

## Genetic analysis of quantitative traits in mungbean

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### ABSTRACT

The experiment comprising 28  $F_1$  and 8 parents was laid out in a randomized block design with three replications. Observations were recorded on days to flower and maturity, plant height, number of primary branches, number of pods per plant, number of grains per pod, pod length, 100-grain weight, yield per plant and protein content. Components of genetic variance were worked out through diallel cross analysis excluding reciprocals. Dominant alleles were more frequent for most of the traits. Positive and negative alleles among parents were distributed asymmetrically for all the characters; one or two major gene groups controlled the characters. Additive and non-additive gene actions were found important in the inheritance of most of the traits.

Key words: Diallel, Mungbean, Quantitative traits, *Vigna radiata*

Mungbean [*Vigna radiata* (L.) Wilczek] is an important pulse crop extensively grown in the country under varying climatic conditions. In mungbean, genetic enhancement was based on selection from locally adapted varieties. The world's annual pulse production must be increased with reference to increased population. Exploitation of hybrid vigour and selection of parents on the basis of their combining ability have opened a new avenue in crop improvement. Among various techniques developed, diallel analysis is a very convenient one for gathering information about the study of combining ability which helps in selection of parents for hybridization and ultimately the isolation and development of superior genotypes. The present study was undertaken to understand genetic architecture of yield and its components through diallel analysis.

### MATERIALS AND METHODS

A diallel set of crosses involving eight diverse cultivars of mungbean, namely K 851, PDM 54, PDM 139, NDM 5-3, K 146-1, GM 84-4, MH 85-61 and Pusa 9131 was used in this investigation. Eight parents and 28  $F_1$  were sown in a randomized block design with three replications at C. S. Azad University of Agriculture and Technology, Kanpur during summer 2000. Each entry comprised a single row of three m length, 40 cm apart with plant-to-plant distance of 10 cm. Observations were recorded on 10 metric traits (days to flower and maturity, plant height, number of primary branches, number of pods/plant, number of grains/ pod, pod length, 100-grain weight, grain yield/ plant and protein content) from five randomly taken plants for all the treatments in each

replication. The mean values were used for the analysis to determine genetic components of variation following Hayman (2).

### RESULTS AND DISCUSSION

Nonsignificant values of  $t^2$  for all the characters indicated validity of the hypotheses. Regression coefficient 'b' did not deviate significantly from unity for all the characters which indicated the importance of additive gene effects in the inheritance of the traits (Table 1).

Table 1. Values of b,  $S_b$ ,  $b-0/S_b$ ,  $b-1/S_b$  and  $t^2$ , for 10 characters in  $8 \times 8$  diallel cross of mungbean

Character	b	$S_b$	$(b-0)/S_b$	$(b-1)/S_b$	$t^2$
Days to flower	0.617	0.146	4.22**	-2.610*	2.803
Days to maturity	0.894	0.340	2.630*	-0.310	0.513
Plant height (cm)	0.347	0.212	1.640	-3.070*	2.053
Number of primary branches per plant	0.976	0.231	4.210**	-0.100	0.355
Number of pods per plant	0.415	0.179	2.820*	-3.260*	3.129
Number of grains per pod	0.381	0.301	1.270	-2.050	0.264
Pod length (cm)	0.693	0.344	2.010	-0.890	0.079
100-grain weight (g)	0.940	0.156	6.020**	-0.380	0.009
Grain yield per plant (g)	0.191	0.293	0.650	-2.750*	0.575
Protein content (%)	-0.540	0.347	-1.550	-4.430**	0.007

\*,\*\* Significant at 5 and 1 per cent levels

Estimates of all components of variation (D,  $H_1$ ,  $H_2$ ,  $F^1$ ,  $h^2$  and E) along with their standard error are presented in Table 2. Dominant components ( $H_1$  and  $H_2$ ) were highly significant for all the characters except plant height, number of grains/pod, grain yield/plant and protein content which showed non-significant response to additive (D) component of variance. The magnitude of  $H_1$  and  $H_2$  were found higher than the value of D for all the characters showing predominance of non-additive variance in the genetic control of these traits. Similarly, the magnitude of  $H_1$  was higher than  $H_2$  indicating unequal distribution of positive and negative genes for all the characters.

The proportion of genes with positive and negative effect in parents ( $H_2/4H_1$ ) was less than 0.25 for all the

Table 2. Estimates of variance components for 10 characters in 8-parent diallel cross in mungbean

Character	Genetic Parameters						Related Parameters				
	D	H <sub>1</sub>	H <sub>2</sub>	F	h <sup>2</sup>	E	(H <sub>1</sub> /D) <sup>0.5</sup>	H <sub>2</sub> /4H <sub>1</sub>	$\frac{[(4DH_1)^{0.5}+F]}{[(4DH_1)^{0.5}-F]}$	$\frac{h^2/H_2}{h^2/H_2}$	'r' between (Wr + Vr) and Vr
Days to flower	5.33**	14.58**	12.04**	5.14	-0.29	0.67	1.67	0.20	1.82	-0.02	0.75
	±1.13	±2.61	±2.27	±2.68	±1.52	±0.38					
Day to maturity	16.62**	38.53**	28.15**	19.50**	1.32	0.46	1.52	0.18	2.25	0.05	0.80
	±3.19	±7.34	±6.38	±7.54	±4.28	±1.06					
Plant height (cm)	2.80	10.03**	8.95**	1.13	7.39**	0.92	1.89	0.22	1.24	0.83	-0.32
	±1.98	±4.55	±3.96	±4.68	±2.66	±0.66					
Number of primary branches	0.14**	0.51**	0.47**	0.07	-0.05	0.14**	1.89	0.23	1.29	-0.10	-0.23
	±0.05	±0.11	±0.09	±0.11	±0.06	±0.02					
Number of pods per plant	54.69**	79.95**	61.18**	57.75**	137.10**	2.43	1.21	0.19	2.55	2.24	-0.77
	±6.94	±15.96	±13.89	±16.41	±9.31	±2.31					
Number of grains per pod	0.10	0.87	0.64**	0.24	0.06	0.16**	2.92	0.18	2.35	0.10	-0.33
	±0.09	±0.21	±0.18	±0.22	±0.12	±0.03					
Pod length (cm)	0.20**	0.34**	0.28**	0.17	0.12**	0.08**	1.29	0.20	1.92	0.45	0.13
	±0.04	±0.09	±0.08	±0.09	±0.05	±0.01					
100-grain weight (g)	0.28**	0.50**	0.30**	0.43**	0.16**	0.00	1.33	0.15	3.73	0.54	-0.90
	±0.03	±0.06	±0.05	±0.06	±0.04	±0.01					
Grain yield per plant (g)	0.55	11.28**	10.41**	0.35	40.76**	0.10	4.53	0.23	1.15	3.91	-0.54
	±0.50	±1.14	±0.99	±1.17	±0.66	±0.17					
Protein content (%)	4.39	26.57**	18.11**	10.38	10.94**	0.08	2.46	0.17	2.85	0.60	0.32
	±2.30	±5.30	±4.61	±5.44	±3.09	±0.77					

\*,\*\* Significant at 5 and 1 per cent levels

characters showing that the positive and negative alleles are unequally distributed in parents. The mean degree of dominance  $(H_1/D)^{0.5}$  values was found to be more than unity for all the characters indicating presence of overdominance. Similarly, the ratio of dominance and recessive genes  $[(4DH_1)^{0.5} + F] / [(4DH_1)^{0.5} - F]$  was more than unity for all the traits, showing that the dominance genes were more frequent than recessive ones. These findings were in accordance with Giriraj (1) and Pandey *et al.* (3).

The ratio  $h^2/H_2$  of gene groups was found less than unity for all the traits except for number of pods per plant and grain yield per plant. It indicated one major gene group governing the inheritance of these traits whereas number of pods per plant and grain yield per plant indicated the presence of more than one major gene groups.

The correlation coefficient (r) between parental order of dominance  $(Wr + Vr)$  and parental measurement  $(Vr)$  was negative for plant height, number of primary branches, number of pods/plant, number of grains per pod, 100-grain weight and grain yield per plant. It indicated that dominance alleles contributed positively for the expression of these traits. On

the other hand, days to flowering, days to maturity, pod length and protein content recorded positive 'r' values indicating their expression through recessive genes. Thimappa (4) also observed similar findings.

Considering these results, it may be concluded that characters under study are mostly governed by non-additive genetic variance. These characters may be improved through bi-parental mating followed by bulk pedigree method of selection.

#### LITERATURE CITED

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