Gene Action and Heritability Estimates of Some Quantitative Traits in Mung*

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ABSTRACT

The parents, F_1, F_2, F_3 and backcross generations of two crosses (1) T.44×Anand 101—4, and (2) T.44×Sonamung were studied to determine heritability values and gene actions controlling the traits (i) days to flower, (ii) plant height, (iii) number of branches, (iv) pods per plant, (v) pod length, (vi) seeds per pod, (vii) pod yield, (viii) grain yield and (ix) test weight of *mung*.

The findings revealed that all characters excepting number of branches and test weight were not much influenced by environmental factors. The narrow sense heritability estimates for days to flower, plant height, pod yield and grain yield were low. The *dd* gene action was involved to a considerable extent in the expression of all characters of both crosses excepting number of branches, pod length and test weight of cross 2, of which first two were greatly influenced by *d*; and *d*, *dd* and *aa* gene actions, respectively. The latter was influenced by all types of gene actions studied except *d*.

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INTRODUCTION

MUNG (*Phaseolus aureus* Roxb.) is an important pulse crop of India, Southeast Asia and Phillipines. All programmes for its improvement will have to be tailored according to the nature of gene actions involved in the expression of the characters in question. The available information indicates the occurrence of heterosis for pods per plant, pod length, seeds per pod and seed yield (Bhatnagar and Singh, 1964). Empig, Lantican and Escuro (1970) obtained high heritability estimate (broad sense) for days to flower; medium value for seed weight; and low estimates for plant height, pods per plant, seeds per pod and seed yield.

This study was undertaken to determine heritability values and the nature of gene actions involved in the expression of days to flower, plant height and yield contributing traits.

MATERIALS AND METHODS

The parents, F_1, F_2, F_3 and backcross generations of two crosses detailed below were used in this investigation.

Cross No.	Parentage
1	T. 44×Anand 101-4
2	T. 44×Sonamung

Following characters were studied on individual plant basis.

1. *Days to flower:* Days taken from seeding to initiation of first flowering.
2. *Plant height:* Height measured in cm from ground level to the tip of main stem at the time of pod ripening.
3. *Number of branches:* Primary branches

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per plant were counted; main stem was not taken into account.

4. *Pods per plant:* Dried pods of each plant were harvested three times at 10 days interval and the total pods were counted.
5. *Pod length:* Five randomly selected dried pods were measured to the accuracy of 0·1 cm and the average pod length was used for statistical purposes.
6. *Seeds per pod:* Five pods selected for pod length measurements were used. Seeds of individual pods were counted separately and the mean value was computed.
7. *Pod yield:* Dry pods harvested from each plant were weighed in gram (g).
8. *Grain yield:* Cleaned grains obtained from individual plants were weighed in g.
9. *Test weight:* 100 seeds selected at random per plant were weighed to the accuracy of 0·1 g.

The broad and narrow sense heritability estimates, and the nature of gene actions of individual traits were determined as outlined below:

Broad sense heritability (H):

This was estimated by using variances of the parents, F_1 and F_2 generations of cross Nos. 1 and 2. Ten plants of each parent, 12 plants of each F_1, and 385 and 317 plants of F_2 generations of cross Nos. 1 and 2, respectively, were used for this purpose. Heritability was calculated by using the formula:

$$H = \frac{V_{F_2} - \text{mean } V_{P_1P_2F_1}}{V_{F_2}}$$

where mean $V_{P_1P_2F_1}$ is the pooled mean variance of the parent-P_1, parent-P_2 and F_1 populations, and V_{F_2} is the variance of the F_2 population.

Narrow sense heritability (h^2):

The F_2 and F_3 generations were used for this purpose. Each F_3 progeny consisted of 20 to 24 plants. The F_3 progeny means were regressed on the phenotypic value of the corresponding F_2 parent to estimate narrow sense heritability. Since the F_2 and F_3 generations were grown in two different seasons, heritability values were calculated in standard units (Frey and Horner, 1957). This method has the virtue of removing the bias caused by expansion or contraction of the phenotypic scale of measurement due to change in environment. The heritability values were tested for homogeneity (Steel and Torrie, 1960) and pooled values were calculated for homogeneous estimates.

Estimation of gene action:

The mean (m) and the genetic parameters viz., additive (a), dominance (d), additive × additive (aa), additive × dominance (ad) and dominance × dominance (dd) were estimated by the procedure suggested by Gamble (1962). The experiment was carried out at the Institute of Agriculture, Anand; now, Anand Campus of the Gujarat Agricultural University. The parents, F_1, F_2 and backcross generations were studied during monsoon 1969, while the F_3 generation was studied during summer 1970. The

material was space planted at 60 cm interval in rows 90 cm apart.

RESULTS AND DISCUSSION

Heritability:

The estimates of *H* obtained for all characters under study for both the crosses were homogeneous and high except for the number of branches (0·57) and test weight (0·61) having moderate estimates (Table 1) suggesting that all characters studied excepting two mentioned above were not much influenced by environmental factors. The *H* estimates of days to flower and test weight are in agreement to those of

TABLE 1.

Broad and narrow sense heritability estimates of various characters.

Character	*Broad sense heritability@*			*Narrow sense heritability*		
	1	2	*Pooled*	1	2	*Pooled*
Days to flower	0·68**	0·71**	0·69**	0·17	0·46*	0·31*
Plant height	0·75**	0·74**	0·75**	0·02	0·39*	0·19
Number of branches	0·59**	0·54**	0·57**			
Pods per plant	0·82**	0·71**	0·78**			
Pod length	0·79**	0·67**	0·74**			
Seeds per pod	0·77**	0·80**	0·78**			
Pod yield	0·75**	0·71**	0·73**	—0·26	0·10	—0·10
Grain yield	0·73**	0·77**	0·75**	0·18	0·09	0·14
Test weight	0·55**	0·67**	0·61**			

@, 1 and 2 refer to cross numbers.
* and ** refer to the 5 and 1% levels of significance, respectively.

TABLE 2.

Estimates of genetic components of various characters based on mean values.

Character	*Cross No.*	*m*	*a*	*d*	*aa*	*ad*	*dd*
Days to flower	1	48·7	0·4	—1·6	— 2·4	3·9	—21·0
	2	54·8	19·2	—11·1	—14·4	11·8	22·0
Plant height	1	26·5	— 2·7	2·7	— 3·0	7·1	14·5
	2	29·9	11·8	— 7·8	— 8·4	— 4·0	41·4
Number of branches	1	3·4	0·9	0·1	— 0·6	1·0	5·4
	2	3·6	0·5	2·3	1·8	— 0·1	1·3
Pods per plant	1	44·3	11·2	—58·5	—70·8	16·2	238·8
	2	58·0	20·0	— 5·1	—40·0	25·0	200·0
Pod length	1	6·9	0·6	— 0·9	— 1·2	0·3	4·5
	2	7·5	0·1	1·0	0·6	0·1	— 0·9
Seeds per pod	1	10·8	1·2	— 3·6	— 4·0	1·1	11·5
	2	12·2	1·6	— 0·7	— 1·6	0·3	4·6
Pod yield	1	25·1	5·5	—37·5	—45·4	1·0	166·4
	2	34·0	6·0	—15·8	—33·2	14·6	129·0
Grain yield	1	14·8	3·7	—22·8	—22·7	4·5	101·5
	2	21·0	12·4	— 5·5	—21·6	9·7	80·5
Test weight	1	3·4	0·3	1·4	1·4	0·4	— 2·4
	2	3·5	0·6	0·0	— 0·4	— 0·2	0·4

Empig *et al.*, (1970), while the estimates of plant height, pods per plant, seeds per pod and grain yield are higher than those obtained by these workers.

The h^2 estimates (Table 1) for days to flower, plant height, pod yield and grain yield obtained from two populations were also homogeneous but low suggesting that the nonadditive variance was predominating for these characters in the two populations. These findings are supported by the estimates of gene action for these traits.

Estimates of gene effects:

Data presented in Table 2 reveal that the *dd* gene action was involved to a considerable extent in the expression of all characters in both crosses excepting number of branches, pod length and test weight of cross 2. The two crosses under study differed for the relative contributions of different types of gene actions in the expression of various characters under investigation. The number of pods per plant, seeds per pod, pod yield, grain yield and test weight of cross 1 were largely influenced by *dd* gene action. The *aa* and *d* gene actions also influenced these traits to some extent. The order of contribution of various gene actions in the expression of days to flower and plant height of cross 1 was *dd*, *ad*, *aa*, *d* and *a*. The number of branches of first cross was mainly influenced by *dd* gene action. The *ad*, *a* and *aa* gene action had very low effects, while the contribution of *d* gene action was negligible. The pod length of cross 1 was largely under the influence of *dd* gene action, the *aa*, *d* and *a* gene effects had low contributions.

The plant height and seeds per pod of cross 2 were largely influenced by *dd* gene action, the *a*, *aa* and *d* gene actions had low contributions. All types of gene actions were important in the expression of days to flower of cross 2, the *dd* gene action having more influence on this trait than the rest. The *d* had greater influence than *aa* and *dd* gene actions on the number of branches of cross 2. The contributions of *a* and *ad* types of gene actions were either very low or negligible. The number of pods per plant of cross 2 was mainly influenced by *dd* gene action, the *aa*, *ad* and *a* gene actions had low effects. The *d*, *dd* and *aa* gene effects were involved in the expression of pod length of cross 2. The pod and grain yields of this cross were primarily influenced by *dd*, the *aa* gene action had also influenced these traits to some extent. The test weight was influenced by all types of gene actions studied except *d*.

These findings suggest that the use of F_1 hybrids would be the best method to commercially exploit the presence of epistatic gene actions. Till it becomes feasible, the next alternative would be to conserve the frequency of desirable genes influencing yield contributing traits by following cyclic method of breeding.

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