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Gene action for yield and yield contributing traits in blackgram through generation mean analysis

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Abstract
Generation mean analysis was worked out for three crosses of blackgram *viz.,* VBN(Bg) 4 x CO 5, VBN(Bg) 4 x APK 1 and VBN(Bg) 4 x Mash 1008. Five parameter model was utilized in this study to identify the gene actions of various yield and yield contributing traits. Most of the traits recorded the presence of epistasis gene action. The traits *viz.,* pod length, the number of seeds per pod recorded additive-dominance model in the cross VBN(Bg) 4 x APK 1. Significant additive–dominance model for 100-seed weight recorded in the cross VBN(Bg) 4 x CO 5. Hence, these traits can be improved through pedigree breeding and simple selection. Significant additive or additive x additive gene action was observed for days to flowering, plant height, the number of pods per cluster and 100-seed weight in all crosses. The selection needs to be delayed due to the presence of additive or additive x additive gene action with an epistatic model. 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 followed for each cross based on the gene action.

Key words: Blackgram, Generation mean analysis, Additive-dominance model, Epistatic model.

INTRODUCTION

Blackgram is an important food legume and is mostly cultivated in south and southeast Asia. It is used as the best nutritive food for vegetarian people. It is a rich source of protein and phosphoric acid. Blackgram has been domesticated in India from its wild progenitor *V. mungo* var. *sylvestris* (Chandel *et al.,* 1984). Blackgram is short duration crop, hence it fits well in mixed crop and crop rotation. And also, it can be used as a green manure crop. It helps to enrich the soil nitrogen by an associate relationship with specific soil bacterium. Improvement of yield is the basic objective of the breeding programme. Yield is a complex trait controlled by a various genetic and environmental factor. Identification of gene action and inheritance pattern is important to improve the particular trait. Gene action has been estimated through generation mean analysis by Hayman (1954) and Jinks (1954). Such analysis is more useful for obtaining the gene action of the various genetic system involved and for fixing selection indices for speedy gains in segregating generations. Therefore, this study was conducted to identify the gene action of yield and yield contributing traits through generation mean analysis in three crosses of blackgram.

MATERIALS AND METHODS

Four genotypes *viz.,* VBN(Bg) 4, CO 5, APK 1 and Mash 1008 were utilized as parents to develop three crosses namely, VBN(Bg) 4 x CO 5, VBN(Bg) 4 x APK 1 and VBN(Bg) 4 x Mash 1008 (**Table 1**). Selected parents

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were crossed during the summer, 2019 at National Pulses Research Centre, Vamban. F_1 of the three crosses were sown during *kharif*, 2019. True F_1 plants were selfed to produce an F_2 population. The F_2 population was raised during *rabi,* 2019 to obtain F_3 seeds. All generations *viz.,* P_1, P_2, F_1, F_2 and F_3 were raised during summer, 2020. Sowing was carried out in a row of 3 m length with the plant to plant distance of 10 cm and row to row distance of 30 cm. Observations were recorded on 50 random plants of both the parents and F_1s. Observations *viz.,* days to flowering, plant height (cm), the number of branches per plant, the number of clusters per plant, the number of pods per cluster, the number of pods per plant, pod length (cm), the number of seeds per pod, 100 – seed weight (g) and seed yield per plant (g) were recorded on the plants. The presence or absence of non-allelic interaction is estimated by the scaling test (Mather, 1949). The generation mean analysis of five parameter model given by Hayman (1958) was followed. Five parameter model does not provide information about the additive x dominance (j) type of interaction. Generation mean analysis was computed using the software TNAUSTAT (Manivannan, 2014).

Table 1. List of parental material

S. No.	Genotype	Parentage	Source
1	VBN(Bg) 4	CO 4 x PDU 102	NPRC, Vamban
2	CO 5	Pureline selection from Musiri local	TNAU, Coimbatore
3	APK 1	ADT 2 x RU 1	RRS, Arupukkottai
4	Mash 1008	SML-32 x Mash-1	PAU, Ludhiana

RESULTS AND DISCUSSION

Generation mean and gene action of various generations and traits are presented in **Table 2** and **Table 3**, respectively. For the trait, days to flowering, the female parent VBN(Bg) 4 was late flowering compared to male parents. The mean performance among the traits of VBN(Bg) 4 x CO 5 cross showed that the generations i.e., F_1, F_2 and F_3 had intermediate performance considering the parental forms for the traits, days to flowering, plant height, the number of pods per cluster, the number of seeds per pod and hundred seed weight. Whereas, the traits, the number of branches per plant, the number of clusters per plant, the number of pods per plant, pod length and seed yield per plant showed increased effects among the generations of the cross compared to the parental forms involved in the crosses. Among the various generation of the VBN(Bg) 4 x APK 1 cross, the majority of the traits recorded intermediate performance within the parental forms except for the number of branches per plant, the number of clusters per plant, the number of pods per plant, pod length and seed yield per plant. Which showed increased performances over the parents. The mean effects among the various generations of cross VBN(Bg) 4 x Mash 1008 recorded increased effects than the parents for the traits *viz.*, the number of branches per plant, the number of clusters per plant, the thnumber of pods per cluster, the number of pods per plant and seed yield per plant. The remaining traits showed average effects within the range of parental forms.

All crosses recorded significant C scale indicates the presence of epistasis gene action for the trait days to flowering. Additive and additive x additive genetic components were significant in all crosses. Dominance and dominance x dominance components were significant in VBN(Bg) 4 x Mash 1008. This cross had a same sign for dominance and dominance x dominance components which indicates the presence of complementary gene interaction. The cross VBN(Bg) 4 x APK 1 had a significant component of dominance x dominance. Hence, simple selection in the later generation will be effective to improve this trait due to the presence of additive and presence of epistasis gene action. Panigrahi *et al.* (2020) also observed similar findings in blackgram. The presence of a significant scaling test in all crosses indicates the inadequacy of the additive-dominance model for plant height. For plant height additive, additive x additive and dominance x dominance gene interactions were significant in VBN(Bg) 4 x CO 5 and VBN(Bg) 4 x APK 1. VBN(Bg) 4 x Mash 1008 had significant additive and dominance x dominance components. Similar results were reported by Haque *et al*. (2013) in blackgram crosses. Simple selection in the later generations will be effective in these crosses due to the presence of additive as well as epistasis gene action. The significance of the scaling test for the number of branches indicated the presence of epistasis gene action in all crosses. Dominance and additive x additive gene interaction were significant in VBN(Bg) 4 x CO 5. Dominance, additive x additive and dominance x dominance interaction were significant in VBN(Bg) 4 x APK 1 and VBN(Bg) 4 x Mash 1008 crosses. Dominance and dominance × dominance gene effects of VBN(Bg) 4 x APK 1 and VBN(Bg) 4 x Mash 1008 crosses had opposite signs indicating the presence of duplicate epistasis. Postponement of selection at later generations will be helpful to improve this trait due to the presence of additive x additive gene action of epistasis. Latha *et al*. (2018) and Panigrahi *et al.* (2020) reported similar findings among various blackgram crosses.

Inadequacy of additive-dominance model was observed for all crosses for the number of clusters per plant. Significant additive and additive x additive genetic components were observed in VBN(Bg) 4 x APK 1. Additive, dominance, additive x additive and dominance x dominance components were significant in VBN(Bg) 4 x Mash 1008, dominance and additive x additive components were significant in VBN(Bg) 4 x CO 5. Selection in the later generation will be effective in the crosses VBN(Bg) 4 x APK 1 and VBN(Bg) 4 x Mash 1008 due to the presence of additive and epistatic components. Opposite signs of dominance and dominance x dominance interaction in the cross VBN(Bg) 4 x Mash 1008 indicates the presence of duplicate gene interaction. Similar results were reported by Vandodariya *et al.* (2020) in blackgram. Non- significant scaling test was observed in the cross VBN(Bg) 4 x Mash 1008 which indicated the presence of additive-dominance model. VBN(Bg) 4 x Mash 1008 had significant additive gene action. A simple selection technique may improve this trait in this cross. However, a non-additive model was observed in the other two crosses VBN(Bg) 4 x CO 5 and VBN(Bg) 4 x APK 1. The additive gene effect was significant in all the crosses. Dominance, additive x additive and dominance x dominance genetic components were significant in VBN(Bg) 4 x CO 5. Both additive x additive and dominance x dominance genetic components were significant in the cross VBN(Bg) 4 x APK 1. The opposite sign of dominance and dominance x dominance genetic components were observed in the cross VBN(Bg) 4 x CO 5 which indicated the presence of duplicate gene interaction. Vadivel *et al.* (2019) reported similar findings in a various set of crosses of blackgram. Simple selection in the later generations will be effective in these crosses due to the presence of additive as well

Table 2. 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	42.19 ± 0.22	34.67 ± 0.15	37.17 ± 0.11	38.53 ± 0.26	38.72 ± 0.28
	C2	42.19 ± 0.22	34.84 ± 0.18	35.96 ± 0.16	38.95 ± 0.27	39.35 ± 0.29
	C3	42.19 ± 0.22	34.76 ± 0.09	36.83 ± 0.13	38.54 ± 0.26	38.40 ± 0.29
Plant height (cm)	C1	27.56 ± 0.43	36.26 ± 0.72	31.60 ± 0.77	29.20 ± 0.55	30.59 ± 0.70
	C2	27.56 ± 0.43	30.08 ± 0.62	32.16 ± 0.77	27.80 ± 0.53	28.05 ± 0.55
	C3	27.56 ± 0.43	24.30 ± 0.30	29.60 ± 0.51	25.08 ± 0.45	26.75 ± 0.47
Number of branches per plant	C1	2.00 ± 0.13	1.90 ± 0.12	1.60 ± 0.12	2.29 ± 0.10	2.54 ± 0.09
	C2	2.06 ± 0.13	1.82 ± 0.14	2.50 ± 0.10	2.61 ± 0.12	1.95 ± 0.10
	C3	2.06 ± 0.13	1.96 ± 0.12	2.56 ± 0.20	1.98 ± 0.15	3.07 ± 0.17
Number of clusters per plant	C1	8.38 ± 0.31	8.87 ± 0.12	8.80 ± 0.41	11.17 ± 0.41	12.37 ± 0.51
	C2	8.38 ± 0.31	10.60 ± 0.49	11.70 ± 0.72	10.80 ± 0.52	11.51 ± 0.55
	C3	8.38 ± 0.31	9.50 ± 0.36	8.73 ± 0.52	9.23 ± 0.38	13.38 ± 0.40
Number of pods per cluster	C1	3.34 ± 0.11	2.96 ± 0.06	3.13 ± 0.12	2.70 ± 0.07	3.48 ± 0.05
	C2	3.34 ± 0.11	2.36 ± 0.08	3.13 ± 0.10	3.57 ± 0.09	3.30 ± 0.07
	C3	3.34 ± 0.11	2.64 ± 0.09	3.43 ± 0.12	3.41 ± 0.08	3.31 ± 0.08
Number of pods per plant	C1	26.78 ± 1.27	26.10 ± 0.89	22.60 ± 1.71	28.61 ± 1.24	33.61 ± 1.49
	C2	26.78 ± 1.27	27.90 ± 1.01	32.90 ± 1.25	33.44 ± 0.94	34.69 ± 1.04
	C3	26.78 ± 1.27	27.34 ± 1.43	29.43 ± 2.00	27.93 ± 1.42	37.42 ± 1.71
Pod length (cm)	C1	5.21 ± 0.12	5.11 ± 0.08	5.43 ± 0.13	5.33 ± 0.07	5.45 ± 0.56
	C2	5.21 ± 0.12	5.53 ± 0.14	6.03 ± 0.18	5.67 ± 0.16	5.31 ± 0.17
	C3	5.21 ± 0.12	4.80 ± 0.09	5.26 ± 0.12	4.63 ± 0.08	5.08 ± 0.09
Number of seeds per pod	C1	6.71 ± 0.12	6.85 ± 0.13	7.17 ± 0.14	6.89 ± 0.14	6.42 ± 0.14
	C2	6.71 ± 0.12	6.36 ± 0.11	6.53 ± 0.14	6.45 ± 0.09	6.49 ± 0.08
	C3	6.71 ± 0.12	6.22 ± 0.09	6.86 ± 0.16	6.25 ± 0.09	6.58 ± 0.08
100 - seed weight (g)	C1	4.25 ± 0.08	4.54 ± 0.05	4.34 ± 0.07	4.15 ± 0.08	4.29 ± 0.04
	C2	4.25 ± 0.08	3.98 ± 0.08	3.91 ± 0.07	4.37 ± 0.06	4.23 ± 0.05
	C3	4.25 ± 0.08	3.76 ± 0.09	4.31 ± 0.11	3.94 ± 0.06	4.13 ± 0.04
Seed yield per plant (g)	C1	6.01 ± 0.45	6.06 ± 0.31	6.07 ± 0.48	6.04 ± 0.27	7.51 ± 0.36
	C2	6.01 ± 0.45	5.88 ± 0.43	6.82 ± 0.40	8.08 ± 0.42	6.85 ± 0.34
	C3	6.01 ± 0.45	4.85 ± 0.34	6.70 ± 0.56	6.09 ± 0.34	8.05 ± 0.39

C1 – VBN(Bg) 4 x CO 5, C2 – VBN(Bg) 4 x APK 1, C3 – VBN(Bg) 4 x Mash 1008.

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as epistasis gene action. Significance of the scaling test was observed in all three crosses for the trait number of pods per plant which indicates an epistatic model for all crosses. Additive x additive gene interaction was significant in all crosses. The cross VBN(Bg) 4 x CO 5 had a significant dominance component. Dominance and Dominance x dominance interaction were significant in the cross VBN(Bg) 4 x Mash 1008. The opposite sign of dominance and dominance x dominance gene interaction observed in the cross VBN(Bg) 4 x Mash 1008 indicated the presence of duplicate gene interaction. Selection needs to be postponed to a later generation in all crosses due to the presence of a significant additive x additive genetic component. A similar type of results was observed in various blackgram crosses for this trait as reported by Panigrahi *et al.* (2020).

Table 3. 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	2.93** ± 1.09	0.96 ± 1.26	38.53** ± 0.25	3.76** ± 0.13	-1.42 ± 0.91	7.36** ± 0.87	-2.63 ± 2.57
	C2	3.53** ± 1.1	-0.42 ± 1.29	38.54** ± 0.26	3.71** ± 0.12	-0.77 ± 0.93	8.30** ± 0.88	-5.28* ± 2.62
	C3	6.86** ± 1.17	2.49 ± 1.31	38.95** ± 0.27	3.67** ± 0.14	-3.07** ± 0.95	6.83** ± 0.9	-5.82* ± 2.7
Plant height	C1	-10.23** ± 2.8	0.14 ± 3.12	29.20** ± 0.55	-4.35** ± 0.42	-2.11 ± 2.22	-10.50** ± 2.05	13.83* ± 6.1
	C2	-10.78** ± 2.72	-1.02 ± 2.55	27.80** ± 0.53	-1.25** ± 0.38	2.23 ± 1.88	-3.63* ± 1.85	13.00* ± 5.54
	C3	-10.74** ± 2.14	4.98* ± 2.15	25.09** ± 0.45	1.63** ± 0.26	-1.43 ± 1.58	-1.85 ± 1.55	20.96** ± 4.6
Number of branches per plant	C1	2.01** ± 0.51	3.26** ± 0.62	2.29** ± 0.1	0.08 ± 0.09	-2.22** ± 0.43	-1.67** ± 0.41	1.67 ± 1.16
	C2	1.58** ± 0.56	-1.30* ± 0.51	2.62** ± 0.12	0.12 ± 0.1	1.69** ± 0.37	1.37** ± 0.4	-3.83** ± 1.14
	C3	-1.21 ± 0.76	4.30** ± 0.77	1.99** ± 0.15	0.05 ± 0.09	-2.51** ± 0.57	-2.96** ± 0.54	7.34** ± 1.63
Number of clusters per plant	C1	9.81** ± 1.86	9.92** ± 2.23	11.17** ± 0.41	-0.25 ± 0.2	-4.81** ± 1.61	-5.48** ± 1.46	0.14 ± 4.37
	C2	0.86 ± 2.59	5.48* ± 2.5	10.81** ± 0.52	-1.11** ± 0.29	-1.3 ± 1.86	-5.74** ± 1.78	6.17 ± 5.43
	C3	1.59 ± 1.93	17.18** ± 1.87	9.24** ± 0.39	-0.56* ± 0.24	-11.39** ± 1.38	-12.31** ± 1.34	20.79** ± 4.04
Number of pods per cluster	C1	-0.77 ± 0.41	2.20** ± 0.31	2.70** ± 0.08	0.19** ± 0.07	-2.12** ± 0.23	-1.21** ± 0.27	3.97** ± 0.76
	C2	2.31** ± 0.44	0.36 ± 0.39	3.57** ± 0.09	0.49** ± 0.07	0.43 ± 0.29	1.13** ± 0.31	-2.60** ± 0.88
	C3	0.78 ± 0.44	0.47 ± 0.38	3.41** ± 0.08	0.35** ± 0.07	0.26 ± 0.28	-	-
Number of pods per plant	C1	16.37** ± 6.22	24.32** ± 6.64	28.61** ± 1.24	0.34 ± 0.78	-17.33** ± 4.82	-12.81** ± 4.57	10.6 ± 13.49
	C2	13.29* ± 4.83	17.19** ± 4.85	33.44** ± 0.95	-0.56 ± 0.81	-3.69 ± 3.45	-10.36* ± 3.51	5.20 ± 9.96
	C3	-1.25 ± 7.23	39.72** ± 7.65	27.94** ± 1.43	-0.28 ± 0.96	-24.31** ± 5.54	-27.24** ± 5.23	54.62** ± 15.55
Pod length	C1	-0.19 ± 0.45	0.98* ± 0.41	5.25** ± 0.08	0.05 ± 0.07	-0.42 ± 0.29	-0.58* ± 0.31	1.56 ± 0.89
	C2	-0.09 ± 0.75	-0.85 ± 0.66	5.68** ± 0.15	-0.15 ± 0.09	1.21* ± 0.49	-	-
	C3	-2.00** ± 0.43	1.04* ± 0.42	4.64** ± 0.08	0.21** ± 0.07	-0.77* ± 0.3	-0.61* ± 0.31	4.05** ± 0.86
Number of seeds per pod	C1	-0.33 ± 0.65	-1.70** ± 0.65	6.89** ± 0.14	-0.07 ± 0.09	1.46** ± 0.47	0.93* ± 0.47	-1.82 ± 1.39
	C2	-0.33 ± 0.49	-0.02 ± 0.41	6.45** ± 0.09	0.18* ± 0.09	-0.05 ± 0.3	-	-
	C3	-1.65** ± 0.5	0.87* ± 0.4	6.26** ± 0.09	0.25** ± 0.08	-0.46 ± 0.3	-0.36 ± 0.33	3.36** ± 0.92
100 - seed weight	C1	-0.86 ± 0.37	0.05 ± 0.25	4.15** ± 0.08	-0.14** ± 0.05	-0.24 ± 0.20	-	-
	C2	1.41** ± 0.31	-0.03 ± 0.29	4.37** ± 0.06	0.14** ± 0.06	0.06 ± 0.21	0.53* ± 0.22	-1.93** ± 0.62
	C3	-0.86* ± 0.35	0.61*± ± 0.26	3.95** ± 0.06	0.25** ± 0.06	-0.25 ± 0.2	-0.06 ± 0.22	1.96** ± 0.64
Seed yield per plant	C1	1.65 ± 1.55	5.90** ± 1.65	6.04** ± 0.27	-0.02 ± 0.28	-4.49** ± 1.15	-3.71** ± 1.15	5.67 ± 3.16
	C2	6.30* ± 2.04	-1.10 ± 1.75	8.08** ± 0.41	0.30 ± 0.35	2.42 ± 1.27	2.40 ± 1.42	-9.88** ± 4.01
	C3	0.08 ± 1.86	9.17** ± 1.82	6.09** ± 0.34	0.58* ± 0.29	-4.83** ± 1.31	-4.93** ± 1.31	12.11** ± 3.76

*,** Significant at 5 % and 1 % level of probability, respectively. C1 – VBN(Bg) 4 x CO 5, C2 – VBN(Bg) 4 x APK 1, C3 – VBN(Bg) 4 x Mash 1008.

For the trait pod length, the scaling test indicates the presence of an additive-dominance model in the cross VBN(Bg) 4 x APK 1 only. The cross VBN(Bg) 4 x APK 1 had a significant dominance component. The significant additive genetic component was observed in VBN(Bg) 4 x Mash 1008 only. Crosses VBN(Bg) 4 x CO 5 and VBN(Bg) 4 x Mash 1008 had significant additive x additive genetic component. Significant and opposite signs for dominance and dominance x dominance genetic components in the cross VBN(Bg) 4 x Mash 1008 indicated the presence of duplicate gene action. Selection needs to be delayed till the attainment of homozygosity due to the presence of additive x additive genetic components in VBN(Bg) 4 x CO 5 and VBN(Bg) 4 and Mash 1008. Similarly, Vadivel *et al*. (2019) observed the additive and epistatic gene action for pod length among blackgram crosses. The trait number of seeds per pod recorded additive-dominance model for the cross VBN(Bg) 4 x APK 1 only. The additive genetic component was significant in VBN(Bg) 4 x APK 1 and VBN(Bg) 4 x Mash 1008. The cross VBN(Bg) 4 x CO 5 had significant genetic components of dominance and additive x additive. The cross VBN(Bg) 4 x Mash 1008 had significant dominance x dominance genetic component. Immediate selection through the pedigree method can be adopted in the cross VBN(Bg) 4 x APK 1 due to the presence of additive gene action with the additive – dominance model. However, in the other two crosses, the selection needs to be delayed due to the presence of additive or additive x additive gene action with an epistatic model. Similar results were reported by Vadivel *et al.* (2019) and Vandodariya *et al.* (2020) in blackgram. Additive – dominance model was observed for the cross VBN(Bg) 4 x CO 5 for the trait 100-seed weight. Significant additive gene action was observed for all crosses. Additive x additive and dominance x dominance gene interaction were significant in the cross VBN(Bg) 4 x APK 1. Dominance x dominance gene interaction was significant for VBN(Bg) 4 x Mash 1008. Immediate selection through the pedigree method can be adopted in the cross VBN(Bg) 4 x CO 5 due to the presence of additive gene action with the additive – dominance model. However, in the other two crosses, the selection needs to be delayed due to the presence of additive or additive x additive gene action with an epistatic model. Zubair *et al.* (2007) reported similar findings of additive gene action for 100-seed weight in greengram. The significance of the scaling test for the trait seed yield per plant denotes the presence of epistasis gene interaction in all crosses. Additive and additive x additive genetic components were significant in cross VBN(Bg) 4 x Mash 1008. Dominance and additive x additive genetic components were significant in the cross VBN(Bg) 4 x CO 5. A significant dominance x dominance gene interaction was observed in the cross VBN(Bg) 4 x APK 1. Selection needs to be postponed to a later generation in crosses VBN(Bg) 4 x CO 5 and VBN(Bg) 4 x Mash 1008 due to the presence of additive x additive genetic component. A similar type of results was also given by Selvam and Elangaimannan (2010); Prasad and Murugan, (2015) in blackgram.

Generation mean analysis revealed each population had various nature of gene action. Therefore, the selection of breeding methods for each population was effective to improve the trait (Hettiarachchi *et al*., 2009). The effect of “m” was positive and significant for all the cross. Hence, there was a significant difference among generations. Significance of scaling test revealed the presence of digenic and higher order interaction in addition to principle gene effects in these crosses. The traits *viz.,* pod length, the number of seeds per pod recorded additive-dominance model in the cross VBN(Bg) 4 x APK 1. Significant additive–dominance model for 100-seed weight recorded in the cross VBN(Bg) 4 x CO 5. Simple selection may be effective for the improvement of a trait having additive-dominance model. The traits *viz.,* days to flowering, plant height, the number of branches per plant, the number of clusters per plant, the number of pods per cluster, the number of pods per plant and seed yield per plant recorded inadequacy of additive-dominance model for all crosses. A significant additive or additive x additive gene action was observed for days to flowering, plant height, the number of pods per cluster and 100-seed weight in all crosses. The selection needs to be delayed due to the presence of additive or additive x additive gene action with an epistatic model. The other traits *viz.,* the number of branches per plant, the number of clusters per plant, the number of pods per plant and seed yield per plant recorded various epistasis effects for all crosses. An individual breeding method is needed for an individual cross.

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