GENETIC IMPLICATION OF YIELD AND ITS COMPONENTS IN MUNGBEAN *VIGNA RADIATA* (L.) WILCZEK

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Abstract

Gene action and genetic parameters for yield and its components were studied in an 8 parent diallel cross of mungbean. The estimates of components of genetic variation showed that additive genetic effects appeared to be important for pod length and 100 seed weight. The non-additive effects were more pronounced in the genetic control of pods per plant, seeds per pod and grain yield per plant. Directional dominance was observed for pods per plant, seeds per pod and grain yield per plant. The parental lines contained equal number of dominant and recessive genes for all the characters except 100 seed weight for which the genes were distributed asymmetrically among the parents. The graphic analysis revealed partial dominance for all the characters studied. Pod length and 100 seed weight being controlled by additive genetic effects with partial dominance will certainly provide the basis for selection in early segregating generations for improvement in these parameters.

Introduction

The breeding method to be adopted for improvement of a crop depends primarily on the nature of gene action involved in the expression of quantitative traits of economic importance. One of the several biometrical techniques available to plant breeders for evaluating and characterizing genetic variability existing in a crop species is diallel analysis. It is one of the techniques frequently employed to study the nature of genetic variation for particular plant traits and to select the potential parents which would produce the best recombination (Murty, 1975). The technique has been effectively used for such purpose in lentil (Tahir *et al*., 1995), mungbean (Khattak, *et al*., 2002), chickpea (Singh & Bains, 1982; Sarode *et al*., 2001) and cowpea (Sanghwan & Lodhi, 1999). Only a few reports are available on the mode of inheritance of yield and its components in mungbean. The present study is an attempt in this direction.

Materials and Methods

For the inheritance of quantitative characters which are complex in nature, 8x8 parent diallel was conducted. Eight genotypes (NM 20-21, NM 121-25, NM 51, VC 4982, VC 4152, VC 3902, VC 3301 and VC 1163) were crossed in a complete diallel fashion in green house during spring season of 2002. The seeds of 8x8 parent diallel (28 direct crosses and 28 indirect crosses) along with parental lines were planted in the field during July, 2003. The experiment was planted in a Randomised Complete Block Design with three replications at National Agricultural Research Centre, Islamabad. One row of each genotype was dibbled keeping 35 and 10 cm spacing between and within rows, respectively. Basal fertilizer dose @ 25 kg N+60 kg P_2O_5 per hectare was applied and during crop growth period agronomic practices were used as recommended for mungbean crop. Number of pods per plant and grain yield per plant (g) were recorded on 10 guarded

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plants selected randomly and then averaged to per plant basis. Pod length (cm) and seeds per pod were recorded on 10 pods selected at random within each genotype. The seed weight was recorded for each genotype after counting 100 seeds by seed counter and weighed in grams. Analysis of variance was conducted for each character using the average values following the method of Steel & Torrie (1980). Data pertaining to the parental lines, F_1s and reciprocals were also analyzed according to Hayman-Jinks methods (Hayman, 1954; Jinks, 1954) to detect non-allelic interactions by the graphic analysis.

Results and Discussion

Analysis of variance for parents and hybrids are presented in Table 1. Highly significant differences among the parents as well as hybrids were observed for all the traits. Hayman's analysis of variance of diallel tables was conducted for each character under study (Tables 2, 3 and 4) which showed that 'a' and 'b' items were significant for pod length, seeds per pod, 100 seed weight and grain yield per plant suggesting the role of both additive and dominance gene effects in the genetic control of these traits. The analysis of variance of F_1 data for pods per plant revealed non-significant 'a' item and significant 'b' item revealing the role of dominance effects of genes in the development of this trait (Table 2). The significance of 'b_1' item for pods per plant, seeds per pod and grain yield per plant indicated the presence of directional dominance effects. The non-significant 'b_2' item for pods per plant, pod length, seeds per pod and grain yield per plant showed equal distribution of dominant genes among the parents whereas the genes for 100 seed weight were distributed asymmetrically among the parents as 'b_2' item was found to be significant. The significant values of 'b_3' for pods per plant, pod length, seeds per pod, 100 seed weight and grain yield per plant revealed the presence of specific dominance gene action other than attributable to 'b_1' and 'b_2'. The significant 'c' and 'd' items showed the presence of maternal and reciprocal effects in the expression of pods per plant and grain yield per plant. Maternal effects were also present for pod length due to significant 'c' item whereas presence of reciprocal effects was shown by a significant 'd' item for seeds per pod. In case 'c' and 'd' items become significant, the mean squares of 'a' and 'b' items need to be retested against the mean squares of 'c' and 'd' items respectively as suggested by Mather & Jinks (1982). For pods per plant, 'a', 'b_1' and 'b_2' items, when retested against 'c' and 'd' mean squares, remained unchanged. However, significant 'b_3 and 'b' items changed to non-significant, indicating that the properties of dominance genes were masked by the genes with reciprocal effects. In grain yield per plant, significant 'a' item, when retested against 'c' mean square, it reduced to non-significant which revealed that maternal effects masked the additive genetic effects. The significant 'b_3' item also reduced to non-significant revealing the role of reciprocal effects. However, the significant 'b_1' and 'b' items did not alter and thus exhibited the importance of the genes having general dominance coupled with directional dominance. Since 'c' item was significant for pod length, 'a' item was retested against its mean square. After retesting, 'a' item remained unchanged indicating the preponderance of additive gene effects. The significant 'd' item for seeds per pod suggested the need of retesting of 'b' items against mean square of 'd' item. The level of significance of 'b_1' and 'b_2' items remained unchanged after retesting. The values of 'b_3' and 'b' which were previously significant against their own block interactions, reduced to non-significant suggesting that dominance gene effects were masked by the reciprocal gene effects in the inheritance of this trait.

Table 1. Analysis of variance for five characters in 8 parent diallel of mungbean.

Source of variation	Degree of Freedom	Pods per plant	Pod length	Seeds per pod	100 seed weight	Grain yield per plant
Genotypes	63	162.37**	2.08**	1.53**	3.41**	24.50**
Replications	2	495.22**	0.09	5.75**	0.06	53.11**
Error	191	43.42	0.26	0.67	0.44	5.43

Since Hayman's analysis of variance of diallel tables showed that the item (b) was significant for all the five characters under study, the variance (Vr) and covariance (Wr) analysis was further carried out for these traits.

Estimation of genetic parameters and Wr, Vr graphic analyses

Pods per plant: Dominance (H_1, H_2, h^2) genetic variances were found to play an important role in the expression of this character as indicated by the significance of non-additive components against insignificance of additive component (Table 5). A positive F value revealed that dominant alleles were more frequent than the recessive ones. As indicated by the ratio $H_2/4H_1$, positive and negative alleles were asymmetrical at loci showing dominance. The ratio h^2/H_2 indicated that probably three to four groups of genes controlled the character. Partial dominance was noted as the regression line of unit slope intersected the Wr-axis above the point of origin (Fig. 1). The distribution of array points showed the concentration of dominant genes in the parent "VC 3301" followed by "VC 4152", while "NM 51" contained the maximum number of recessive genes. The position of array points showed almost complete dispersion suggesting the greater genotypic variability of the parents.

Pod length: It is obvious from Table 5 that estimates of additive (D) and non-additive (H_1) genetic variances were significant indicating the involvement of both additive and dominance type of gene actions for this character. Higher value of D than H_1 revealed higher degree of additive gene action. Partial degree of dominance was observed by the ratio $(H_1/D)^{1/2}$. Asymmetrical gene distribution in the parents was apparent, as $H_2/4H_1$ ratio deviated from its expected value of 0.25. The ratio KD/KR suggested more dominant alleles in the parents for the trait. Higher narrow sense heritability indicated the greater importance of additive gene action. The results of graphic analysis (Fig. 2) suggested the existence of partial dominance. The position of the arrays on the graph indicated that the parent "NM 121-25" was close to origin having the most dominant genes for pod length, while the parental line "VC 4982" occupied a far position with most recessive genes.

Seeds per pod: Significance of dominance genetic variances (H_1, H_2, h^2) indicated the prevalence of non-additive gene action in the expression of this trait (Table 5). As the $H_2/4H_1$ did not deviate from its expected value of 0.25, the gene distribution was symmetrical. KD/KR revealed that dominant alleles were in excess in the parents which was also supported by the negative correlation between the parental performance and Wr+Vr statistics. The ratio h^2/H_2 indicated that probably three groups of genes exhibiting some degree of dominance controlled the character. The regression line intercepted the Wr-axis above the point of origin indicating the existence of partial dominance (Fig. 3). The position of the arrays on the graph showed that the parental genotypes "NM 121-25", "VC 3301" and "VC 1163" seemed to have the most dominant genes for seeds per pod, while the parent "VC 3902" had the most recessive genes.

Table 2. Hayman's analysis of variance for pods per plant and pod length in an 8x8 complete diallel of mungbean.

		Pods per plant			Retested against				Pod length			Retested against
Item	DF	SS	MS	F. ratio	c	d	Item	DF	SS	MS	F. ratio	c
a	7	865.20	123.60	2.41	0.56		a					10.15**
b_1	1	1436.73	1436.73	74.95*		15.07**	b_1	1	0.24	0.24	2.00	
b_2	7	781.46	111.64	2.57		1.17	b_2	7	3.00	0.43	1.43	
b_3	20	2718.27	135.91	3.25**		1.43	b_3	20	13.23	0.66	3.14**	
b	28	4936.46	176.30	4.26**		1.85	b	28	16.47	0.59	2.57**	
c	7	1551.27	221.61	4.45**			c	7	9.31	1.33	5.32**	
d	21	2002.35	95.35	2.38**			d	21	10.59	0.50	1.67	
t	63	9355.28	148.50	3.46**			t	63	130.87	2.08	8.00**	
a x B	14	717.22	51.23				a x B	14	3.66	0.26		
b_1 x B	2	38.34	19.17				b_1 x B	2	0.25	0.12		
b_2 x B	14	607.04	43.36				b_2 x B	14	4.22	0.30		
b_3 x B	40	1673.98	41.85				b_3 x B	40	8.56	0.21		
b x B	56	2319.36	41.42				b x B	56	13.03	0.23		
c x B	14	696.61	49.76				c x B	14	3.51	0.25		
d x B	42	1681.93	40.05				d x B	42	12.71	0.30		
Error	126	5415.11	42.98				Error	126	32.91	0.26		

**, * = Significant at 1% and 5% probability level, respectively.

Table 3. Hayman's analysis of variance for seeds per pod and 100 seed weight in an 8x8 complete diallel of mungbean.

Item	Seeds per pod				Retested against d	Item	100 seed weight			
	DF	SS	MS	F. ratio	d		DF	SS	MS	F. ratio
a	7	26.32	3.76	2.91*	8.34*	a	7	165.91	23.70	107.73**
b_1	1	9.67	9.67	35.81*	0.66	b_1	1	0.41	0.41	1.95
b_2	7	5.32	0.76	0.99	1.04	b_2	7	9.57	1.37	4.28**
b_3	20	24.24	1.21	1.95*	1.21	b_3	20	15.81	0.79	2.14*
b	28	39.23	1.40	2.19**		b	28	25.78	0.92	2.63**
c	7	6.36	0.91	1.47		c	7	1.03	0.15	0.34
d	21	24.31	1.16	2.23*		d	21	5.09	0.24	0.37
t	63	96.22	1.53	2.28**		t	63	197.80	3.14	7.14**
a x B	14	18.00	1.29			a x B	14	3.11	0.22	
b_1 x B	2	0.55	0.27			b_1 x B	2	0.41	0.21	
b_2 x B	14	10.77	0.77			b_2 x B	14	4.51	0.32	
b_3 x B	40	24.73	0.62			b_3 x B	40	14.89	0.37	
b x B	56	36.05	0.64			b x B	56	19.81	0.35	
c x B	14	8.71	0.62			c x B	14	6.15	0.44	
d x B	42	22.00	0.52			d x B	42	26.90	0.64	
Error	126	84.76	0.67			Error	126	55.97	0.44	

**, * = Significant at 1% and 5% probability level, respectively.

Table 4. Hayman's analysis of variance for grain yield per plant in an 8x8 complete diallel of mungbean.

Item	Df	SS	MS	F. ratio	Retested against	
					c	d
a	7	206.44	29.49	4.04*	1.01	
b_1	1	242.41	242.41	30.15*		21.55**
b_2	7	67.17	9.60	2.34		0.85
b_3	20	408.23	20.41	3.30**		1.81
b	28	717.82	25.64	4.47**		2.28*
c	7	205.31	29.33	4.48**		
d	21	236.25	11.25	2.85**		
t	63	1365.82	21.68	4.01**		
a x B	14	102.15	7.30			
b_1 x B	2	16.07	8.04			
b_2 x B	14	57.52	4.11			
b_3 x B	40	247.07	6.18			
b x B	56	320.66	5.73			
c x B	14	91.58	6.54			
d x B	42	165.67	3.94			
Error	126	680.06	5.40			

**, * = Significant at 1% and 5% probability level, respectively.

Table 5. Estimates of genetic components of variation and proportional values for yield and yield components in an 8x8 complete diallel of mungbean.

Components	Pods per plant	Pod length	Seeds per pod	100 seed weight	Grain yield per plant
D	- 0.186	1.103**	- 0.033	2.435**	- 0.330
	±13.240	±0.048	±0.108	±0.086	±0.935
F	9.130	0.042	- 0.281	0.729**	- 1.412
	±31.284	±0.114	±0.256	±0.203	±2.210
H_1	135.56**	0.262*	0.785**	0.554**	17.519**
	±30.436	±0.111	±0.249	±0.197	±2.150
H_2		0.220*	0.433*	0.322	9.996**
		±0.097	±0.216	±0.172	±1.871
h^2		- 0.002	1.301**	- 0.005	34.456**
		±0.065	±0.145	±0.115	±1.255
E	16.587**	0.086**	0.251**	0.146**	2.048**
	±4.413	±0.016	±0.036	±0.029	±0.312
$(H1/D)^{1/2}$	-	0.448	-	0.477	-
$H_2/4H_1$	0.101	0.210	0.249	-	0.234
KD/KR	0.834	1.082	1.744	1.914	1.836
r(Wr+Vr)Yr	- 0.328	0.149	- 0.855	0.341	- 0.086
r^2	0.108	0.022	0.732	0.116	0.007
h^2/H_2	3.741	-	3.007	-	3.447
Heritability (ns)	0.51	0.80	0.46	0.81	0.48

**, * = Significant at 1% and 5% probability level, respectively.
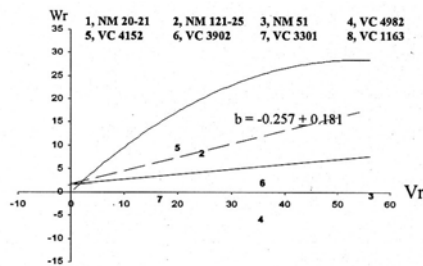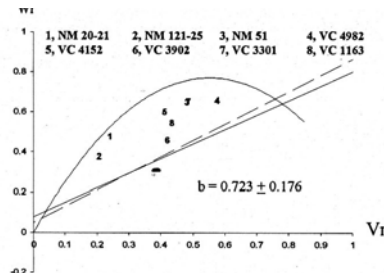
Fig. 1. Wr, Vr graph for pods per plant.
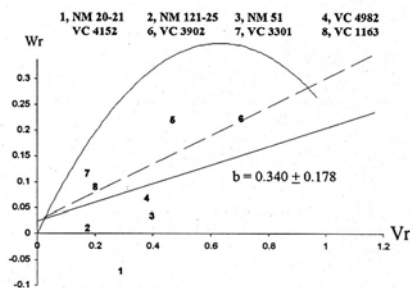

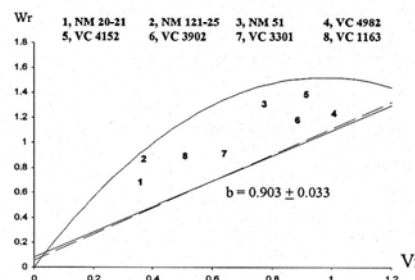Fig. 2. Wr, Vr graph for pod length.

Fig. 3. Wr, Vr graph for seeds per pod.

Fig. 4. Wr, Vr graph for 100-seed weight.
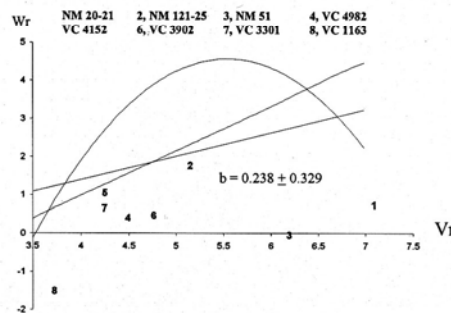

Fig. 5. Wr, Vr graph for grain per plant.

100 seed weight: The significance of components D and H_1 revealed the equal importance of additive as well as non-additive genetic variance, however higher magnitude of D than H_1 indicated more pronounced additive gene action for the trait (Table 5). F was positive and significant indicating an excess of dominant alleles. KD/KR also indicated that dominant alleles were in excess, however partial dominance was revealed on the basis of $(H_1/D)^{1/2}$. High magnitude of narrow sense heritability indicated the greater importance of additive gene action for this trait. The regression line of unit slope for 100-seed weight intersected the Wr-axis above the point of origin which revealed partial dominance for the trait (Fig. 4). The parent "NM 20-21" contained the most dominant genes, whereas "VC 4982" had the most recessive genes.

Grain yield per plant: Significant values of dominance genetic variances and insignificant value of additive component revealed that grain yield per plant was under the influence of dominant gene effects (Table 5). The proportion of genes with positive

and negative effects was close enough to 0.25 indicating symmetry at the loci showing dominance. Dominant alleles were in excess as indicated by the ratio KD/KR and supported by the negative correlation between the parental performance and Wr+Vr statistics. The ratio h^2/H_2 suggested that there might be three groups of genes controlling the character. The regression line cuts the Wr, Vr graph above the point of origin showing partial dominance for the trait (Fig. 5). The distribution of array points along and around the regression line for grain yield per plant indicated that the parents "VC 3301" and "VC 4152" had an excess of dominant genes, whereas "NM 20-21" being farthest from the origin was carrying maximum of recessive genes.

All the analytical techniques followed exhibited the prevalence of both additive and non-additive genetic effects in the inheritance of pod length and 100 seed weight, however additive variance was predominant for these traits. The estimates of components of genetic variance, in contrast to other analyses, depicted the predominant role of non-additive genetic effects together with non-significant additive variance for pods per plant, seeds per plant and grain yield per plant. Importance of additive as well as non-additive genetic effects have been reported in earlier findings in pulse crops (Joseph & Kumar, 2000; Ranwah & Sharma, 2000; Girase & Deshmukh, 2000; Khattak *et al*., 2002). The present study provided useful information by way of indicating the nature of inheritance of various characters. It was further possible to classify the parents on the basis of the type of alleles present in them and this provides useful clues for the selection of parental combinations which are likely to give better segregates.

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