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Assessment of variability in twenty-four lines of blackgram (*Vigna mungo* L.)

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Abstract

Variability, heritability and genetic advance were studied in twenty-four lines of blackgram for seven quantitative traits. The analysis of variance showed significant differences among genotypes for all the traits under study. Replication item was significant for all the traits except LA50%F and NS/P. Interaction (L×R) was significant for NSBFF, NL50%F, LA50%F, NS/P and RL50%F. The phenotypic variation (σ^2_P) was greater than those of σ^2_L, σ^2_{LR} and σ^2_w components of variation for all the traits. The highest phenotypic and genotypic variations were observed for LA50%F followed by NN50%. It is also noticed that phenotypic coefficients of variability (PCV) in general, were higher than the estimates of genotypic coefficients of variability (GCV) for all the traits. The traits viz., LA50%F and NN50% showed high GCV estimates whereas; NN50%, NSBFF, LA50%F, and NL50%F exhibited high PCV. The heritability, genetic advance (GA) and genetic advance as percentage of mean (GAM %) were found to be low.

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Introduction

Blackgram is an erect, fast-growing annual, herbaceous legume reaching 30-100 cm in height. It has a well-developed taproot and its stems are diffusely branched from the base. The leaves are trifoliate with ovate leaflets 4-10 cm long and 2-7 cm wide. It contains 4-10 ellipsoid black or mottled seeds (Jansen, 2006). The seeds are rich in protein (24-26 % DM) and starch (35 %) (Wiryawan, 1997). *Vigna mungo* is a taprooted, N-fixing legume that improves soil fertility and soil physical properties (Parashar, 2006). Its cultivation does not require N fertilization but N fixation is improved by inoculation with local *Rhizobium* strains (Sharma *et al.*, 2011). Blackgram is responsive to P (40 kg/ha) and K (30 kg/ha) and only needs rough tillage and one or two weedings (Baligar *et al.*, 2007).

The knowledge of genetic variability is inevitable for any traits under improvement for the success of any fruitful plant breeding program. The blackgram is the most widespread economically important and genetically diverse cultivated pulse crop in Bangladesh. Variability is more helpful for proving an idea about a particular traits on which greater emphasize should be given during selection (Singh *et al.*, 1981). Heritability of a character is important for the blackgram breeder because it provides an idea of the extent of genetic control for the expression of a particular character (Chopra, 2000). Moreover, heritability serves as a guide to the reliability of phenotypic variability in the selection program and hence determines its success (Hamdi, 1992). Heritability estimates together with genetic advance are more important than heritability alone to predict the resulting effect of selecting the best individuals (Johnson *et al.*, 1955). Genetic advance is also of considerable importance because it indicates the magnitude of the expected genetic gain from one cycle of selection (Hamdi *et al.*, 2003). As a result, the present investigation is undertaken to evaluate variability, heritability and genetic advance of seven agronomical characters in twenty-four blackgram genotypes to provide necessary information that could be useful in blackgram improvement programs desired to improve yield traits.

Materials and methods

Plant materials

Twenty-four blackgram lines were taken as materials. The seeds of blackgram were collected from BARI regional station, Ishurdi, Pabna, Bangladesh. Layout of the experimental field and trial of the lines was conducted under completely randomized block design with 3 replications. The data of seven quantitative traits viz., leaf area at 50% flower (LA50%F), root length at 50% flower (RL50%F), number of nodule at 50% flower (NN50%F), number of leaf at 50% flower (NL50%F), plant height at first flower (PHFF), number of secondary branch at first flower (NSBFF) and number of seed/plant (NS/P) were collected on individual plant basis following C.G.S system.

Table 1. Twenty-four lines of blackgram

SL. No.	AC. No.	SL. No.	AC. No.	SL. No.	AC. No.
1.	E86146	9.	ERU7	17.	E86325
2.	E86287	10.	E86042	18.	E86149
3.	Egen-8	11.	E86107	19.	E86106
4.	EB-34	12.	E86359	20.	E2025
5.	EMLO13	13.	E86376	21.	E86309
6.	E2032	14.	E86006	22.	E86077
7.	E86053	15.	86289	23.	RU181
8.	86317	16.	E9019	24.	EB28

Statistical analysis

Variance analysis: The analysis of variance of a mixed modal was used, where line (L) fixed and replication (R) random. The expectation of mean square (E. M. S) is derived as follows:

Table 2. Analysis of variance (ANOVA).

Item	d. f.	SS	MS	EMS
Treat.	(LS-1)=71	SS_1	MS_1	
Rep. (R)	(R-1)=2	SS_2	MS_2	$\sigma^2_w + LS\sigma^2_R$
Line (L)	(L-1)=23	SS_3	MS_3	$\sigma^2_w + S\sigma^2_{LR} + RS\sigma^2_L$
R × L	(L-1)(R-1)=46	SS_4	MS_4	$\sigma^2_w + S\sigma^2_{LR}$
W. error	LR(S-1)=144	SS_5	MS_5	σ^2_w
Total	(LRS-1)=215			

Where, $LS\ \sigma^2_R$ = Variance due to replication

$RS\ \sigma^2_L$ = Variance due to line

$S\ \sigma^2_{LR}$ = Variance due to L × R

σ^2_w = Variance due to within error

The components of variation were phenotypic ($\sigma^2{}_P$), genotypic ($\sigma^2{}_L$) interaction ($\sigma^2{}_{LR}$) and error variance ($\sigma^2{}_w$). These were measured as follows:

$$\sigma^2{}_L = (MS_3 - MS_4)/_{RS}$$

$$\sigma^2{}_R = (MS_2 - MS_5)/_{LS}$$

$$\sigma^2{}_{LR} = (MS_4 - MS_5)/_R$$

$$\sigma^2{}_W = MS_5$$

Phenotypic variance ($\sigma^2{}_P$) = $\sigma^2{}_L + \sigma^2{}_{LR} + \sigma^2{}_w$

Coefficients of variability: Genotypic (GCV) Phenotypic (PCV) and Within error (ECV) coefficients of variability were computed according to Burton and Devane (1953) and expressed as percentage:

$$PCV = \frac{\sigma_p}{\overline{X}} \times 100$$

$$GCV = \frac{\sigma_g}{\overline{X}} \times 100$$

$$ECV = \frac{\sigma_e}{\overline{X}} \times 100$$

Where, σ_p = Genotypic standard deviation

σ_g = Phenotypic standard deviation

σ_e = Within error standard deviation

$\overline{X}$ = General mean of the trait

PCV and GCV values were categorized as low (0-10%), moderate (10-20%) and high (>20) values as indicated by Sivasubranian and Menon (1973).

Heritability: Heritability (in broad sense) estimates was computed by dividing the genotypic variance with phenotypic variance and then multiplying by 100 as suggested by Warner (1952).

$$h^2{}_b = \frac{\sigma^2{}_g}{\sigma^2{}_p} \times 100$$

Where, $h^2{}_b$ = Heritability in broad sense

$\sigma^2{}_g$ = Genotypic variance

$\sigma^2{}_p$ = Phenotypic variance

Heritability was classified as suggested Robinson *et al.* (1949) into low (0-30%), moderate (30.1-60%) and high (>60%).

Genetic advance: Genetic advance was calculated by the following formula as suggested by Lush (1949).

$$GA = k(\sigma_p) \left(\sigma^2{}_g / \sigma^2{}_p \right)$$

Where, k = The selection differential in standard units for the present study it was 2.06 at 5% level of selection, σ_p = Square root of the phenotypic variance, $\sigma^2{}_p$ = Phenotypic variance and $\sigma^2{}_g$ = Genotypic variance.

Genetic advance as percentage of mean: It was calculated by the following formula.

$$GAM\% = \frac{GA}{\overline{X}} \times 100$$

Where, $\overline{X}$ = Grand mean for a particular trait.

The GAM% was categorized into low (0–10%), moderate (10.1–20%) and high (>20%) as suggested by Johnson *et al.* (1955).

Results and discussion

In the analysis of variance, line (L) item was highly significant for all the traits when it was tested against within error (Table 3). These results indicated that genotypes were significantly and genotypically different from each other and it justified their inclusion in the present investigation as materials. This observation was in accordance with the findings of Hasan and Deb (2013) in chickpea. Replication item was significant for all the traits except LA50%F and NS/P. Khan (2013) got significant R values for all the traits in wheat. Interaction (L×R) was significant for NSBFF, NL50%F, LA50%F, NS/P and RL50%F. These results are in conformity with the findings of Hasan and Deb (2013) in chickpea.

The different components of variation varied differently in different traits. Phenotypic component of variation ($\sigma^2{}_p$) was higher than genotypic ($\sigma^2{}_L$), interactions ($\sigma^2{}_{LR}$) and error ($\sigma^2{}_w$) components of variation (Table 4). The difference between phenotypic and genotypic variation were greater in magnitude for LA50%F followed by NN50% which indicated that the environment had considerable effect on these traits. Azad *et al.* (2011) in lentil got the same results for all studied traits. The pronounced environmental variance for LA50%F and NN50%F indicated that greater portion of the phenotypic

variation was environmental in nature. High environmental variance was observed by Azad *et al.* (2011) in lentil for plant area per plant, number of pod per plant and number of seed per plant.

In the analysis, phenotypic coefficient of variability was greater than genotypic and all other coefficient of variabilities (Table 4). The results are in agreement with the findings of Hefny (2013) in white lupin (*Lupinus albus*). All the traits showed low GCV and PCV values. It indicated that environment had considerable effect on these traits. Sirvastava and Singh (2012) in mungbean observed the same results.

The heritable portion of variability cannot be judged by genetic coefficient of variation alone. The heritability together with genotypic coefficient of variation can give the actual picture in heritable variation. The heritability estimate in the present investigation was found to be low (Table 4). The lowest values of heritability indicated that the environment constituted a major portion of total phenotypic variation for the traits. Bicer and Sakar (2004) found low heritability for biological yield per plant, seed yield per plant, number of pods per plant and number of seeds per plant in lentil. Khan (2013) in wheat also observed low heritability for most of the traits

However, heritability does not provide indication of amount of genetic progress that would result from selecting the best individuals. Johnson *et al.* (1955) in soybean suggested that heritability estimate with genetic gain are more useful for effective improvement. In this study, genetic advance (GA) was low for all the traits under studied. Similar results were obtained by Zeeshan *et al.* (2013) in chickpea. In addition to this, genetic advance as percentage of mean (GAM%) were low for all the traits and supported by the findings of Jonah *et al.* (2013) in groundnut for most of the traits.

Table 3. Analysis of variances among genotypes and its interaction with replication for seven quantitative traits in blackgram.

Items	df	LA50%F		RL50%F		NN50%F		NL50%F	
		F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2
Treatment	71								
Rep. (R)	2	2.44	1.25	20.84**	10.48**	6.145**	5.58**	14.99***	8.52**
Line (L)	23	3.24**	1.65	2.56**	1.29	1.927*	1.75	1.93*	1.09
R×L	46	1.95**		1.98**		1.417		1.75*	
W. Error	144								
Total	215								

Contd....

Items	df	NS/P		NSBFF		PHFF	
		F_1	F_2	F_1	F_2	F_1	F_2
Treatment	71						
Rep. (R)	2	0.136	1.39	7.53**	4.28*	21.536***	8.12*
Line (L)	23	3.025**		1.83*	1.04	3.059*	1.153
R×L	46	2.168**		1.75*		2.652	
W. Error	144						
Total	215						

* and ** indicate significant at 5% and 1% levels, respectively.

Table 4. Phenotypic (σ^2_P), genotypic (σ^2_L), interactions (σ^2_{LR}) and within error (σ^2_W) components of variation and Phenotypic (PCV), genotypic (GCV), within error (ECV) coefficient of variability, and heritability (h^2_b), genetic advance (GA) and genetic advance as percentage of mean (GAM%) for seven quantitative traits in blackgram.

Traits	σ^2_P	σ^2_G	σ^2_{LR}	σ^2_W	PCV
LA50%F	112.76	11.03	24.54	77.19	3.734
RL50%F	4.743	0.219	1.12	3.404	2.235
NN50%F	93.61	4.43	10.9	78.28	5.238
NL50%F	19.954	0.254	3.372	13.328	3.750
NS/P	0.706	0.045	0.185	0.476	1.719
NSBFF	0.603	0.0004	0.121	0.482	4.647
PHFF	11.935	0.338	4.118	7.479	2.015
					Contd....
Traits	GCV	ECV	h^2_b	GA	GAM%
LA50%F	1.167	3.089	9.78	2.139	0.752
RL50%F	0.48	1.894	4.617	0.207	0.212
NN50%F	1.139	4.79	4.732	0.943	0.51
NL50%F	0.459	3.324	1.498	1.270	1.162
NS/P	0.434	1.41	6.373	0.11	0.225
NSBFF	0.119	4.155	0.024	0.00106	0.00634
PHFF	0.339	1.595	2.832	0.201	0.117

Conclusion

The results of the present investigation revealed that the characters included are quantitative in nature and provided environmental factors are to be controlled as for as possible as low PCV, GCV, heritability and GA were observed in these materials.

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