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Anu Bishnoi
MSc Student, Department of
Genetics and Plant Breeding,
SHIATS, Allahabad,
Uttar Pradesh, India

Priyanka Gupta
MSc Student, Department of
Genetics and Plant Breeding,
SHIATS, Allahabad,
Uttar Pradesh, India

DR Meghawal
Ph.D Scholar, Department of
Genetics and Plant Breeding
RCA, MPUA&T, Udaipur,
Rajasthan, India

G.M. Lal
Assistant Professor
Department of Genetics and
Plant Breeding, SHIATS,
Allahabad, Uttar Pradesh, India

Correspondence

Anu Bishnoi
MSc Student, Department of
Genetics and Plant Breeding,
SHIATS, Allahabad,
Uttar Pradesh, India

Evaluation of genetic variability and heritability in blackgram (*Vigna mungo* (L.) Hepper) genotypes

Anu Bishnoi, Priyanka Gupta, DR Meghawal and GM Lal

Abstract

An experiment was conducted to estimate the extent of genetic variability and heritability in blackgram with the use of thirty-six genotypes available at Department of Genetics and Plant breeding, Sam Higginbottom Institute of Agriculture Science and Technology, Allahabad. The genotypes were tested during *Kharif*, 2015 under irrigation condition in randomized block design with three replications. Analysis of variance revealed significant differences for 13 characters studied among the genotypes. High phenotypic coefficient of variation was recorded for clusters/plant while medium values were found in plant height and primary branches per plant. Medium genotypic coefficient of variation was reported in plant height and clusters/plant. High heritability was showed by traits like seed index (0.90), seed yield per plant (0.89), biological yield per plant (0.89), pods per plant (0.67) and harvest index (0.61). The expected genetic advance and genetic advance as % of mean of blackgram genotypes ranges between 0.12 for seeds per pod to 11.24 plant height and 2.02 for days to maturity to 17.10 for seed yield per plant, respectively. Thus, traits showing variability both at genotypic and phenotypic levels and heritability coupled with moderate to high genetic advance need to be paid attention while formulating breeding strategies for improvement of grain yield of blackgram.

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

1. Introduction

Blackgram (*Vigna mungo* (L.) Hepper) is an important nutritious pulse crop occupying unique position in Indian agriculture (Malik, 1994) ^[9] which occupies about 3.7 million ha land with annual production of 1.5-1.9 million tons in India (FAOSTAT, 2015). In U.P., Blackgram is grown in about 3.91 lakh ha land with a total production of 1.87 lakh tones (Anonymous, 2013) ^[1]. This crop is grown in cropping systems as a mixed crop, catch crop, sequential crop besides growing as sole crop under residual moisture conditions after the harvest of rice and also before and after the harvest of other summer crops under semi irrigated and dryland conditions. Its seeds are highly nutritious with protein (25-26%), carbohydrates (60%), fat (1.5%), minerals, amino acids and vitamins. Like other pulses, it also enriches the soil fertility, improves the soil structure and used as green fodder for cattle (Parveen *et al.*, 2011) ^[11].

Per capita availability of pulses per day is only 47g as against the minimum requirement of 104 g as recommended by nutritional experts of World Health Organization/Food and Agriculture Organization (Hariprasanna and Bhatt, 2002) ^[5]. Generally pulses are rich in those amino acids (Lysine and Tryptophan) which are present in traces in cereals. It is a cheap source of dietary protein 23-24%. It also contributes 76% carbohydrate, 3-5% Fiber, 1.74% Fat and a major portion of lysine in the vegetarian diet (Elangaimannan *et al.*, 2008) ^[3]. Lack of stable varieties for higher yield is a major bottleneck for growing of this crop. Therefore for increasing the productivity of blackgram collection and characterization of germplasm from different regions of cultivation need specific emphasis. The improvement in this crop is confined to pure line selection and to a limited extent through hybridization. In the past, there have been attempts to increase the production and productivity of the crop using conventional breeding approaches in different agriculture research centers (Ali and Kumar, 2006) ^[1].

The study 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 is helpful for framing the effective breeding programme. The genetic variability, heritability and genetic advance help to formulate selection criteria for evolving high yielding genotypes in blackgram (Rao *et al.*, 2006) ^[14]. Hence, the present research work was carried out to assess the genetic variability and heritability presence among the blackgram genotypes.

Materials and Methods

The experimental materials comprising of thirty-six blackgram genotypes were grown in a randomized block design with three replications at Field Experimentation Center, Department of Genetics and Plant Breeding, Sam Higginbottom Institute of Agriculture Science and Technology (Deemed-to-be-University), Allahabad, India during *Kharif*, 2015 under irrigated condition. Each plot consisted of single row plot of 2 m length with a spacing of 25×10 cm where 2 seeds per hill were dropped manually. Later, one plant per hill was maintained after thinning. Chemical fertilizers, at the rate of 20:40:20 NPKKg /ha in the form of Urea, Di-ammonium phosphate (DAP) and Murate of potash (MOP), were applied and other standard agronomical operation and plant protection measures were adapted to raise healthy and uniform crops.

Data were recorded on visual observations of plants on plot basis for traits like days to 50% flowering, days to 50% pod setting, and days to maturity while data for plant height (cm), primary branches/plant, no. of clusters/plant, no. of pods/plant, pod length (cm), no. of seeds/pod, seed index (%), seed yield/plant (g), biological yield/plant (g) and harvest index (%) were taken from five randomly selected plants from middle of row of each entry in each replication.

The mean values over replications were subject to analysis of variance as suggested by Panse and Sukhatme (1985) [10]. The variability presence in the genotypes was estimated by phenotypic and genotypic variances and coefficient of variations using the procedure suggested by Burton and De Vane (1953) as follows:

$$\text{Phenotypic variance } (\sigma_p^2) = \sigma_g^2 + \sigma_e^2$$

$$\text{Genotypic variance } (\sigma_g^2) = \frac{MSG - MSE}{r}$$

Where, σ_e^2 = Environmental variance or Error mean square, MSG = Mean square due to genotypes, MSE = Mean square due to error (environment variance), r = Number of replication

$$\text{Phenotypic coefficient of variation (PCV)} = \frac{\sqrt{\sigma_p^2}}{\bar{x}} \times 100$$

$$\text{Genotypic coefficient of variation (GCV)} = \frac{\sqrt{\sigma_g^2}}{\bar{x}} \times 100$$

Where \bar{x} = Population mean of the character being evaluated
Heritability in broad sense (H^2_{bs}) was computed using the formula given by Lush (1949):

$$H^2 = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

The genetic advance (GA) for selection intensity (K) at 5% was calculated by the formula suggested by Johnson *et al.* (1955) [6]: $GA = K \cdot \sigma_p \cdot H^2$

Where, σ_p = Phenotypic standard deviation on mean basis and K = Selection differential (= 2.06 at 5% selection intensity)
Genetic advance as percentage of mean (GA as % of mean) was derived to compare the extent of predicted genetic advance of different traits under selection using the formula:

$$GA (\% \text{ of mean}) = \frac{GA}{\bar{x}} \times 100$$

Results and Discussion

Analysis of variance

The analysis of variance (Table 1) revealed significant differences among the genotypes for all the traits studied suggesting the presence of genetic variability among the genotypes for the characters studied which shows an ample scope for selection of promising genotype from the present gene pool for increasing yield of blackgram. The presence of large amount of variability might be due to diverse source of material taken as well as environmental influence affecting the phenotypes.

Table 1: Analysis of variance for 13 different quantitative characters in 36 genotypes of Blackgram

Characters	Sources of variation			CV (%)
	Replication (df=2)	Genotypes (df=35)	Error (df=70)	
Days to 50% flowering	4.08	14.65**	3.64	4.58
Days to 50% pod setting	0.71	20.19**	5.40	4.64
Plant height	6.28	256.91**	69.05	11.83
Number of primary branches	0.03	0.36**	0.12	8.69
Number of clusters per plant	37.47	28.42*	15.22	21.95
Pods per plant	0.78	15.88**	2.21	2.37
Pod length	0.00	0.04**	0.01	1.98
Number of seeds per pod	0.03	0.14*	0.08	4.91
Days to maturity	0.66	4.43**	1.33	1.67
Seed index	0.02	0.20**	0.01	1.87
Harvest index	4.88	17.77**	3.12	4.40
Biological yield	0.12	22.78**	0.94	2.74
Seed yield per plant	0.22	4.82**	0.18	3.02

*and** significant of 5% and 1%, respectively

Per se mean performance of genotypes

The *per se* mean performance of various genotypes exhibited wide range of variation for most of the traits studied (Table 2). Despite that some traits showed more variation like as plant height (41.82-85.91cm), clusters/plant (8.87-25.13),

pods/plant (59.07-72.47), days to 50% flowering (35.67-45.67 days), days to 50% pod setting (45.67-55.33 days), days to maturity (67.00-71.67 days), harvest index (32.51-44.73%), biological yield/plant (27.87-39.83), seed yield/plant (11.42-15.91g), etc. indicates sufficient variation among the

genotypes for the traits studied. The mean value for grain yield was found 14.16g with standard error of 0.25. This reflected that there is greater opportunity to improve the yield and its related traits in blackgram.

Phenotypic and genotypic variations

The estimates of variability parameters for various yield and yield related traits are presented in (Table 2). The phenotypic and genotypic variances were ranges from 0.02 - 131.67 and 0.01 - 62.62, respectively (Table 2). Comparatively higher phenotypic variance value of 131.67 for plant ht, 19.62 for cluster/plant and 10.33 for days to 50% pod setting & seed yield/plant were recorded in this study. Similarly, higher genotypic variances values were observed for the same traits pointed out that genotype could be reflected by phenotype and the effectiveness of selection of genotypes based on phenotypic performance of these traits. The PCV values were revolved around 2.23% for days to maturity to 24.91% for clusters/plant and GCV values were ranged from 1.48% to 11.79% for the same traits (Table 2). High PCV was recorded for clusters/plant while medium PCV was found in traits like plant ht. and primary branches/plant. In addition, medium GCV was reported in traits such as plant ht., clusters/plant. The selection of genotypes based on these traits would be effective. The nominal variation between PCV and GCV in the traits like as seed index (0.30), pods/plant (0.74), and days to maturity (0.75) and pod length (0.82) showed there was considerably low influence of environment for the expression of the traits. Konda *et al.* (2009) [7] also reported high value of PCV for pods per plant, number of branches per plant and plant height. Moreover, Umadevi and Ganesan (2006) [17], Samad *et al.* (2013) [15] also reported high GCV values for the number of clusters per plant, number of pods per plant, pod length and number of seeds per pod in blackgram and

suggested for a greater scope of selection for these traits.

Heritability (broad sense) and expected genetic advance

In the present study high estimates of heritability were observed for seed index (90%), followed by seed yield per plant (89%), biological yield per plant (89%), pods per plant (67%) and harvest index (61%) (Table2). High heritability estimates for these traits indicating that these traits are more likely to be controlled by additive genetic component. Sowmini and Jayamani (2013) [16], Wani *et al.* (2007) [18] reported high heritability for the traits such as number of pods per plant, number of pods per cluster, plant height and seed yield per plant and suggested the additive genetic control in the inheritance of these characters.

The expected genetic advance and genetic advance as % of mean by selecting top 5% (high yielder) of blackgram genotypes arranged between 0.12 for seeds per pod to 11.24 plant ht. and 2.02 for days to maturity to 17.10 for seed yield/plant, respectively (Table 2). Estimated of genetic advance and genetic advance as percentage of mean, respectively were moderately high for plant height (11.24 & 16.00). Other traits like as cluster per plant (11.50%), seed index (11.29%), biological yield per plant (14.83%) and seed yield/plant (17.10%) also exhibited moderately high genetic advance as % of mean. The results of present study were also supported by the finding of Ramya (2014) [13], Konda *et al.* (2009) [7] and Prasad & Prasad (2013) [12].

Jonson *et al.* (1955) [6] and Panse & Sukhatme (1985) [10] suggested high estimates of heritability and genetic advance as per cent of mean should be taken into consideration for selection for base improvement. Heritability along provides no indication of the amount of genetic improvement that would result from selection of the individual genotypes.

Table2: Estimate of range, mean and other variability components of various characters for 36 Blackgram genotypes

Characters	Range	Mean±SEm	VG	VP	GCV	PCV	h ² (bs)	GA	GA as % of mean
Days to 50 % flowering	35.67-45.67	41.65±1.10	3.67	7.31	4.60	6.49	0.50	2.80	6.71
Days to 50 % pod setting	45.67-55.33	50.07±1.34	4.93	10.33	4.43	6.42	0.48	3.16	6.31
Plant height	41.82-85.91	70.24±4.80	62.62	131.67	11.27	16.34	0.48	11.24	16.00
Primary branches/plant	3.47-5.07	3.91±0.20	0.08	0.20	7.36	11.39	0.42	0.38	9.79
Clusters/ plant	8.87-25.13	17.78±2.25	4.40	19.62	11.79	24.91	0.22	2.05	11.50
Pods/ plant	59.07-72.47	62.84±0.86	4.56	6.77	3.40	4.14	0.67	3.61	5.74
Pod length	4.61-5.09	4.81±0.06	0.01	0.02	1.98	2.80	0.50	0.14	2.88
Seeds/ pod	5.47-6.47	5.90±0.17	0.02	0.10	2.36	5.45	0.19	0.12	2.12
Days to maturity	67.00-71.67	68.90±0.67	1.04	2.36	1.48	2.23	0.44	1.39	2.02
Seed index	3.85-4.79	4.46±0.05	0.07	0.07	5.76	6.06	0.90	0.50	11.29
harvest index	32.51-44.73	40.19±1.02	4.88	8.01	5.50	7.04	0.61	3.56	8.85
Biological yield/ plant	27.87-39.83	35.29±0.56	7.28	8.21	7.64	8.12	0.89	5.23	14.83
Seed yield/ plant	11.42-15.91	14.16±0.25	1.54	1.72	8.77	9.28	0.89	2.42	17.10

Conclusion

Existence of variability among the blackgram genotypes shows the selection will be effective in enhancing the seed yield. While selecting genotypes of blackgram for formulating breeding strategies traits like clusters per plant, seed index, biological yield/plant, seed yield/plant, harvest index, etc. should give higher priority as they have high variability and heritability.

References

1. Ali M, Kumar S. Paradigm shift in Planning needed. *The Hindu Survey of Anonymous*. 2013. Directorate of Pulse Research, Department of Agriculture and Cooperation, Ministry of Agriculture, Govt. of UP, 2006.
2. Burton GW, De Vane EH. Estimation of heritability in

Tall Festuca (*Festuca arundinacea*) from replicated clonal material. *Agronomy Journal*. 1953; 45:478-481.

3. Elangaimannan R, Anbuselvam Y, Karthikeyan P. Genetic diversity in Blackgram (*Vigna mungo* (L.) Hepper). *Legume research*. 2008; 31(1):57-59.
4. FAO STAT. Online Ineractive Database on Agriculture *FAO STAT*, 2015. [Retrieved from www.fao.org.]
5. Hariprasanna K, Bhatt J. Pulse's production looking at constraints and prospects. *Agriculture Today*. 2002, 49-53.
6. Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybeans. *Agronomy Journal*. 1955; 47:314-318.
7. Konda CR, Salimath PM, Mishra MN. Genetic variability studies for productivity and its components in blackgram

- [*Vigna munga* (L.) Hepper]. Legume research. 2009; 32(1):59-61.
8. Lush JL. Intra-site, correlation and regression of offspring on dams as a method of estimating heritability of characters. Proceeding of American Society of Animal Production. 1949; 33:293-301.
 9. Malik BA. Grain legumes. In: Crop Production (Ed.): National Book Foundation. 1994, 301.
 10. Panse VG, Sukhatme PV. Statistical methodology for agricultural workers. ICAR Publications, New Delhi, 1985.
 11. Parveen SI, Sekhar MR, Reddy DM, Sudhakar P. Correlation and path coefficient analysis for yield and yield components in blackgram (*Vigna mungo* (L.) Hepper) International Journal of Applied Biology and Pharmaceutical Technology. 2011; 2:619-625.
 12. Prasad BVV, Prasad GS. Genetic variability, trait association and path analysis of yield and yield components in *Vigna radiata* L. International Journal of Bio-resource and Stress Management. 2013; 4(2):251-254.
 13. Ramya B, Nallathambi G, Ram GS. Genetic variability, heritability and genetic advance in induced mutagenesis black gram (*Vigna mungo* L. Hepper) Plant Archives. 2014; 14(1):139-141.
 14. Rao CM, Rao YK, Reddy M. Genetic variability and path analysis in mungbean. Legume Research. 2006; 29:216-208.
 15. Samad MA, Sarker N, Sarker JK, Azad AK, Deb AC. Assessment of variability in twenty-four lines of blackgram (*Vigna mungo* L.) International Journal of Biosciences. 2013; 3(8):307-312
 16. Sowmini K, Jayamani P. Genetic variability studies for yield and its component traits in RIL population of blackgram (*Vigna mungo* (L.) Hepper). Electronic Journal of Plant Breeding. 2013; 4(1):1050-1055.
 17. Umadevi M, Ganesan NM. Variability, correlation and path analysis for yield and yield components in blackgram [*Vigna mungo* (L.) Hepper]. Crop Research (Hisar). 2006; 31(2):253-257.
 18. Wani BA, Marker S, Lavanya GR. Genetic variability, correlation and path analysis in green gram. Journal of Maharashtra Agricultural Universities. 2007; 32(2):216-219.