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# Generation Mean Analysis for Seed Yield and Its Contributing Traits in the Inter-varietal Cross of Blackgram [*Vigna mungo* (L.) Hepper]

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## ABSTRACT

**Background:** Blackgram is being cultivated as an indispensable pulse crop and a rich source of vitamins and minerals. Though the requirement for blackgram is high, the productivity is low. The ultimate aim of any plant breeder in a crop improvement program is to increase seed yield/ productivity. With this background, the current study was focused to investigate genetic variability/effects on important yield and its contributing traits of blackgram.

**Methods:** The research material comprised of $P_1$, $P_2$, $F_1$, $F_2$ and $F_3$ obtained from a cross between CO 6 and LBG 17 varieties in blackgram. Observations on nine biometrical traits were recorded from all these five populations for generation mean analysis. By employing Mather and Jinks (1971) scaling test of C and D, the suitability nature of the simple additive-dominance model can be identified. Following Hayman (1958) perfect fit solution, the mean of five generations ($P_1$, $P_2$, $F_1$, $F_2$ and $F_3$) was utilized to calculate five parameters.

**Result:** Fitted genetic model revealed as important yield and yield contributing traits governed by dominance and epistasis in this study, it indicates the selection may be postponed to later generations with greater homozygosity.

**Key words:** Crop improvement, Five generations, Genetic model, Genetic variation, Selection, Yield.

## INTRODUCTION

Pulses serve as an integral component in the human diet especially in developing countries, like Africa and South East Asia (Ofuya and Akhidue, 2005) where other animal-based proteins are scarce and costly. Nevertheless, demand for pulses is on the rise due to the ever-growing population and change in the preference of dietary patterns towards the health concern in developing and developed countries. Blackgram is being cultivated as an indispensable pulse crop mainly in tropical countries like India, South-East Asia, Iran, East Africa and Greece. It is a source of slowly digestible starch, soluble fibers, rich in iron which helps in the maintenance of insulin and plasma glucose levels in postprandial conditions, secretion of bile, prevents anemia and boosts energy (Jenkins *et al.,* 1986). Though the requirement for blackgram is high, the productivity is low due to the absence of variability, ideal ideotypes and highly prone to pests and disease attacks.

The ultimate aim of any plant breeder is to enhance seed yield/ productivity. The genetic enhancement of any population or trait depends upon the mode or nature of gene action for choosing an appropriate breeding procedure. Since, yield is a complex trait, plant breeders require more information about gene action governing the yield and its component characters. Different genic models are given for the estimation of the genetic effects (Kumar and Ganesan, 2004; Kumar *et al.,* 2020). The reports on epistasis/ inter allelic interaction in blackgram are limited since variations due to epistasis with dominance effects could not be successfully manipulated in blackgram. The knowledge on epistatic genetic interactions offers great scope for planning breeding strategies in the blackgram.

Generation mean analysis (Hayman, 1958) used as a powerful tool to estimate gene effects in polygenic traits and it can also be used to determine whether or not epistasis gene interactions exist and determine the individual's

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genotypic values through estimating gene effects such as additive, dominance deviations effects and epistasis genetic interactions. The scaling test (Scale C and D) was carried out utilizing mean measurements of observed traits in different generations. In light of this, the current research used a five-parameter model of generation mean analysis to investigate gene interaction for yield attributing traits in blackgram.

## MATERIALS AND METHODS

The research material comprising $P_1$, $P_2$, $F_1$, $F_2$ and $F_3$ was obtained from a cross between CO 6 and LBG 17 varieties in blackgram. The field study was carried out at Millet Breeding Station and New Area (MBS and NA) farm, Tamil Nadu Agricultural University, Coimbatore during Summer 2020 by adopting Augmented Design II. Each progeny was raised in a plot size of 8.1 square meters with 30 cm between rows and 10 cm between plants. The observations on biometric characters namely plant height (cm), number of branches /plant, number of clusters /plant, number of pods /cluster, number of pods/plant, pod length (cm), number of seeds/pod, 100-seed weight (g) and seed yield/plant (g) were observed for about 250 single plants in each population except for $F_1$ (population size is 50). The standard agronomical practices were followed throughout the crop period.

### Scaling test

The suitability of the simple additive-dominance model in a generation was determined using C and D scaling tests (Mather and Jinks, 1971), which were suitable for the populations studied.

$$C = 4\overline{F2} - 2\overline{F1} - \overline{P1} - \overline{P2} = 0$$

$$D = 8\overline{F3} - 2\overline{F1} - 3\overline{P1} - 3\overline{P2} = 0$$

Where,

$\overline{P1}$, $\overline{P2}$, $\overline{F1}$, $\overline{F2}$, $\overline{F3}$ are average values of CO 6 ($1^{st}$ parent), LBG 17 ( $2^{nd}$ parent ), $F_1$, $F_2$ and $F_3$ generation.

Tests of significance were performed employing the variances of different generations for the corresponding mean. The variances of scales C and D were determined as follows:

$$V_C = 16V\overline{F2} + 4V\overline{F1} + V\overline{P1} + V\overline{P2}$$

$$V_D = 64\,V\overline{F3} + 4V\overline{F1} + 9\,V\overline{P1} + 9\,V\overline{P2}$$

Where,

$V\overline{F3} + V\overline{F1} + V\overline{P1} + V\overline{P2}$ = variance of the means of the corresponding generation.

The standard errors were calculated as the square roots of the corresponding variances.

$$\text{SE of C} = (V_C)^{1/2}$$

$$\text{SE of D} = (V_D)^{1/2}$$

At a 5% or 1% level of significance, the observed t values for ratios C / SE of C and D / SE of D were compared to the 't' table. The degrees of freedom in each test is the sum of the degrees of freedom of the different generations involved. If one of the two scales deviated substantially from zero, the additive-dominance model was found inadequate.

### Components of the mean estimation

Following Hayman (1958) perfect fit solution, the mean of five generations ($P_1$, $P_2$, $F_1$, $F_2$ and $F_3$) was utilized to measure five parameters and equations are as follows,

$$(\widehat{m}) = \overline{F2}$$

$$(\widehat{d}) = 1/2\ \overline{P1} - 1/2\ \overline{P2}$$

$$(\widehat{h}) = 1/6\ (4\ \overline{F1} + 12\ \overline{F2} - 16\ \overline{F3})$$

$$(\widehat{i}) = \overline{P1} - \overline{F2} - 1/2\ (\overline{P1} - \overline{P2})$$

$$(\widehat{j}) = 1/3\ (16\ \overline{F3} - 24\ \overline{F2} + 8\ \overline{F1})$$

The following are the variances of these parameter estimates:

$$(Vm) = V\overline{F2}$$

$$(Vd) = 1/4\ (V\overline{P1} + V\overline{P2})$$

$$(Vh) = 1/36\ (16\ V\overline{F1} + 144\ V\overline{F2} + 256\ V\overline{F3})$$

$$(Vi) = V\ \overline{P1} + V\ \overline{F2} + 1/4\ (V\ \overline{P1} + V\overline{P2} + V\overline{h}) + 1/16\ \overline{V1}$$

$$(V1) = 1/9\ (256\ V\overline{F3} - 576\ V\overline{F2} + 64\ V\overline{F1})$$

The square root of the corresponding variances was used to calculate the standard errors of these assessments.

S.E of m = $(V_m)^{1/2}$

S.E of d = $(V_d)^{1/2}$

S.E of h = $(V_h)^{1/2}$

S.E of i = $(V_i)^{1/2}$

SE of 1 = $(V_1)^{1/2}$

The different estimates of 't' values were calculated as follows:

t(m) = m/S.E (m)

t(d) =d/S.E (d)

t(h) =h/S.E (h)

t(i) =h/S.E (i)

t(1) =h/S.E (1)

## RESULTS AND DISCUSSION

### Assessment of genetic parameters

The mean and standard error worked out for nine characters in various generations *viz.*, $P_1$, $P_2$, $F_1$, $F_2$ and $F_3$ of the cross CO 6 × LBG 17 were given in Table 1. Results on scaling test and genetic parameters for the same cross is given in Table 2.

### Plant height (cm)

The suitability nature on generation mean analysis to the plant height showed the contribution of gene effects *viz.*, additive, dominance and epistasis. It displayed a mean height of 46.25 cm and predominant nature of the dominant gene effect (12.08) than the additive effects (-3.76). The dominance × dominance parameter (32.35) had a higher magnitude over the non-significant additive × additive component (-1.56). The same sign for dominance (h) and dominance × dominance (l) signifying that this trait is governed by complementary epistasis. It is akin to the findings of Vadivel *et al.* (2019) and Kanchana Rani (2008).

### Number of branches/plant

The scale C and D exhibited non-significance for branches/ plant, indicated fitness of the basic additive-dominance model. The mean (3.16) and dominant (4.26) (h) effects were significant and accounted for the expression of a trait. Vadivel *et al.* (2019) and Latha *et al.* (2018) recorded additive gene action, whereas Prasad and Murugan (2015) reported dominant gene action.

### Number of clusters/plant

The dominance (h) and dominant × dominant (l) epistatic effects significant for number of clusters per plant, whereas non-significance was observed for additive (d) and additive × additive (i) components. The mean value was 13.05 and the dominant × dominant (l) epistasis (10.88), dominant (-3.81) effect recorded the high value with contrary signs. This indicated that the trait was controlled by a duplicate type of non-allelic interaction. It was in accordance with the findings of Thamodharan *et al.* (2017); Vadivel *et al.* (2019).

### Number of pods/cluster

This trait recorded a significant mean of 4.38 and additive gene effects (d) (0.29) were lower than the dominant effects (1.13). The additive × additive (i) component (1.69) recorded a higher value than the dominance × dominance (l) component (-2.50). The presence of a contrary sign indicated that the character is under the control of duplicate epistasis. Vadivel *et al.* (2019) and Thamodharan *et al.* (2017) reported that the trait was governed by non-additive gene action with epistasis interaction.

### Number of pods/plant

It registered a significant mean of 46.04 pods per plant and additive genetic components (7.20) exhibited a higher value over the dominant gene effect (-14.74). The dominance × dominance component (64.92) had higher values over the additive × additive component (-14.74). This implies that this character was governed by additive and epistatic type of gene actions (dominant × dominant). These results were in line with the earlier reports by Vadivel *et al.* (2019); Panigrahi *et al.* (2015); Kanchana Rani (2008). The presence of a contrary sign for dominance and dominance × dominance indicated the trait is governed by duplicate epistasis.

**Table 1:** Mean performance of different generations of the cross CO 6 × LBG 17 for nine quantitative traits.

| Characters | $P_1$ | $P_2$ | $F_1$ | $F_2$ | $F_3$ |
|---|---|---|---|---|---|
| PH (cm) | 50.50±0.31 | 58.03± 0.15 | 60.38±0.61 | 46.25±0.64 | 45.25±0.56 |
| NBP | 3.40±0.11 | 3.35±0.11 | 3.60±0.16 | 3.17±0.06 | 3.19±0.04 |
| NCP | 15.05±0.15 | 11.65±0.11 | 13.60±0.34 | 13.05±0.26 | 14.62±0.21 |
| NPC | 4.60± 0.03 | 4.00±0.03 | 4.33±0.05 | 4.39±0.03 | 3.95±0.04 |
| NPP | 51.00±0.29 | 46.60±0.39 | 54.90±1.07 | 46.04±0.91 | 53.78±0.78 |
| PL (cm) | 4.90±0.03 | 4.95±0.03 | 5.26±0.05 | 4.85±0.04 | 4.76±0.03 |
| NSP | 4.85±0.03 | 4.83±0.03 | 5.08±0.06 | 4.34±0.04 | 4.51±0.03 |
| HSW (g) | 4.97±0.06 | 4.74±0.05 | 4.93±0.06 | 4.86±0.01 | 4.93±0.03 |
| SPY (g) | 13.46±0.11 | 11.54±0.11 | 14.51±0.16 | 11.38±0.21 | 12.33±0.16 |

$P_1$- CO 6, $P_2$ - LBG 17

PH (cm)- Plant height, NBP- Number of branches per plant, NCP- Number of clusters per plant,

NPC- Number of pods per cluster, NPP- Number of pods per plant, PL (cm)- Pod length, NSP- Number of seeds per pod, HSW (g) - Hundred seed weight, SPY (g)- Single plant yield

**Table 2:** Estimation of scaling test and gene effects of five generations of the cross CO 6 × LBG 17 for various quantitative traits.

| | Scales | | Genetic parameters. | | | | |
|---|---|---|---|---|---|---|---|
| Characters | C | D | m | d | h | i | l |
| PH (cm) | -44.28+2.86** | -20.01+2.60** | 46.25+0.64 ** | -3.76+0.17** | 12.08+2.00** | -1.56+1.97 $^{ns}$ | 32.35+6.15** |
| NBP | -0.42+0.44 $^{ns}$ | -0.31+0.26 $^{ns}$ | 3.16+0.06 ** | 0.20+0.15 $^{ns}$ | 4.26+0.23 ** | 0.42+0.38 $^{ns}$ | 1.28+0.85 $^{ns}$ |
| NCP | -1.68+1.24 $^{ns}$ | 5.67+0.98 ** | 13.05+0.25 ** | 1.70+0.09 $^{ns}$ | -3.81+0.78** | -0.66+0.79 $^{ns}$ | 10.88+2.49 ** |
| NPC | 0.29+0.17 $^{ns}$ | -1.58+0.17 ** | 4.38+0.03 ** | 0.29+0.02 ** | 1.13+0.12 ** | 1.69+0.12 ** | -2.50+0.37 ** |
| NPP | -13.04+ 4.25 ** | 35.45+3.63 ** | 46.04+0.91 ** | 7.20+0.24 ** | -14.74+2.84 ** | -11.44+2.81 ** | 64.92+8.85 ** |
| PL (cm) | -0.96+0.18** | -0.53+0.15 ** | 4.85+0.03 ** | -0.02+0.02 $^{ns}$ | 0.52+0.11 ** | 0.14+0.12 $^{ns}$ | 1.70+0.37 ** |
| NSP | -0. 25+0.19 ** | -0.33+0.15 * | 4.34+0.03 ** | 0.007 +0.02 $^{ns}$ | 0.04+0.12 $^{ns}$ | -0.17+0.12 $^{ns}$ | 2.82 +0.38 ** |
| HSW (g) | -0.13+0.14 $^{ns}$ | 0.28+0.15 $^{ns}$ | 4.85+0.01 ** | 0.11+0.03 ** | -0.13+0.09 $^{ns}$ | 0.01+0.10 $^{ns}$ | 0.23+0.34 $^{ns}$ |
| SPY (g) | -8.57+0.92 ** | 5.06+0.79 ** | 10.78+0.21 ** | 2.12+0.07 ** | -1.63+0.62 ** | -0.56+0.63 $^{ns}$ | 18.18+2.1.97 ** |

PH (cm)- Plant height, NBP- Number of branches per plant, NCP- Number of clusters per plant, NPC- Number of pods per cluster, NPP- Number of pods per plant, PL (cm)- Pod length, NSP- Number of seeds per pod, HSW (g) - Hundred seed weight, SPY (g)- Single plant yield *-Significance at 5% level; **- Significance at 1% level; ns- Non- significance.

### Pod length (cm)

Significance was observed for a mean (4.85) and dominance (h) (0.52); dominance × dominance gene effects (1.70) whereas the remaining components *viz.,* additive (d) and additive × additive (0.14), showed non-significance. This indicated the existence of dominance and dominance × dominance epistatic gene actions on the expression of the character. This was in agreement with the findings of Latha *et al.* (2018) and disagreed with the reports by Kanchana Rani (2008) and Vadivel *et al.* (2019).

### Number of seeds/pod

The mean (4.34) and dominant × dominant (l) (2.82) epistasis were high and significant and showed a more proportion of dominant gene effects. Vadivel *et al.* (2019) and Latha *et al.* (2018) reported similar findings, while Zubair *et al.* (2007) reported additive gene action is governing the trait.

### Hundred seed weight (cm)

All of the scales were non-significant, indicating that the basic additive-dominance model was adequate. Hundred seed weight exhibited significant mean (4.85) and additive (0.11) (d) effects. Vadivel *et al.* (2019) and Zubair *et al.* (2007) reported similar findings.

### Single plant yield

All the forms of gene action were found in the cross except additive × additive (i) gene effects. The mean value for this character is 10.78, the additive (2.12) gene effect was higher than the dominance (-1.63) gene effects. The components dominance (-1.63) and dominance × dominance (18.18) recorded different signs, exhibiting the presence of duplicate epistasis. This implied that single plant yield was governed by additive with epistasis gene action. Vadivel *et al.* (2019); Latha *et al.* (2018) noted an akin result.

In the present study, significantly non-additive genetic was found to be observed in all biometrical traits except for number of pods/plant, hundred seed weight and single plant yield. The importance of additive gene effects for the expression of these traits inferred that the homozygous recombinants could be isolated from the segregating populations suggesting that the pedigree method may be recommended for the enhancement of these characters.

Plant height, number of branches/plant, number of clusters/plant, number of pods/cluster and pod length, exerted non-additive genetic effects with epistasis. In the present study, it has been demonstrated that epistasis cannot be overlooked as the fundamental component as adoption of a breeding method based on the main gene effect (additive and dominant) may mislead the results. The non-fixable (dominant) gene effect was greater than the fixable (additive) gene effect, showing preponderance of dominant gene effects for these traits, which indicated that such a trait could be improved by recurrent selection such as bi-parental mating or diallel selective mating in an early generation.

Among the traits, number of clusters/plant and number of pods/cluster showed negative significance. Epistatic gene action may respond to dominance with negative estimates. Hence, this study indicated that the selection in later (advanced) generations could be more desirable. Early generation selection could be effective when the trait is influenced by additive gene action. The different types of predicted gene effects offer scope for the improvement of desirable traits to develop superior blackgram varieties.

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