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Assessment of genetic variability parameters in blackgram [*Vigna mungo* (L.) Hepper] germplasm for yield and physiological traits

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Abstract

The present investigation was carried out on 40 Blackgram genotypes to study about genetic variability, heritability and genetic advance for 9 characters. High GCV and PCV was observed in SLA followed by Pods per plant. High heritability coupled high genetic advance as percent of mean were observed for Plant height (cm), number of pods per plant, SLA and Seed yield (kg/ha) suggesting the functioning of additive gene action in the inheritance of these traits. Therefore, simple phenotypic selection is sufficient for improving these traits.

Keywords: PCV, GCV, heritability and genetic advance as percent of mean

Introduction

Blackgram is an annual leguminous crop belongs to family Fabaceae and sub-family Papilionaceae with a chromosome number $2n=22$ (Dana, 1980) and originated from Indian continent [De Candolle, 1882, Vavilov, 1926]. It is popularly known as “urd bean and mash” is an important short duration and self-pollinated Kharif legume crop and is an important part of Indian diet. It is rich source of protein (25-28%), carbohydrates (62-65%), fibre (3.5-4.5%), ash (4.5-5.5%), oil (0.5- 1.5%), amino acids like lysine, vitamins like thiamine, niacin, riboflavin and much needed iron and phosphorus Sohel *et al.*, (2016) [27]. Being a leguminous crop, it restores the soil fertility by fixing atmospheric nitrogen and thus prevents soil erosion. India is the largest producer as well as consumer of blackgram. The major producing states are Andhra Pradesh, Maharashtra, Madhya Pradesh, Tamil Nadu, Uttar Pradesh. Despite its great importance, blackgram cultivation is neglected as little attention is given towards its improvement. There are various reasons for the low production of crop like lack of genetic variability, absence of suitable ideotype, susceptibility to biotic and abiotic stresses and planting in marginal areas of farming. Hence, it is vital to improve the productivity of blackgram. This can be achieved by studying the genetic architecture of the crop.

The knowledge of the inheritance of various quantitative and qualitative traits through estimation of genetic parameters like phenotypic and genotypic coefficients of variability, heritability, and genetic advance is a prerequisite in conducting an effective breeding programme. Before starting any breeding programme, it is necessary to access the nature and magnitude of genetic variability in the population to improve the yield and its component traits Singh *et al.*, (2016) [26].

Along with genetic variability, knowledge of heritability and genetic advance is essential to formulate selection criteria for improvement of seed yield. Heritability is the heritable portion of phenotypic variance which is good index of transmission of traits from parents to their offspring.

Heritability in broad sense provides an idea about the additive and non-additive gene action in the expression of traits. The estimates of heritability along with genetic advance are more important than genetic advance alone to know the resulting effect of the best individuals Johnson *et al.*, (1955) [11]. Keeping in view these points, the present investigation is conducted to assess the variability, heritability, in broad sense and genetic advance in blackgram germplasm.

The extent of variability is measured by phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV), which provides the information about relative amount of variation in different characters. Since heritability is also influenced by environment, the information on heritability alone may not help in pin pointing the characters enforcing selection. Nevertheless, the heritability estimates in conjunction with the predicted genetic advance will be more reliable (Johnson *et al.*, 1955) [11].

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Materials and Methods

The experimental material for present investigation was carried out during *Kharif*, 2020 at Agricultural research station, Podalakur, Nellore district.

Experimental material consists of 40 blackgram genotypes were sown in RBD in 3 replications, 1 row of each genotype in each replication with 4m length. Row to row and plant to plant distance was kept at 30cm and 10cm, respectively. All the recommended package of practices was followed to raise a healthy crop.

Data was recorded on 10 quantitative characters *viz.*, days to 50% flowering, plant height, number of clusters per plant, number of pods per plant, days to maturity, 100 seed weight, SLA, SCMR and seed yield per plant. The observations for days to 50% flowering and days to maturity were observations recorded for whole plot basis. The various genetic parameters *viz.*, GCV and PCV were calculated by adopting the formulae suggested by Burton (1952), while heritability, GA as % mean were calculated by adopting the formulae given by Johnson *et al.*, (1955)^[11].

Table 1: Analysis of variance for the characters studied

Sl. No.	Character(s)	Mean sum of squares		
		Replications (df: 2)	Treatments (df: 39)	Error (df: 78)
1	Days to 50% flowering	52.51**	2.65**	4.69**
2	Days to maturity	51.85**	32.58**	5.49**
3	Plant height (cm)	84.88**	66.93**	7.46**
4	Pods per plant	28.67**	83.56**	7.02**
5	Clusters per plant	10.20	18.73	6.24
6	100 seed weight	0.54**	0.66**	0.14**
7	SCMR	19.82**	24.17**	11.91**
8	SLA	1994.72	3826.93	316.63
9	Seed yield (kg/ha)	2156.86	13805.75	1229.23

* Significant at 5% level

** Significant at 1% level

Table 2: Mean, Coefficient of variability, Heritability (broad sense), Genetic advance as per cent of mean for nine characters of Black gram

Sl. No.	Character(s)	Mean	Range		Variance		Coefficient of Variation		Heritability (Broad sense) (%)	Genetic Advance as percent of mean (%)
			Min.	Max.	Genotypic	Phenotypic	Genotypic	Phenotypic		
1	Days to 50% flowering	42.53	36	51	6.98	11.68	6.21	8.03	59.79	9.89
2	Days to maturity	77.56	69	86	9.02	14.52	3.87	4.91	62.14	6.29
3	Plant height (cm)	38.74	24.4	48.7	19.82	27.28	11.49	13.48	72.63	20.17
4	Pods per plant	25.67	15	37	25.51	32.53	19.67	22.21	78.40	35.88
5	Clusters per plant	11.36	5	20	4.16	10.40	17.95	28.37	40.01	23.38
6	100 seed weight	4.51	2.8	6	0.17	0.317	9.22	12.48	54.66	14.05
7	SCMR	42.35	34	56	4.08	16.97	4.77	9.44	25.54	4.96
8	SLA	157.77	98	300	1170.09	1486.73	21.68	24.43	78.70	39.62
9	Seed yield (kg/ha)	342.43	156	485	4192.17	5421.39	18.90	21.50	77.32	34.25

Results and Discussion

The ANOVA revealed that mean squares due to genotypes were highly significant for all the traits (Table 1) under evaluation connoting the existence of wider genetic diversity among the genotypes. The PCV was higher than GCV for all the characters under study which indicated that the environmental factors influencing the characters studied. The present findings are in accordance with the findings of Panigrahi *et al.*, (2014)^[18], Deepshika *et al.*, (2014)^[7], Babu *et al.*, (2016)^[2], Priyanka *et al.*, (2016)^[20] and Hemalatha *et al.*, (2017)^[10]. The GCV and PCV were categorized as low (less than 10%), moderate (10-20%) and high (more than 20%) as suggested by Burton and Devane (1953)^[4]. The estimated GCV and PCV helped in getting a clear understanding of the variability present among various genotypes. Higher magnitude of GCV was recorded for SLA followed by Pods per plant. Higher magnitude of PCV was recorded in number of clusters per plant, SLA followed number of pods per plant and Seed yield (kg/ha). The estimates of variability parameters revealed that the phenotypic coefficient of variation along with least difference from genotypic coefficient of variation observed for most of

the characters indicating the greater role of genetic factors influencing the expression of these characters. Thus it indicates the utility of these characters in the selection programme.

The estimates of heritability in broadsense for yield and attributing characters have been presented in Table 2. In the present study high estimates of heritability were observed for SLA, number of primary branches per plant, Seed yield (kg/ha) and Plant height (cm) had high estimates of heritability. Similar findings were reported by Hemalatha *et al.*, (2017)^[10].

Genetic advance as percent of mean were recorded higher value for SLA, number of pods per plant, Seed yield (kg/ha), no of clusters per plant and Plant height (cm). These findings are in accordance with the result of Rajashekhar *et al.*, (2017)^[22]. High heritability coupled high genetic advance as percent of mean were recorded for SLA, number of pods per plant, Seed yield (kg/ha) and Plant height (cm). Selection of these traits was useful for further improvement in plant breeding programme. These findings are in accordance with the result of Dharmendra *et al.*, (2017)^[18].

References

1. Anonymous. Indian Institute of Pulses Research, Kanpur (U.P.); c2016.

2. Babu JS, Reni YP, Ramana MV. Character correlation and path coefficient in blackgram [*Vigna mungo* (L.) Hepper]. International Research Journal of Natural and Applied Sciences. 2016;3:178-185.
3. Burton GM. Quantitative inheritance in grasses. Sixth International Grassland Congress. 1952;1:277-283.
4. Burton GW, Devane EM. Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. Agronomy Journal. 1953;45:478-481.
5. Dana S. Genomic relationship in the genus *Vigna* and its implications in the breeding programme. Breeding methods for improvement of pulse crops; c1980. p. 357-367.
6. De Candolle A, L'origine des plantes cultives, Paris, 330. (English translation: Origin of cultivated plants, London; c1882-1884. p. 411-415.
7. Deepshika, Lavanya GR, Kumar S. Assessment of genetic variability for yield and its contributing traits in Blackgram. Trends in Biosciences. 2014;7:2835-2838.
8. Dharmendra Kumar R, Mahrndra Kumar J, Deva Ram M, Lal GM. Studies on genetic variability in blackgram (*Vigna mungo* (L.) Hepper) germplasm Journal of Pharmacognosy and Phytochemistry. 2017;6(4):1506-1508.
9. Gupta P, Semwal BD, Gupta D. Genetic variability, heritability and genetic advance for some traits in blackgram (*Vigna mungo* L. Hepper). Progressive Agriculture. 2012;6:164-166.
10. Hemalatha K, Lal SS, Lal GM. Study on genetic variability and correlation in blackgram (*Vigna mungo* L. Hepper). Journal of Pharmacognosy and Phytochemistry. 2017;6:674-676.
11. Johnson HW, Robinson HF, Comstock RF. Estimation of genetic environmental variability in soya bean. Agronomy Journal. 1955;47:314-318.
12. Konda CR, Salimath PM, Mishra MN. Genetic variability studies for productivity and its components in blackgram. Legume Research. 2009;32:59-61.
13. Kumar VG, Vanaja M, Abraham B, Anitha Y, Jyothi Laxmi N, Maheshwari M. Variability, heritability and genetic advance for quantitative traits in Blackgram. International Journal of Current Sciences. 2015;17:37-42.
14. Lukoki L, Marechal R, Otoul E. The wild ancestors of the cultivated beans, *V. radiata* and *V. mung*. Bulletin du Jardin Botanique National de Belgique. 1980;28:23-30.
15. Meshram MP, Ali RI, Patil AN, Meena S. Variability studies in M3 generation in blackgram (*Vigna mungo* (L.) Hepper). International Quarterly Journal of Life Science. 2013;8:1357-1361.
16. Naga N, Sharma SK, Kant A. Agronomic evaluation of some induced mutants of blackgram. SABRAO Journal of Breeding and Genetics. 2006;38:29-38.
17. Ozukum C, Sharma MB. Variability among urdbean (*Vigna mungo* L. Hepper) for yield and yield components. International Journal of Research and Innovation in Applied Science. 2017;2:26-28.
18. Panigrahi KK, Mohanty A, BAisakh B. genetic divergence, Variability and character association in landraces of blackgram (*Vigna mungo* L. Hepper) from Odisha. Journal of Crop and Weed. 2014;10:155-165.
19. Patel RV, Patil SS, Patel SR, Jadhav BD. Genetic variability and character association in blackgram (*Vigna mungo* (L.) Hepper) during summer. Trends in Biosciences. 2014;7:3795-3798.
20. Priyanka S, Rangaiah S, Showkath Babu BM. Genetic variability estimates of quantitative and qualitative traits in blackgram. International Journal of Agriculture Sciences. 2016;40:1821-1824.
21. Punia SS, Gautam NK, Jain NK, Koli NR, Jat VS. Genetic variability and correlation studies in urdbean (*Vigna mungo* (L.) Hepper). Legume Research. 2013;37:580-584.
22. Rajasekhar D, Sapna S Lal, Gabriel M Lal. Character association and path analysis for seed yield and its components in blackgram (*Vigna mungo* (L.) Hepper). Plant Archives. 2017;17(1):467-471.
23. Reni YP, Rao YK, Satish Y, Babu JS. Estimates of genetic parameters and path analysis in blackgram. International Journal of Plant, Animal and Environmental Sciences. 2013;3:231-234.
24. Robinson HF, Comstock RE, Harvey PH. Estimates of heritability and the degree of dominance in corn. Agronomy Journal. 1949;41:353-359.
25. Singh K, Gautam RK, Singh PK, Kumar N, Swain S. Estimation of genetic variability and association analysis in the indigenous landraces of blackgram of Andaman islands. Vegetos. 2014;27:113-122.
26. Singh M, Swamp I, Gaikwad PD, Singh J. Variability and heritability analysis in blackgram. Advances of Life Sciences. 2016;5:2619-2621.
27. Sohel MH, Miah MR, Mohiuddin SJ, Islam AKMS, Rahman MM, Haque MA. Correlation and path coefficient analysis of blackgram (*Vigna mungo* (L.) Hepper). Journal of Bioscience and Agriculture Research. 2017;7:621-629.