



ISSN (E): 2277- 7695
ISSN (P): 2349-8242
NAAS Rating: 5.23
TPI 2021; 10(9): 1447-1451
© 2021 TPI
www.thepharmajournal.com
Received: 13-07-2021
Accepted: 23-08-2021

Pallavi Yergude

Department of Agricultural
Botany, Post Graduate Institute,
Dr. Panjabrao Deshmukh Krishi
Vidyapeeth, Akola,
Maharashtra, India

MB Rakshe

Department of Agricultural
Botany, Post Graduate Institute,
Dr. Panjabrao Deshmukh Krishi
Vidyapeeth, Akola,
Maharashtra, India

VV Ujjainkar

Department of Agricultural
Botany, Post Graduate Institute,
Dr. Panjabrao Deshmukh Krishi
Vidyapeeth, Akola,
Maharashtra, India

Genetic variability analysis in Blackgram [*Vigna mungo* L. Hepper]

Pallavi Yergude, MB Rakshe and VV Ujjainkar

Abstract

The present investigation was undertaken for evaluating the genetic analysis of thirty-six blackgram genotypes during *kharif*, 2014 at Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola using randomized block design. Analysis of variance indicated significant differences among the genotypes for all morphological characters investigated. The phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV). The high values of GCV and PCV observed for the number of primary branches per plant, pod weight per plant, seed yield per plot, days to 50-percent flowering, 100 seed weight, the number of pod per plant, high heritability coupled with the high genetic advance was observed to shelling percent, days to 50% flowering, days to maturity, plant height. The yield per plant was significant and positively correlated with plant height, the number of primary branches per plant, days to maturity, 100 seed weight, the number of seed per pod, the number of pod per plant, pod weight per plant, the number of cluster per plant, the number of pod per cluster. Promising genotypes in present study *viz.*, AKU-15, AKU-10-2 and AKU-11-6 having high seed yielding capacity coupled protein percent above the mean performance and top four genotypes *viz.*, AKU-15 and AKU-10-1 exhibited higher performances for almost all the character among all thirty-six genotypes studied.

Keywords: Black gram, broad sense heritability, genetic advance, GAM, genetic variability

1. Introduction

Pulses are the main sources of protein for the predominant vegetarian population in India. They are also used as fodder and concentrate to the cattle. The vital role of pulses in fixation of atmospheric nitrogen needs no emphasis, which is fact very crucial in light up the price hike of nitrogenous fertilizers. As compared to growth in food grain production consequent to the Green Revolution, the growth in production of pulses is rather disappointing, leading to a rise in the prices of pulses. In any other crops the growth in production of pulses is largely determined by the growth under cultivation in area an improvement in productivity levels or combination of both.

Black gram is the major pulse in Asia since ancient time (Paroda and Thomas, 1987) [9]. Blackgram (*Vigna mungo* L. Hepper), also known as urid, urd and blackgram. White *et al.* (1953) [14] reported that the legumes are being grown as the economic crop since 6000 year ago the most important pulse crop grown in India. Black gram has originated from Indian continent (Vavilov, 1926) [12] having chromosome number $2n=22$ (Dana, 1980) [3]. It the warm season crop grown in *kharif*, *rabi* and spring/summer season in the country including India, Pakistan, Bangladesh, Thailand and Korea, and widely cultivated in the country as sole, mix or intercrop with cotton, sorghum, maize, pigeon pea, pearl millet, groundnut and sesamum.

It is an erect, semi-erect or trailing, densely hairy annual herb. The tap root produces a branched root system with smooth, rounded nodules. The pods are narrow, cylindrical and up to 6 cm. long, the stem is diffused, furrowed and much branched at the base and entire plant is covered with rough reddish brown hairs. The flowers are small, yellow and born on auxillary inflorescence in clusters (5-6 florets). Pods do not shatter much and contain 3- 10 seeds per pod. It is the self-pollinated crop, however, sometimes cross pollination occurs due to insects.

It is the main source of protein, amino acids in the vegetarian diet. It contains about 24-26 per cent protein, 56 per cent carbohydrates and 2 per cent fat. It is the rich source of calcium, iron and niacin. Pulses have good ability to fix atmospheric nitrogen and improve soil fertility. They are mostly useful as fodder and concentrates in cattle feed. Because of the special features of pulses they are mostly used as green manure.

Gloabally, it is proved that narrow genetic base coupled with low utilization of genetic

Corresponding Author:

Pallavi Yergude

Department of Agricultural
Botany, Post Graduate Institute,
Dr. Panjabrao Deshmukh Krishi
Vidyapeeth, Akola,
Maharashtra, India

resources are the principal limiting factors for achieving the target of quality legume production (Marawar and Ujjainkar, 2019) [7]. The knowledge of heritability and genetic advance is essential along with genetic variability estimates for formulating the selection criteria for improvement of seed yield. Heritability is the heritable portion of phenotypic variance which is the good index of transmission of characters from parents to their subsequent generations further in broad sense estimates, it 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 for further utilization of crop improvement (Johnson *et al.* 1955) [5].

Table 1: List of thirty-six genotypes of blackgram and their sources

Sr. No.	Source	No of genotypes	Genotypes
1.	Dr. PDKV, Akola	18	AKU-15, AKU-10-1, AKU-10-2, AKU-11-6, AKU-11-2, AKU-12-28, AKU-11-15, AKU-12-1, AKU-12-3, AKU-11-1, AKU-11-3, AKU-11-18, AKU-11-13, AKU-12-27, AKU-13-1, AKU-12-21, AKU-14-1, AKU-12-22, TAU-1.
2.	MPKV, Rahuri	5	Phule U-0014, Phule U-502-17 Phule U-502-14, Phule U-401-3, TPU-4.
3.	VNMAU, Parbhani	2	BDU-1, BDU-2012-1.
4.	IIPR, Kanpur	3	IPU-10-17, KU-323, IPU-7-19

The data were collected from the replicated experiment was analyzed as per standard procedures for the estimation of ANOVA, Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV), heritability and genetic advance.

Results and Discussion

Genetic variability in any crop is pre-requisite for selection of superior genotype over the existing cultivars. Variance analysis for all the characters revealed significant variation among the genotypes studied (Table-2). The analysis of variance showed significant differences among 36 black gram genotypes for all the characters under study, indicates that there is ample scope for selection of promising genotypes from present germplasm for yield improvement.

The mean performance of various genotypes exhibited a wide range of variation for most of the traits studied (Table 3). Despite some traits showed more variation like as Days to 50% flowering (29 to 94 days) Plant height (cm) (13.4 to 46.2 cm), No of primary branches per plant (4.26 to 8.53), Days to maturity (64 days to 127.66 days), 100 seed weight (g) (2.33 g to 6.60 g), Pod length (cm) (3.65 cm to 5 cm), No. of seeds per pod (4.86 to 6.20), Shelling (%) (43.23% to 83.73%), the no. of pod per plant (4.2 to 7.2), Pod weight per plant (g) (3.55 to 12.42), the no. of cluster per plant (1.52 to 6.49), the no. of pods per cluster (2.60 to 4.13), Protein (%) (23.31 to 26 (%)), Seed yield per plot (g) (153.6 g to 688.66) and Seed yield per plant (g) (2.64 g to 8.13) etc. indicates sufficient variation among the genotypes for the traits studied.

Genotypic and phenotypic coefficient of variation

Phenotypic variance was higher than the genotypic variances for all the characters thus indicating the influence of the environmental factors on these traits. The genotypic and phenotypic variations were obtained for different characters, and they are presented in Table 3 (Fig. 1). The maximum (103.13 and 112.56) genotypic variation (Vg) and phenotypic variation (Vp) were obtained from the days to 50-percent

Material and Methods

The present investigation entitled, "Genetic variability, correlation and path studies in Black gram (*Vigna mungo L. Hepper*) conducted in the field of Agricultural Botany, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola, Maharashtra state during the *kharif* season, 2014. Akola situated in the tropical belt at 307.4 meters above mean sea level. The geographical situation is 20.42°N latitude and 77.02°E longitude. The soil was medium black, with clay, fairly leveled and uniform in topography with appropriate drainage. The present study comprising of thirty-six diverse genotypes of blackgram collected throughout the pulse research stations of country.

flowering followed by Days to maturity (99.39 and 106.75), respectively. Similar findings were reported by Konda *et al* 2009 [6]. The lowest value were recorded in the number of seed per pod had the lowest genotypic variance (0.1053) and the character number of seed per pod had the lowest phenotypic (0.14) variance respectively. The lowest value shows that there was considerable low influence of the environment for the expression of a traits. A comparison by the estimates of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) suggested that estimates PCV were higher than the estimates of GCV for all the characters (Table 3). This may be due to the involvement of environment and genotype environment interaction effects of characters expression. The estimates of GCV and PCV maximum for the number of cluster per plant (45.42, 53.37) followed by Pod weight per plant (38.29, 38.63), Seed yield per plant (g) (30.61, 34.98), Days to 50% flowering (28.69, 29.98), 100 seed weight (g) (21.81, 22.78) and lowest Protein (%) (3.12, 3.26), followed by the no of seed per pod (5.57, 6.45) respectively. Moreover, Uma devi and Ganesan (2006) [11], Samad *et al* (2013) also reported high GCV values for the number of clusters per plant, the number of pods per plant, pod length and number of seeds per pod of black gram and suggested for a greater scope of selection for these traits.

Heritability and Genetic Advance:

Knowledge in heritability of character is important as it indicates the possibility and extent to which improvement is possible through selection. It is a measure of genetic relationship between parents to progeny and has been widely used to assess the degree to which a character may be transmitted from parents to off springs. In the present study high estimates of heritability in percentage and were observed for the heritability estimates presented in (Table 3 and Fig 2) indicated that different traits showed a wide range of heritability (h²) from 68.77% to that number of primary branches per plant to 98% plant height, shelling percent, pod weight per plant. The considerably high estimates of

heritability were obtained for plant height (98%), shelling percent (98%), pod length (90%), pod weight per plant (98%). High heritability estimates for these traits indicating that these traits are more likely to be controlled by additive genetic component. Sowmini and Jayamani (2013) ^[10], Wani *et al.* (2007) ^[13] reported high heritability for a traits such as the number of pods per plant, the number of pods per cluster, plant height and seed yield per plant and suggested the additive genetic control in the inheritance of these characters. High heritability, genetic advance and per cent of mean were observed for traits seed yield per plant, biological yield per plant, harvest index and seed index. Wani *et al.*, (2007) ^[13] also reported high heritability for plant height. Konda *et al*

2009 ^[6] also reported high genetic advance for cluster per plant. Jonson *et al.* (1995) and Panse & Sukhatme (1985) ^[8] 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. The highest magnitude of the genetic advance was observed for days to 50% flowering (20.02) followed by days to maturity (19.81), shelling percent (17.64), the lowest magnitudes of genetic advance were reported for the number of pod per cluster (0.79), pod length (0.91), the number of seed per plot (0.57).

Table 2: Analysis of variance for the mean sum of squares for various characters in the blackgram

Sr. No.	Characters	Replication	Treatment	Error
	Degree of freedom	2	35	70
1	Days to 50% flowering	6.027	318.828**	9.437
2	Plant height (cm)	1.260	108.609**	0.600
3	No. of primary branches per plant	0.692	3.050**	0.401
4	Days to maturity	9.750	305.530**	7.359
5	100 seed weight (g)	0.094	2.348**	0.068
6	Pod length (cm)	0.002	0.680**	0.022
7	No of seed per pod	0.107	0.352**	0.036
8	Shelling (%)	0.620	225.344**	1.333
9	No of pod per plant	0.147	2.147**	0.052
10	Pod weight per plant (g)	0.178	22.656**	0.134
11	No. of clusters per plant	0.140	6.362**	0.716
12	No. of pod per cluster	0.042	0.509**	0.015
13	Protein (%)	0.009	1.849**	0.055
14	Seed yield per plant (g)	0.279	6.252**	0.579
15	Seed yield per plot (g)	6332.791	47974.507	14433.122

*Significance at 5% level, **Significance at 1% level

Table 3: Estimates of genetic parameters in blackgram

Sr. No.	Characters	Range	Genotypic variance	Phenotypic variance	GCV %	PCV %	Heritability (h ²) (BS) (%)	Genetic Advancement (GA)	GAM (%)
1	Days to 50% flowering	29.00-94.00	103.13	112.56	28.69	29.98	91.61	20.02	56.58
2	Plant height (cm)	13.40-46.20	36.02	36.60	19.11	19.27	98.36	12.25	39.05
3	No. of primary branches per plant	4.26-8.53	0.88	1.28	14.79	17.83	68.77	1.60	25.26
4	Days to maturity	64.00-127.66	99.39	106.75	13.83	14.33	93.11	19.81	27.49
5	100 seed weight (g)	2.33-6.60	0.75	0.82	21.81	22.78	91.68	1.71	43.02
6	Pod length (cm)	3.65-5.00	0.21	0.24	9.91	10.41	90.62	0.91	19.43
7	No of seed per pod	4.86-6.20	0.10	0.14	5.57	6.45	74.44	0.57	9.90
8	Shelling (%)	43.22-83.73	74.67	76.03	13.10	13.21	98.25	17.64	26.75
9	No of pod per plant	4.20-7.20	0.69	0.75	14.79	15.35	92.95	1.65	29.39
10	Pod weight per plant	3.55-12.42	7.50	7.64	38.29	38.63	98.24	5.59	78.18
11	No. of cluster per plant	1.52-6.63	1.88	2.59	45.42	53.37	72.42	2.40	79.62
12	No. of pod per cluster	2.60-4.13	0.16	0.18	12.08	12.63	91.48	0.79	23.81
13	Protein (%)	23.31-26.00	0.59	0.65	3.12	3.26	91.57	1.52	6.15
14	Seed yield per plant (g)	2.64-8.13	1.89	2.47	30.613	34.98	76.56	2.47	55.17

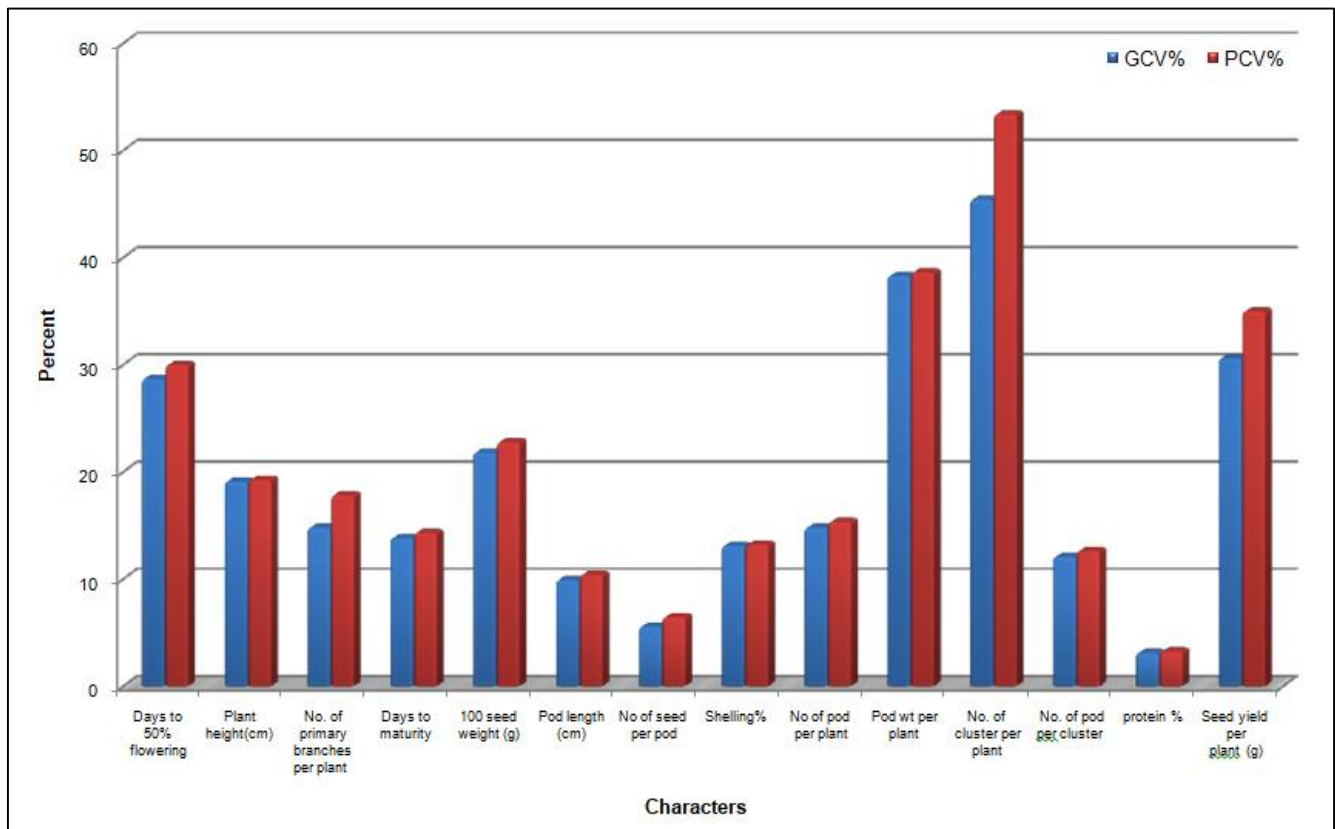


Fig 1: GCV and PCV estimates for various characters in black gram

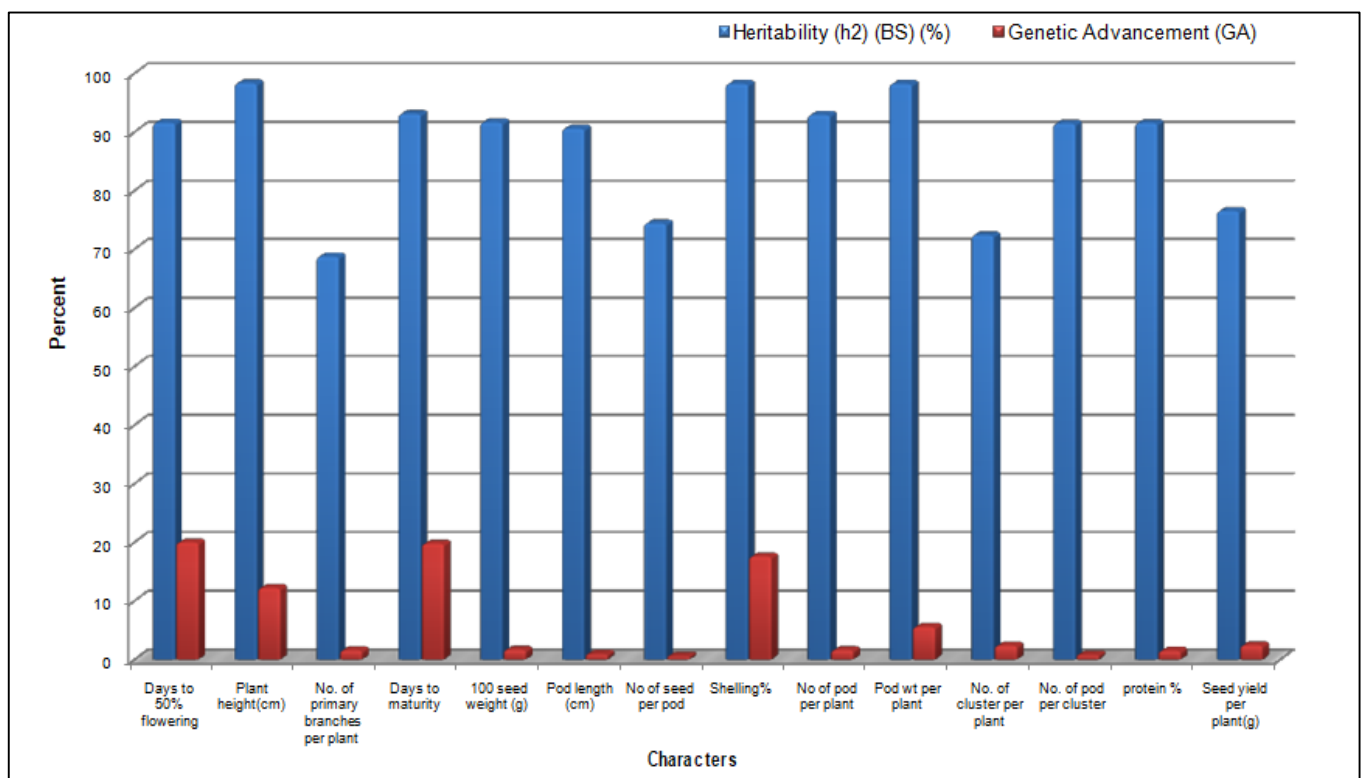


Fig 2: Heritability and genetic advance estimates for various characters in black gram

Conclusions

High heritability coupled with high genetic advance as percent of mean was observed for the number of seed per pod, the number of pod per plant, the number of cluster per plant, the number of pod per cluster, seed yield per plant indicating the preponderance of additive gene action and selection may be rewarding. the promising genotypes in present study viz.,

‘AKU-15, AKU-10-2, AKU-11-6, AKU-11-2, AKU-12-28, AKU-12-1, KKB-05011, NDU-07-25, BDU-1 and BDU-2012-1’ having high seed yielding capacity coupled with protein percent above the mean performance and top four genotypes viz., ‘AKU-15, AKU-10-1, TAU-1, NUL-7’ exhibited higher performances for almost all the character among all thirty-six genotypes studied.

Acknowledgement

Authors are thankful to the Senior Research Scientist, Pulses Research Unit, Dr. PDKV, Akola and the Head, Department of Agricultural Botany, their staff members for their co-operation of conducting this experiment alongwith providing all necessary material and technical assistance for present investigation.

References

1. Burton GW, De Vane EM. Estimating heritability in tall fesses from replicated cloned material. *Journals of Agronomy* 1953;45(3):474-481.
2. Burton GW. Quantitative inheritance in grasses Proc. 6th int. Grassland cong 1952;1:227-283.
3. Dana S. Genomic relationship in the genus vigna and its implications in the breeding programme. *Crop Improvement* 1980;22(1):357-367.
4. Fisher RA. Statistical tables for biological, agricultural and mendelian inheriatance. France Royal Society of Edinburgh 1938;52:399-433.
5. Johnson HW, Robinson HF, Comstock RE. Genotypic and Phenotypic Correlations in Soybean and their implications in selection *Agronomy* 1955;47:477-438.
6. Konda CR, Salimath PM, Mishra MN. Genetic variability studies for productivity and its components in blackgram (*Vigna mungo* (L.) Hepper). *Legume Research* 2009;32(1):59-61.
7. Marawar MW, Ujjainkar VV. Role of Pigeonpea in Indian Food Security. *Remarking An Analisation* 2019;4(2):E-461-466
8. Panse VG, Sukhatme PV. Statistical methodology for agricultural workers. ICAR Publications, New Delhi 1985.
9. Paroda RS, Thomas TA. Genetic resources of mungbean (*Vigna radiate* L. Wilczek) in India. In, mungbean, Proceeding of 2nd international symposium, 16-20 November, 1987, Bangkok, Thiland 1987.
10. 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.
11. 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.
12. Vavilove NI. Studies on the origin of cultivated plant. *Bull. Appl. Bot* 1926;16:139-148.
13. Wani BA, Marker S, Lavanya GR. Genetic variability, correlation and path analysis in green gram. *Journal of Maharashtra Agricultural Universities* 2007;32(2):216219.
14. White RO, Nelsonand LG, Trumble NG. Legumes in Agric. F.A.O. *Wikungen der Rontegenstrahkha. Biochem. Z* 1953;128:326-358.