Research Article

GENETIC VARIABILITY ESTIMATES OF QUANTITATIVE AND QUALITATIVE TRAITS IN BLACK GRAM

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Abstract- Black gram (*Vigna mungo* L.) has the potential of supplying a major portion of dietary protein demand and restoring the soil health at the same time. Research on genetic variability studies of the genotypes may increase the opportunity to exploit its potential which will help to meet the demand of high yield and nutrition supply. In this connection, an experiment was conducted to estimate the genetic variability of quantitative and qualitative traits in 24 lines of black gram. Genetic parameters like genotypic and phenotypic variance, coefficient of variation, heritability and genetic advance were estimated. Except for days to maturity a significant variation was noted for all the traits. The genotypes were highly variable for cluster plant^{-1}, pods plant^{-1}, seeds pod^{-1} and seed yield plant^{-1}. In general phenotypic coefficient of variability was greater than their corresponding genotypic coefficient of variability. Broad-sense heritability was higher for all the traits except for days to 50 per cent flowering and branches plant^{-1}. High heritability coupled with high GAM was observed for the characters pods cluster^{-1}, pod length, test weight, seeds pod^{-1} and seed yield plant^{-1} indicating that these characters are mainly controlled by additive genes and selection of such traits might be effective for the improvement of grain yield. The genotypes with dull seed luster were highly frequent than shiny seed luster. Globular seeds producing genotypes were more frequent than those producing drum shaped and globular seeds.

Keywords- Black gram, Broad sense heritability, Genetic advance, GAM, Variability

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Introduction

Black gram (*Vigna mungo* (L.) Hepper) is one of the most ancient and important legume crop of India and contributes 70% of world's total production. It is suitable for cultivation under different farming situations. Urd bean occupies an important position due to its high seed protein (25-26%, carbohydrates (60%), fat (1.5%), minerals, amino acids and vitamins and ability to restore the soil fertility through symbiotic nitrogen fixation [1]. Hence, it is usually known as "poor man's meat" particularly in the vegetarian population of the Indian subcontinent. The yield of pulses in general and black gram in particular remains at low level and there is a need for improvement. The yield is a complex character and is associated with various other contributing characters, which are interrelated among them. The study of inheritance of various quantitative and qualitative traits through the estimation of different genetic parameters like components of variances, genotypic and phenotypic coefficients of variability, heritability and genetic advance is a prerequisite for a plant breeder in conducting effective breeding programme. In this connection, variability is one such estimate provides a clear-cut idea about a particular traits on which greater emphasize should be given during selection [2]. According to Chopra [3] heritability of a character provides an idea of the extent of genetic control for the expression of a particular character. Moreover, heritability serves as a guide to the reliability of phenotypic variability in the selection program and hence determines its success [4]. Johnson *et al.*, [5] reported that heritability estimates along with genetic advance are more reliable than heritability alone to the predict effect of selecting the best individuals. Genetic advance indicates the magnitude of the expected genetic gain from one cycle of selection [6]. In this

regards, the present investigation was undertaken to evaluate variability, heritability and genetic advance of 11 quantitative and 3 qualitative characters in 24 black gram genotypes to provide necessary information that could be useful to improve yield traits.

Materials and Methods
Quantitative Traits

The material for the present study comprised of 24 black gram (*Vigna mungo* L. Hepper) germplasm collected from NBPGR, Hyderabad, Akola, ANGRAU, IIPR Kanpur, TNAU and ARS, Bidar [Table-1]. These lines were evaluated in randomized block design with two replications at the experimental plots of Department of GPB, 'K' block, GKVK, UAS, Bangalore during *Rabi* 2014 for their yield and yield attributes performance. All the recommended crop production and protection practices were followed to raise a healthy crop. Data on the 11 different quantitative traits *viz.*, days to 50% flowering, days to maturity, plant height (cm), number of branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, pod length (cm), number of seeds per pod, hundred grain weight (g) and Seed yield per plant (g) were recorded on five randomly selected competitive plants.

In order to assess and estimate the variability among the genotypes, the statistical analysis was carried out using WINDOSTAT 8.1 package. Phenotypic and genotypic components of variance estimated by applying the formula as suggested by [7].

Phenotypic variance $(\sigma^2 p) = \sigma^2 g + \sigma^2 e$ (EMSS from ANOVA)
Genotypic variance $(\sigma^2 g) = MSS\ (G) - EMSSr$
Error variance $(\sigma^2 e) = EMSS$

Genotypic coefficient of variance (GCV) = $\dfrac{\sigma^2 g}{\bar{X}}$ x 100

Phenotypic coefficient of variance (PCV) = $\dfrac{\sigma^2 p}{\bar{X}}$ x 100

Coefficients of variations: Phenotypic and genotypic coefficients of variability were computed as per the method suggested by [8].

PCV and GCV values were categorized as low (0-10%), moderate (10-20%) and high (>20) values as indicated by [9].

Table-1 *List of 24 black gram genotypes evaluated in the present study*

Sl. No	Genotype	Source	Sl. No	Genotype	Source
1	IC-282007	NBPGR	13	K.951	TNAU
2	IC-282006	NBPGR	14	GP-702	ARS, Bidar
3	IC-436753	NBPGR	15	MDU.992	TNAU
4	IC-436758	NBPGR	16	AC.43	TNAU
5	IC-436778	NBPGR	17	LBG-645	ARS, Bidar
6	IC-436765	NBPGR	18	LBG-20	ARS, Bidar
7	AKU-07-4	Akola	19	K-5-572	ARS, Bidar
8	AKU-10-04	Akola	20	GP-723	ARS, Bidar
9	LBG-685	ANGRAU	21	G.333	TNAU
10	K-07-07	ARS, Bidar	22	IPU-07.03	IIPR
11	PU-1	ANGRU	23	DU-1	ANGRAU
12	BDU-3-04	ARS, Bidar	24	RASHMI	ARS, Bidar

Heritability: The broad sense heritability $(h^2 bs)$ was estimated for all the characters as the ratio of genotypic variance to the total variance as suggested by [10].

$$h^2 bs = \frac{\sigma^2 g}{\sigma^2 p} \text{ X } 100$$

Heritability was classified as suggested Robinson *et al.* [11] into low (0-30%), moderate (30.1-60%) and high (>60%).

Genetic advance (GA)
It was predicted by using the formula provided by [4].

$$GA = h^2_{(bs)} \times \sigma^2 p \times k$$

Where, $h^2_{(bs)}$ = Heritability in broad sense, $\sigma^2 p$ = Phenotypic standard deviation of the trait, k = Standard selection differential which is 2.06 at 5 per cent selection intensity

Genetic advance as per cent mean (GAM): It was calculated by the following formula.

$$GAM\ (\%) = \frac{GA}{\bar{X}} \text{ X } 100$$

The GAM% was categorized into low (0–10%), moderate (10.1–20%) and high (>20%) as suggested by [5].

Qualitative traits
Data were recorded on five randomly tagged plants on 3 qualitative traits based on visual rating/scoring [Table-2] using appropriate scale depending on the trait in each germplasm accession and check entry following the descriptors developed by Protection of Plant Variety and Farmers Right Authority (PPV & FR), Government of India.

Table-2 *Protocol followed to record data on qualitative (seed) traits in black gram*

Sl. No	Traits	Crop stage for recording data	Score	Classified as
1	Seed color	Mature seeds	1	Green
			2	Greenish brown
			3	Brown
			4	Black
			5	Mottled
2	Seed shape	Mature seeds	1	Globluse
			2	Oval
			3	Drum shaped
3	Seed luster	Mature seeds	1	Dull
			2	Shiny

Results and Discussion
Quantitative traits
Analysis of variance revealed highly significant mean of squares due to genotypes for all traits *viz.*, days to 50 per cent flowering, branches plant[-1], cluster plant[-1], pods per cluster, pods plant[-1], plant height, pod length seed yield plant[-1] except for trait days to maturity [Table-3]. Highly significant mean squares indicated substantial variability not only among the genotypes but also among the check varieties for most of the quantitative traits as indicated by analysis of variance which indicate the scope for selection of desirable genetic material for further improvement. The overall mean of the parents for each characters are given below in [Table-4]. The mean values for quantitative traits such as, days to 50 per cent flowering (49.17 days), days to maturity (68.63 days), plant height (31.58 cm), branches plant[-1] (5.96), clusters plant[-1] (10.35), pods cluster[-1] (4.15), pod length (4.53 cm), pods plant[-1] (46.7), seeds pod[-1] (4.93), seed yield plant[-1] (6.83 g) and test weight was recorded (4.81 g).

Knowledge on the relative contribution of genetic and non-genetic sources on the quantitative trait variability is useful in formulating appropriate selection strategies to breed improved black gram cultivars. The estimates of the range provide clues about the occurrence of genotypes with extreme expression, which varied with the trait. Among the genotypes, the trait days to 50 per cent flowering varied from 45.50 days (K-951) to 51 days (AC-43) and the days to maturity ranged from 66.00 days (G.333) to 71.00 days (AC-43). However, plant height varied from 18.00 cm (G.333) to 38.70 cm (GP-723). The genotype AKU-07-04 exhibited a minimum number of branches plant[-1] of 4.00 and the maximum numbers of branches plant[-1] of 8.20 was exhibited by G-333. The genotype AC-43 exhibited a minimum number of clusters plant[-1] (5.80) while, maximum number of clusters

plant[-1] was developed by DU-1 (17.5). The number of pods cluster[-1] was minimum (2.90) in genotype LBG-645 and maximum in MDU-992 (5.10) [Table-4]. The number of pods plant[-1] was minimum in BDU-03-04 (28.50) and maximum in IC-436765 (72.18). The genotype K-5-572 exhibited minimum pod length (3.79 cm) while, genotype RASHMI recorded maximum pod length of 5.37 cm. Number of seeds per pod varied from 3.30 (MDU-992) to 8.40 (RASHMI). Seed yield per plant with a minimum of 3.2 g was recorded in AKU-07-04 and a maximum of 14.12 g in RASHMI was noticed. 100-grain weight showed considerable variation with a minimum yield of 3.50 g (K-951) to a maximum of 7.85 g (IC-282006) [Table-4]. However, range *per se* does not reflect variability in the expression of all the genotypes.

Table-3 *Analysis of variance for 11 quantitative traits in 24 blackgram genotypes*

Sources of variance	df	Days to flowering	Days to maturity	Plant height (cm)	Branches plant[-1]	Clusters plant[-1]	Pods Cluster[-1]	Pods plant[-1]	Pod length (cm)	Seeds pod[-1]	Seed yield plant[-1] (g)	Test weight (g)
Replication	1	0.08	1.33	3.22	0.001	0.06	0.13	4.74	0.001	0.12	0.47	0.06
Genotypes	23	3.12*	2.49	41.62**	2.07**	25.59**	0.57**	273.35**	0.34**	3.23**	20.05**	1.56**
Error	23	1.23	1.77	1.20	0.67	0.01	0.13	45.88	0.02	0.08	0.61	0.03

*Significant at $P \leq 0.05$ level, ** Significant at $P \leq 0.01$ level.

Table-4 *Estimates of genetic variability components for 11 quantitative traits in 24 blackgram genotypes*

Sl. No	Traits	Grand Mean	Range Lowest	Range Highest	GCV %	PCV %	h² % (Broad sense)	GAM %
1	Days to flowering	49.17	45.50	51.00	1.96	3.01	42.50	1.16
2	Days to maturity	68.63	66.00	71.00	0.87	2.13	16.94	0.21
3	Plant height (cm)	31.58	18.00	38.70	14.12	14.77	91.40	5.70
4	Branches plant[-1]	5.96	4.00	8.20	14.06	19.62	51.38	12.72
5	Clusters plant[-1]	10.35	5.80	17.50	34.56	34.58	99.87	19.87
6	Pods cluster[-1]	4.15	2.90	5.10	11.66	14.11	68.32	28.04
7	Pods plant[-1]	46.70	28.50	72.18	22.84	27.05	71.26	2.65
8	Pod length (cm)	4.53	3.79	5.37	8.29	9.12	82.60	34.15
9	Test weight (g)	4.81	3.50	7.85	18.77	18.82	99.43	42.49
10	Seeds pod[-1]	4.93	3.30	8.40	25.70	26.35	95.15	38.82
11	Seed yield plant[-1] (g)	6.83	3.20	14.12	45.62	47.03	94.10	27.51

The estimates of GCV and PCV which reflect average inter-genotype differences are more useful tools to understand variability among the genotypes. In general phenotypic coefficient of variability was greater than their corresponding genotypic coefficient of variability. The genotypes were highly variable for cluster plant[-1], pods plant[-1], seeds pod[-1] and seed yield plant[-1] as indicated by the estimates of PCV (>20%) suggesting that these characters are under the influence of genetic control. The genotypes were moderately variable for [10.1 ≤ PCV ≤ 19.62 %] plant height, branches plant[-1], and pods cluster[-1] and test weight. These results are in accordance with Murthy *et al.* [12] in green gram, [13-15] in black gram. The genotypes showed least variable for days to 50 per cent flowering, days to maturity and pod length (PCV=9.12%). These results are in accordance with Medhi *et al.* [16] in green gram and [17] in cowpea.

The broad-sense heritability reported in the present study provide only a broad idea about the extent to which the traits are heritable and assessing the degree to which the traits are fixable require development and evaluation of carefully planned experimental populations. Broad-sense heritability was higher (>60%) for all the traits *viz.*, plant height (91.40%), clusters plant[-1] (99.87%), pods cluster[-1] (68.32%), pods plant[-1] (71.26%), pod length (82.60%), test weight (99.43%), seeds pod[-1] (95.15%) and seed yield plant[-1] (94.10%) while, days to 50 per cent flowering (42.50%) and branches plant[-1] (51.38%) heritability were found to be moderate. Whereas, for days to maturity (16.94%) recorded least heritability and the results are in accordance with [13, 14, 18, 19] in black gram.

The estimates of expected GAM were higher for pods cluster[-1] (28.04), pod length (34.15%), test weight (42.49%), seeds pod[-1] (38.82%) and seed yield plant[-1] (27.51%). While, GAM were moderate for branches plant[-1] (12.72%) and clusters plant[-1] (19.87%). The traits days to maturity (0.21%), days to 50% flowering (1.16%), plant height (5.70%) and pods plant[-1] (2.65%) exhibited least estimates of expected GAM [Table-4]. In the present study, high heritability coupled with high GAM was observed for the characters pods cluster[-1], pod length, test weight, seeds pod[-1] and seed yield plant[-1] and high heritability coupled with moderate GAM for the branches plant[-1] and clusters plant[-1] indicating that these characters are mainly controlled by additive genes and selection of such traits might be effective for the improvement of grain yield, hence are amenable for simple selection. The moderately high heritability and low GAM for remaining characters indicates the presence of non additive gene action and role of environment in the expression of these traits. Therefore, priority should be given to those traits which recorded higher estimates of genetic advance as per cent mean while deciding selection strategies and selection based on these characters may be useful in realizing better gain by selection. The genotypes such as K-951 and G-333 with fewer days to 50 per cent flowering, and IC-436765, IC-436753, IC-436758, and IC-282006 with more pods plant[-1], DU-1, IC-282006 and RASHMI with high seed yield plant[-1] are useful in breeding short duration cultivars with higher productivity.

Qualitative Traits
Seed traits were recorded separately for the 23 black gram genotypes [Table-5]. Genotypes with black coloured seed (19) were more frequent than those with brown seeds (5). Genotypes with brown coloured dry seeds were represented in higher frequency than those with black, greenish brown and green coloured dry seeds. The seed colour is a highly polymorphic yet another useful trait for germplasm characterization. As is true with other qualitative traits seed coat colour being monogenic/oligogenic trait [20-22], it could be used as a morphological marker for germplasm characterization, purity assessment and identification of true F_1s. Monogenic markers are useful in estimating the rate of crossing in predominantly self-pollinated crops like black gram [23].

Table-5 *Variability for qualitative traits and their frequency among 23 black gram genotypes*

Sl. No	Traits	Classified as	Frequency	Per cent
1	Seed color	Green	0	0
		Greenish brown	0	0
		Brown	5	20.83
		Black	19	79.16
		Mottled	0	0
2	Seed shape	Globular	17	70.83
		Oval	0	0
		Drum shaped	7	29.16
3	Seed luster	Dull	18	75.00
		Shiny	6	25.00

Genotypes having globular shaped seeds (17) were frequent than those with drum shaped seeds (7). Globular seeds producing genotypes were more frequent than those producing drum shaped and globular seeds. Genotypes that produced dull

seeds (18) were more frequent compared to shiny seeded ones (6). The genotypes with dull seed luster were highly frequent than shiny seed luster. The inheritance of black and seed colour in mungbean was controlled by one gene and seed lustre possibly control by two or more genes [24].

Conclusion

Black gram is predominantly a self-pollinated crop, the genotypes are a mixture of pure lines, each of which possess a slightly different combination of traits and hence are better adapted to different production environment and/or a combination of production environments. Through increased use of landraces, black gram cultivars that are suitable for diverse production constraints, especially those of abiotic stresses whose occurrence are expected to vary in timing, intensity and duration, and crop growth stage could be developed. Qualitative trait polymorphism has been attributed to diversity in phylogeny [25]. A few of the polymorphic traits such as seed coat colour could be used as diagnostic descriptor for germplasm characterization, purity assessment and genetic studies. Further, heritability reported in the present study are based on single season data resulting in biased estimates unless genotype-by-environment interaction is negligible in non-crossover types, which is rarely true for quantitative traits of agronomic importance [26]. Thus, heritability estimates reported in the present study need to be confirmed from data collected in multiple locations and years representing the target environments.

Conflict of Interest: None declared

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