Original Research Article

Studies on Genetic Variability in Black gram genotypes [*Vigna mungo* (L.) Hepper]

Abstract

An investigation was carried out with 12 diverse genotypes of black gram (*Vigna mungo* (L.) Hepper) to gain and insight into the existing pattern of variability for quantitative traits to find out the high yielding superior genotypes. The analysis of variance study revealed that all the genotypes were differed significantly among themselves for all the characters. The PCV value was found to be higher than GCV for all the ten characters. The traits *viz*., number of seeds per pod, number of pods per plant and pod length had moderate estimates of genotypic coefficient of variation. Pod length recorded the highest heritability followed by single plant yield, number of pods per plant, days to 50% flowering and number of seeds per pod. The moderate heritability was observed for plant height, hundred seed weight, number of clusters per plant, number of branches per plant and days to maturity. Hence these characters could be given importance during selection programme for developing high yielding varieties.

Key words: Variability, Heritability, Genetic Advance, Blackgram

Comment [sj1]: Need to identify the problem or brief introduction then move to the objective – need to set the tone of the study to win readership.

Comment [sj2]: Should be 'an'

Comment [sj3]: High-yielding - hyphenated

Comment [sj4]: No need for 'were'

Comment [sj5]: Need to expand on this, since it is being used for the first time.

Comment [sj6]: need to expand on this, since it is being used for the first time

Comment [sj7]: No need for the article 'the'

Comment [sj8]: Value?

Comment [sj9]: Place in alpa order

Introduction

Pulses belonging to the sub family of Fabaceae and the seeds are food especially for the vegetarian people. They are rich in protein content than cereals and other crops. Pulses are also rich in lysine content with an average of 65 ± 7 mg/g of protein as compared to 29 ± 7 mg/g in cereals. In developing countries, pulses serve as a major source of protein when compared to greater dependence of animal protein (56 %) in developed countries.

Black gram is a highly priced pulse, very rich in phosphoric acid. India currently represents the largest producer of Black gram accounting for more than 70% of the global production. India is followed by Myanmar and Pakistan. In India during kharif 2020 - 2022, area covered under black gram is 37.52 lakhs ha. The states of Madhya Pradesh, Uttar Pradesh, Rajasthan, Maharastra, Karnataka and Andhra Pradesh are the major producers of black gram in India. The production of pulses such as tur, urad and other lentils across India was estimated to be around 25 million metric tons in financial year 2022. It produces about 24.5 lakh tonnes of urad annually from about 4.6 million ha of area, with an average productivity of 533 kg per ha in

Comment [sj10]: Source?

Comment [sj11]: Source?

Comment [sj12]: Why expand?

Comment [sj13]: No need for 'per' use the forward slash

UNDER PEER REVIEW

2020 - 2022. Blackgram is generally cultivated as follow-up crop after rice cultivation. However, its productivity is very low and the major constraints in achieving higher yield of this crop are low yield potential and narrow genetic base of existing cultivars, absence of suitable genotypes for different cropping system, poor harvest index and susceptibility to diseases (Swathi Das *et al.*, 2014). Lack of suitable varieties and genotypes with adaptation to local condition is among the factors that also affects the production. To improve such important pulse crop through breeding, study on genetic variability of important traits responsible for seed yield. Knowledge on heritability and genetic advance of the character indicate the scope for the improvement of a trait through selection. Heritability estimates along with genetic advance are also helpful in predicting the gain under selection (Johnson *et al.*, 1955).

Material and Methods

The present study was carried out in the college farm, Adhiparasakthi Agriculture College, G.B. Nagar, Kalavai, Ranipet district during May to July 2022.The experimental material consisted of twelve genotypes of black gram which were collected from National Pulses Research Centre, Vamban. The details of the genotypes used in this study were given in Table 1. The genotypes were raised in plat bed method with a spacing of 30 x 10 cm in randomized block design under irrigated condition with two replications. Observations will be recorded on Days to 50 % flowering, Days to maturity Plant height, Number of clusters per plant, Number of pods per cluster, Number of pods per plant, Pod length (cm), Number of seeds per pod, 100 seed weight (g), Seed yield per plant (g) using five randomly selected plants from each replication for all the characters. The data were subjected to statistical analysis for parameters of variability *viz.*, GCV & PCV, heritability, genetic advance. Variability that existed in the population for various characters was estimated by the method suggested by Burton (1952). Heritability in broad sense was estimated by the formula of Devane and Burton (1953). The genetic advance of the genotypes at 5% selection pressure was calculated using the formula suggested by Johnson *et al.*, *(*1955).

Comment [sj14]: Why two when the standard is three? Justify why two.

Comment [sj15]: How you measure 50% flowering?

Comment [sj16]: Need to explain the applicability of GCV and PCV in this experiment.

Comment [sj17]: How?

Comment [sj18]: Is this formula used here? How effective? Explain.

Comment [sj19]: Should mention the formula here.

Table 1. Details of the genotypes of black gram used for this study

Comment [sj20]: In 'this study' is understood.

UNDER PEER REVIEW

S. No	Genotypes	Parentage	Source
1.	VBN 2	Spontaneous mutant	NPRC, Vamban, TN
2.	VBN 3	LBG 402 × LBG 17	NPRC, Vamban, TN
3.	VBN 5	VBN 1 × LBG 20	NPRC, Vamban, TN
4.	VBN 6	VBN1 × *Vigna mungo var. silvestris*	NPRC, Vamban, TN
5.	VBN 7	VBN 3 x *Vigna mungo var. silvestris*	NPRC, Vamban, TN
6.	VBN 8	VBN 3 × VBG 04-008	NPRC, Vamban, TN
7.	VBN 9	Mash114 x VBN 3	NPRC, Vamban, TN
8.	VBN 10	VBN 1 x UH04-04	NPRC, Vamban, TN
9.	VBN 11	PU31 x CO 6	NPRC, Vamban, TN
10.	ADT 5	Selection from Kanpur Variety	NPRC, Vamban, TN
11.	ADT 6	Vamban 1 × VBG 04-2006	NPRC, Vamban, TN
12.	CO 6	DU 2 × VB 20	NPRC, Vamban, TN

RESULTS AND DISCUSSION

Analysis of variance

Analysis of variance was carried out for ten quantitative characters in 12 black gram genotypes and was furnished in **Table 2**. The study revealed that all the genotypes were differed significantly among themselves for all the characters.

Table 2. Analysis of variance for different quantitative characters

Characters	Mean sum of squares		
	Replication	Genotype	Error
Days to 50 per cent flowering	0.479	12.840**	2.113
Plant height	6.545	10.203**	2.763
Number of branches per plant	0.387	0.325**	0.128
Number of clusters per plant	0.583	0.630**	0.214
Number of pods per plant	2.701	19.237**	2.601
Pod length	0.115	0.814**	0.035
Number of seeds per pod	0.100	0.923**	0.214
Days to maturity	111.415	73.001**	30.719
Hundred seed weight	0.661	0.359**	0.119
Single plant yield	0.559	0.521**	0.033

* Significant at 5% level

Mean performance for quantitative traits in black gram

UNDER PEER REVIEW

The mean performance can be used as a criterion for selecting desirable plants and for eliminating undesirable types. The results on mean performance of parents for different characters are presented in the **Table 3.** The genotype CO 6 was found to be superior and registered maximum mean value for plant height, number of clusters per panicle, days to and hundred seed weight. The genotype VBN 10 registered maximum mean value for number of branches per plant, number of pods per plant and single plant yield. The genotype VBN 11 recorded higher mean values for number of seeds per pods. Based on the mean values for various quantitative traits the genotypes *viz*., CO 6, VBN 10 and VBN 11 were found to be superior. Hence these genotypes may be utilized for improvement of yield and other useful traits.

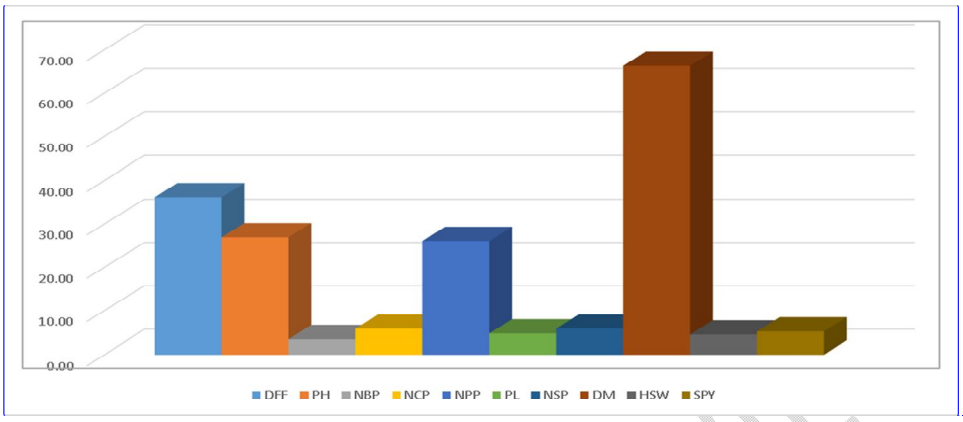
Table 3. Mean performance of ten quantitative traits of 12 genotypes in black gram

S.No	Genotypes	DFF	PH	NBP	NCP	NPP	PL	NSP	DM	HSW	SPY
1	VBN 2	32.54	22.5	2.65	3.67	20.7	4.25	4.37	58.75	3.86	4.84
2	VBN 3	36.05	29.06	3.02	4.91	24.53	4.12	4.06	70.57	4.29	4.95
3	VBN 5	37.10	29.30	2.91	6.03	28.45	4.78	5.67	70.26	5.11	5.00
4	VBN 6	32.84	24.65	3.01	6.00	22.06	4.17	5.89	62.66	3.76	4.19
5	VBN 7	38.4	21.76	2.34	5.54	23.65	5.02	6.32	64.65	4.24	5.07
6	VBN 8	34.66	24.30	3.05	6.03	27.49	4.10	5.43	47.98	4.45	5.59
7	VBN 9	36.73	30.67	4.05	5.87	26.50	5.24	7.05	65.42	4.38	5.43
8	VBN 10	38.0	27.5	5.56	6.5	30.45	5.32	6.35	72.52	4.63	6.52
9	VBN 11	35.8	28.54	4.76	6.34	29.54	4.64	7.26	70.72	4.57	6.04
10	ADT 5	37.82	26.34	3.00	6.04	25.81	5.77	6.36	68.83	4.49	4.03
11	ADT 6	38.45	26.48	3.39	6.05	29.33	4.25	5.24	70.37	4.53	5.26
12	CO 6	35.75	32.0	3.52	7.23	24.4	5.34	6.46	73.0	5.77	5.73
	Mean	**36.18**	**26.93**	**3.44**	**5.85**	**26.08**	**4.75**	**5.86**	**66.31**	**4.50**	**5.22**
	SE d	**1.45**	**1.66**	**0.35**	**0.46**	**1.61**	**0.18**	**0.46**	**5.54**	**0.34**	**0.18**
	CD (5 %)	**3.08**	**3.52**	**0.76**	**0.98**	**3.41**	**0.39**	**0.98**	**11.75**	**0.73**	**0.38**

Fig. 1. Mean performance of black gram genotypes for different Quantitative traits

Comment [sj21]: This goes below the figure, above only in tables.

UNDER PEER REVIEW



Comment [sj22]: Graph has not titles on the axes.

Phenotypic and genotypic co-efficient of variation

A total of 12 genotypes of black gram were studied for variability in ten quantitative traits. The data were subjected to analysis of variance and it was found that the germplasm differed significantly for all the characters studied. The estimates of genotypic and phenotypic variances were worked out for all the characters. The phenotypic coefficient of variation was slightly higher than the genotypic coefficient of variation for all the characters suggesting the presence of environmental influence to some extent in the expression of these characters. Moderate GCV estimates were observed for pod length, number of pods per plant, number of seeds per pod and single plant yield. It indicates the availability of abundant variability for these characters in black gram. These results are in accordance with the findings of Panigrahi *et al.* (2014) for pod length; Gowsalya *et al.* (2016) for number of pods per plant; Ramya *et al.* (2014) and Sowmini and Jayamani (2013) for number of seeds per pod; Arul Balachandran *et al.* (2010) and Senapati and Misha (2010) for single plant yield.

Comment [sj23]: How much? What are the results as compared with yours? PLEASE APPLY TO ALL THE OTHERS

Heritability and genetic advance

Estimates of heritability (h^2), genetic advance and GA as percentage of mean for traits of crop are furnished in **Table 4**. The genotypes under study showed high heritability values for most of the characters under study. Estimates of heritability ranged from 40.77 to 91.74 per cent. Pod length (91.74 %) recorded the highest heritability followed by single plant yield (88.10 %), number of pods per plant (76.17 %), days to 50% flowering (71.73

Comment [sj24]: expand

Comment [sj25]: Table 4 in parenthesis is ok, not this .....

Comment [sj26]: %

UNDER PEER REVIEW

%) and number of seeds per pod (62.61 %). The moderate heritability was observed for plant height (57.38 %), hundred seed weight (50.05 %), number of clusters per plant (49.22 %), number of branches per plant (43.39 %) and days to maturity (40.77 %). None of the character was found have low amount of heritability.

Table 4. Estimates of Variability, heritability and genetic advance as per cent of mean for ten quantitative characters in black gram

Characters	Mean	Range	PCV (%)	GCV (%)	h^2 (BS) (%)	GAM
Days to 50% flowering	36.18	32.54 – 38.45	7.34	6.22	71.73	10.85
Plant height	26.93	21.76 – 32.00	9.28	7.03	57.38	10.97
Number of branches per plant	3.44	2.34 – 5.56	15.02	9.89	43.39	13.42
Number of clusters per plant	7.20	3.67 – 7.20	11.02	7.73	49.22	11.18
Number of pods per plant	26.08	20.70 – 30.45	12.69	11.07	76.17	19.91
Pod length	4.75	4.10 – 5.77	14.22	13.62	91.74	26.88
Number of seeds per pod	5.86	4.06 – 7.20	13.88	10.98	62.61	17.90
Days to maturity	66.31	47.98 – 73.00	10.49	6.69	40.77	8.81
Hundred seed weight	4.50	3.76 – 5.70	11.18	7.91	50.05	11.53
Single plant yield	5.22	4.03 – 6.52	11.19	10.50	88.10	20.31

UNDER PEER REVIEW

Figure 2 : Selection of Good Genotypes in Project Field

Early flowering- VBN 2 **Single plant yield – VBN 10**

All the ten characters studied, recorded high heritability indicating lesser environmental influence. Among the characters studied, pod length and single plant yield recorded high heritability with high genetic advance, suggesting these characters are governed by additive genetic effect to a great extent and improvement of these characters would be effective through phenotypic selection. Similar results were observed by Priyanka *et al.* (2016) for pod length; Thanga Hemavathy *et al.* (2013), Panigrahi *et al.* (2014), Ramya *et al.* (2014), Gowsalya *et al.* (2016), Reena mehra *et al.* (2016), Kondagari Hemalatha *et al.* (2017) and Panda *et al.* (2017) for single plant yield.

Comment [sj27]: How you measure this? The environmental influence

The GAM ranged from 8.81 to 26.88 per cent. The highest magnitude of genetic advance was recorded by pod length (26.88 %) and single plant yield (20.31 %). The moderate amount of GAM was observed for number of pods per plant (19.91 %), number of seeds per pod (17.90 %), number of branches per plant (13.42 %), hundred seed weight (11.53 %), %), number of clusters per plant (11.18 %), plant height (10.97 %) and days to 50% flowering (10.85 %). Days to maturity (8.81 %) exhibited lowest amount of genetic advance as percentage of mean. Result indicates that the high heritability estimate indicates less influence of environment on respective characters. Low heritability (broad sense) indicates predominance of no additive gene action indicating the scope for breeding. High estimates of GA coupled with substantial amount of heritability indicate that selection for such characters would result in the improvement of characters in the desired direction as

Comment [sj28]: %

UNDER PEER REVIEW

the character is governed by additive genes. High heritability coupled with low genetic advance indicates non-additive gene action. The heritability exhibited due to favorable influence of environment rather than genotypes and selection for such traits may not be rewarding. If, low heritability coupled with low genetic advance indicates such character was highly influenced by environment and selection would be ineffective for those traits.

Comment [sj29]: Need a conclusion as per journal requirement,

References:

Arulbalachandran, D., L. Mullainathan, S. Velu and C. Thilagavathi. 2010. Genetic variability, Heritability and genetic advance of quantitative traits in black gram by effects of Mutation in field trail. African Journal of Biotechnology, 9(19): 2731-2735.

Burton, G.M. 1952. Quantitative inheritance in grasses. Sixth International Grassland Congress, 1: 277-283.

Gowsalya, P., D. Kumaresan, D. Packiaraj and J.R. Kannan Bapu. 2016. Genetic variability and character association for biometrical traits in Blackgram (*Vigna mungo* (L.) Hepper). Electronic Journal of Plant Breeding, 7(2): 1-8.

Johnson, H.W., H.F. Robinson and R.E. Comstock. 1955. Estimation of genetic variability and Environmental variability in soybean. Agron. J., 47: 314-318.

Kondagari Hemalatha, Sapna S Lal and Gabrial M Lal. 2017. Study on Genetic Variability and Correlation in Blackgram (*Vigna mungo* (L.) Hepper). Journal of Pharmacognosy and Phytochemistry, 6(4): 674- 676.

Lush, J.L. 1949. Heritability of quantitative characters in farm animals. Heridates; 35: 356-375.

Sowmini, K. and P. Jayamani. 2013. Genetic variability studies for yield and its component traits in RIL population of blackgram (*Vigna mungo* (L.) Hepper). Electronic Journal of Plant Breeding, 4(1): 1050- 1055.

Senapati, N. and R.C. Misha. 2010. Genetic divergence and variability studies among micromutants in blackgram (*Vigna mungo* (L.) Hepper). Legume Research, 33(2):108-113.

Thanga Hemavathy, A., N. Shunmugavalli and G. Anand. 2015. Genetic variability, Correlation and path co-efficient studies on yield and its components in mungbean (*Vigna radiata* (L.) Wilezek). Legume Research, 38(4): 442-446.

Panda, D.P., D. Lenka, A.P. Dashi, S.K. Tripathy, C. Behera and B. Baisakh. 2017. Genetic variability and heritability studies in relation to seed yield and its component traits in black gram (*Vigna mungo* (L.) Hepper). Trends in Biosciences, 10(6): 1412-1414.

Comment [sj30]: Kindly review the format on 'instructions to authors' and comply consistently.

UNDER PEER REVIEW

Punia, S.S., N.K. Gautam, Baldev Ram, Preeti Verma, Meenakshi Dheer, N.K. Jain, N.R. Koli, Rajesh Mahavar and V.S. Jat. 2014. Genetic variability and correlation studies in urdbean (*Vigna mungo* (L.)). Legume Res., 37 (6): 580-584.

Panigrahi, K.K., A. Mohanty and B. Baisakh. 2014. Genetic divergence, variability and character association in landraces of blackgram (*Vigna mungo* (L.) Hepper). Journal of Crop and Weed, 10(2): 155-165.

Priyanka, S., S. Rangaiah and B. Showkath babu. 2016. Genetic variability estimates of Quantitative and qualitative traits in black gram. International Journal of Agriculture Sciences, 8(40): 1821-1824.

Ramya, B., G. Nallathambi and S. Ganesh Ram. 2014. Genetic variability, heritability and genetic advance in induced mutagenesis black gram (*Vigna mungo* (L.) Hepper). PlantArchives, 14(1): 139-141.

Reena Mehra, A., N. Tikle, Ashok Saxena, Ashok Munjal, Rekhakhandia and Mahipal Singh. 2016. Correlation, path-coefficient and genetic diversity in Blackgram (*Vigina mungo* (L.) Hepper). Int. Res. J. Plant Sci., 7(1): 001-011.

UNDER PEER REVIEW