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Generation mean analysis using five parameters genetic model for quantitative traits in black gram (*Vigna mungo* L. Hepper)

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Abstract
Generation mean analysis was employed in a cross between B-3-8-8 x Keonjhar Local of black gram to partition the mean into various components *viz*., additive, dominance and epistasis. Five generations *viz*., P_1, P_2, F_1, F_2 and F_3 of this cross were evaluated. The scaling tests were applied to the data to detect the presence or absence of non-allelic interactions. The results of the scaling test showed significant values of C & D scales for majority of traits under study. In several traits the additive gene effects were negative and significant additive gene effects were found for days to 50% flowering, days to maturity, plant height, number of clusters/plant, number of seeds/pod and yield/plant. Similarly, dominant gene effects were negative for days to 50% flowering, plant height, number of primary branches/plant, number of pods/plant. Significant positive dominant gene effects were found for pod length and yield/plant. Epistasis was present in all of the characters under study. Additive × additive gene effects were found for plant heights, number of primary branches /plant, number of clusters/plant and number of seeds/pod. Significant dominance × dominance gene interaction were found for days to maturity, number of primary branches/plant and number of clusters/plant.

Keywords: Generation mean analysis, black gram, scaling test & five parameters

Introduction
Vigna, a pantropical 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 (Rahman *et al.*, 2003) [20s]. It is an important short duration crop and widely cultivated in India. It gives us an excellent source of easily digestible good quality 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) [23]. 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) [14].

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 (Kearsey and Pooni, 1996) [7]. Development of hybrids is an important phase of crop improvement; Generation mean analysis (Mather and Jinks, 1982) [11] 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 (aa), dominance x dominance (dd) and additive x dominance (ad) 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 & methods
To understand the genetic nature of 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 in Randomized Block Design (RBD) replicated three times. The experimental material for this investigation was two black gram varieties namely, B-3-8-8 (popular high yielding released cultivar of black gram) and Keonjhar Local (a local promising genotype of Odisha). Within each replicate, cross populations were first randomized and separate randomization was followed for all the replications. Generations within crosses / populations were also randomized separately. Single row of 3 m length and 30 cm apart were planted for generations *i.e.*, P_1, P_2 and F_1 were grown in five rows each where as F_2 & F_3 generation in 15 rows each were grown. Irrigation at sowing was given to ensure complete seed germination. Thereafter, irrigation, weeding and other agronomical operations were adopted for normal growth of the plant. Scaling test was conducted as suggested by Mather (1949) [13]. The adequacy of simple additive-dominance model was detected by employing C and D scaling test suggested by Mather and Jinks (1971) [12]. 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) [4].

Result & Discussion

Quantitative characters which are of great interest, are governed by large number of genes having their own effects. These are too modified by several environmental factors (Johansen, 1926) [5]. Thus, analysis at the level of individual genes become impractical and whole genome analysis over the totality of the gene should be undertaken (Wright, 1956) [24]. The genetic variability, thus, should be partitioned into its broad components. The present study was planned to estimate the nature and magnitude of allelic and non-allelic interactions in black gram.

The result of scaling test either both or C and D alone revealed significant values indicates the additive-dominance model was not found adequate for all traits in this cross. The failure of additive-dominance model was attributed mainly due to the epistasis. 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 this cross were presented in (Table 1, 2 and 3).

Table 1: Mean performance of the five generations (P_1, P_2, F_1, F_2 and F_3) of the cross B-3-8-8 × Keonjhar Local (KL)

S. No.	Generations/Traits	P_1	P_2	F_1	F_2	F_3
1	Days to 50% Flowering	38.4000 ± 0.5099	40.6000 ± 0.6782	35.4000 ± 0.5099	41.1333 ± 0.6005	41.9000 ± 0.8226
2	Days to Maturity	74.2000 ± 0.8000	76.6000 ± 0.6782	72.0000 ± 0.7071	83.8667 ± 1.1500	82.7000 ± 1.3828
3	Plant height (cm)	22.5180 ± 0.4076	25.2580 ± 0.7141	20.3400 ± 0.3288	23.9747 ± 0.5171	24.8990 ± 0.1925
4	Number of Primary branches/plant	1.4640 ± 0.0866	1.6300 ± 0.0765	1.5880 ± 0.0883	1.5280 ± 0.0558	1.7630 ± 0.0677
5	Number of clusters/plant	5.1120 ± 0.0706	5.9720 ± 0.0672	5.2840 ± 0.1304	6.0327 ± 0.0311	5.9160 ± 0.0887
6	Number of Pods/ plant	23.6880 ± 1.0375	25.2080 ± 0.4944	23.9700 ± 0.2782	24.8673 ± 0.4730	26.3630 ± 0.2711
7	Number of Seeds/pod	5.5540 ± 0.1708	6.1780 ± 0.1162	6.0580 ± 0.0706	6.0553 ± 0.0870	5.8640 ± 0.1191
8	Pod length (cm)	5.4580 ± 0.1682	5.8080 ± 0.1575	6.1200 ± 0.0614	5.9253 ± 0.0325	5.6760 ± 0.0925
9	100 seed weight (g)	4.3460 ± 0.1794	4.3700 ± 0.1597	4.7320 ± 0.0394	4.3293 ± 0.0673	4.3830 ± 0.1156
10	Yield/plant (g)	4.3560 ± 0.1655	4.8380 ± 0.0464	5.4380 ± 0.2162	5.0813 ± 0.0807	4.7940 ± 0.1227

Table 2: Estimation of scaling test of five generations viz., P_1, P_2, F_1, F_2 and F_3 of the cross B-3-8-8 × Keonjhar Local (KL)

S. No.	Traits/ Parameters	Scaling test	
		C	D
1	Days to 50% Flowering	14.7333± 2.7441**	6.3333 ± 1.7573
2	Days to Maturity	40.6667 ± 4.9255**	12.2667 ± 6.0816*
3	Plant height (cm)	7.4427 ± 2.3208**	3.8707 ± 1.5291**
4	Number of Primary branches/plant	-0.1580 ± 0.3073	0.9020 ± 0.3147**
5	Number of clusters/plant	2.4787 ± 0.3050**	0.5147 ± 0.3730
6	Number of Pods/ plant	2.6333 ± 2.2826	6.8213 ± 1.8417**
7	Number of Seeds/pod	0.3733 ± 0.4286	-0.3867 ± 0.5475
8	Pod length (cm)	0.1953 ± 0.2917	-0.4127 ± 0.4408
9	100 seed weight (g)	-0.8627 ± 0.3694*	0.1573 ± 0.5381
10	Yield/plant (g)	0.2553 ± 0.5663	-0.1807 ± 0.5444

Table 3: Estimation of gene effects based on performance of five generations viz., P_1, P_2, F_1, F_2 and F_3 of the cross B-3-8-8 × Keonjhar Local (KL)

S. No.	Traits/ Parameters	Generation mean analysis					Epistasis
		m	d	h	i	l	
		(Hayman)	(Hayman)	(Hayman)	(Add × Add)	(Dom × Dom)	
1	Days to 50% Flowering	41.1333 ± 0.6005**	-1.1000 ± 0.4243*	-5.8667 ± 2.5239*	-3.9667 ± 2.2703	-11.2000 ± 6.6466	C
2	Days to Maturity	83.8667 ± 1.1500**	-1.2000 ± 0.5244*	-4.8000 ± 4.3715	-3.8000 ± 3.9909	-37.8667 ± 11.9411*	C
3	Plant height (cm)	23.9747 ± 0.5171**	-1.3700 ± 0.4111**	-4.8880 ± 1.1751**	-4.0800 ± 1.4598**	-4.7627 ± 4.3512	C
4	Number of Primary branches/plant	1.5280 ± 0.0558**	-0.0830 ± 0.0578	-0.5867 ± 0.2202**	-0.7937 ± 0.2239**	1.4133 ± 0.6205*	D
5	Number of clusters/plant	6.0327 ± 0.0311**	-0.4300 ± 0.0487**	-0.1880 ± 0.2595	-0.7900 ± 0.2249**	-2.6187 ± 0.6376**	C
6	Number of Pods/ plant	24.8673 ± 0.4730**	-0.7600 ± 0.5746	-4.5867 ± 1.2050**	-5.6287 ± 1.7474**	5.5840 ± 4.1183	D
7	Number of Seeds/pod	6.0553 ± 0.0870**	-0.3120 ± 0.1033**	0.5120 ± 0.3651	-0.3040 ± 0.3720	-1.0133 ± 0.9606	D
8	Pod length (cm)	5.9253 ± 0.0325**	-0.1750 ± 0.1152	0.7947 ± 0.2584**	-0.0423 ± 0.2836	-0.8107 ± 0.5812	D
9	100 seed weight (g)	4.3293 ± 0.0673**	-0.0120 ± 0.1201	0.1253 ± 0.3374	-0.2727 ± 0.3495	1.3600 ± 0.8254	C
10	Yield/plant (g)	5.0813 ± 0.0807**	-0.2410 ± 0.0860**	1.0040 ± 0.3922*	-0.3190 ± 0.3916	-0.5813 ± 1.0849	D

C = Complementary; D = Duplicate; *Significant at P=0.05, **Significant at P=0.01 respectively.

Days to 50% flowering
This character recorded significant values for three components as revealed by the five parameter model. It recorded a mean days to 50% flowering (41.13) days where additive gene effect (-1.10) were predominant over dominant gene effects (-5.86). Additive × additive component (-3.96) had higher values over dominance × dominance component (-11.20). Dominance and dominance × dominance gene effects have same sign indicating that the trait is governed by complementary epistasis. However, dominance and dominance × dominance effects were predominant (Bhor and Dhumbre, 1998) [2] in this cross for most of the traits. Hence accordingly more reliance should be placed on simple selection between the families or recurrent selection can be advocated for improvement of this cross.

Days to Maturity
Significant values for days to maturity was observed for 'm', 'd' and 'l' components in the five parameter model except 'h' & 'i' components which was non-significant. Dominant gene effects (-4.80) were lower than additive gene effects (-1.20). Dominance × dominance component (-37.86) had lower values in comparison with the additive × additive component of epistasis (-3.80). Days to maturity also falls under category of complementary type of epistasis as revealed by negative signs for both dominant and dominance × dominance gene effects. Similar findings were also reported by Patil *et al.* (1996) [17], Kute and Deshmukh (2003) [8], Ammavasai *et al.* (2005) [1] and Singh *et al*. (2007) [21].

Plant height (cm)
Black gram genotypes with three generation when analysed for five parameter model of generation mean analysis registered significant values for this character. Mean performance was 23.97 for this character with negative additive gene effect (-1.37) and additive × additive component (-4.08). Similarly, negative dominant gene effect (-4.88) and dominance × dominance effect was found for plant height. This trait is also governed by complementary gene action. Similarly, Kanchana Rani (2008) [6] and Thamodharan *et al.,* (2015) [22] recorded additive and non-additive gene action respectively.

Number of Primary branches/plant
This character recorded significant values for four components i: e; mean performance, dominant gene effect, additive × additive and dominance × dominance components of epistasis. Whereas additive gene effect was found non-significant. A mean of 1.52 number of primary branches per plant with additive effect (-0.08) were higher than dominant effects (-0.58). Dominance × dominance component (1.41) had higher value over additive × additive component (-0.79). Dominant and dominance × dominance gene effects have opposite signs indicating the presence of duplicate epistasis. Same results of additive and non-additive gene action were given by Latha *et al*., (2018) [9] and Prasad and Murugan (2015) [19] respectively.

Number of clusters/plant
This character also recorded significant values for four components 'm','d' 'i' and 'l' except 'h'. A mean of 6.03 clusters/plant with additive effect (-0.43) was recorded. additive × additive component (-0.79) had higher values over dominance × dominance component (-2.61) of epistasis. Dominant and dominance × dominance values with same sign indicating that the trait is governed by complementary epistasis. Similarly, non-additive gene action was reported by Thamodharan *et al.,* (2015) [22].

Number of Pods/ plant
Five parameters as analysed considering mean numbers of pods/plant is 24.86 for three generations along with their two parents. It's dominant (-4.58), additive (-0.76) and additive × additive components (-5.62) of epistasis were negative and significant except for dominance × dominance gene effect (5.58) which was non-significant. Dominant and dominance × dominance were found values with different signs indicating that the trait is governed by duplicate epistasis. Being a complex character this is on the expected line as also reported by Mehta and Zaveri (1999) [15] and Bhor and Dhumbre (1998) [2]. Hence, approaches like biparental mating and mass selections are suggested for improving this trait in this population.

Number of Seeds/pod
Number of seeds /pod recorded significant values for mean and additive gene effects. The mean number of seeds/pod for all generation is 6.05. The dominant gene effects (0.51) were higher than additive gene effects (-0.31). Dominance × dominance component (-1.01) had lower values in comparison with the additive × additive component of epistasis (-0.30). Number of seeds /pod falls under the category of duplicate epistasis. Similarly gene action was observed by Zubair *et al.,* (2007) [25] and Latha *et al.,* (2018) [9] respectively.

Pod length (cm)
Significant values for two components 'm' and 'h' revealed by the five parameters model whereas 'd', 'i' and 'l' components were found negative and non-significant. All the generations on an average having pod length of 5.92 cm. with dominant effects (0.79) were higher than additive effects (-0.17). Additive × additive components (-0.04) had higher value than dominance × dominance component (-0.81). Dominance and dominance × dominance gene effects have different sign indicating that the trait is governed by duplicate epistasis. Marangappanavar (1984) [10] and Chakraborty and Borua (1998) [3] also suggested the same operation of additive, dominance as well as epistatic gene action in cowpea.

100 seed weight (g)
Five parameters as analysed considering a mean 100 seed weight of 4.32 gm. for three generations along with their two parents. It's dominant (0.12) as well as dominance × dominance (1.36) component of epistasis were positive. Additive gene effects (-0.01) and additive × additive gene effects (-0.27) of epistasis recorded negative values. Signs of 'h' and 'l' signifying complementary epistasis. Non-additive gene action was reported by Panigrahi *et al.,* (2015) [16] and Vadivel *et al*., (2019) [23].

Yield/plant (g)
This character recorded significant values for three components i:e; mean, additive and dominant gene effects. A mean value of 5.08 g/plant was recorded for all generations. Additive and dominant gene effects were significant. The dominant gene effects (1.00) were higher than additive gene effects (-0.24). Additive × additive component (-0.31) had

higher values over dominance × dominance component (-0.58). Dominant and dominance × dominance gene effects have opposite signs indicating the presence of duplicate epistasis. Non-additive gene action was reported by Payasi *et al*., (2010) [18] and Latha *et al.*, (2018) [9].

The results of this study showed that as a consequence of higher magnitude of interactions, the non-fixable gene effects were higher than the fixable indicating the major role of non-additive gene effects. In view of high magnitude of gene interactions the successful breeding methods will be the ones, which can mop-up the genes to form superior gene constellations interacting in a favourable manner. Some forms of recurrent selection namely, diallele selective mating or biparental mating in early segregating generations and selections followed by hybridization might prove to be effective alternative approaches.

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