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Genetic variability studies on yield component characters and physiological traits in rice fallow black gram [*Vigna mungo* (L.) Hepper]

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Abstract

Fifty genotypes of black gram were evaluated during rabi 2018-19 at ARS, Ghantasala, Krishna district, Andhra Pradesh in RBD with three replications under rice fallow situation. The phenotypic coefficient of variation was found superior than the genotypic coefficient of variation for all traits studied, showing that the variation is not only genetic but also influenced by growing environments in the expression of the traits. The genotypes were highly variable for No. of branches per plant, No. of clusters per plant, No. of pods per plant, seed yield per plant, total biomass per plant, harvest index, No. of nodules per plant and leaf area index. Broad sense heritability was higher for all the traits except days to maturity, plant height, 100 seed weight and pod length. High heritability coupled with high genetic advance as per cent of mean was observed for No. of branches per plant, No. of clusters per plant, No. of pods per plant, No. of seeds per pod, seed yield per plant, specific leaf weight, leaf nitrogen content, total biomass per plant, harvest index, No. of nodules per plant, weight of nodules, leaf area index and specific leaf area.

Keywords: Variability, heritability, genetic advance, black gram and rice fallow

Introduction

Black gram [*Vigna mungo* (L.) Hepper, 2n=22] is an important grain legume which occupies a unique position in Indian agriculture. It is mainly known for its nutritional quality, soil nitrogen fixing ability and suitability to different cropping systems. It is popularly known as urdbean, urd or mash.

In India black gram occupies an area of 44.78 lakh hectares producing 28.31 lakh tons with a productivity of 632 kg/ha (www.Indiastat.com, 2016-17) ^[3]. Black gram cultivation has been very popular in rice fallows cultivation in large area particularly in coastal Andhra Pradesh and certain areas of Tamil Nadu and Odisha. In Andhra Pradesh it is cultivated in an area of 5.00 lakh ha, with a production and productivity of 3.29 lakh tons and 658 kg/ha, respectively (www.Indiastat.com, 2016-17) ^[3].

It is felt by breeders that lack of cultivars with high yield potential and stability is the key point for low productivity in pulses, as a whole. In order to develop varieties with higher yield suitable to various seasons and cropping systems, it is essential to generate wider variability.

The study of mode of inheritance of various developmental and productive traits through the estimation of different genetic parameters like components of variances, genotypic and phenotypic coefficients of variability, heritability and genetic advance as per cent of mean is helpful for framing the effective breeding programme.

Material and Methods

Fifty genotypes of black gram were sown on 26th and 27th December, 2018 in plot no. 22 of ARS, Ghantasala using RBD with three replications during the rabi 2018-19. Each genotype was sown in 6 rows of 4m length with a spacing of 30 cm between the rows and 10 cm between the plants.

Data was collected at the time of harvest for plant height (cm), number of branches per plant, number of clusters per plant, number of pods per plant, number of seed per pod, 100-seed weight (g), pod length (cm), seed yield per plant (g), leaf nitrogen content (g m⁻²), total biomass per plant (g), harvest index in per cent, number of nodules, weight of nodules (mg); for specific leaf weight (g cm⁻²) (SLW), leaf area index (LAI) and specific leaf area (cm² g⁻¹) (SLA) data was collected at a regular intervals of 40 DAS & 60 DAS and for days to 50% flowering and days to maturity data collected at that time.

Data was recorded from five randomly selected plants of each genotype per replication and the average was taken for analysis. Standard statistical procedures were used for the analysis variance due to different sources that was worked out according to Panse and Sukhatme (1967) ^[9], genetic variability estimates of quantitative traits such as PCV and GCV was calculated using the formula given by Burton (1952) ^[11] and categorization of the range of variation was done as proposed by Sivasubramanian and Madhavamenon (1978) ^[12]. Broad sense heritability (h^2) was computed according to Lush (1949) ^[6] and genetic advance was worked out as per Johnson *et al.*, (1955) ^[4].

Results and Discussion

Analysis of variance (ANOVA) was carried out for 18 characters and the results are presented in Table I. The variance due to treatments was highly significant for all the eighteen characters and the variation due to replication was non significant for all characters. The genotypic and phenotypic coefficient of variability, heritability (broad sense) and genetic advance as per cent of mean are presented in Table II and Figure I. Among the eighteen quantitative characters, the range of variation was found to be maximum in No. of pods per plant (16.60-41.96) in quantitative characters and specific leaf area among physiological characters (169.56-376.43). MBG-1069, MBG-1050 and TGBG-26 were found to be the three best performers in respect to seed yield per plant.

The estimates of genetic parameters revealed that high phenotypic and genotypic coefficient of variation was found for No. of branches per plant, No. of clusters per plant, No. of pods per plant, seed yield per plant, total biomass per plant, harvest index, No. of nodules per plant, leaf area index (40 DAS) and leaf area index (60 DAS). Estimates of moderate genotypic and high phenotypic coefficient of variation are

shown by plant height, specific leaf weight (40 DAS), specific leaf weight (60 DAS), leaf nitrogen content, weight of nodules per plant, specific leaf area (40 DAS) and specific leaf area (60 DAS). And other characters like days to 50 % flowering, days to maturity, number of seeds per pod, 100 seed weight and pod length expressed low variability. These results are in conformity with the findings of Kumar *et al.* (2018) ^[5], Susmitharaj *et al.* (2018) ^[13], Priyadarsini *et al.* (2017) ^[11], Mohankumar *et al.* (2011) ^[7] and Neemar *et al.* (2007) ^[8].

High heritability coupled with high genetic advance as per cent of mean was observed for No. of branches per plant, No. of clusters per plant, No. of pods per plant, seed yield per plant, specific leaf weight (40 DAS), specific leaf weight (60 DAS), leaf nitrogen content, total biomass per plant, harvest index, No. of nodules per plant, weight of nodules per plant, leaf area index (40 DAS), leaf area index (60 DAS), specific leaf area (40 DAS) and specific leaf area (60 DAS). This indicated the governance of additive gene action in the inheritance of these characters. Hence, these characters can be fixed since they respond better to selection.

However the characters days to 50 % flowering and No. of seeds per pod had high heritability along with moderate genetic advance as per cent of mean, which might be due to abundance of non-additive gene effects. Moderate heritability and genetic advance as per cent of mean was observed for plant height and moderate heritability with low genetic advance as per cent of mean for days to maturity and 100 seed weight. Low heritability and low genetic advance as per cent of mean was observed for pod length indicating the role of non additive gene action. These results were in agreement the findings of Hadimani *et al.* (2015) ^[2], Kumar *et al.* (2018) ^[5], Priyadarsini *et al.* (2017) ^[11], Neemar *et al.* (2007) ^[8] and Patil and Salimath (2003) ^[10].

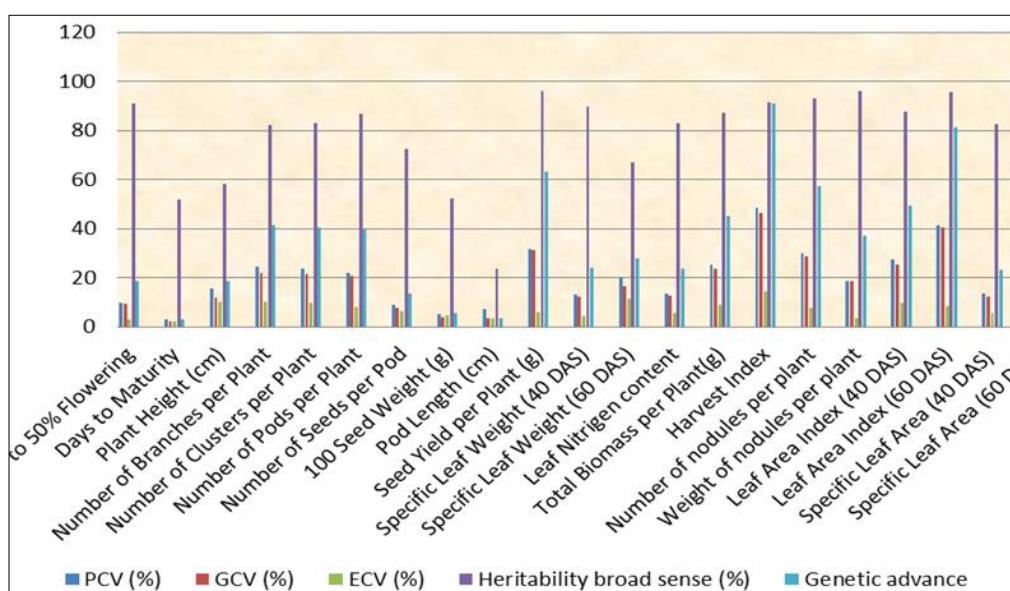
Table 1: Analysis of Variance (ANOVA) for different yield and physiological characters in rice fallow black gram [*Vigna mungo* (L.) Hepper]

| S. No | Character | Mean sum of squares | | |
|-------|-------------------------------|---------------------|----------------------|----------------------|
| | | Replications (df=2) | Replications (df=49) | Replications (df=98) |
| 1. | Days to 50% Flowering | 0.72 | 53.83** | 1.71 |
| 2. | Days to Maturity | 2.28 | 10.53** | 2.48 |
| 3. | Plant Height (cm) | 4.71 | 20.37** | 3.96 |
| 4. | Number of Branches per Plant | 0.07 | 0.74** | 0.05 |
| 5. | Number of Clusters per Plant | 0.06 | 2.45** | 0.15 |
| 6. | Number of Pods per Plant | 4.65 | 106.44** | 5.10 |
| 7. | Number of Seeds per Pod | 0.07 | 0.44** | 0.04 |
| 8. | 100 Seed Weight (g) | 0.04 | 0.44** | 0.04 |
| 9. | Pod Length (cm) | 0.02 | 0.11** | 0.02 |
| 10. | Seed Yield per Plant (g) | 0.22 | 13.47** | 0.17 |
| 11. | Specific Leaf Weight (40 DAS) | 0.14 | 45.01** | 0.03 |
| 12. | Specific Leaf Weight (60 DAS) | 0.67 | 3.99** | 0.56 |
| 13. | Leaf Nitrogen content | 0.008 | 0.22** | 0.01 |
| 14. | Total Biomass per Plant(g) | 3.48 | 52.52** | 2.47 |
| 15. | Harvest Index | 10.18 | 1218.51** | 37.56 |
| 16. | Number of nodules per plant | 10.00 | 150.40** | 3.57 |
| 17. | Weight of nodules per plant | 26.00 | 889.62** | 11.54 |
| 18. | Leaf Area Index (40 DAS) | - | 0.01** | - |
| 19. | Leaf Area Index (60 DAS) | 0.01 | 0.58** | - |
| 20. | Specific leaf area (40 DAS) | 331.79 | 2680.21** | 177.69 |
| 21. | Specific leaf area (60 DAS) | 668.90 | 1990.96** | 238.32 |

** significant at 1 per cent level; -: low estimate of error mean square.

Table 2: Estimates of variability, heritability (broad sense) and genetic advance as per cent of mean for yield and physiological characters in Black gram [*Vigna mungo* (L.) Hepper] under rice fallow situation

| Character | Mean | Range | | Coefficient of variation | | | Heritability broad sense (%) | Genetic advance as per cent of mean |
|-------------------------------|--------|---------|---------|--------------------------|---------|---------|------------------------------|-------------------------------------|
| | | Minimum | Maximum | PCV (%) | GCV (%) | ECV (%) | | |
| Days to 50% Flowering | 44.34 | 37.33 | 53.66 | 9.85 | 9.39 | 2.95 | 91.09 | 18.46 |
| Days to Maturity | 75.58 | 71 | 79.33 | 3.00 | 2.16 | 2.08 | 51.94 | 3.21 |
| Plant Height (cm) | 19.79 | 14.20 | 24.56 | 15.51 | 11.81 | 10.05 | 58.00 | 18.52 |
| Number of Branches per Plant | 2.17 | 1.13 | 3.63 | 24.39 | 22.10 | 10.32 | 82.14 | 41.24 |
| Number of Clusters per Plant | 4.02 | 2.63 | 6.73 | 23.82 | 21.70 | 9.83 | 83.00 | 40.72 |
| Number of Pods per Plant | 28.26 | 16.60 | 41.96 | 22.06 | 20.56 | 7.99 | 86.94 | 39.48 |
| Number of Seeds per Pod | 6.53 | 5.93 | 7.13 | 7.47 | 3.65 | 6.51 | 23.90 | 3.68 |
| 100 Seed Weight (g) | 4.65 | 3.49 | 5.72 | 9.16 | 7.81 | 4.80 | 72.67 | 13.70 |
| Pod Length (cm) | 4.53 | 4.16 | 4.98 | 5.23 | 3.78 | 3.61 | 52.35 | 5.64 |
| Seed Yield per Plant (g) | 6.73 | 3.07 | 10.92 | 31.84 | 31.24 | 6.16 | 96.26 | 63.14 |
| Specific Leaf Weight (40 DAS) | 4.38 | 2.80 | 6.60 | 13.08 | 12.38 | 4.22 | 89.66 | 24.14 |
| Specific Leaf Weight (60 DAS) | 6.47 | 2.83 | 9.67 | 20.19 | 16.53 | 11.59 | 67.07 | 27.89 |
| Leaf Nitrogen content | 2.09 | 1.53 | 2.67 | 13.78 | 12.55 | 5.69 | 82.92 | 23.55 |
| Total Biomass per Plant(g) | 17.36 | 10.66 | 27.33 | 25.20 | 23.51 | 9.05 | 87.14 | 45.21 |
| Harvest Index | 42.85 | 13.67 | 88.34 | 48.45 | 46.29 | 14.30 | 91.28 | 91.12 |
| Number of nodules per plant | 24.22 | 11.33 | 43.33 | 29.91 | 28.87 | 7.80 | 93.27 | 57.42 |
| Weight of nodules per plant | 92.63 | 47.66 | 133.33 | 18.83 | 18.46 | 3.66 | 96.20 | 37.31 |
| Leaf Area Index (40 DAS) | 0.29 | 0.15 | 0.48 | 27.30 | 25.54 | 9.64 | 87.50 | 49.23 |
| Leaf Area Index (60 DAS) | 1.08 | 0.55 | 2.14 | 41.23 | 40.33 | 8.55 | 95.74 | 81.28 |
| Specific leaf area (40 DAS) | 232.96 | 169.56 | 376.43 | 13.65 | 12.39 | 5.72 | 82.43 | 23.18 |
| Specific leaf area (60 DAS) | 155.43 | 110.48 | 244.29 | 18.54 | 15.50 | 9.93 | 71.02 | 26.99 |

**Fig 1:** Genetic parameters of different quantitative and physiological characters in black gram [*Vigna mungo* (L.) Hepper] under rice fallow situation

Conclusion

From the present investigation, it is suggested that the genotypes i.e., MBG-1069, MBG-1050, VBG 13-003 and TGBG-26 which are varying greatly among themselves regarding means among yield component characters and physiological characters may further be used in the future breeding programmes as divergent parents. Higher heritability estimates for most of the characters studied indicates that the selection on phenotypic value would give good response.

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