

GENETIC STUDY OF SOME AGRONOMICAL TRAITS THROUGH SINGLE CROSS ANALYSIS IN BLACKGRAM [*Vigna mungo* (L.) Hepper]

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Accepted for publication on 15 July 2010

ABSTRACT

Nahar K, Deb AC, Samad MA, Khaleque MA (2010) Genetic study of yield and yield components through single cross analysis in blackgram [*Vigna mungo* (L.) Hepper]. *Int. J. Sustain. Crop Prod.* 5(3), 22-28.

The present investigation deals with the genetic study of six agronomic characters namely shoot weight (SHW), root weight (RW), number of pods per plant (NPdPP), pod weight per plant (PdWPP), number of seeds per plant (NSPP) and seed weight per plant (SWPP) in two crosses viz. cross I (line-21×line-17) and cross II (line-21×line-20) between three lines of blackgram. In Mather's scaling test, A, B and C were non-significant in most of the cases. The potence values were observed non-significant for all the characters, except for NPdPP in cross II where it was significant. In the Joint scaling test, the non-significant χ^2 values was found in cross I for SHW, PdWPP and SWPP. In RW non-significant χ^2 was found in both of the crosses. Non-significant χ^2 values indicated that the presence of only additive-dominance relationship in these characters. For estimates of the components of variation, D and H for all the characters in both of the crosses expressed negative values, except for NPdPP and NSPP where D were positive. In almost all the cases over dominance was found in negative direction. In these materials due to the low and negative genetic components of variation, heritability and genetic advance were found to be low and negative. However, high and moderate heritability with 77% and 35% for NPdPP and NSPP, respectively were found in cross II. Selection practices may be fruitful with these characters and crosses as they also showed positive and moderate genetic advance.

Key words: agronomical traits, single cross, blackgram

INTRODUCTION

Blackgram [*Vigna mungo* (L.) Hepper] is one of the important pulse crop grown in Bangladesh. It is an important source of plant protein and contains approximately 25% protein in grain. It contains not only protein, minerals and vitamin-B, but also dry seed contain about 9.7% water, 23.4% proteins, 1% fats, 57.3% carbohydrates, 3.8% fibers and 4.5% ash (Purseglove 1968). The yield and yield contributing characters of blackgram and other crops are controlled by polygenic system. In this system both additive and non-additive gene actions and interactions are found to be operative. Yield of blackgram is a compound character, which depends on morphological, physiological and developmental components. Genetic information on the inheritance of quantitative characters is necessary for the preparation of effective and meaningful breeding programmes on any crop for its improvement.

Quantitative characters require more elaborate statistical methods. Mather (1949) and Hayman and Mather (1955) developed the scaling test and three-parameter model for the estimation of the components of generation means of the quantitative character. In model fitting adequacy of scale must satisfy that genes are independent in action (no non-allelic interaction) and independent in distribution (no linkage) and also independence of heritable components form non-heritable ones. Hayman (1958) and Jinks and Jones (1958) gave six-parameter model for the estimation of various genetic components including non-allelic interaction, viz, additive-additive, additive-dominance and dominance-dominance. Heritability is a measure of the amount of genetic variability. Estimates of heritability in relation to genetic interpretation are important in determining the response to selection for the traits under observation.

As the yield of blackgram per acre is low, extensive research effort is necessary for the improvement of this crop in our country. For the improvement of yield and its components, estimation of additive and dominance components is also necessary. Hence, the objective of this research is the improvement of this crop through proper knowledge of genetic information on the inheritance of quantitative traits.

MATERIALS AND METHODS

Materials used in this study comprised three lines of blackgram [*Vigna mungo* (L.) Hepper] namely E 86325, E 2025, E 86309 with access number 17,20 and 21 respectively, used as parents. Two single crosses [cross I (line-21× line-17) and cross II (line-21× line-20)] were made with reciprocals between the selected parents. The experiment was done in research field, behind the 3rd Science Building, University of Rajshahi containing a randomized complete block design with three blocks following individual plant randomization in August, 2005. Data were collected on individual plant basis for six yield and yield components viz. shoot weight (SHW), root weight (RW), number of pods per plant (NPdPP), pod weight per plant (PdWPP), number of seeds per plant (NSPP) and seed weight per plant (SWPP).

The collected data were analyzed following biometrical techniques as suggested by Mather (1949) based on mathematical models of Fisher *et al.* (1932) and that of Hayman and Mather (1955), Cavalli (1952), Warner (1952) and Lush (1949).

The techniques that have been used are described in the following sub-heads:

The analysis of variance (ANOVA) is done for testing the significant differences among the population. Variance analysis for the six generations *ie.* P₁, P₂, F₁, F₂, B₁ and B₂ was carried out separately for the six characters of two crosses in blackgram. Since P₁ and P₂ are different parents, in this way P₁, P₂, F₁, F₂, B₁ and B₂ constitute six generations. The variance due to different sources such as replicates, within, reciprocals and types were analyzed in the present study.

Mather's scaling test was done according to Mather (1949) and Hayman and Mather (1955).

Test of potence could be done by comparing F₁ and F₂ means as calculated by following formula:

$$\bar{F}_1 - \bar{F}_2 = 1/2[h]$$

Test of significance done by 't' test as follows:

$$t = \text{Estimated value of } \bar{F}_1 - \bar{F}_2 / \text{standard error of mean}$$

Joint scaling test was done based on 3-parameter model for six generations. For testing the adequacy of additive-dominance model following weighted least square technique was done as proposed by Cavalli (1952). The significance of the three parameters m, [d] and [h] are tested against their standard errors as:

$$t = \text{Estimated value of the parameter} / \text{standard error of the parameter}$$

Here, 'm' measures the mean of base population, [d] measures the additive gene effects and [h] measures the dominance gene effects. Testing the goodness of fit of the 3-parameter model for six generations following two steps are involved:

(a) Computation of the expected means of these six families using estimates of m, [d] and [h] in a manner given below:

$$\bar{P}_1 = m + [d], \quad \bar{P}_2 = m - [d]$$

$$\bar{F}_1 = m + [h], \quad \bar{F}_2 = m + 1/2[h]$$

$$\bar{B}_1 = m + 1/2[d] + 1/2[h]$$

$$\bar{B}_2 = m - 1/2[d] + 1/2[h]$$

(b) Calculation of the square of deviations of the observed mean from the expected mean for each family and computation of χ^2 values was done following Cavalli's (1952) joint scaling test.

The techniques of Mather (1949) were followed to estimate components of variation according to the formulae:

$$V(F_2) = 1/2D + 1/4H + E \dots\dots\dots (i)$$

$$V(B_1) + V(B_2) = 1/2D + 1/2H + 2E \dots\dots\dots (ii)$$

$$V(P_1) + V(P_2) + V(F_1) / 3 = E \dots\dots\dots (iii)$$

Where, V(F₁) = Variance of F₁, V(F₂) = Variance of F₂, V(P₁) = Variance of P₁

V(P₂) = Variance of P₂, V(B₁) = Variance of B₁, V(B₂) = Variance of B₂

Here, D = Additive component of variation, H = Dominance component of variation and

E = Environmental variation.

Dominance ratio was calculated suggested by Mather (1949) as:

$$\text{Dominance ratio} = \sqrt{H/D}$$

Heritability was calculated in two different ways following Mather (1949) as follows:

i. Narrow sense heritability (h^2_n):

$$h^2_n = 1/2D / (1/2D + 1/4H + E)$$

Here, D, H and E are the estimates of components of variation.

ii. Broad sense heritability (h^2_b):

$$h^2_b = (1/2D + 1/4H) / (1/2D + 1/4H + E)$$

Here, $\sigma^2_g = (1/2D + 1/4H)$ and $\sigma^2_p = (1/2D + 1/4H + E)$

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

$$GA = K \times \sigma_p \times h^2_b \text{ or } h^2_n$$

Where,

K = The selection differential in standard unit. According to Lush (1949), the value of K is 2.06 at 5% level of selection.

σ_p = Standard deviation of the phenotypic variance of F₂

h^2_b = Heritability in broad sense

h^2_n = Heritability in narrow sense.

RESULTS AND DISCUSSION

Genetic information on the inheritance of quantitative traits is necessary for the preparation of effective and meaningful breeding programmes in any crops for its improvement. Quantitative characters controlled by polygenes, show continuous variation and follow the normal distribution in each case indicated that the biometrical techniques developed to study the quantitative characters would be suitable for the inheritance of these characters. In the analysis of variance replicates item for all the generations were found to be non-significant in most of the cases (Table 1) indicated that there was no significant difference between the replications. The reciprocals item for F_1 and F_2 were also found to be non-significant in all the cases. The types item for B_1 and B_2 were significant for all the characters, except in NPdPP, PdWPP and SWPP where B_2 of cross I were non-significant. Significant types item indicated that the difference between the parents and maternal effects were present.

In Mather's scaling test, A, B and C were non-significant in most of the cases except SWPP in cross II (Table 2). Scale C was significant for all the characters in cross II and non-significant for all the characters in cross I except NSPP. A was significant only in cross II for PdWPP and for SWPP it was non-significant for all other characters in both of the crosses. Significant B was found for NPdPP and NSPP in cross I. On the other hand for SWPP, scale A, B and C were significant in cross II. Non-significant values indicated the adequacy of additive-dominance model and significant values indicated the inadequacy of the model. Shahid (1996), Deb and Khaleque (2009) and Samad *et al.* (2009) obtained a result from Mather's scaling test on different crops and observed that additive-dominance model was inadequate in most of the cases.

Non-significant potence was found for all the characters in both of the crosses, except for NPdPP in cross II where significant potence was found (Table 2). Non-significant potence shows that dominance may be ambidirectional.

Again, it was noted from Table 3 that the χ^2 values were found to be non-significant in cross I for SHW, PdWPP and SWPP. In the character RW, the χ^2 value was non-significant in both crosses. It exhibited the presence of only additive dominance relationship for those characters and crosses would likely help in doing successful breeding plan easily for the development of potential lines in blackgram. Deb and Khaleque (2009) found similar result in some cases in chickpea. The χ^2 values following joint scaling test in the rest of the characters, such as NPdPP and NSPP were significant in both crosses. In cross II, the χ^2 values for SHW, PdWPP and SWPP were found to be significant, which indicates the inadequacy of additive dominance model. In this context, non-allelic interaction and linkage may play a part with the additive dominance gene effects in the inheritance of these characters.

The estimates of H component were negative in all the cases (Table 4). These results corroborate with the findings of Samad (1991) in rapeseed and Samad *et al.* (2009) in blackgram. The magnitude of D was negative for all the cases, except in NPdPP and NSPP in both crosses. Among the three components, component E exhibited positive value in all the characters and crosses and hence it showed the highest value for NSPP in both crosses indicated that this character is highly influenced by the environment. Negative estimates of components of variation, however might be arised from sampling errors (Mather 1949) or genotype-environment interaction (Hill 1966).

The highest and the lowest values of dominance ratio $\sqrt{H/D}$ was found in cross I for RW and SWPP, respectively (Table 4). In this investigation, all the characters showed over dominance and in both the crosses it was negative for NPdPP and NSPP, which indicated dominance effect towards decreasing parent. Degree of dominance for most of the characters ranged from partial to over dominance in majority of the crosses observed by Khaleque (1975) in rice. Uddin (1983), Rahman (1984), Deb and Khaleque (2009) and Samad *et al.* (2009) also reported over dominance for different characters in their cross materials in wheat, erisilkworm, chickpea and blackgram, respectively.

In the present study, low and negative values of heritability were found in all the characters, except in NPdPP and NSPP where positive narrow sense (h^2_n) heritability was obtained in both of the crosses (Table 4). The negative heritability values in these materials were due to the fact that dominance is increasingly negative. These results is supported by the various researchers viz. Paroda and Joshi (1970a), Sharma *et al.* (1979), Shamsuddin (1982), Shahid (1996), Deb and Khaleque (2009), Hussain *et al.* (2009).

Genetic advance (GA) was lower and negative in most of the cases (Table 4). Positive genetic advance followed by h^2_n was found in NPdPP and NSPP for both of the crosses. Nahar (1997) obtained low values of GA for cane height, cane diameter, number of tiller/clump, millable cane/clump, field brix, and cane yield/clump in sugar cane. Hussain (1997) and Samad *et al.* (2009) found similar results in some cases while working on chilli and blackgram, respectively.

Table 1. Mean sum squares from ANOVA for six agronomic characters in two crosses of blackgram

Generations	Items	SHW				RW			
		Cross I		Cross II		Cross I		Cross II	
		MS	P	MS	P	MS	P	MS	P
P ₁	Replicates	0.656	>5%	0.655	>5%	0.028	>5%	0.028	>5%
	Within	4.895		4.895		0.106		0.106	
P ₂	Replicates	61.425	>5%	36.516	>5%	0.479	>5%	0.045	>5%
	Within	18.365		11.721		0.118		0.374	
F ₁	Reciprocals	4.115	>5%	60.1784	>5%	0.041	>5%	0.034	>5%
	Replicates	11.647	>5%	7.969	>5%	0.147	>5%	0.019	>5%
	Within	9.475		19.099		0.335		0.155	
F ₂	Reciprocals	75.948	>5%	17.169	>5%	0.217	>5%	0.082	>5%
	Replicates	41.455	>5%	1.220	>5%	0.150	>5%	0.426	>5%
	Within	28.456		17.020		1.249		0.217	
B ₁	Types	57.895	<5%	57.698	<1%	0.357	<1%	0.955	<1%
	Replicates	25.073	>5%	18.002	>5%	0.115	<5%	0.246	>5%
	Within	19.818		7.427		1.120		0.124	
B ₂	Types	57.082	<1%	92.339	<1%	0.397	<1%	1.841	<1%
	Replicates	10.940	>5%	18.228	>5%	0.077	<1%	0.282	>5%
	Within	13.666		10.449				0.120	

Generations	Items	NPdPP				PdWPP			
		Cross I		Cross II		Cross I		Cross II	
		MS	P	MS	P	MS	P	MS	P
P ₁	Replicates	0.341	>5%	0.341	>5%	0.351	>5%	0.351	>5%
	Within	12.138		12.138		1.412		1.412	
P ₂	Replicates	20.969	>5%	56.518	>5%	0.793	>5%	5.005	>5%
	Within	51.668		32.978		7.171		3.631	
F ₁	Reciprocals	115.080	>5%	22.161	>5%	14.004	>5%	1.677	>5%
	Replicates	176.465	<5%	21.015	>5%	11.610	>5%	4.185	>5%
	Within	46.418		40.102		5.827		5.552	
F ₂	Reciprocals	38.867	>5%	102.836	>5%	0.268	>5%	0.104	>5%
	Replicates	54.286	>5%	19.943	>5%	18.473	>5%	17.189	>5%
	Within	41.622		62.853		5.895		8.685	
B ₁	Types	69.376	<5%	68.045	<1%	25.156	<1%	51.905	<1%
	Replicates	44.490	>5%	47.682	<5%	13.107	>5%	7.913	<5%
	Within	23.393		13.720		5.403		2.713	
B ₂	Types	35.409	>5%	150.761	<1%	12.459	>5%	33.199	<1%
	Replicates	21.239	>5%	86.622	<1%	1.730	>5%	4.276	>5%
	Within	15.374		22.952		4.329		5.881	

Generations	Items	NSPP				SWPP			
		Cross I		Cross II		Cross I		Cross II	
		MS	P	MS	P	MS	P	MS	P
P ₁	Replicates	1189.388	<5%	1189.388	<5%	0.001	>5%	0.001	>5%
	Within	214.478		214.478		0.929		0.929	
P ₂	Replicates	985.837	>5%	4268.700	>5%	0.584	>5%	5.961	>5%
	Within	1296.285		1036.299		3.914		1.919	
F ₁	Reciprocals	691.971	>5%	326.161	>5%	4.294	>5%	1.002	>5%
	Replicates	1487.953	>5%	427.265	>5%	4.943	>5%	0.534	>5%
	Within	513.941		847.042		3.314		2.841	
F ₂	Reciprocals	5848.152	<5%	20.315	>5%	0.479	>5%	2.142	>5%
	Replicates	2225.847	>5%	608.298	>5%	17.807	<5%	9.191	>5%
	Within	1058.113		1040.498		3.852		4.879	
B ₁	Types	2284.254	<5%	1439.766	<1%	17.847	<1%	7.786	<1%
	Replicates	725.059	>5%	3441.349	<1%	8.192	>5%	5.556	<5%
	Within	609.002		309.288		3.553		1.791	
B ₂	Types	1522.153	<1%	2470.178	<1%	4.423	>5%	20.645	<1%
	Replicates	618.588	>5%	2348.897	<1%	1.682	>5%	1.659	>5%
	Within	365.860		503.577		3.163		3.703	

Table 2. Analysis of Mather's scaling test and test of potence for six agronomic characters in two crosses of blackgram

Characters	Parameters	Cross I		Cross II	
		Value±Se	Probability	Value±Se	Probability
SHW	A	1.344±2.145	0.20-0.10	1.263±1.234	0.30-0.20
	B	0.283±1.373	0.80-0.70	1.145±1.315	0.30-0.20
	C	0.820±4.16	0.50-0.40	2.163±2.365	0.05-0.01
	Potence	0.413	0.70-0.60	0.885	0.40-0.30
RW	A	1.301±0.128	0.20-0.10	1.487±0.143	0.20-0.10
	B	0.309±0.118	0.80-0.70	1.096±0.159	0.30-0.20
	C	1.398±0.217	0.20-0.10	2.269±0.259	0.05-0.01
	Potence	1.006	0.30-0.20	1.7111	0.10-0.05
NPdPP	A	0.839±1.912	0.50-0.40	1.215±1.771	0.30-0.20
	B	1.997±2.143	0.05-0.01	0.328±2.000	0.80-0.70
	C	0.681±3.808	0.50-0.40	2.776±3.939	P< 0.01
	Potence	0.402	0.70-0.60	2.033	0.05-0.01
PdWPP	A	1.491±0.776	0.20-0.10	2.895±0.698	P< 0.01
	B	0.437±0.868	0.70-0.60	1.385±0.819	0.20-0.10
	C	0.695±1.388	0.50-0.40	2.275±1.448	0.05-0.01
	Potence	0.342	0.80-0.70	0.463	0.70-0.60
NSPP	A	1.462±8.071	0.20-0.10	0.982±8.116	0.40-0.30
	B	1.804±9.482	0.10-0.05	0.665±9.906	0.60-0.50
	C	2.057±16.283	0.05-0.01	1.889±17.397	0.10-0.05
	Potence	1.766	0.10-0.05	0.996	0.30-0.20
SWPP	A	2.513±0.614	0.05-0.01	3.384±0.539	P< 0.01
	B	0.218±0.682	0.90-0.80	1.973±0.620	0.05-0.01
	C	0.893±1.076	0.30-0.20	3.123±1.067	P< 0.01
	Potence	0.789	0.50-0.40	1.928	0.10-0.05

Table 3. Analysis of joint scaling test for six agronomic characters in two crosses of blackgram

Characters	Joint scales	Cross I		Cross II	
		Value±Se	Probability	Value±Se	Probability
SHW	m	9.623±0.220		9.914±0.186	
	d	-0.789±0.360		-0.513±0.316	
	h				
	χ^2	7.044	0.20-0.10	11.134	0.05-0.01
RW	m	0.795±0.019		0.845±0.022	
	d	-0.017±0.036		-0.073±0.043	
	h				
	χ^2	2.859	0.70-0.50	5.737	0.30-0.20
NPdPP	m	10.733±0.278		11.057±0.587	
	d	-0.303±0.496		-1.150±0.502	
	h			1.003±1.187	
	χ^2	12.393	0.05-0.01	9.556	0.05-0.01
PdWPP	m	4.147±0.121		4.464±0.120	
	d	-0.509±0.202		-0.415±0.186	
	h				
	χ^2	4.678	0.50-0.30	21.039	P< 0.01
NSPP	m	49.041±1.324		52.703±1.348	
	d	-0.360±2.292		-4.200±2.287	
	h				
	χ^2	18.634	P< 0.01	11.008	0.05-0.01
SWPP	m	2.852±0.098		3.038±0.093	
	d	-0.386±0.162		-0.283±0.145	
	h				
	χ^2	7.935	0.10-0.05	23.034	P< 0.01

Table 4. Analysis of components of variations (D, H & E), dominance ratio ($\sqrt{H/D}$), heritability (h^2_n & h^2_b) and genetic advance ($GA_{(n)}$ & $GA_{(b)}$) for six agronomic characters in two crosses of blackgram

Parameters	SHW		RW		NPdPP	
	Cross I	Cross II	Cross I	Cross II	Cross I	Cross II
D	-0.1362	-0.0634	-0.0012	-0.0016	0.1120	0.7534
H	-0.5164	-1.1636	-0.0116	-0.0212	-4.5128	-3.9028
E	0.4178	0.4545	0.0047	0.0078	1.3948	1.0862
$\sqrt{H/D}$	1.9472	4.2840	9.8640	3.6180	-6.3477	-2.2760
h^2_n	-0.3087	-0.2400	-0.5090	-0.4820	0.1736	0.7730
h^2_b	-0.8939	-2.4460	-3.0170	-3.6370	-3.3236	-1.2290
$GA_{(n)}$	-0.2987	-0.1790	-0.0357	-0.0406	0.2030	1.1113
$GA_{(b)}$	-0.8649	-1.8290	-0.2113	-0.3060	-3.8880	-1.7669

Parameters	PdWPP		NSPP		SWPP	
	Cross I	Cross II	Cross I	Cross II	Cross I	Cross II
D	-0.1136	-0.0050	3.1960	5.7068	-0.0852	-0.0248
H	-0.3188	-0.2600	-75.9760	-85.1532	-0.1232	-0.0900
E	0.1822	0.1348	25.598	26.5008	0.1033	0.0727
$\sqrt{H/D}$	1.6750	7.2110	-4.8757	-3.8628	1.4460	1.9050
h^2_n	-1.2429	-0.0370	0.1948	0.3538	-1.4250	-0.3280
h^2_b	-2.9870	-1.0029	-2.1209	-2.2860	-2.4550	-0.9230
$GA_{(n)}$	-0.5474	-0.0198	1.1492	2.0690	-0.5080	-0.1314
$GA_{(b)}$	-1.3160	-0.5359	-12.5125	-13.3740	-0.8740	-0.3696

CONCLUSION

In this work of genetic study of yield and yield components of blackgram, additive-dominance relationship in different generations was found only in cross I for SHW, PdWPP and SWPP. The components of variation were mostly either low or negative but E was high and positive, which reflected in the estimation of heritability and genetic advance. These values were low and negative. All these might be due to high environmental variance influenced by unusual vegetative growth due to late sowing in mid of August. However, the cross I with characters PdWPP and SWPP may be considered for further breeding research with care for timely sowing. It may also be concluded that selection practices may be done with the characters, NPdPP and NSPP in cross II as they showed high to moderate positive narrow sense heritability and genetic advance.

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