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Assesment of genetic parameters for yield and it's components in blackgram (*Vigna mungo* (L.) Hepper)

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Abstract

Estimation of genetic parameters like Mean, Range, Variance, Genotypic coefficient of variation, Phenotypic coefficient of variation, Heritability, Genetic advance and Genetic advance as per cent of mean for ten yield and its related traits like height of the plant, number of branches, number of clusters, number of pods per plant, length of the pod, number of seeds per pod, days to 50 per cent flowering, days to maturity, single plant yield and 100 seed weight in two replications were performed in 177 plants of F_{2:3} population of blackgram derived from cross MBG-207 × PU-31 during *summer* season 2018-19 at ARS, Madhira, Khammam. Random block design (RBD) analysis was carried out and observations from ANOVA table were considered to know the variations as high and low values in different traits that will contribute to yield in blackgram crop.

Keywords: Mean, range, GCV, PCV, heritability, genetic advance and RBD

1. Introduction

Black gram or Urad bean (*Vigna mungo* (L.) Hepper) is one of the most highly prized pulse crop in the world. In India, it was in cultivation across the states (Delic *et al.*, 2009) [2], this leguminous pulse crop has inevitably marked itself as the most popular pulse and can be most appropriately referred to as the "king of the pulses". India is the largest producer and consumer of black gram cultivated in an area about 39.43 lakh hectares (AICRP Report 2021). The coastal Andhra region in Andhra Pradesh is famous for black gram after paddy (INDIASTAT 2021).

The Guntur District ranks first in Andhra Pradesh for the production of black gram. Black gram is very nutritious as it contains high levels of protein (25g/100g), potassium (983 mg/100g), calcium (138 mg/100g), iron (7.57 mg/100g), niacin (1.447 mg/100g), Thiamine (0.273 mg/100g) and riboflavin (0.254 mg/100g) (Karamany 2006) [3]. Blackgram complements the essential amino acids provided in most cereals.

Being a proper leguminous crop, black gram has all the essential nutrients which it makes to turn into a fertilizer with its ability to fix nitrogen it restores soil fertility as well. It proves to be a great rotation crop enhancing the yield of the main crop as well. The low yield levels are due to several biotic and abiotic factors.

Mungbean Yellow Mosaic Virus (MYMV) is a significant biotic stress causing profound yield loss in blackgram. MYMV belongs to the genus Begomovirus and transmitted by the vector whitefly, *Bemisia tabaci*. Yield loss due to this disease varies from 5 to 100 per cent depending upon disease severity, susceptibility of cultivars and population of whitefly (Nene, 1972) [5]. The estimates of genetic components of variation would be very useful to adopt suitable breeding method and to find the appropriate generation for the improvement of traits (Khattak *et al.*, 2001) [4]. With these backgrounds, the present investigation was carried out to find out the gene action for yield and its related components.

2. Materials and Methods

2.1 Experiment location

Phenotyping of F_{2:3} population of 177 plants was carried out in field level at ARS, Madhira, Khammam.

2.2 Development of mapping population

Crosses were made between susceptible and resistant MBG 207 and PU31 parents of blackgram respectively under shade net at Institute of Biotechnology (IBT), PJTSAU during *Kharif* 2017. Obtained F₁'s were selfed to produce F₂ population during *Rabi* 2017-18 at IBT. F₂ seeds from molecularly confirmed F₁'s were selfed to produce F_{2:3} populations during *Rabi* 2018-19 at ARS, Madhira. During Summer 2018-19, 177 plants of F_{2:3} were sown in field for analysis of genetic parameters for morphological traits.

2.3 Field layout

In field along with parents 177 plants of F_{2:3} mapping population were sown in plots in two replications. MBG 207 is used as a susceptible check and sown after every ten rows and also around the plots to increase the incidence of yellow mosaic virus disease.

2.4 Statistical analysis

The data recorded in replications for the yield and its related traits were subjected to the following statistical analysis to find the nature of various genetic parameters.

2.4.1 Genotypic and phenotypic coefficient of variation

The genotypic and phenotypic coefficient of variation was computed according to Burton and Devane (1953).

$$\text{Genotypic coefficient of variation (GCV)} = \frac{\sqrt{\sigma^2g}}{\text{Mean}} \times 100$$

$$\text{Phenotypic coefficient of variation (PCV)} = \frac{\sqrt{\sigma^2p}}{\text{Mean}} \times 100$$

Where

s²g = Genotypic variance

s²p = Phenotypic variance and X = General mean of the character

2.4.2 Heritability

Heritability in broad sense was estimated as the ratio of genotypic to phenotypic variance and expressed in percentage (Hanson *et al.*, 1956).

$$h^2(\text{bs}) = \frac{\sigma^2g}{\sigma^2p}$$

Where

h²(bs) = heritability in broad sense

s²g = Genotypic variance

s²p = Phenotypic variance

As suggested by Johnson *et al.* (1955) (h²) estimates were categorized as:

Low: 0-30%

Medium: 30-60%

High: above 60%

2.4.3 Genetic advance (GA)

This was worked out as per the formula proposed by Johnson *et al.* (1955).

$$GA = k. s^2p. H.$$

Where

k = Intensity of selection

s²p Phenotypic standard deviation

H = Heritability in broad sense

The value of 'k' was taken as 2.06 assuming 5 per cent selection intensity.

2.4.4 Genetic advance expressed as percentage over mean (GAM)

In order to visualize the relative utility of genetic advance among the characters, genetic advance as percent for mean was computed.

$$\text{Genetic advance as percent of mean} = \frac{GA}{\text{Grand mean}} \times 100$$

The range of genetic advance as percent of mean was classified as suggested by Johnson *et al.* (1955)

Low: Less than 10%

Moderate: 10-20%

High: More than 20%

3. Results and Discussions

Phenotypic data recorded for various morphological traits is subjected to statistical analysis of various genetic parameters and results were evaluated within and among the traits to find out their contribution and effect on final yield of each plant of the population. In order to assess the worth of the population for isolating high yielding lines besides looking for resistance to YMV the following are the various genetic parameters calculated and analysed for various morphological traits (Table 1).

3.1 Mean

Mean values were high for days to maturity (72.79), days to 50% flowering (38.70), plant height (22.25), number of pods per plant (17.54). Low mean values were observed in other traits, lowest mean was observed in number of branches per plant (3.27).

3.2 Range

Height of the plant ranged from 20 to 32 with a mean of 22.25, Number of branches per plant ranged from 4 to 5 with a mean of 3.27, Number of clusters ranged from 3 to 9 with a mean of 6.04, Days to 50% flowering ranged from 38 to 50 with a mean of 38.7, Number of pods per plant ranged from 10 to 21 with a mean of 17.54, Pod length ranged from 4.0 to 8.0 with a mean of 4.29, Number of seeds per pod ranged from 3 to 6 with a mean of 5.56, days to maturity ranged from 70 to 75 with a mean of 72.79, Seed yield per plant ranged from 2.12 to 4.43 with a mean of 3.98 and 100 seed weight ranged from 2.59 to 3.69 with a mean of 3.72.

3.3 Variance

High variance observed for number of clusters (22.67), number of pods per plant (20.59), number of branches per plant (10.57), and single plant yield (8.78). Less variance was observed for the remaining traits and the lowest variation was observed for the trait days to maturity (1.29).

The increase in mean values as a result of hybridization indicates, scope for further improvement in traits like number of pods per plant, number of seeds per pod, pod length and other characters in subsequent generations, there by

facilitating selection of transgressive segregants in later generations. The results are in line with the findings of Basamma *et al.* (2011)^[1].

The critical parameters are range and variance which decide the higher extreme value of the cross. The range observed was wider for number of pods per plant, number of seeds per pod, pod length, number of branches per plant, plant height, number of clusters, days to 50% flowering and single plant yield in F_{2:3} population. Similar results were obtained by Salimath *et al.* (2007)^[6] in F₂ and F₃ population of cowpea.

3.4 Genetic variability parameters

The genetic gain through selection depends on the quantum of variability and extent to which it is heritable. The following are the variability parameters analysed for the observed traits.

3.5 Phenotypic coefficient of variation (PCV)

High PCV estimates were observed for number of clusters (37.23), number of pods per plant (30.30), single plant yield (27.95). Lowest estimates were observed for days to maturity (1.24).

3.6 Genotypic Coefficient of Variation (GCV)

High GCV estimates were observed for number of clusters (29.52), single plant yield (26.53), Number of pods per plant (22.23). Moderate estimates were observed for plant height (13.94), pod length (9.00), number of branches per plant (7.23). Lowest estimates for days to maturity (0.36).

The genotypic coefficients of variation for all characters obtained were lesser than phenotypic coefficient of variation indicating masking effects of environment showing greater influence of environment on these traits. These results are in accordance with the finding of Singh *et al.* (2009). Low to moderate GCV and PCV values for above characters indicate the influence of the environment on these traits and also limited scope of selection for improvement of these characters.

The high, medium and low PCV and GCV indicate the potentiality with which the characters express. However, GCV is considered to be more useful than PCV for assessing variability since, it depends on the heritable portion of variability. The results of the above experiments showed that variability can be created by hybridization (Basamma, 2011)^[1]. However, the variability generated to a large extent depends on the parental genotype and the trait under study.

3.7. Heritability

Heritability in broad sense was high for single plant yield (90.1), plant height (73.6), pod length (65.9), number of clusters (62.9), days to 50% flowering (60.0). Moderate values were observed for number of seeds per pod (48.0), number of pods per plant (53.8). Lowest values were observed for 100 seed weight (30.7).

3.8 Genetic advance

Genetic advance was high for number of pods per plant (5.89), plant height (5.48), number of clusters (2.91) and single plant yield (2.06). Low values observed for days to 50% flowering (1.59) and number of branches per plant (0.27).

3.9 Genetic advance as percent of mean

Genetic advance as percent of mean was high for single plant yield (51.89), number of clusters (48.24), Number of pods per plant (33.60). Low values were observed for plant height (24.63) and pod length (15.06).

In this study heritability in broad sense and genetic advance as percent of mean was high for single plant yield and number of clusters indicating that these traits were controlled by additive genes indicating the availability of sufficient heritable variation that could be made use in the selection programme and can easily be transferred to succeeding generations. Similar results were found by Rajwani *et al.* (2021)^[7].

Table 1: Estimates of genetic parameters for different morphological traits of F_{2:3} population of cross MBG 207× PU 31 in blackgram.

Morphological trait	M	R	Variance	PCV	GCV	h ² %	GA 5%	GAM 5%
Plant height (cm)	22.25	8	8.36	16.25	13.94	73.6	5.48	24.63
Number of branches per plant	3.27	3	10.57	12.81	7.23	31.9	0.27	8.42
Number of clusters (cm)	6.04	3	22.67	37.23	29.52	62.9	2.91	48.24
Pod length (cm)	4.29	4	6.47	11.09	9.00	65.9	0.64	15.06
Number of pods per plant	17.54	11	20.59	30.30	22.23	53.8	5.89	33.60
No of seeds per pod	5.56	3	8.21	11.39	7.9	48	0.62	11.27
Days to 50% flowering	38.70	12	2.07	3.28	2.54	60	1.57	4.05
Single plant yield (g)	3.98	1.95	8.78	27.95	26.53	90.1	2.06	51.89
Days to maturity	72.79	2.45	1.29	1.24	0.36	8	0.16	0.28
100 seed weight	3.72	1.12	6.35	7.6	4.22	30.7	0.18	6.18

M= Mean, R= Range, V= Variance, PCV= Phenotypic coefficient of variation, GCV= Genotypic coefficient of variation, h²%= heritability (broad sense), GA= Genetic advance GAM= Genetic advance as percent mean.

4. Conclusions

It can be concluded that traits like single plant yield, number of branches per plant, number of clusters per plant, number of pods per plant may respond more to the selection since these traits showed high heritability along with high genetic advance as percent of mean. Therefore, these traits could be considered during selection for yield improvement of this crop at desired level.

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