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Gene effects of some agronomic traits through single cross analysis in blackgram (*Vigna mungo* L. Hepper)

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Abstract

A trait is control by one or more than one gene. Proper knowledge about gene effects of different traits is a must in fruitful breeding programme. As a biometrical tools generation mean analysis provides the estimates of main gene effects (additive and dominance) along with epistasis and helps in understanding the nature of gene effects involved in different trait concern. The present study revealed the adequacy of additive-dominance model for A, B and C for most of the traits in both of the crosses. It indicated that most of the traits under study governed by only additive and dominance genes. Potence was non-significant for different traits and crosses. The χ^2 value was significant for PHF, DT50%F and PHH in both of the crosses and for NL50%F in cross 1 which expressed the involvement of epitasis gene effects for these traits. Component of variation D and H for all the traits in both of the crosses exhibited positive to negative values. Negative sign was due to large sampling variation and genotype-environment interaction. In all cases low to complete dominance were found whereas, effective factors K was always less than 1.

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Introduction

Among pulses crop, blackgram is important crop in Bangladesh. It is a good 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). Being a short duration crop, it fits well in mixtures and crop rotation and it can beused as green manure crop or as a combined cash and soil improvement crop with residues incorporated into soil after pods have been harvested. It helps to enrich the soil by symbiotic relationship with specific soil rhizobia of the genus *Bradyrhizobium*. It also helps in soil conservation through thick canopy. The traits of blackgram and other crops are controlled by polygenic system in where both additive and non-additive gene actions and interactions are found to be operative. Genetic information on the inheritance of quantitative traits is inevitable for fruitful breeding programmes on any crop for its improvement. Quantitative traits need 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 traits. 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. As the yield of blackgram per acre is being low day by in bangladesh, necessary steps should be taken for the improvement of this crop in our country. Hence, the present study was done to see whether the traits under study were governed by only additive-dominance or not .

Materials and methods

Plant materials

Materials used in this study comprised three lines of blackgram namely EML 013, EH 6376, E 86309 with access number 5, 13 and 21 respectively, used as parents. Two single crosses [cross I (line-5×line-13) and cross II (line-5× line-21)] were made with reciprocals between the selected parents. The experiment was done in the research field of the department of Botany, University of Rajshahi containing a randomized complete block design with three blocks following individual plant randomization. Data were collected on individual plant basis for six quantitative traits viz., plant height at first flower (PHFF), number of secondary branches at first flower (NSBFF), days to 50% flower (DT50%), number of leaf 50% flower (NL50%F), leaf area 50% flower (LA50%F) and plant height at harvest (PHH) flowing C.G.S. system.

Statistical analysis

The analysis of variance (ANOVA) is done for testing the significant differences among the population. Variance analysis for the six generations *ie.* P_1, P_2, F_1, F_2, B_1 and B_2 was carried out separately for the six characters of two crosses in blackgram. Since P_1 and P_2 are different parents, in this way P_1, P_2, F_1, F_2, B_1 and B_2 constitute six generations. The variance due to different sources such a+s replicates, within, reciprocals and types were analyzed in the present study.

Mather's scaling test

The presence or absence of epistasis in studied characters was detected by using A, B and C scaling test as suggested by Mather (1949) and Hayman and Mather (1955) which is given below:

Scales

$$A = 2\overline{B}_1 - \overline{P}_1 - \overline{F}_1$$

$$B = 2\overline{B}_2 - \overline{P}_1 - \overline{F}_1$$

$$C = 4\overline{F}_2 - 2\overline{F}_1 - \overline{P}_1 - \overline{P}_2$$

Standard error of Scales

$$V_A = 4V(\overline{B}_1) + V(\overline{P}_1) + V(\overline{F}_1)$$

$$V_B = 4V(\overline{B}_2) + V(\overline{P}_2) + V(\overline{F}_1)$$

$$V_C = 16\,V(\overline{F}_2) + 4V(\overline{F}_1) + V(\overline{P}_1) + V(\overline{P}_2)$$

VP_1, VP_2, VF_1, VF_2, VB_1 and VB_2 are the variances of $\overline{P}_1$, $\overline{P}_2$, $\overline{F}_1$, $\overline{F}_2$, $\overline{B}_1$ and $\overline{B}_2$ populations, respectively. Significance of any of these scales indicated the presence of epistasis. When the scale is adequate, the values of A, B and C should be zero within the limits of their respective standard errors.

Potence:

Potence was done by comparing F_1 and F_2 means and is calculated by the following formula.

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

Potence was test by t-test. Non-significance of this test will indicate no difference between F_1 and F_2 and there will be no potence.

Joint scaling test

For testing the adequacy of additive-dominance model following weighted least square technique was done as proposed by Cavalli (1952). Here, 2-parameter model (m and d) is done with five generations when potence is non-significant whereas, 3-parameter (m, d and h) model is appropriate with significant potence values. The χ^2 test was employed to test the goodness of fit of observed generation means with expected means. If the χ^2 value is significant, it indicates that the additive-dominance model is inadequate and the estimates of the 2 and 3-parameter model are biased to an unknown extent by the effects not attributable to the additive and dominance actions of the genes.

Variance analysis, degree of dominance and number of effective factors

Heritable [additive (D)] and non-heritable [dominance (H) and Environment (E)] components of variance were estimated for each cross separately as per the formula suggested by Mather (1949) and are given below.

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

$V(B_1) + V(B_2) = ½ D + ½ H + 2 E$

$\{V(P_1) + V(P_2) + V(F_1)\} / 3 = E$

Where, $V(F_1)$ = Variance of F_1, $V(F_2)$ = Variance of F_2, $V(P_1)$ = Variance of P_1, $V(P_2)$ = Variance of P_2, $V(B_1)$ = Variance of B_1 and $V(B_2)$ = Variance of B_2.

The average degree of dominance over all loci was determined by the square root of the ratio between H and D (Mather, 1949). Here, D is the additive component of varianc and H is the dominance component of variance.

$$\text{Degree of dominance} = \sqrt{\frac{H}{D}}$$

The numbers of effective factors were estimated by the following formula (Mather, 1949). Where, D = Least square estimate of component of genetic variation.

$$K = \frac{\frac{1}{4}(\bar{P}_1 - \bar{P}_2)^2}{D}$$

Results and discussion

For successful breeding research in any crop, genetic information are of utmost importance regarding the nature, relative magnitude any types of gene action following proper genetic model. The quantitative characters controlled by polygenes, showed continuous variation which follow the normal distribution. It indicated that the biometircal techniques developed to study the quantitative characters would be suitable in the inheritance of the characters under study. In the analysis of variance replicates item for all the generations were found to be significant in most of the cases (Table 1) indicated that there was significant difference between the replications. The reciprocals item for F_1 and F_2 were also found to be non-significant in most of the cases. The types item for B_1 and B_2 were significant for all the traits. Significant types item indicated that the difference between the parents and maternal effects were present. Nahar *et al.* in blackgram (2010) got the same resutls. The result of Mather's scaling test (Table 2) indicated the adequacy of additive-dominance model for A, B and C for most of the traits in both the crosses. Samad *et al.* in blackgram (2009), Rahman and Saad in *Vigna sesquipedalis*, (2000) and Sharmila *et al.* (2007) in sesame observed the adequacy of additive-dominance model in most of the cases. Non-significant potence was found for different traits and crosses. Non-significant potence shows that dominance may be ambi-directional.

Table 1. Mean sum squares from ANOVA for six quantitative traits in two crosses of blackgram

Generations	**Items**	**PHFF**				**NSBFF**			
		Cross I		Cross II		Cross I		Cross II	
		MS	P	MS	P	MS	P	MS	P
P_1	Replicates	145.3	<5%	145.3	<5%	10.3	<5%	10.3	<5%
	Within	9.013		9.013		1.455		1.455	
P_2	Replicates	172.24	<5%	225.55	<5%	1.38	> 5%	0.01	NS
	Within	9.671		7.721		0.717		0.9004	
F_1	Reciprocals	-81.81	<5%	3.116	NS	39.53	<5%	2.29	> 5%
	Replicates	69.21	<1%	176.24	<5%	16.1	<1%	21.285	<1%
	Within	11.90		15.62		1.431		2.035	
F_2	Reciprocals	-0.717	NS	714.79	<5%	0.020	NS	0.05	NS
	Replicates	571.95	<5%	479.65	<5%	6.51	<1%	30.54	<1%
	Within	15.34		15.915		1.90		1.473	
B_1	Types	198.88	<5%	160.38	<5%	24.54	<5%	22.56	<5%
	Replicates	182.96	<1%	252.58	<5%	6.07	<1%	3.782	<1%
	Within	9.510		4.664		0.7476		0.425	
B_2	Types	139.4	<5%	3583.27	<5%	28.47	<5%	15.05	<5%
	Replicates	139.46	<5%	2835.21	<1%	2.61	<1%	0.867	<1%
	Within	9.78		3.53		0.5922		0.799	

Generations	Items	DT50%F				NL50%F			
		Cross I		Cross II		Cross I		Cross II	
		MS	P	MS	P	MS	P	MS	P
P_1	Replicates	36.95	>5%	36.95	>5%	238.35	<5%	4.973	NS
	Within	11.73		11.73		27.82		27.82	
P_2	Replicates	89.27	<5%	0.57	NS	258.84	<5%	24.85	NS
	Within	10.291		23.173		36.00		41.92	
F_1	Reciprocals	13.44	>5%	3.82	NS	96.01	>5%	40.90	NS
	Replicates	8.89	>1%	6.165	NS	293.38	<1%	43074	NS
	Within	5.785		7.134		38.08		48.61	
F_2	Reciprocals	61.45	>5%	16.71	>5%	69.71	>5%	366.45	<5%
	Replicates	171.33	<1%	89.88	<1%	295.44	>1%	45.50	NS
	Within	17.311		9.742		37.34		57.001	
B_1	Types	190.95	<5%	170.54	<5%	965.07	<5%	1209.16	<5%
	Replicates	19.175	<1%	25.09	>1%	236.21	<1%	165.19	<1%
	Within	4.468		8.457		19.804		19.24	
B_2	Types	170.54	<5%	233.55	<5%	1308.52	<5%	1878.38	<5%
	Replicates	25.092	<1%	94.12	<1%	145.24	<1%	250.70	<1%
	Within	8.328		12.464		20.73		31.88	

Generations	Items	LA50%F				PHH			
		Cross I		Cross II		Cross I		Cross II	
		MS	P	MS	P	MS	P	MS	P
P_1	Replicates	30.43	>5%	30.43	>5%	1863.35	<5%	1863.35	<5%
	Within	15.73		15.73		230.54		230.54	
P_2	Replicates	6.09	NS	148.64	<5%	84.0	NS	105.90	NS
	Within	11.470		23.696		202.86		160.97	
F_1	Reciprocals	6.62	NS	0.31	NS	98.20	NS	121.49	>5%
	Replicates	29.25	>1%	95.14	>1%	30.71	NS	195.94	>1%
	Within	9.565		12.561		165.67		63.93	
F_2	Reciprocals	4.21	NS	149.95	<5%	876.59	>5%	0.91	NS
	Replicates	21.265	NS	524.07	<1%	190.83	NS	502.7	>1%
	Within	27.39		23.127		262.68		222.48	
B_1	Types	343.06	<5%	414.64	<5%	3805.68	<5%	2723.0	<5%
	Replicates	105.27	<1%	84.96	<1%	61.79	NS	12.76	NS
	Within	9.160		19.417		66.33		85.70	
B_2	Types	397.89	<5%	349.21	<5%	782.01	<5%	1932.9	<5%
	Replicates	21.46	>1%	221.18	<1%	20.90	>1%	183.95	>1%
	Within	14.808		12.170		60.76		73.24	

Table 2. Scaling tests, potence, gene effects for six quantitative traits in two single crosses of blackgram

Traits	Crosses	Scales			Potence	2 and 3-parameter			
		A	B	C		m	[d]	[h]	χ^2
PHFF	Cross I	3.298^{**}	0.674^{NS}	1.024^{NS}	1.1^{NS}	34.41^{**}	0.61^{NS}	-	15.55^{**}
	Cross II	1.739^{NS}	1.73^{NS}	2.822^{NS}	1.45^{NS}	34.59^{**}	1.60^{**}	-	42.017^{**}
NSBFF	Cross I	$.6704^{NS}$	1.7916^{**}	0.333^{NS}	0.37^{NS}	4.26^{**}	0.13^{NS}	-	6.9708^{NS}
	Cross II	0.203^{NS}	1.331^{NS}	0.716^{NS}	-0.59^{*}	4.62^{**}	0.12^{NS}	-1^{**}	6.1014^{NS}
DT50%F	Cross I	0.552^{NS}	3.30^{**}	3.883^{**}	-1.87^{**}	44.65^{**}	1.68^{**}	0.62^{NS}	35.098^{**}
	Cross II	2.940^{**}	2.134^{NS}	0.152^{NS}	1.33^{**}	42.12^{**}	-0.63^{NS}	-1.56^{NS}	12.179^{**}
NL50%F	Cross I	0.685^{NS}	0.684^{NS}	0.409^{NS}	-0.12^{NS}	21.31^{**}	$2^{**}\pm$	-	11.72^{*}
	Cross II	1.003^{NS}	0.607^{NS}	0.740^{NS}	-0.06^{NS}	22.25^{**}	0.48^{NS}	-	4.568^{NS}
LA50%F	Cross I	1.259^{NS}	1.113^{NS}	2.818^{NS}	-1.25^{NS}	19.74^{**}	-0.25^{NS}	-	12.311^{*}
	Cross II	0.922^{NS}	1.275^{NS}	3.774^{NS}	-3.29^{**}	21.99^{**}	-0.73^{NS}	-1.38^{NS}	16.268^{**}
PHH	Cross I	1.527^{NS}	0.446^{NS}	1.721^{NS}	-5^{NS}	64.62^{**}	1.68^{NS}	-	6.878^{NS}
	Cross II	2.96^{NS}	3.451^{NS}	3.136^{NS}	5.51^{**}	64.95^{**}	4.15^{**}	4.85^{**}	7.291^{NS}

Cross I= line-5×line-13 and cross II= line-5× line-21. A, B and C Mather's scaling test and χ^2 joint scaling test. m= mean of the base population, d= additive gene effect and h= dominance gene effect. *, ** significant at P≤0.05 and P≤0.01, respectively.

Table 3. Components of variation (D, H and E), degree of dominance ($\sqrt{H/D}$) and effective factors (K) for six quantitative traits in two single crosses of blackgram.

Traits	Crosses	D	H	E	$\sqrt{H/D}$	K
PHFF	Cross I	-17.668	23.176	1.825	1.145317	-0.0327
	Cross II	-1.754	0.242	0.434	0.371444	-6E-05
NSBFF	Cross I	1.444	-0.952	0.129	0.81196	0.04328
	Cross II	1.447	0.17	0.0555	0.34276	0.00062
DT50%F	Cross I	-0.4	-0.226	0.341	0.751665	-0.3706
	Cross II	-1.528	-0.23	0.581	0.387974	-0.1873
NL50%F	Cross I	-4.384	0.204	-0.994	0.215715	-0.0101
	Cross II	-5.348	0.318	1.613	0.243847	-0.0099
LA50%F	Cross I	-2.293	-0.5734	0.488	0.500065	-0.0092
	Cross II	-1.82	-0.118	0.699	0.254628	-0.6409
PHH	Cross I	-64.74	44.38	8.07	0.827956	-0.0279
	Cross II	-22.176	2.354	6.206	0.325808	-0.084

Again, it was noted from table 2 that the χ^2 values were found to be non-significant for NSBFF, PHH in both of the crosses and NL 50%F in cross II. It indicated the presence of only additive dominance relationship for those traitss and crosses would likely help in doing successful breeding plan easily for the development of potential lines in blackgram. Deb and Khaleque (2009) in chickpea found similar result in some cases in chickpea. The χ^2 value was significant for PHF, DT50%F and PHH in both of the crosses and for NL50%F in cross 1, 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. Shoba *et al.* (2010) in groundnut, Kumar *et al.* (2011) in sweet sorghum and Ajay *et al.* (2012) in pigeonpea observed the same results. The estimates of D and H component were positive and negative in in this study (Table 3). These results corroborate with the findings of Samad *et al.* (2009) in blackgram. In all cases low to dominance were found whereas, effective factors K was always less than 1. It indicated that all traits under study governed by one group of gene. This results were supported by the findings of Deb and Khaleque (2009) in chickpea.

Conclusion

Scaling and joint scaling test have revealed that traits like NSBFF, PHH in both of the crosses and NL 50%F in cross II controled by only additive and dominance gene. So, these traits would likely help in doing fruitful breeding plan easily for the development of potential lines in blackgram.

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