Received: 21 Oct 2021 | Revised: 09 Dec 2021 | Accepted: 15 Dec 2021

Electronic Journal of Plant Breeding

Research Article

Estimation of genetic parameters and gene action among crosses of blackgram (*Vigna mungo* (L.) Hepper) for seed yield and its component traits

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Abstract

Generation mean analysis was employed among the crosses of MDU1 x TU68, VBN6 x TU68 and VBN8 x TU68 of blackgram to partition the mean into various genetic components *viz*., additive, dominance and epistasis. Five generations *viz.,* P_1, P_2, F_1, F_2 and F_3 obtained from the above three cross combinations were evaluated. The results of the scaling test showed that number of branches per plant in MDU 1 x TU 68, number of branches per plant and number of pods per cluster in VBN 6 x TU 68 and days to flowering and pod length in VBN 8 x TU 68 recorded additive gene action. Hence, these traits can be improved through pedigree breeding and simple selection. All other traits showed non additive model as one or both scales of C and D had significance. Days to flowering, plant height, number of branches per plant, number of clusters per plant, pod length, number of seeds per pod, 100-seed weight and single plant yield had additive gene action. In the case of epistasis, days to flowering had additive x additive type gene action in MDU 1 x TU68 and VBN6 x TU68 crosses, while the cross VBN8 x TU68 had additive gene action alone. Hence, the selection at later generations is effective to improve these traits. Other traits had differential gene action in each cross. Based on the results, it can be concluded that an appropriate selection programme needs to be devised for each cross based on the gene action.

Key words: Blackgram, Generation mean analysis, Epistasis, Five parameters, Seed Yield.

INTRODUCTION

Blackgram (*Vigna mungo* (L.) Hepper) is one of the important food legume crop of India. It gains its importance due to the short duration nature and wide spread cultivation in India. Blackgram is an excellent source of easily digestible good quality protein and it has its importance in restoring soil fertility through symbiotic soil - nitrogen fixation. Blackgram seeds possess 24-26% of protein, 60% of carbohydrates, 1.5 % of fat, minerals, amino acids and vitamins (Mehra *et al.,* 2016). The choice of an efficient breeding program depends mainly on the knowledge of the type of gene action involved in the expression of the character. Whereas, dominant gene action would favor the production of hybrids, additive gene action indicates that standard selection procedures would effectively bring about advantageous changes in characters (Edwards *et al.*, 1975). Generation mean analysis (GMA) has proved to be a potential technique to estimate gene action through different genetic parameters

https://doi.org/10.37992/2021.1204.170

(Kearsey and Pooni, 1996). The concept of generation mean analysis was initially developed by Hayman (1958) to estimate genetic components of variation. With this background, the present investigation was carried out to determine the gene action for seed yield and other yield component traits through generation mean analysis in blackgram.

MATERIALS AND METHODS

The experimental material comprising of the P_1, P_2, F_1, F_2 and F_3 derived from three crosses of blackgram *viz.,* MDU 1 x TU68, VBN6 x TU68 and VBN8 x TU68. The variety, MDU 1 was released from Agriculture College and Research Institute, Tamil Nadu Agricultural University, Madurai for commercial cultivation. VBN 6 and VBN 8 were released from National Pulses Research Centre, Tamil Nadu Agricultural University, Vamban. The genotype TU 68 was developed from the cross TU 94-2 x *Vigna mungo* var. *silvestris* by Bhabha Atomic Research Centre (BARC), Trombay. Five generations *viz.,* P_1, P_2, F_1, F_2 and F_3 of these three crosses were evaluated during *rabi,* 2019 with a plot size of 3 m length and a spacing of 30 cm as between row and 10 cm as within row. Recommended agronomic packages of practices were followed to raise the crop. Observations were recorded on individuals plant in respect of days to flowering, plant height (cm), number of branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, pod length (cm), number of seeds per pod, 100-seed weight (g) and seed yield per plant (g). Observations were documented on individual plants in respect to 10 quantitative traits. The mean of five generations *viz.,* P_1, P_2, F_1, F_2 and F_3 were used to estimate genetic parameters. The details of all the generations of the crosses are as follows.

Generations	MDU1 x TU68 (C1)	VBN6 x TU68 (C2)	VBN8 x TU68 (C3)
P_1	20	20	20
P_2	20	20	20
F_1	22	21	17
F_2	124	126	85
F_3	410	170	120

The scaling test for the GMA was performed as suggested by Mather (1949). The additive-dominance model of the population can be detected by employing a scaling test with C & D scales as suggested by Mather and Jinks (1971). The additive-dominance model was deliberated unsatisfactory when any one of the scales *viz*., C & D were found significant. Genetic parameters were assessed based on the suggestion of Hayman (1958). Five parameter model does not provide information about the additive x dominance (j) type of interaction. The data were analysed using the software TNAUSTAT statistical package (Manivannan, 2014).

RESULTS AND DISCUSSION

The generation mean analysis was implemented to detect the non-allelic interaction of the mean component in the phenotypic distribution of the yield traits. The mean and the standard errors of each cross among various generations are summarized in **Table 1**. The results of the scaling test and genetic parameters of various yield traits among each cross are presented in **Table 2**.

In the present investigation, three crosses *viz*., MDU1 x TU68, VBN6 x TU68 and VBN8 x TU68 were involved for the generation mean analysis. A good understanding of the genetic mechanisms regulating the expression of yield traits facilitates in selecting suitable efficient breeding procedures (Gopikannan and Ganesh, 2013; Mangaldeep *et al.,* 2015). The majority of the traits among any one of the crosses showed significant for both the scale C and D which indicates the presence of non- allelic interaction for the traits. The mean performance among the traits of MDU1 x TU68 cross showed that the generations i.e., F_1, F_2 and F_3 had intermittent performances considering the parental forms for the traits, days to flowering, plant height, number of pods per cluster, number of seeds per pod, hundred seed weight and seed yield per plant. Whereas, the traits number of clusters per plant, number of pods per plant and pod length showed increased effects among the generations of the cross comparing the parental forms involved in the crosses. The cross MDU1 x TU68 recorded a simple additive-dominance model for the trait number of branches per plant. Similarly, Latha *et al.* (2018) recorded an additive - dominance model for number of branches per plant in greengram. Hence, selection can be planned at early generation to improve the mean performance of progenies for this trait. Traits *viz.,* days to flowering, plant height, number of pods per cluster, pod length and number of seeds per pod had both additive as well as additive x additive gene action. Kanchana Rani (2008) and Vadivel *et al.* (2019) observed a similar type of additive and epistatic interaction in blackgram. Hence, these traits can be improved by postpone the selection to later generations. Traits *viz.,* number of clusters per plant, number of pods per plant, 100-seed weight and seed yield per plant had epistatic or dominance gene action. The results agree with Panigrahi *et al.* (2015) in blackgram. Hence, selection may not be effective for these traits. Epistatic gene or inter allelic interaction effects may be considered either complementary or duplicate gene action, depending on whether the additive x additive and dominance x dominance interactions are all significant and positive / negative or all significant with one negative and the other on positive direction. Two epistatic gene effects with the same sign are complementary, whereas different signs indicate duplicate epistasis (Kearsey and Pooni, 1996). The significant differential expression on the traits *viz.,* plant height, pod length, hundred seed weight and seed yield per plant showed duplicate epistasis among the traits involved in the study.

https://doi.org/10.37992/2021.1204.170

Table 1. Mean and standard error for yield and yield contributing traits in various generations among the different crosses of blackgram

Traits		P_1	P_2	F_1	F_2	F_3
Days to flowering	C1	36.15 ± 0.34	26.00 ± 0.26	31.95 ± 0.30	32.26 ± 0.27	32.41 ± 0.14
	C2	34.20 ± 0.31	26.05 ± 0.23	31.57 ± 0.33	31.17 ± 0.27	31.28 ± 0.23
	C3	34.30 ± 0.30	25.46 ± 0.33	31.25 ± 0.37	30.93 ± 0.34	31.10 ± 0.29
Plant height (cm)	C1	39.00 ± 0.99	21.61 ± 0.79	29.32 ± 0.81	24.39 ± 0.44	30.47 ± 0.37
	C2	28.80 ± 0.63	24.70 ± 0.69	26.10 ± 0.88	25.09 ± 0.44	27.71 ± 0.46
	C3	24.20 ± 0.91	21.62 ± 1.17	22.42 ± 1.21	19.84 ± 0.54	25.48 ± 0.50
Number of branches per plant	C1	2.00 ± 0.14	3.50 ± 0.17	1.73 ± 0.13	2.19 ± 0.07	2.32 ± 0.04
	C2	2.25 ± 0.14	3.85 ± 0.20	2.33 ± 0.14	2.47 ± 0.10	2.56 ± 0.09
	C3	2.25 ± 0.14	2.77 ± 0.20	2.50 ± 0.23	3.02 ± 0.15	2.71 ± 0.09
Number of clusters per plant	C1	6.20 ± 0.41	6.67 ± 0.48	6.64 ± 0.47	8.29 ± 0.21	7.85 ± 0.15
	C2	7.35 ± 0.42	12.45 ± 0.52	10.38 ± 0.67	10.72 ± 0.37	10.11 ± 0.29
	C3	7.80 ± 0.55	10.15 ± 0.70	7.75 ± 0.93	10.05 ± 0.38	12.58 ± 0.33
Number of pods per cluster	C1	3.40 ± 0.11	3.11 ± 0.14	3.14 ± 0.12	3.20 ± 0.05	3.07 ± 0.03
	C2	2.75 ± 0.10	2.35 ± 0.11	2.67 ± 0.11	3.02 ± 0.06	3.40 ± 0.05
	C3	2.70 ± 0.11	2.38 ± 0.14	2.50 ± 0.15	2.29 ± 0.08	2.63 ± 0.05
Number of pods per plant	C1	20.75 ± 1.68	20.11 ± 1.65	19.55 ± 1.44	26.11 ± 0.74	23.87 ± 0.49
	C2	23.70 ± 2.34	28.35 ± 2.59	26.76 ± 2.69	31.12 ± 1.27	31.86 ± 0.99
	C3	19.65 ± 2.01	21.92 ± 2.42	18.17 ± 1.95	22.72 ± 1.17	33.03 ± 0.99
Pod length (cm)	C1	4.72 ± 0.11	4.23 ± 0.06	5.13 ± 0.11	5.09 ± 0.05	4.81 ± 0.03
	C2	5.54 ± 0.08	4.92 ± 0.11	5.63 ± 0.10	4.86 ± 0.08	4.56 ± 0.05
	C3	5.52 ± 0.08	4.91 ± 0.11	5.39 ± 0.10	5.34 ± 0.05	5.39 ± 0.04
Number of seeds per pod	C1	6.95 ± 0.17	5.44 ± 0.22	6.91 ± 0.19	6.36 ± 0.09	6.48 ± 0.05
	C2	6.55 ± 0.11	5.45 ± 0.11	7.14 ± 0.14	6.81 ± 0.06	6.37 ± 0.07
	C3	6.55 ± 0.14	5.85 ± 0.15	6.17 ± 0.17	6.06 ± 0.07	6.39 ± 0.07
100 - seed weight (g)	C1	3.94 ± 0.09	2.56 ± 0.07	3.91 ± 0.08	2.85 ± 0.04	3.41 ± 0.03
	C2	3.45 ± 0.07	2.77 ± 0.07	3.06 ± 0.07	2.78 ± 0.03	2.94 ± 0.03
	C3	3.80 ± 0.07	2.56 ± 0.08	2.89 ± 0.09	3.11 ± 0.10	3.51 ± 0.06
Seed yield per plant (g)	C1	5.17 ± 0.19	3.65 ± 0.20	5.25 ± 0.25	4.48 ± 0.17	5.24 ± 0.11
	C2	5.02 ± 0.24	4.46 ± 0.34	4.19 ± 0.41	5.19 ± 0.21	5.92 ± 0.21
	C3	4.94 ± 0.33	3.44 ± 0.36	3.92 ± 0.45	5.16 ± 0.24	8.17 ± 0.36

C1=MDU 1 x TU 68; C2= VBN 6 x TU 68; C3=VBN 8 x TU 68

Among the various generation of the VBN6 x TU68 cross, the majority of the traits recorded intermittent performances within the parental forms except number of pods per cluster, number of pods per plant and number of seeds per pod. Which showed increased performances over the parents. The genetic parameters of cross VBN6 x TU68 showed that the traits, number of branches per plant and number of clusters per plant recorded a simple additive-dominance model (Latha *et al.,* 2018) and Vadivel *et al.* (2019). Hence, selection at earlier generation itself will be effective in improving the mean performance of the progenies for these trait. Days to flowering, number of pods per cluster, number of pods per plant, pod length, number of seeds per pod, 100-seed weight and seed yield per plant weight had both additive as well as additive x additive gene action. Hence, the selection needs to be practiced at later generations for these traits. Plant height recorded epistatic or dominance gene action. Non-additive gene action was reported by Panigrahi *et al.* (2015) for this trait in blackgram. These traits are not amenable for improvement through selection. Plant height, number of pods per cluster and seed yield per plant showed different signs among the epistatic genes specifying the presence of duplicate gene action for those traits.

Table 2. Scaling test and estimates of genetic parameters for various yield and yield contributing traits in blackgram

Traits		Scales		Parameters				
		C	D	m	d	h	i	l
Days to flowering	C1	3.0* ± 1.3	3.0** ± 0.9	32.3** ± 0.3	5.1** ± 0.2	-0.6 ± 0.7	8.7** ± 0.9	0.0 ± 2.4
	C2	1.3 ± 1.3	2.5* ± 1.1	31.2** ± 0.3	4.1** ± 0.2	0.0 ± 0.8	6.7** ± 0.9	1.7 ± 2.7
	C3	1.5 ± 1.6	2.8 ± 1.4	30.9** ± 0.3	4.4** ± 0.2	-0.2 ± 1.1	-	-
Plant height	C1	-21.7** ± 2.7	12.5** ± 2.2	24.4** ± 0.4	8.7** ± 0.6	-12.9** ± 1.4	5.4** ± 1.9	45.6** ± 4.6
	C2	-5.3* ± 2.7	7.2** ± 2.2	25.1** ± 0.4	2.1** ± 0.5	-6.3** ± 1.6	-1.6 ± 1.7	16.7** ± 4.9
	C3	-11.3** ± 3.6	16.4** ± 2.7	19.8** ± 0.5	1.3 ± 0.7	-13.3** ± 1.9	-10.3** ± 2.2	37.0** ± 6.0
Number of branches per plant	C1	-0.2 ± 0.4	-0.6 ± 0.3	2.2** ± 0.1	-0.8** ± 0.1	-0.7** ± 0.2	-	-
	C2	-0.9 ± 0.5	-0.8 ± 0.5	2.5** ± 0.1	-0.8** ± 0.1	-0.3 ± 0.3	-	-
	C3	2.1** ± 0.8	-0.2 ± 0.5	3.0** ± 0.1	-0.3* ± 0.1	0.5 ± 0.4	0.0 ± 0.5	-3.1* ± 1.4
Number of clusters per plant	C1	7.0** ± 1.4	1.9* ± 1.0	8.3** ± 0.2	-0.2 ± 0.3	0.1 ± 0.7	-0.6 ± 0.9	-6.8** ± 2.3
	C2	2.3 ± 2.1	-0.8 ± 1.5	10.7** ± 0.4	-2.6** ± 0.3	1.4 ± 1.2	-	-
	C3	6.7** ± 2.6	12.3** ± 1.8	10.0** ± 0.4	-1.2* ± 0.4	-8.3** ± 1.3	-9.4** ± 1.5	7.4 ± 4.3
Number of pods per cluster	C1	0.0 ± 0.4	-0.6* ± 0.2	3.2** ± 0.1	0.1 ± 0.1	0.3 ± 0.2	0.7** ± 0.2	-0.9 ± 0.6
	C2	1.7** ± 0.4	2.5** ± 0.3	3.0** ± 0.1	0.2** ± 0.1	-1.2** ± 0.2	-1.0** ± 0.2	1.1 ± 0.6
	C3	-0.9 ± 0.5	0.9** ± 0.3	2.3** ± 0.1	0.2 ± 0.1	-0.8** ± 0.2	-0.4 ± 0.3	2.4** ± 0.8
Number of pods per plant	C1	24.5** ± 4.8	2.4 ± 3.4	26.1** ± 0.7	0.3 ± 1.2	1.6 ± 2.2	3.1 ± 3.1	-29.5** ± 7.5
	C2	18.9* ± 8.2	13.1* ± 5.9	31.1** ± 1.3	-2.3 ± 1.7	-4.9 ± 4.1	-10.3* ± 5.1	-7.7 ± 13.5
	C3	13.0 ± 6.9	45.1** ± 5.6	22.7** ± 1.2	-1.1 ± 1.6	-30.5** ± 3.8	-30.2** ± 4.5	42.8** ± 12.0
Pod length	C1	1.2** ± 0.3	0.1 ± 0.2	5.1** ± 0.1	0.2** ± 0.1	0.8** ± 0.1	0.6* ± 0.2	-1.4* ± 0.5
	C2	-2.3** ± 0.4	-2.1** ± 0.3	4.9** ± 0.1	0.3** ± 0.1	1.4** ± 0.2	1.6** ± 0.3	0.3 ± 0.8
	C3	0.1 ± 0.3	0.5 ± 0.2	5.3** ± 0.0	0.3** ± 0.1	-0.1 ± 0.2	-	-
Number of seeds per pod	C1	-0.8 ± 0.6	0.8* ± 0.4	6.4** ± 0.1	0.8** ± 0.1	0.1 ± 0.3	0.9* ± 0.4	2.1* ± 0.9
	C2	1.0* ± 0.4	-0.1 ± 0.3	6.8** ± 0.1	0.6** ± 0.1	1.4** ± 0.2	1.3** ± 0.3	-1.5 ± 0.7
	C3	-0.5 ± 0.5	1.1** ± 0.4	6.1** ± 0.1	0.4** ± 0.1	-0.8** ± 0.3	-0.1 ± 0.3	2.1* ± 0.8
100 - seed weight	C1	-2.9** ± 0.3	1.4** ± 0.2	2.8** ± 0.0	0.7** ± 0.1	-0.8** ± 0.1	-0.1 ± 0.2	5.8** ± 0.4
	C2	-1.2** ± 0.2	0.0 ± 0.2	2.8** ± 0.0	0.3** ± 0.0	-0.2* ± 0.1	0.5** ± 0.1	1.6** ± 0.4
	C3	0.3 ± 0.4	1.5** ± 0.3	3.1** ± 0.1	0.6** ± 0.1	-1.2** ± 0.3	0.3 ± 0.3	1.6* ± 0.9
Seed yield per plant	C1	-1.4 ± 0.9	3.2** ± 0.6	4.5** ± 0.2	0.8** ± 0.1	-1.5** ± 0.5	-0.8 ± 0.6	6.1** ± 1.6
	C2	2.7* ± 1.3	3.8** ± 1.0	5.2** ± 0.2	0.3 ± 0.2	-2.6** ± 0.8	-1.6* ± 0.8	1.5 ± 2.4
	C3	4.4** ± 1.4	14.0** ± 1.6	5.2** ± 0.2	0.7** ± 0.2	-8.8** ± 1.1	-7.1** ± 1.0	12.7** ± 3.0

*,** Significant at 5 % and 1 % level of probability, respectively. C1=MDU 1 x TU 68; C2=VBN 6 x TU 68; C3=VBN 8 x TU 68.

The mean effects among the various generations recorded increased effects than the parents for the traits *viz.*, number of clusters per plant, number of pods per plant and seed yield per plant. The remaining traits showed an average effects within the range of parental forms. The generation mean analysis of the cross VBN8 x TU68 recorded a simple additive-dominance model for days to flowering and pod length. Hence, selection can be performed at early generation to improve the mean performance of progenies for these traits. Number of cluster per plant and seed yield per plant had both additive and additive x additive gene action. Hence, selection needs to be postponed to the later generations for these traits. Plant height, number of branches per plant, number of pods per cluster, number of pods per plant, number of seeds per pod and 100-seed weight had recorded epistatic or dominance gene action. These traits are not amenable for selection. These results are in agreement with Pal *et al.* (2007), Subhiah *et al.* (2013) and Thamodharan *et al.* (2015). Based on the epistatic gene expression, the traits *viz.,* plant height, number of pods per cluster, number of pods per plant, number of seeds per pod, 100 – seed weight and seed yield per plant had different sign indicating duplicate epistasis.

Based on the preceding discussion, it can be concluded that number of branches per plant in MDU 1 x TU 68, number of branches per plant and number of pods per cluster in VBN 6 x TU 68 and days to flowering and pod length in VBN 8 x TU 68 had additive gene action. A. similar type of results was also given by Selvam and Elangaimannan (2010); Prasad and Murugan, (2015). Hence, these traits can be improved through pedigree breeding and simple selection. All other traits showed non additive model as one or both scales of C and D had significance. Apart from this, days to flowering, plant height, number of branches per plant, number of clusters per plant, pod length, number of seeds per pod, 100-seed weight and single plant yield had additive gene action. In the case of epistasis, days to flowering had additive x additive type gene action in two crosses MDU 1 x TU68 and VBN6 x TU68, while the other cross VBN8 x TU68 had additive gene action alone. Additive gene action was found predominant over dominant gene action among the crosses involved in the study. Hence, the selection at later generations is effective to improve these traits. Other traits had differential gene action in each cross. Thus, an appropriate selection programme needs to be devised for each cross based on the gene action.

ACKNOWLEDGEMENT

The Authors are admitting the assistance rendered by Mr. Arul Doss, Agricultural Supervisor, NPRC, Vamban in the field trials.

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