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## ASSESSMENT OF GENETIC VARIABILITY THROUGH COMBINED HYBRIDIZATION AND MUTATION IN F<sub>3</sub>M<sub>2</sub> GENERATION OF BLACKGRAM (*Vigna mungo* L. HEPPER)

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### ABSTRACT

A field experiment was carried during *Rabi* 2020 at ZAHRS, Shivamogga, to determine the genetic parameters among 400 progeny lines of F<sub>3</sub>M<sub>2</sub> blackgram, which are generated by hybridization between PU31 × Rashmi than F<sub>2</sub> seeds are treated with gamma irradiation (20kr) at IIHR, Bangalore. Significant variations in progeny lines were documented for most of the traits from analysis of variance, showing the vast genetic variability. High phenotypic coefficient of variation (PCV) was documented for the trait seed yield per plant and moderate genotypic coefficient of variation (GCV) were observed for the traits, number of branches per plant, number of seeds per pod, number of pods per plant, and seed yield per plant. The estimated GCV and PCV depict the level of variability present in the population, estimation of high values of PCV indicates more variability for the character seed yield per plant in the population and the narrow range between GCV and PCV, which implies the lesser influence of the environmental effects on the expression of traits. High heritability combined with the high genetic advance as *per cent* of mean was documented for trait number of pods per plant. This reveal that more effective selection can be made for these traits.

**Keywords :** Heritability, Irradiation, Population, Variability, Yield

### Introduction

Blackgram was originated in India (Vavilov, 1926). The progenitor of blackgram is believed to be *Vigna mungo* var. *silvestris*, (Lukoki *et al.*, 1980). It is a staple pulse crop in central and South-East Asia. However, it is extensively used across India and now grown in the Southern United States, West Indies, Japan and other tropics (Delic *et al.*, 2009).

Blackgram accounts for 13 *per cent* of total pulse area and 10 *per cent* of total pulse production in India. It occupies an area of about 5.44 m ha, with a production of 3.56 mt and productivity of 604 kg ha<sup>-1</sup>. Karnataka is one of the major blackgram growing states of India with an area of 0.81 lakh hectares, with a production of 0.45 lakh tonnes and productivity of 821.5 kg ha<sup>-1</sup> (Anonymous, 2020).

The variability available in the segregating population helps in selecting the superior plant types.

Heritability shows the relative success of selection as it measures the relative amount of heritable portion of variability. High heritability combined with high genetic advance is more useful in selection of traits than heritability alone in predicting the resultant effect on selecting the best individual (Johnson *et al.*, 1955).

Thorough knowledge of the genetic parameters such as variability, heritability, and genetic advance in the segregating population will provide a systematic approach for identifying the high yielding progeny lines. Therefore, by keeping all these in the view, the present study in blackgram was undertaken with F<sub>3</sub>M<sub>2</sub> populations derived from than F<sub>2</sub> seeds are treated with gamma irradiation (20kr) at IIHR, Bangalore. Individual plats in F<sub>2</sub> were selected based on high mean performance for seed yield. With this premise, the present investigation was undertaken

## Materials and Methods

The present investigation was undertaken to study genetic variability in  $F_3M_2$  population of blackgram [*Vigna mungo* (L.) Hepper] along with four checks. The experiment was conducted during Rabi 2020 at Zonal Agricultural and Horticultural Research Station (ZAHRS), Navile, Shivamogga, Keladi Shivappa Nayaka University of Agricultural and Horticultural Sciences, Shivamogga, Karnataka, India. Which is situated in 13.28° North latitude and 75.34° East

longitude and at an altitude of 617.0 meters above mean sea level.

The experimental material consisted of 400  $F_3M_2$  progeny lines of developed by hybridization between (PU31 × Rashmi) and mutation by 20 Kr gamma irradiation in blackgram [*Vigna mungo* (L.) Hepper] along with four checks (PU31, Rashmi, DBGV5 and DU1). The experiment was done by using Augmented with ten blocks and for checks were replicated in all ten blocks. Pod characteristics and seed characteristics of parents shown in plate 1.



**Plate 1: (a)** Pod characteristics of parents,

**(b)** Seed characteristics of parents

**Table 1 :** Experimental material for seed yield and its component traits for  $F_3M_2$  blackgram [*Vigna mungo* (L.) Hepper]

|   |                                       |           |
|---|---------------------------------------|-----------|
| 1 | Number of genotypes                   | 400       |
| 2 | Experimental design                   | Augmented |
| 3 | Number of blocks                      | 10        |
| 4 | Number of checks                      | 04        |
| 5 | Number of genotypes in a block        | 40        |
| 6 | Row length                            | 4 m       |
| 7 | Spacing between the rows              | 0.3 m     |
| 8 | Spacing between the plants within row | 0.1 m     |

**Table 2 :** Characteristics of parents.

| S. No. | Parents | Characteristics                                                                                                                           |
|--------|---------|-------------------------------------------------------------------------------------------------------------------------------------------|
| 1.     | Rashmi  | Long duration variety (70-75days) susceptible to YMV, pods are hairy with shiny seeds, which produces potential yield of 600 – 900 kg/ha. |
| 2      | PU31    | Medium duration variety tolerant to YMV, pods are non-hairy with dull seeds, which produces potential yield of 600-700 kg/ha.             |

The experimental data from the augmented design was used in analysis of variability by using R software version 4.1.0 with Augmented design package. Statistical analysis was performed on the traits mean

values of data recorded from 15 selected plants in each progeny line for yield and its attributing traits.

## Results and Discussion

Analysis of variance was carried out for yield and its attributing traits in 400  $F_3M_2$  progeny lines along with four checks. Analysis of variance disclosed significant differences among the progeny lines for all the traits studied, indicating the presence of sufficient amount of genetic variability and the choice of the material for the investigation was appropriate.

The  $F_3M_2$  generation of cross (PU31 × Rashmi) exhibited a considerable amount of variability for all ten characters individually (Table 4.2). The range is 37 to 47 for days to 50 per cent flowering, 24 cm to 37 cm range for plant height, 2.40 to 4.12 range for number of branches, number of clusters per plant ranges from 11 to 19, number of pods per cluster ranges from 2.80 to 4.70, for number of pods per plant range is 31 to 58, pod length ranges from 3.8 cm to 6 cm, range for number of seeds per pod is 4.10 to 7, for 100 seed weight range is 2.98 g to 5.30 g and total seed yield per plant showing the range of 5.2 g to 16.40 g.

Traits showing skewed distribution indicates that genes controlling the character are predominantly dominant irrespective of enhancing or inhibiting effects on the expression of the trait. In general, the distribution pattern of  $F_3M_2$  generation suggested

dominance and dominance based epistasis as the major causes for significant variation and asymmetrical distribution of the majority of the traits investigated in the present study.

The traits with platykurtic distribution are controlled by fewer and a large number of genes.

Kurtosis is negative or close to zero in absence of gene interactions and is positive in the presence of gene interactions (Pooni *et al.*, 1977; Choo and Reinbergs 1982). The inferences on the relative number of genes and nature of genetic control of different traits in  $F_3M_2$  generation of blackgram.

**Table 3 :** Estimates of parameters specifying variability for seed yield and its component traits in  $F_3M_2$  blackgram [*Vigna mungo* (L.) Hepper]

| Sl No | Traits                                 | Mean  | Range   |         | GCV (%) | PCV (%) | $h^2_{bs}$ (%) | GAM (%) | Skewness | Kurtosis | Kurtosis type |
|-------|----------------------------------------|-------|---------|---------|---------|---------|----------------|---------|----------|----------|---------------|
|       |                                        |       | Minimum | Maximum |         |         |                |         |          |          |               |
| 1     | Days to 50 % flowering                 | 42.16 | 37.00   | 47.00   | 3.56    | 4.29    | 68.92          | 6.09    | -0.119   | 0.335    | P             |
| 2     | Plant height (cm)                      | 30.82 | 24.00   | 37.00   | 6.02    | 8.68    | 48.04          | 8.6     | -0.100   | 0.014    | P             |
| 3     | Number of branches plant <sup>-1</sup> | 3.33  | 2.40    | 4.12    | 10.39   | 11.75   | 78.2           | 18.96   | -0.037   | -0.354   | P             |
| 4     | Number of clusters plant <sup>-1</sup> | 15.72 | 11.00   | 19.00   | 9.18    | 10.68   | 73.9           | 16.28   | -0.460   | -0.115   | P             |
| 5     | Number of pods cluster <sup>-1</sup>   | 3.70  | 2.80    | 4.70    | 9.00    | 10.28   | 76.79          | 16.28   | 0.077    | -0.703   | P             |
| 6     | Number of pods plant <sup>-1</sup>     | 45.16 | 31.00   | 58.00   | 11.61   | 13.53   | 73.55          | 20.54   | -0.137   | -0.518   | P             |
| 7     | Pod length (cm)                        | 4.86  | 3.80    | 6.00    | 7.07    | 9.23    | 58.74          | 11.18   | 0.241    | -0.346   | P             |
| 8     | Number of seeds pod <sup>-1</sup>      | 5.39  | 4.10    | 7.00    | 10.74   | 12.46   | 74.3           | 19.1    | -0.617   | -0.346   | P             |
| 9     | 100 seed weight (g)                    | 4.61  | 2.98    | 5.30    | 7.88    | 8.76    | 80.9           | 14.62   | -0.683   | 1.168    | P             |
| 10    | Seed yield plant <sup>-1</sup> (g)     | 10.48 | 5.20    | 16.40   | 15.45   | 20.26   | 58.13          | 24.3    | 0.045    | -0.099   | P             |

GCV = Genotypic coefficient of variation

PCV = Phenotypic coefficient of variation

$h^2_{bs}$  = Broad sense heritability

GAM = Genetic advance as per cent mean

Out of ten yield and yield attributing traits evaluated, three characters viz, number of pods per cluster, pod length and seed yield per plant showed positive skewness with platykurtic distribution which is an evidence for involvement of moderate number of genes among which equal frequency of genes had increasing and decreasing effects with complementary type of epistasis on the expression of the traits. Similar findings were obtained by the previous studies conducted by Vadivel (2019), Kuralarasan and Jayamani. (2021).

In the  $F_3M_2$  segregating lines studied, The PCV estimates were relatively high for seed yield per plant and moderate PCV values were observed for number of branches per plant, number of clusters per plant, number of pods per cluster, number of pods plant and number of seeds per pod and low PCV values were recorded for days to 50 per cent flowering, plant height, pod length and test weight. These findings were in close agreement with the reports of Punia *et al.* (2013); Deepshikha *et al.* (2014); Kumar *et al.* (2015) and Singh *et al.* (2016).

In the results of the current experiment, the PCV values were higher than their corresponding GCV values for all the component traits studied. These findings were in close agreement with the reports of Panigrahi *et al.* (2014); Gandhi *et al.* (2018) and Surekha *et al.* (2020).

Number of branches per plant, number of pods per plant, number of seeds per pod showed moderate GCV

and PCV. These findings were in close agreement with the reports of Reni *et al.* (2013); Deepshikha *et al.* (2014); Singh *et al.* (2014), Sushmitharaj *et al.* (2018) and Patidar *et al.* (2018).

Days to 50 per cent flowering, plant height, pod length and 100 seed weight showed low GCV and PCV. These findings were in close agreement with the reports of Singh *et al.* (2016); Priyanka *et al.* (2016); Gowsalya *et al.* (2016) and Teja *et al.* (2021).

Number of clusters per plant and number of pods per cluster showed low GCV and moderate PCV. These findings were in close agreement with the reports of Konda *et al.* (2008); Chouhan *et al.* (2018); Tank *et al.* (2018) and Sathees *et al.* (2019).

Greater heritability values were noticed for the Days to 50 per cent flowering, number of branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, number of seeds per pod and 100 seed weight. This indicates that effective selection can be made for these traits.

## Conclusion

Heritability estimates indicate both additive and non-additive gene action. So high heritability does not always imply high genetic gain. Heritability, along with genetic advance, can be used as efficient selection parameters instead of heritability alone as both together implies the heritability due to additive gene effects.

In the present F<sub>3</sub>M<sub>2</sub> segregating population, high heritability associated with more genetic advance as per cent of mean was documented for days to 50 per cent flowering, plant height, number of branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, 100 seed weight, pod length, number of seeds per pod, seed yield per plant. Parallel results were obtained by Chaithanya *et al.* (2019); Chowdhury *et al.* (2020); Singh *et al.* (2020) and Rehman *et al.* (2021).

It is very clear from the findings of the present field experiment that the Number of clusters per plant, number of pods per cluster, number of pods per plant, number of seeds per pod and seed yield per plant exhibited the greater values of PCV, GCV, heritability and genetic advance. It is highly insisted to select these traits to attain increased yield.

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