high per se performance for number of pods per plant and 100 seed weight. These crosses could be further exploited to obtain transgressive segregants in the breeding programme.

Keywords: Specific combining ability, Blackgram, Transgressive segregants

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Introduction

Food legumes are a vital source of protein, especially for the poor who often cannot afford animal products. These crops also contain high amounts of macro and micronutrients (Ca, P, K, Fe and Zn), vitamins (niacin, Vitamin A, Ascorbic Acid, Inositol), fibre and carbohydrate for balanced nutrition. They are rich in lysine, an essential amino acid which is low in cereal protein. Blackgram (*Vigna mungo* (L.) Hepper) is an important pulse crop of India cultivated over a wide range of agro-climatic zones of the country. Apart from an excellent source of high-quality dietary protein, it also has good digestibility. It contributes a major portion of lysine in vegetarian diet and fairly a good quantity of vitamins and much needed iron and phosphorus [1]. Hence, there is a strong need to improve the productivity of blackgram. This could be achieved by studying the genetic architecture of this crop. Genetic information on yield and yield attributes is a pre-requisite for any crop improvement programme. However, success depends primarily upon identification of the best parental lines which may produce desirable gene combinations. The knowledge of gene action and combining ability helps in the selection of suitable parents for hybridization and F1s for identification of transgressive segregants in segregating generation for further exploitation in breeding program. The present study was therefore, carried out to know the type of gene action and combining ability for yield and yield contributing traits.

Materials and Methods

The experimental material for the present study comprised 20 F1's of blackgram involving four lines; ACM-16-023, ACM-16-14, ACM-16-017 and MDU1 (derived from different mutagens) and five diverse testers; VBN6, VBN8, KKM1, ADT6 and CO6.

The testers VBN6, VBN8, KKM1, ADT6 and CO6 are commercial varieties, whereas, ACM-16-023, ACM-16-014 and ACM-16-017 are advanced breeding lines (mutant lines). These 29 genotypes (20 F1's and 9 parents) were sown in *kharif* 2017 in a randomized block design with two replications and each genotype was sown in 3 m long single row spaced 30 cm apart. Within rows, seeds were sown at 10 cm distance. Observations were recorded on ten randomly selected plants from each F1 and parents on nine quantitative traits viz., days to 50% flowering, plant height (cm), number of primary branches per plant, number of clusters per plant, number of pods per plant, number of seeds per pod, pod length (cm), 100-seed weight (g) and single plant yield (g). Observations on days to 50% flowering, days to maturity were based on all plants of a plot. The statistical analysis was done as per procedure given by Kaushik *et al* (1984) for combining ability analysis using fixed effect model [2].

Result and Discussion

The analysis of variance for general (gca) and specific (sca) combining ability for various traits are presented in [Table-2]. The variance due to lines and testers showed highly significant for all the characters viz., days to 50% flowering, plant height, number of branches, number of clusters per plant, number of pods per plant, number of seeds per pod, pod length, 100 seed weight and single plant yield. The variance due to line x tester was highly significant for all the traits under study except number of branches per plant. The significant differences among different genotypes of blackgram and their F1 hybrids for grain yield and other component traits in different sets of material were also reported by Singh Mohar (2008) [3] and Baradhan and Thangavel (2011) [5].

Table-1 Analysis of variance for different quantitative traits in parents and crosses

Source	df	Mean square								
		DF	PH	NBR	NCP	NPP	PL	NSP	HSW	SPY
Parents										
Replications	1	0.89	0.05	0.03	0.04	0.01	0.01	0.09	0.03	0.01
Parents	8	6.21	95.54*	0.13*	26.31*	20.57*	0.13*	0.23*	0.60*	4.44*
Error	8	1.12	0.39	0.02	0.16	1.15	0.01	0.03	0.01	0.03
Crosses										
Replications	1	0.6	3.84	0.03	1.49	5.24	0.03	0.05	0.07	1.38
Crosses	19	3.94*	23.46*	0.16*	13.65*	36.63*	0.07*	0.23*	0.29*	5.47*
Error	19	0.69	4.44	0.01	0.5	3.23	0.01	0.01	0.01	2.29

*Significant at 5% level

Table-2 Analysis of variance for combining ability for different quantitative traits

Source	df	Mean square								
		DF	PH	NBR	NCP	NPP	PL	NSP	HSW	SPY
Lines	3	6.63*	21.81*	0.15*	22.92*	86.59*	0.12*	0.42*	0.74*	12.38*
Testers	4	21.02*	209.08*	0.50*	11.02*	47.72*	0.04*	0.22*	0.17*	2.67*
L x T interaction	12	0.88*	5.73*	0.13*	9.28*	10.54*	0.04*	0.13*	0.07*	2.29*
Error	19	0.69	4.44	0.01	0.5	3.23	0.01	0.01	0.01	0.31

*Significant at 5% level

Table-3 Combining ability variance and gene action for different traits

Variance	DF	PH	NBR	NCP	NPP	PL	NSP	HSW	SPY
GCA	0.08	0.45	0.01	0.11	0.67	0.06	0.02	0.01	0.08
SCA	0.09	0.71	0.06	4.39	3.66	0.2	0.06	0.03	0.99
σ^2A (F=1)	0.16	0.91	0.02	0.22	1.34	0.12	0.05	0.03	0.16
σ^2D (F=1)	0.09	0.71	0.06	4.39	3.66	0.02	0.06	0.03	0.99
σ^2A / σ^2D	1.59	1.29	0.39	0.05	0.37	0.61	0.79	0.72	0.16

Table-4 Per se expression of different traits in parents

Parents	DF	PH	NBR	NCP	NPP	PL	NSP	HSW	SPY
Lines									
ACM-16-023	33.5	35.20*	2.57	17	33.2	4.64	6.50*	4.76*	7.87*
AM-16-014	34	36.10*	2.53	17.1	34.30*	4.79	6.1	4.74*	7.88*
ACM-16-017	34.5	40.3	3.30*	20.10*	36.50*	4.73*	6.50*	5.00*	9.18*
MDU1	33	32.30*	2.5	14.5	31.30*	4.71	6.15	4.32	7.04
Testers									
VBN6	33	51	2.9	13.1	31.7	4.26	6.3	4.79*	6.89
VBN8	33	19.10*	2.55	21.40*	34.00*	4.95*	5.7	4.98*	8.90*
CO5	35	37.2	2.55	18.1	26.65	4.93*	5.65	3.79	4.81
ADT6	30.50*	35.80*	2.3	13.4	31.1	4.63	5.7	4.49	6.69
KKM1	30.5	36.2	2.5	19.7	33.5	4.53	5.85	4.56	8.09
Mean	33.31	41.18	2.55	16.13	31.23	4.59	5.92	4.29	6.7
SE _d ±	0.45	2.26	0.06	0.83	0.92	0.06	0.09	0.12	0.4
CD	2.28	1.34	0.29	0.85	2.31	0.09	0.38	0.12	0.37

*Significant at 5% level

Table-5 Per se performance of different traits in F₁'s

F ₁ 's	DF	PH	NBR	NCP	NPP	PL	NSP	HSW	SPY
ACM-16-023 x VBN6	32.00	36.23	2.67	15.93	34.88	4.70	6.70*	3.84	9.82
ACM-16-023 x VBN8	31.50	32.95	2.46	18.40*	40.10*	4.68	6.55	4.72	8.80
ACM-16-023 x CO5	33.50	37.45	2.76*	17.84*	34.25	4.82*	6.21	4.70	8.39
ACM-16-023 x ADT6	34.00	34.50	2.37	12.70	32.10	4.69	6.56	4.09	7.96
ACM-16-023 x KKM1	33.50	36.60	2.90	16.85	39.25	4.56	6.35	4.71	9.24
ACM-16-014 x VBN6	34.00	39.10	2.64	16.20*	38.00	4.70	6.75*	4.60	8.64
ACM-16-014 x VBN8	32.50	36.90	2.38	16.00*	40.95*	4.77	6.37	4.83*	11.24
ACM-16-014 x CO5	33.50	32.59	2.36	16.90*	37.35	4.75	6.77*	5.21*	12.11*
ACM-16-014 x ADT6	34.00	30.00	2.67	12.67	32.63	4.69	6.69*	4.54	9.67
ACM-16-014 x KKM1	34.50	37.60	2.37	12.90	40.25*	5.07*	6.73*	4.77*	11.05
ACM-16-017 x VBN6	31.50	42.30	2.67	16.63	39.55*	4.60	6.51	4.70	8.98
ACM-16-017 x VBN8	33.50	36.40	3.63*	24.00*	44.50*	5.31*	6.92*	4.76*	13.98*
ACM-16-017 x CO5	30.50*	30.75*	2.63	14.70	36.40	4.64	6.38	3.60	8.45
ACM-16-017 x ADT6	29.50*	34.65	2.37	16.02*	39.27*	4.60	6.94*	5.00*	9.85
ACM-16-017 x KKM1	33.50	32.59	2.36	16.90*	37.35	4.75	6.77*	5.21*	12.11*
MDU1 x VBN6	34.00	30.00	2.67	12.60	32.63	4.69	6.69*	4.63	8.43
MDU1 x VBN8	32.50	31.92	2.46	12.60	37.48	4.59	6.45	5.11*	10.35*
MDU1 x CO5	34.50	35.50	2.47	11.63	34.10	4.36	6.13	4.49	8.44
MDU1 x ADT6	31.50	33.70	2.45	11.10	33.40	4.80	6.04	4.23	8.02
MDU1 x KKM1	32.00	29.38	2.33	13.10	35.10*	4.62	6.68*	4.90*	9.59
Mean	33.11	34.76	2.51	13.62	35.37	4.66	6.36	4.40	9.16
SE _d ±	0.24	0.75	0.04	0.43	0.53	0.02	0.04	0.08	0.22
CD (0.05)	1.28	2.49	0.16	1.03	2.66	0.13	0.21	0.16	3.08

*Significant at 5% level

Table-6 General combining ability effects of parents for different traits

Parents	DF	PH	NBR	NCP	NPP	PL	NSP	HSW	SPY
Lines									
ACM-16-023	0.97*	2.04*	-0.08*	-0.49*	0.10	-0.001	0.08*	-0.08*	0.03
AM-16-014	-1.30*	0.43	0.28*	2.08*	3.38*	0.32*	0.36*	0.11*	1.95*
ACM-16-017	0.47	1.65	0.22*	1.65*	4.73*	0.17*	0.22*	0.41*	2.72*
MDU1	0.14	-1.61	-0.06	-1.74*	-4.66*	0.13*	0.23*	0.03*	1.43*
SE	0.12	0.82	0.09	1.05	2.09	0.08	0.04	0.10	0.69
Testers									
VBN6	0.02	-3.55*	-0.10*	-0.32*	-1.52*	-0.04*	-0.11*	0.09*	-0.36*
VBN8	-1.70*	-2.06*	0.20*	1.37*	2.50*	0.09*	0.29*	0.47*	1.12*
CO5	0.30	-0.43	0.09*	1.07*	3.20*	-0.07*	0.09*	0.23*	-0.02
ADT6	-0.03	-0.56	-0.16*	-3.84*	-0.88	-0.17*	-0.25*	-0.21*	-0.50*
KKM1	-0.98*	1.51*	0.17*	0.81*	1.42*	0.05*	0.04	-0.02	0.33*
SE	0.08	0.04	0.08	1.07	1.06	0.05	0.10	0.13	0.28

*Significant at 5% level

Table-7 Specific combining ability effects of F1's for different traits

F1's	DF	PH	NBR	NCP	NPP	PL	NSP	HSW	SPY
ACM-16-023 x VBN6	0.03	0.19	-0.34*	-0.15	2.21	0.02	0.27*	-0.19*	0.54
ACM-16-023 x VBN8	0.20	0.51	-0.49*	1.38*	0.89	0.01	0.17*	0.03	1.05*
ACM-16-023 x CO5	-0.52	-1.36	-0.16*	1.15*	1.92*	0.23*	0.15*	-0.08	-0.56
ACM-16-023 x ADT6	-0.02	1.60	0.04	0.48	1.82	-0.08	0.26*	-0.16*	0.40
ACM-16-023 x KKM1	0.48	0.70	-0.07	0.31	0.01	0.04	0.40*	0.12*	0.79*
ACM-16-014 x VBN6	-0.64	1.40	0.02	0.02	0.42	-0.03	0.36*	-0.22*	0.28
ACM-16-014 x VBN8	-0.68	0.26	0.20*	0.83*	2.79*	0.22*	0.12*	0.31*	1.34*
ACM-16-014 x CO5	0.15	0.07	-0.18*	-2.00*	-1.06	-0.03	0.33*	0.08	0.31
ACM-16-014 x ADT6	-0.52	-0.89	0.40*	0.45	-2.21	-0.06	0.12	0.30*	0.25
ACM-16-014 x KKM1	0.32	0.58	-0.07	0.80	2.70	0.03	0.18*	0.29*	1.39*
ACM-16-017 x VBN6	0.82	-1.17	0.05	-0.05	1.31*	0.05	0.37*	0.15*	0.32
ACM-16-017 x VBN8	0.15	0.41	0.58*	5.82*	4.91*	0.26*	0.12	0.14*	2.95*
ACM-16-017 x CO5	0.20	1.55	0.08	2.70	-1.58	-0.03	-1.18*	0.05	-0.49
ACM-16-017 x ADT6	-0.35	-1.62	0.10	-0.71	2.64	0.07	-0.15*	-0.14*	0.18
ACM-16-017 x KKM1	0.35	0.93	0.10	4.44*	4.02*	0.27*	0.04*	0.11	1.90*
MDU1 x VBN6	-0.85	-1.62	-0.04	1.65*	2.40	0.07	0.06	-0.05	0.36
MDU1 x VBN8	-0.30	1.36	0.20*	0.52	0.54	0.06	0.08	0.14*	0.97*
MDU1 x CO5	0.15	-0.82	-0.22*	-0.43	-1.71	0.02	0.17*	0.12*	0.11
MDU1 x ADT6	0.53	-0.24	0.11*	0.67	0.10	-0.15*	-0.10	0.24*	0.16
MDU1 x KKM1	-0.02	0.44	0.09	1.96*	-0.65	-0.07	0.25*	0.18*	1.01*
SE	0.10	0.23	0.02	0.19	0.37	0.01	0.02	0.02	0.08

*Significant at 5% level

The relative estimates of variance due to sca were higher than variance due to gca for days to 50% flowering, plant height, number of clusters per plant, number of pods per plant and single plant yield. Normally the sca effects do not contribute tangibly in the improvement of self pollinated crops, except where commercial exploitation of heterosis is feasible. Breeder's interest therefore rests in obtaining transgressive segregants through crosses by producing more potent homozygous [5]. Non-additive gene effects for plant height and number of pods per plants were also reported in urdbean by Baradhan and Thangavel (2011). Barad *et al* (2008) reported additive gene action in the control of days to 50% flowering, days to maturity and grain yield per plant in mung bean [6]. Whereas, plant height, number of clusters per plant, pods per plant, 100 seed weight and protein content were under the control of non-additive gene action. However, Singh *et al* (2003) reported the importance of both additive and non-additive components for plant height and grain yield per plant in urdbean [7]. The estimates of gca and per se performance of parents are given in [Table-4]. The parents with good per se performance and significant gca effects are considered as good general combiners for deriving desirable transgressive segregants in self pollinated crops. The parent ACM-16-014, VBN8, ADT6 and KKM1 were recorded significant desirable negative gca effects for days to 50% flowering, suggesting that these parents are good general combiners for breeding for earliness. The lines ACM-16-014 and testers VBN8 and KKM1 are also good general combiners for breeding for early maturity as they showed high negative gca effect. For plant height, line MDU1, ADT6, VBN6, VBN8 and CO5 showed significant negative gca effect indicating that it is a good general combiner for reduced plant height in blackgram during *kharif* season. For number of branches per plant lines, ACM-16-014, ACM-16-017 and tester KKM1 were good general combiners as they showed positive significant gca effects and their mean values were also high.

The lines ACM-16-014, ACM-16-017 and testers VBN8, KKM1 highly significant positive gca effects and high mean values for number of clusters per plant, number of pods per plant, number of seeds per pod, hundred seed weight and single plant yield, indicating that these genotypes are good general combiners for this important yield component. In the present investigation, the gca effects of lines indicated that the parent ACM-16-017, ACM-16-014, VBN8 and KKM1 were good general combiner for grain yield per plant, days to 50% flowering, number of pods per plant, number of clusters per pod, number of seeds per pod, pod length, 100 seed weight and single plant yield. The high gca effects are associated with additive and additive x additive interaction effects [8] hence, these good general combiners can be used in the varietal improvement programme of urdbean during *kharif* season.

Conclusion

The sca effect is an important criterion for the evaluation of hybrids. Among the various gene interactions contributing towards sca, the additive x additive type of gene interaction is fixable in later generations in self-pollinated crops like urdbean. Thus, the ultimate aim of a breeder is to generate desirable transgressive segregants to develop potential homozygous lines through hybridization. The cross combinations with significant desirable sca effects along with mean performance and gca effects of the parents for various traits are listed in [Table-6]. The cross ACM-16-017 x VBN8 and ACM-16-017 x KKM1 recorded significant positive sca effects and high per se performance for number of branches per plant, number of clusters per plant, number of pods per plant, number of seeds per pod, pod length, hundred seed weight and single plant yield. The crosses ACM-16-014 x VBN8 and ACM-16-014 x KKM1 recorded significant positive effects for number of branches per plant, number of pods per plant, number of

pods per plant, hundred seed weight and single plant yield. For days to 50% flowering and plant height, the crosses ACM-16-023 x ADT6, ACM-16-023 x CO5, ACM-16-014 x VBN6, MDU1 x KKM1 and MDU1 x VBN6 recorded negative sca effects as well as low mean values indicating early maturity.

Application of research: The present study described the importance of both additive and non-additive components of inheritance for yield and its parent traits. Therefore, breeding strategies like simple selection can be useful where particular cross combinations show additive component of variance.

Research Category: Plant Breeding and Genetics

Abbreviations:

DF – Days to 50% flowering
 PL – Pod length
 PH – Plant height
 NSP – number of seeds per pod
 NBR – Number of branches per plant
 HSW – hundred seed weight
 NCP – Number of clusters per plant
 SPY – Single plant yield
 NPP – Number of pods per plant
 GCA – General combining ability
 SCA – Specific combining ability

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Study area / Sample Collection: Research farm, Agricultural College and Research Institute, Coimbatore, 641003

Cultivar / Variety / Breed name: Blackgram (*Vigna mungo* (L.) Hepper)

Conflict of Interest: None declared

Ethical approval: This article does not contain any studies with human participants or animals performed by any of the authors.
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