

STUDY OF GENETIC CONTROL OF SOLUBLE PROTEIN IN ROOT NODULES AND SEEDS IN BLACKGRAM (*Vigna mungo* (L.) Hepper)

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ABSTRACT

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The genetic control of soluble protein in root nodules and seeds per plant in four lines of blackgram (*Vigna mungo* (L.) Hepper) in two different crosses (cross I: 5×21 & cross II: 17×20) were studied separately. Additive-dominance relationships for soluble protein in root nodules in cross II and also for soluble protein in seeds in both of the crosses were non-significant. Potence values were significant in all the cases except for soluble protein in seeds in cross I. Components of variation, D and H for both of the characters and crosses expressed positive and negative values. Negative sign was due to large sampling variation and genotype-environmental interaction. Dominance ratio showed complete to over dominance in negative direction, which indicated dominance towards decreasing parent. The narrow sense heritability, being high mostly, indicated that selection might be fruitful for soluble protein in nodules in cross I and for soluble protein in seeds in cross II. Genetic advance (GA) was negative in most of the cases, but in some cases it showed positive genetic advance. Positive genetic advance in narrow sense for the characters in root nodules in cross I and for the same in seeds in cross II accompanied by high narrow sense heritability was obtained. This indicated that selection of soluble protein in nodules and seeds in these crosses would likely be fruitful in an advance generations.

Keywords: Blackgram, genetic control, single cross, soluble protein

INTRODUCTION

Pulses are one of the most important leguminous crops that have been cultivated in many countries all over the world by human being since the early ages of history. Among pulses, blackgram (*Vigna mungo* L. Hepper) is one of the important edible pulse crops of Bangladesh which provides adequate nutritional elements, specifically protein, remaining a vital role in the increment, and compensation of its economy. Locally it is known as "Mashkalai" and its dry seeds are called "Dhal". It stands 4th regarding its importance (Anonymous, 1998) among the crops after rape and mustard on the basis of production and 3rd on rank by dint of yield production and seed protein. Apart from Bangladesh, it is also a staple crop in India, Burma, Pakistan, and Thailand due to its importance (Lawn and Ahn, 1985; Rubatzky and Yamaguchi, 1997). Besides in the presence of nodule on the roots of blackgram as symbiotic association, containing nitrogen fixation bacteria (*Rhizobia* sp.) which help in management of soil fertility as well as save nitrate leaching during precipitation (Jones, 1939). It is needless to say that blackgram, being an important staple crop, is much neglected and a few works are being done for the improvement of this crop dealing with the problem genetic control of different quantitative characters in early days in our country. Hence, extensive research efforts are necessary for the improvement of blackgram through meaningful breeding programme whereas, proper knowledge of genetic information on the inheritance of quantitative characters controlled by polygenic system having both additive and non-additive gene effect is essential.

MATERIALS AND METHODS

In the present study, four lines of blackgram [*Vigna mungo* (L.) Hepper] viz. line-5, line-17, line-20 and line-21 were collected from Regional Agricultural Research Station (RARS), Ishurdi, Pabna, Bangladesh. The experiment was done in the research field of Botanical garden of the Department of Botany, Rajshahi University. Lay out of the experimental field was done following completely randomized block design. Two single crosses were made without reciprocals between the selected parents in 2005 as shown in the following table:

Table 1. Single crosses of four lines blackgram

SL. No.	Crosses	P ₁	P ₂	F ₁	F ₂	B ₁	B ₂
1	5×21	EMLO13	E86309	EMLO13	EMLO13	EMLO13	EMLO13
				×	×	×	×
				E86309	E86309	E86309	E86309
				×	×	×	×
				E86309	E86309	E86309	E86309
2	17×20	E86325	E2025	E86325	E86325	E86325	E86325
				×	×	×	×
				E2025	E2025	E2025	E2025
				×	×	×	×
				E2025	E2025	E2025	E2025

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Root nodules and seeds were collected in individual plant basis under three replications. The experimental data were analyzed by means of biometrical technique as suggested by Mather (1949) based on the mathematical models of Fisher *et al.* (1932) and that of Hayman and Mather (1955), Warner (1952) and Lush (1949) along with biochemical analysis through the Lowry *et al.* (1951) method.

RESULTS AND DISCUSSION

For successful breeding research in any crop, genetic information is of utmost importance regarding the nature, relative magnitude and types of gene action following proper genetic model. The result of Mather’s scaling test shown in Table 2 which indicated the adequacy of additive-dominance model for A, B and C for both characters and crosses except for B for root nodules per plant in cross I. Shahid (1996) following Mather’s scaling test and obtained inadequacy of additive-dominance model in wheat. Deb and Khaleque (2009) also found adequacy of additive-dominance model in some of the cases in chickpea. Since each test has its own expectation in terms of type and magnitude of epistatic effects, agreement should not necessary be expected among these test.

Joint scaling test of Cavalli (1952) is more effective than any other test in detecting the adequacy of model, since it uses information from of all the generations available from each cross at a time. In the joint scaling test, the χ^2 values were found to be non-significant for soluble protein in both of the characters and crosses (Table 2). The non-significant χ^2 value indicated the presence of only additive-dominance effects in the inheritance of these characters and crosses. This result also indicated that with only the additive-dominance relationship for soluble protein of those characters and crosses would likely help in future breeding programme for the development of good lines in blackgram. This result corroborate with the findings of Islam (1980) in eggplant, Shahid (1996) in wheat and Deb and Khaleque (2009) in chickpea.

For soluble protein in both of the characters the potences were significant except in seeds per plant in cross I as shown in Tale 2. These results reflect to some extent in calculation of dominance ratio. These show that dominance is predominance but which was negative direction in these characters and crosses.

Table 2. Analysis of Mather’s scaling test (A, B & C) and joint scaling test (m, d, h & χ^2) for soluble protein in root nodules and seeds per plant in four lines of blackgram

Crosses	Scaling test	Soluble protein in root nodule per plant		Soluble protein in seeds per plant	
		Values with SE	Probability	Values with SE	Probability
Cross I: Line-EML013 × Line- E86309	A	0.3246±5.0805	.70-.80	-0.0569±2.5951	P>.90
	B	2.1764±3.5118	.05-.01	1.1486±3.3503	.20-.30
	C	1.3661±12.1744	.10-.20	0.2344±4.1600	.80-.90
	m	9.5927±0.7866		5.7638±0.4522	
	d	-0.8580±0.7777		0.5040±0.4266	
	h	-1.3899±0.7254		1.4843±0.5144	
	χ^2	5.6433	.10-.20	1.6536	.50-.70
	Potence		-4.3810±0.8089		0.2315±0.3303
Cross II: Line-E86325 × Line- E2025	A	0.6670±5.7647	.50-.60	0.5229±2.9940	.60-.70
	B	0.2645±6.4039	.70-.80	-0.4692±2.7868	P>.90
	C	0.7780±11.0240	.40-.50	-0.6170±5.8647	P>.90
	m	11.5000±1.1883		7.9350±0.6818	
	d	0.3984±1.2205		-1.1556±0.6221	
	h	-2.7635±0.6741		0.1089±0.7165	
	χ^2	0.8952	.80-.90	1.0809	.70-.80
	Potence		-3.5160±0.7878		0.9498±0.4592

Table 3. Components of variation (D, H & E), dominance ratio ($\sqrt{H/D}$), heritability (h^2_b & h^2_n) and genetic advance ($GA_{(b)}$ & $GA_{(n)}$) for soluble protein in root nodules and seeds per plant in four lines of blackgram

Crosses	Parameters	Soluble protein in root nodule per plant		Soluble protein in seeds per plant	
Cross I: Line-EML013 × Line- E86309	Components of variation	D	19.9204		-3.7250
		H	-18.4792		3.4472
		E	3.0840		1.5877
	Dominance ratio	$\sqrt{H/D}$	-0.9631		-0.9619
	Heritability	h^2_b	63.3900		-170.4700
		h^2_n	118.23		-317.29
	Genetic advance	$GA_{(b)}$	3.7900		-2.6902
		$GA_{(n)}$	7.0689		-5.0070
Cross II: Line-E86325 × Line- E2025	Components of variation	D	-13.7600		1.5696
		H	27.7200		-7.1992
		E	5.8949		2.3811
	Dominance ratio	$\sqrt{H/D}$	-1.4193		-2.1416
	Heritability	h^2_b	-0.8500		-74.2900
		h^2_n	-117.80		57.4400
	Genetic advance	$GA_{(b)}$	-0.0423		-1.7887
		$GA_{(n)}$	-5.8643		1.3829

Table 3 showed that the estimates of H component in soluble protein in both of the characters and crosses were negative and positive. Similar results were obtained in maize by Moll *et al.* (1960), Lindsey *et al.* (1962) and Williams (1960), in mustard by Joarder and Eunus (1968) and Joarder *et al.* (1977), in rapeseed by Samad (1991), in chilli by Husain (1997), and in sugarcane by Nahar (1997). The magnitude of D was also negative and positive in few cases. Similar results were noted by Paul *et al.* (1976b), and Samad (1991) in rapeseed and Deb and Khaleque (2009) in chickpea. In the present investigation, the additive and dominance components of variation were found to be negative in few cases, which might be due to large sampling variation and genotype-environmental interaction as were indicated by Mather (1949) and Hill (1966).

Dominance ratio showed complete to over dominance but in negative direction in these characters and crosses (Table 3). The negative sign may be due to the fact that the decreasing parents are dominant. Samad (1991) recorded similar results in rapeseed, Nahar (1997) in sugarcane and Husain (1997) in chilli for different characters. Eunus (1964) observed over dominance in three different crosses viz. Atsel×Tulate, Frontier×Bonneville and Montclam×Beecher. Singh and Ramanujam (1972) observed over dominance for PB, SB, DF and F/U in cross S.15×S.10 and PH, PB, SB and Y/P in cross S.15×PSWF. Sharma *et al.* (1979) in BIP's of pearl millet reported the presence of over dominance. Islam (1980) observed over dominance in majority of the characters of five crosses of brinjal (*Solanum melongena* L.).

For soluble protein in root nodules and seeds per plant the heritability estimates both in broad and narrow senses were found to be high mostly and low only in one case for soluble protein in nodules in cross II (Table 3). Coyne (1968) estimated a low heritability for seed yield and yield components in field bean. Husain *et al.* (2000) obtained low narrow and broad sense heritability in chilli following triple test cross (TTC). Nahar and Khaleque (2000) found high narrow and broad sense heritability in some of the cases in sugarcane following BIP's. The magnitude of high narrow sense heritabilities (h_n^2) for soluble protein in nodules in cross I and seeds in cross II indicated that the genetic progress under selection for the characters studied would be fruitful. The higher magnitude of narrow sense and broad sense heritabilities in the present materials indicated respectively the preponderance of more additive and non-additive genetic variation in the inheritance of soluble protein of root nodules per plant.

In the present investigation, the genetic advance (GA) was negative in most of the cases, but in some cases it showed positive genetic advance (Table 3). Ramana Rao *et al.* (1974), Deb (1994) and Husain (1997) also found the same result in chilli and Deb and Khaleque (2009) in chickpea. Positive genetic advance in narrow sense for the characters in root nodules in cross I and for the same in seeds in cross II accompanied by high narrow sense heritability was obtained. This indicated that selection of soluble protein in nodules and seeds in these crosses would likely be fruitful in advance generation. Kritisingh *et al.* (1972) also reported high heritability accompanied by high genetic advance for fruit size in chilli. According to Panse (1957), high heritability and high genetic advance are the indication of additive gene effects.

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