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Generation mean analysis for yield, yield components in blackgram [*Vigna mungo* (L). Hepper]

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Abstract
Using the means of P_1, P_2, F_1, F_2 and F_3 generations in each cross, estimates of various gene effects were obtained by partitioning method of five crosses for thirteen characters. Additive dominance model is failed in all the cases, hence five parameter model was applied which gave the information about the Digenic interactions between the genes at different loci. The nature of gene action for seed yield and yield attributing traits were assessed in five crosses. An experiment was conducted to fulfill the objective of estimation of Heterosis and understands genetic nature of seed yield and contributing traits have been carried out by growing the parents, P_1 and P_2 along with F_1, F_2 and F_3 during Rabi 2018 in Randomized complete block design replicated three times. A total of five populations (5 crosses) and five generations of each cross were grown. The mean data of populations were subjected to joint scale test. The results of generation mean analysis indicated varying nature of genes under different genetic backgrounds.

Keywords: Generation mean analysis, five parameter model, yield, blackgram

Introduction
Vigna, a pan tropical genus comprises about 150 species, most of which are found in Asia and Africa. Only seven species of *Vigna* are cultivated as pulse crop, of which two are African and five are of Asiatic origin, in which black gram (*Vigna mungo* L. Hepper) is an ancient and well known crop in Asia particularly in the Indian subcontinent and is now becoming popular in other continents. It is an important short duration crop and widely cultivated in India. It is an excellent source of easily digestible good quality vegetable protein and ability to restore the fertility of soil through symbiotic nitrogen fixation. Seeds are highly nutritious with protein (24-26%), carbohydrates (60%), fat (1.5%), minerals, amino acids and vitamins (Vadivel *et al*., 2019) [12]. The biological value improves greatly, when wheat or rice is combined with blackgram because of the complementary relationship of the essential amino acids such as arginine, Leucine, lysine, isoleucine, Valine and phenylalanine, etc. (Mehra *et al*., 2016) [8]. Generation mean analysis is one such useful tool for estimation of gene effects for polygenic traits which can estimate epistatic gene effects such as additive × additive, dominance × dominance and additive × dominance effects. Generation mean analysis provides information on the relative importance of average effects of the genes (additive effects), dominance deviations and effects due to non-allelic genetic interactions such as additive x additive (*i*) and dominance x dominance (*l*) effects to determining genotypic values of the individuals and consequently mean genotypic values of families and generations. Such analysis is very useful for rapidly obtaining the overall information on the various genetic system involving and for fixing selection indices for speedy gains in segregating generations. Therefore, in the present study gene interaction was estimated for yield attributing characters in blackgram by using generation mean analysis.

Material and Methods
To understand the genetic nature of seed yield and its contributing traits have been carried out by growing the parents, $P_1$and P_2 along with F_1, F_2 and F_3. A total of five populations (5 crosses) and five generations of each cross were grown. Within each replication, cross populations were first randomized and separate randomization was followed for all the replications. Generations within crosses/populations were also randomized separately. Two rows of 4 m length and 30 cm apart were planted for generations *i.e*., P_1 and P_2 and F_1 were grown where as F_2 & F_3 generations in 8 rows each were grown. Irrigation at sowing was given to ensure complete seed germination. Thereafter, irrigation, weeding and other agronomical operations were adopted to raise good crop. Scaling test was conducted as suggested by Mather (1949) [6].

The adequacy of simple additive-dominance model was detected by employing C and D scaling test suggested by Mather and Jinks (1971) [7]. The additive-dominance model was considered inadequate when any one of the two scales was found to deviate significantly from zero. Genetic parameters were estimated following Hayman (1958) [2].

Results and Discussion

Using the means of P_1, P_2, F_1, F_2 and F_3 generations in each cross, estimates of various gene effects were obtained by portioned method of weighted least square analysis of three parameter model fitted to five generation means of each cross for thirteen characters. Both the scaling tests 'C' and 'D' were found significant for all the crosses indicating the inadequacy of simple additive- dominance model for explaining the inheritance of traits and also indicating the involvement of non-allelic gene effects. The two interaction effects namely "*i*" explain the sum of additive x additive effects of genes and *l* sum of dominance x dominance effects of genes were estimated in five parameter model along with *m*, *d* and *h*. It will therefore, be convenient to present the results of this analysis separately for each cross combination for all thirteen characters of five crosses.

A good knowledge on the genetic systems controlling expression of the characters facilitates the choice of the most efficient breeding and selection procedure (Mangaldeep *et al*., 2015) [5]. The generation mean analysis was adopted to detect non-allelic interaction component of the mean of the phenotypic distribution. The results of scaling test and genetic parameters in each cross were presented in (Table 1, 2, 3, 4 and 5).

The present study was planned to estimate the nature and magnitude of allelic and non-allelic interactions in blackgram. Eight elite genotypes differing in many quantitative characters were chosen to create variability in five crosses. The five generation of these crosses were grown and observations were recorded on thirteen characters. The discussions on the results obtained with regard to nature of gene actions are reported here cross wise.

LBG 20 x P 1070

The estimates of scaling tests C and D were found significant for all the traits indicating the inadequacy of simple additive-dominance model for explain the traits. In this cross both additive and dominant gene effects were found significant for all the traits except pod length, number of seed per pod and chlorophyll content. The magnitude of additive gene effects were higher than the dominance gene effects for majority of the characters except number pods per plant and number of seeds per pod indicating the role of additive gene effects in expression of traits in this cross. Duplicate type of epistasis was observed in most of the traits in this cross except for number of clusters per plant, pod length and 100 seed weight. Both type of inert actions (additive x additive, dominance x dominance) were found significant majority of the traits. Additive x additive type of non-allelic interaction was positively significant for days to 50% flowering, plant height, leaf area and SPAD. Further it can be observed that, the dominance x dominance component of gene interaction is having higher magnitude than the additive x additive for most of the characters showing the predominance of non-fixable genetic variance. Preponderance of duplicate type of non-allelic interactions for most of the traits were also reported earlier by Satya *et al*., (2021) [9] Vadodariya *et al*., (2020) [13] and Raghul *et al*. (2021) [10]. Although, additive x additive gene effects are significant for most of the traits under study, non-additive gene effects appear to be over power them. In this situation Biparental mating or recurrent selection followed by conventional selection procedures are appear to be appropriate for improvement traits in this cross.

LBG 752 x P 1053

The estimates of scaling tests and gene effects in five parameter model were presented in table 2. The scaling tests were found significant for all the traits indicating the simple additive dominance model is not adequate for explaining the inheritance of traits and involvement of non-allelic interaction. Both additive and dominance gene effects were found significant for all the traits except for number of branches per plant (Durga prasada *et al*., 2015) [1]. The magnitude of additive gene effects is higher than the dominance gene effects for most of the traits except pod length, number of seeds pod, days to maturity, leaf area and chlorophyll content. It indicates the importance additive gene effects in the inheritance traits in this cross. Further, the magnitude of dominance x dominance (*l*) non allelic interaction is larger than the either additive gene effects (d) or additive x additive (*i*) gene interaction. It clearly indicates the presence of dominance x dominance gene effects in the expression of the traits. The sign of dominance x dominance was negative for pod length, days to maturity and leaf area suggesting the dominance at one loci is in negative direction *ie*., shorter pods, short duration and less leaf area. But the cumulative effects of all loci are in positive direction. Duplicate type of epistasis is predominant for most of the characters under study. In spite of significant additive and additive x additive gene effects were significant for all the traits but non additive gene effects appears to be over power them which is evident from its magnitude. Predominance of non-additive gene effects for expression of traits were in accordance with Singh *et al*., (2016) [11].

MBG 207 x PU 31

The scaling tests C and D were significant for all the traits except for chlorophyll content which is having significant for D scaling test alone, 100 seed weight and leaf are found to be significant for C test alone. Thus scaling tests indicates the involvement of non-allelic inter action on the inheritance of traits. Out of thirteen traits studied, days to 50% flowering, plant height, number of clusters per plant, number of pods per plant, pod length, number of seed per pod, 100 seed weight, days to maturity, leaf area, SPAD and seed yield are found to be significant and higher additive gene effects than the dominance gene effects indicating the role of additive gene effects in the expression of these traits. Further the magnitude of dominance x dominance non allelic inter action is larger than additive or additive x additive gene effects for majority of the traits under study. Preponderance of additive x additive type non allelic inter action for most the traits were earlier reported by Singh *et al*. (2016) [11]. The sign of dominance x dominance inter actions is in negative directions suggesting that dominance at some of the loci are in negative direction.

TBG 104 x PU 31

In this cross, both additive and dominance gene effects were significant for most of the traits under study except for days to

50% flowering and chlorophyll content. In case of chlorophyll content both the gene effects were non-significant where as significant negative dominance gene effects were recorded for plant height, number of clusters per plant, number of branches per plant, number of pods per plant and seed yield per plant. Duplicate type epistasis was recorded for majority of the crosses except for days to 50% flowering, number of seed per plant, 100 seed weight, SPAD and chlorophyll content. Both additive x additive and dominance x dominance gene inter actions were significant for all the traits except for pod length. Preponderance of duplicate types of non-allelic interaction for most the traits was also earlier reported by Kachave *et al*., (2015) [4]. Although, additive, additive x additive were significant for most of the traits in this cross, non-additive gene effects appears to be over power them for this reason a breeding procedure like Heterosis breeding which could exploit the kind of gene action would be appropriate for improvement of traits under study. In the present situation biparental mating or recurrent selection followed by convention selection procedures (DSMS) are to be appropriate for improvement of traits under study.

TU 68 x P 1053

The scaling test C and D were found to be significant for all the traits indicating the inadequacy of simple additive dominance model and presence of epistatic interaction. Significant positive additive gene effects were recorded for days to 50% flowering, plant height, pod length, days to maturity, SPAD and seed yield per plant where as number of branches per plant and leaf area exhibited negative significant gene effects. Negative significant dominance gene effects were recorded for most of the traits where as positive significant gene effects were recorded for plant height, number seed per pod, leaf area, SPAD and chlorophyll content. Further, it is observed that, the magnitude of dominance x dominance non allelic interactions is also larger than either additive gene effects or additive x additive gene effects. This clearly indicates the presence of non-allelic interaction in the expression of traits in this cross. The component means suggests that involvement of non-allelic interactions for most of the traits. The *h* and *l* are same direction for majority of the crosses indicates the presence of complementary types of epistatic inter action. This type preponderance of non-allelic interaction was also earlier reported by Jagadish and Jayalaxmi (2014) [3].

This can be concluded from the present findings that seed yield and its related characters are under the control of duplicate types epistasis mostly. The results further indicated varying expression of the genes under different genetic background. Significant inbreeding depression also gave an indication of prevalence of dominance genetic variance along with duplicate types of epistasis for most of the traits under study. Under such circumstances intermating or recurrent selection should be followed for genetic enhancement of grain yield in blackgram

Table 1: Estimates of gene effects for different traits in LBG 20 x P 1070

S. No	Characters	Scaling		Gene effects in 5 parameter model scaling test					
		C	D	*m* (Hayman)	*d* (Hayman)	*h* (Hayman)	*I* (Add x Add)	*l* (Dom x Dom)	Type of epitasis
1	Days to 50% flowering	-2.65**	-2.80**	36.37**	0.53*	0.16*	2.49**	-0.21*	D
2	Plant height (cm)	-0.22*	0.14*	58.78**	0.8*	-3.92**	1.14*	3.14*	D
3	No. of branches per plant	4.40**	4.32**	4.29**	0.2*	-1.61*	-1.69*	-0.10	C
4	No. of Clusters per plant	1.29**	3.28**	8.76**	0.91*	-0.79*	-0.13	2.65**	D
5	No. of Pods per plant	6.80**	20.66**	33.25**	0.7*	-7.74**	-11.24**	18.47**	D
6	Pod length (cm)	0.18*	0.12*	4.79**	-0.11	0.04	-0.33*	0.03	C
7	No. of Seeds per pod	-0.49*	0.2*	5.88**	-0.02	-0.24*	-0.26*	0.94*	D
8	100 seed weight (g)	1.77**	0.54**	4.70**	0.38*	-0.52*	-0.70*	-1.64*	C
9	Days to maturity	4.26**	17.91**	80.33**	1.13**	-10.16**	-8.96**	18.20**	D
10	Leaf area (cm^2)	369.05**	13.12**	595.84**	-7.30*	142.12**	38.15**	-474.56**	D
11	SPAD	5.46**	-0.95*	41.83**	0.70*	3.44**	3.95*	-8.45*	D
12	Chlorophyll content (mg g-1)	0.44**	0.30*	1.32**	-0.86*	0.02	-0.46*	-0.18	D
13	YMV	5.35**	7.71**	2.99**	1.30*	-5.92**	-1.29*	2.43**	D
14	Seed yield per plant (g)	-0.53*	5.91**	7.95**	1.84**	-1.80*	-2.34**	8.60**	D

Table 2: Estimates of gene effects for different traits in LBG 752 x P 1053

S. No	Characters	Scaling		Gene effects in 5 parameter model scaling test					
		C	D	*m* (Hayman)	*d* (Hayman)	*h* (Hayman)	*i* (Add. x Add.)	*L* (Dom. x Dom.)	Type of epitasis
1	Days to 50% flowering	-7.76*	-6.26**	36.05**	1.33**	0.47*	5.54**	2.05**	C
2	Plant height (cm)	-0.97*	30.26**	67.60**	8.76**	-16.57**	-2.80*	41.65**	D
3	No. of branches per plant	0.13	0.20*	2.52*	0.07	-0.07	0.04	0.09	D
4	No. of Clusters per plant	0.25*	1.01*	6.73**	0.72*	-1.33*	0.75*	1.13*	D
5	No. of Pods per plant	4.54**	7.84**	26.25**	2.29**	-5.19**	0.10	4.39**	D
6	Pod length (cm)	-0.36*	-0.41*	4.98**	0.11*	-0.18*	0.45*	-0.07	D
7	No. of Seeds per pod	-3.39**	-1.61*	5.20**	0.15*	0.61*	0.82*	2.37**	C
8	100 seed weight (g)	-0.10	0.50*	4.57**	0.20*	0.07	0.37*	0.15*	C
9	Days to maturity	-7.03**	-11.61**	75.46**	1.70*	4.42**	9.96**	-6.10**	D
10	Leaf area (cm^2)	12.21**	-3.26**	423.05**	-1.86*	6.08**	0.48*	-20.64**	D
11	SPAD	-9.52**	6.20**	31.96**	4.16**	1.98*	10.88**	4.42**	C
12	Chlorophyll content (mg g-1)	-0.94**	-0.53*	0.98*	0.02	0.16*	0.25*	0.53*	C
13	YMV	12.55**	1.40*	4.73**	1.06*	1.96*	5.16**	-18.61**	D
14	Seed yield per plant (g)	-0.07	4.16**	6.28**	0.48*	-3.11**	1.94*	6.61**	D

Table 3: Estimates of gene effects for different traits in MBG 207 x PU 31

S. No	Characters	Scaling		Gene effects in 5 parameter model scaling test					
		C	D	*m* (Hayman)	*d* (Hayman)	*h* (Hayman)	*i* (Add. x Add.)	*l* (Dom. x Dom.)	Type of epitasis
1	Days to 50% flowering	1.21*	1.45*	38.45**	2.56**	-1.60*	4.36**	0.32	D
2	Plant height (cm)	4.51**	12.73**	58.81**	3.90**	-2.83**	0.06	10.75**	D
3	No. of branches per plant	-0.86*	-0.18*	2.12*	-0.44*	-0.11	-0.90*	0.90*	D
4	No. of Clusters per plant	1.83*	2.68**	7.24**	-0.58*	-0.90*	-2.64**	1.13*	D
5	No. of Pods per plant	9.54**	13.25**	28.89**	-3.50**	-3.81**	-14.24**	4.93**	D
6	Pod length (cm)	0.12	0.17*	4.98**	0.30*	0.21*	0.50	0.07	C
7	No. of Seeds per pod	-0.41*	0.27*	5.87**	0.61*	0.07	0.11	0.03	C
8	100 seed weight (g)	-0.20*	-0.02	4.73**	0.24*	0.06	0.48	0.03	C
9	Days to maturity	-8.19**	-3.65*	77.03**	3.30**	1.37*	7.73**	6.06**	C
10	Leaf area (cm^2)	32.87**	2.52**	430.59**	20.98**	-27.33**	45.66**	-40.48**	C
11	SPAD	-29.26**	-14.11**	29.83**	-2.50*	6.23**	-0.46	20.20**	C
12	Chlorophyll content (mg g-1)	-0.05	0.14	1.13*	-0.22**	-0.01	-0.54	0.25	D
13	YMV	4.26**	0.11	3.08*	1.96**	-1.40*	4.53**	-5.53**	C
14	Seed yield per plant (g)	3.27**	3.17	8.05**	-1.11*	-0.13	-3.80**	-0.12	C

Table 4: Estimates of gene effects for different traits in TBG 104 x PU 31

S. No	Characters	Scaling		Gene effects in 5 parameter model scaling test					
		C	D	*m* (Hayman)	*d* (Hayman)	*h* (Hayman)	*i* (Add. x Add.)	*l* (Dom. x Dom.)	Type of epitasis
1	Days to 50% flowering	0.56*	1.13*	37.10**	0.1\06	1.67*	0.52*	0.75*	C
2	Plant height (cm)	9.42**	39.55**	62.10**	4.56**	-19.36**	-15.66**	40.16**	D
3	No. of branches per plant	-2.61*	-0.16	3.09**	0.50	-0.66*	3.26**	0.67*	D
4	No. of Clusters per plant	1.84*	6.85**	7.99**	1.23*	-4.09**	-1.71*	6.67**	D
5	No. of Pods per plant	7.39**	27.40**	31.98**	4.99**	-16.36**	-7.16**	26.37**	D
6	Pod length (cm)	-0.31	0.37	4.96**	0.12	0.09	0.43	-0.07	D
7	No. of Seeds per pod	0.50	0.21*	5.95**	0.24	0.23	0.75*	0.22	C
8	100 seed weight (g)	0.48	-0.32*	4.67**	0.31	0.23	0.75*	0.22	C
9	Days to maturity	3.63**	0.66*	80.15**	2.15*	5.15**	4.47**	-3.96**	D
10	Leaf area (cm^2)	-88.42**	-103.80**	393.26**	20.30**	10.60**	95.06**	-20.51**	D
11	SPAD	-14.16**	-10.36**	33.86**	1.30*	2.77*	7.07**	5.67*	C
12	Chlorophyll content (mg g-1)	-0.75*	-0.64*	0.95*	0.01	0.07	0.32	0.14	C
13	YMV	8.25**	3.02**	3.17**	-0.03	-0.74*	-0.70*	6.96**	D
14	Seed yield per plant (g)	3.02*	8.63**	8.96**	1.70*	-4.45**	1.83*	7.47**	D

Table 5: Estimates of gene effects for different traits in TU68 X P 1053

S. No	Characters	Scaling		Gene effects in 5 parameter model scaling test					
		C	D	*m* (Hayman)	*d* (Hayman)	*h* (Hayman)	*i* (Add. x Add.)	*l* (Dom. x Dom.)	Type of epitasis
1	Days to 50% flowering	1.57*	2.02*	37.44**	0.40*	-1.36*	-0.29	0.66*	D
2	Plant height (cm)	13.27**	0.19*	61.86**	0.10	8.71**	2.28*	-17.43**	D
3	No. of branches per plant	1.20*	0.44*	3.01*	-0.18	-0.13	-0.46*	-1.02*	C
4	No. of Clusters per plant	3.18**	1.98*	6.69**	-0.03	-0.67*	-0.86*	-1.60*	C
5	No. of Pods per plant	11.25**	10.93**	26.10**	0.44*	-4.39**	-4.57**	-0.34	C
6	Pod length (cm)	0.61*	0.52*	5.01**	0.14	-0.23	-0.04	-0.12	C
7	No. of Seeds per pod	-0.97*	-0.65*	5.76**	0.03	0.34	0.26	0.45*	C
8	100 seed weight (g)	0.16	0.27*	4.66**	-0.07	-0.15	-0.29	0.14	D
9	Days to maturity	3.45**	4.43**	78.64**	0.96*	-2.81*	-0.45*	1.30*	D
10	Leaf area (cm^2)	-341.22**	-160.80**	406.62**	-36.73**	76.50**	-23.09**	240.48**	C
11	SPAD	-10.48**	-7.88**	35.39**	0.50*	2.27*	4.51**	3.46**	C
12	Chlorophyll content (mg g-1)	-0.76*	-0.47*	1.09*	0.02	0.14	0.24	0.39	C
13	YMV	11.85**	5.82**	3.97**	0.03	-1.94*	-8.03**	-1.84*	C
14	Seed yield per plant (g)	3.95**	5.57**	7.04**	0.86*	-3.12**	-1.32*	2.17**	D

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