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Genetic Basis of Synchrony in Pod Maturity in Mungbean (*Vigna radiata* (L.) Wilczek)

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ABSTRACT

The inheritance of early flowering, early pod maturity and synchrony in pod maturity was studied in six diverse mungbean genotypes through the diallel crossing design. The genotype NM 92 was the best general combiner for early flowering and early pod maturity, whereas accession ML-5 was the best general combiner for more synchrony in pod maturity. The best specific combination for early flowering and early pod maturity was NM 92 x NM 89 and for highest synchrony in pod maturity was NM 92 x ML-5. The days to first pod and 90% pod maturity, and degree of indetermination from first flower to 90% pod maturity (DDd_1) were controlled by both additive and dominance gene effects with predominant effect of additive component. Only additive and dominance gene effects controlled the days to first flower and degree of indetermination from first pod maturity to 90% pod maturity (DDd_2), respectively.

The high narrow and broad sense heritability for days to first flower, days to first pod maturity and 90% pod maturity revealed more proportion of their genetic variation due to additive gene effects. The selection for synchrony in pod maturity is suggested to be made in advanced generation due to the low narrow sense heritability for degree of indetermination from first flower to 90% pod maturity.

Key words: mungbean, synchrony, dominant, recessive, combining ability

INTRODUCTION

In mungbean flowering continues for long period of time in consecutive flushes. In rainy season, due to high humidity, the flowering once started goes right till harvesting and plants may flower even thereafter if left standing in the field (Tickoo *et al*., 1996). In spring/summer season the newly short stature and early maturing varieties can be manipulated to a great extent to have synchronous flowering and maturity by controlled irrigation, provided there are no rains. But seed yield of these new varieties in spring/summer season is low compared with those of kharif season because they developed pods only from a single flush. The variation in period from first flower initiation to 90% pod maturity in mungbean has been described as degree of indetermination of growth duration (Na Lampang *et al*., 1988). They reported correlation between post flowering increase in plant height and degree of indetermination of growth duration in the dry season, but were not apparent in the rainy season.

The genotypes with early and highest synchrony in pod maturity are not only essential for mungbean to survive as a main kharif pulse crop in Asian countries, but also would fill the gaps in the high input farming systems in fertile lands with

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available irrigation without competing directly with major crops like wheat, rice and cotton. The inheritance of synchrony in pod maturity would help to adopt suitable and efficient breeding methods to develop mungbean genotypes with uniform pod maturity. But no information is available regarding the genetic architecture of synchrony in mungbean. Thus in the present investigation the inheritance of synchrony in mungbean pod maturity has been studied in terms of the degree of indetermination of growth duration (DDd).

MATERIAL AND METHODS

Three local (NM 92, 6601 and NM 89) and three exotic (VC 1560D, VC 3902 A and ML-5) mungbean genotypes exhibiting wide range of variation were crossed among each other in a diallel fashion, excluding reciprocals, during kharif 1997. The parents and F_1s were sown in spring/summer 1998 in a randomized complete block design with three replications. The plot size of 0.6 m^2 (2 row of 1-m length) was assigned for each entry per replication. Ten plants of uniform size were randomly selected to record data for the following characters :

1. Days to first flower (D_1)
2. Days to first pod maturity (D_2)
3. Days to 90% pod maturity (D_3)
4. Degree of indetermination (DD) for pod maturity (DDd) was calculated as below :

i. DDd from first flower to 90% pod maturity (DDd_1) = $\frac{D_3 - D_1}{D_3} \times 100$

ii. DDd from first pod maturity to 90% pod maturity (DDd_2) = $\frac{D_3 - D_1}{D_3} \times 100$

The data collected were subjected to analysis of variance according to Steel and Torrie (1980). The combining ability analysis was carried out using Method II of Griffing (1956), i.e., including parents, and their F_1s.

To fulfil the assumptions of absence of epistasis, no multiple allelism and independent gene distribution, data were subjected to two tests (the uniformity of *Wr* and *Vr* test (t^2) and the analysis of regression coefficient test) as described by Singh and Chaudhary (1985). Failure of both the tests completely invalidates the additive-dominance model. However, if one of them fulfils the assumption, the additive-dominance model was considered partially adequate (Wilson *et al*., 1978; Azhar and McNeilly, 1988).

The genetic components of variance, i.e., additive variance (*D*), variance due to dominant effect of genes (H_1), variance due to dominant effect of genes correlated for gene distribution (H_2), relative frequency of dominant and recessive alleles (*F*), over-dominance effect of heterozygous loci (h^2), environmental variance (*E*), proportion of genes with positive and negative effects in the parents ($H_2/4H_1$), proportion of dominant and recessive genes in the parents (*KD/KR*) and heritability both in broad sense ($h^2 B$) and narrow sence ($h^2 N$) were calculated using the procedures given by Hayman (1954), and Mather and Jinks (1982).

RESULTS AND DISCUSSION

The analysis of variance for genotypic differences and combining ability for flowering, maturity and degree of indetermination for growth duration (DDd) is presented in Table 1. There was a significant genotypic variation for all the traits studied. The *GCA* and *SCA* mean squares revealed that the days to first pod maturity, days to 90% pod maturity and degree of indetermination from first flower to 90% pod maturity (DDd_1) were controlled both by additive and dominance gene effects whereas days to first flower and degree of indetermination from first pod maturity to 90% pod maturity (DDd_2) showed only additive and dominance gene action, respectively. The higher *GCA* variance for days to first flower, first pod maturity and 90% pod maturity

resulted in a high additive variance indicating the importance of additive genetic control for these traits, whereas the high SCA variance for DDd_1 and DDd_2 resulted in a high dominant variance indicating the preponderance of dominant genetic control for DDd_1 and DDd_2. The additive gene action for days to flowering in mungbean have also been reported by Malik and Singh (1983), Wilson *et al*. (1985), and Singh and Singh (1996). However, Rao *et al*. (1984) and Tiwari *et al*. (1993) have reported only additive and non-additive gene action, respectively, for 90% pod maturity in mungbean.

The early pods maturity and low degree of indetermination of pods maturity are of great significant in the sense that early mungbean genotypes with uniform pods maturity will help to grow mungbean as a catch crop in already available gaps without competing with major crops like cotton, wheat, and rice etc. With the objective of early pods maturity, the variety NM 92 was the best general combiner for days to first flower, first pod maturity and 90% pod maturity. The accession VC 1560D and genotype NM 89 were the best general combiner for DDd_1 and DDd_2 with maximum negative GCA value (Table 3). The best cross combination on the basis of *SCA* effects (Table 4) was NM 92 x NM 89 for days to first flower, days to first pod maturity and days to 90% pods maturity with higher negative *SCA* value. The best specific performance was indicated by the hybrids NM 92 x ML-5 and NM 92

Table 1 Analysis of variance for genotypic difference and combining ability of days to flower and maturity, and degree of indetermination of maturity (DDd).

Source	df	Mean squares				
		Days taken to			DDd	
		First flower	First pod maturity	90% pod maturity	DDd_1	DDd_2
Genotypes	20	54.30**	41.43**	69.06**	31.73**	10.59**
Blocks	2	2.54	7.73	1.30	2.87	6.29
GCA	5	196.25**	134.02**	199.25**	55.22**	6.90
SCA	15	6.99	10.57**	25.56**	23.90**	11.82**
Error	40	6.48	5.24	6.10	5.11	3.01

** = Significant at 0.01 level

Table 2 Estimates of variance components for combining abilities of days to flower and maturity, and degree of indetermination of maturity (DDd).

Characters	s^2g	s^2s	s^2e	s^2A	s^2D
Days to first flower	47.32	0.51	6.48	94.63	0.51
Days to first pod maturity	30.86	5.33	5.24	61.72	5.33
Days to 90% pods maturity	43.50	19.46	6.10	86.99	19.46
DDd_1	7.83	18.79	5.11	15.66	18.79
DDd_2	-1.23	8.82	3.01	-2.46	8.82

Table 3 General combining ability effects of days to flower and maturity, and degree of indetermination of maturity (DDd).

Genotype	Days taken to			DDd	
	First flower	First pod maturity	90% pods maturity	DDd_1	DDd_2
NM 92	-5.58	-4.51	-4.58	2.85	0.05
6601	-0.25	-0.77	-2.61	-0.06	-0.14
NM 89	1.04	1.37	1.15	0.24	-0.79
VC 1560D	2.36	1.39	1.97	-1.32	-0.05
VC 3902A	1.07	1.38	1.65	-1.07	0.04
ML-5	1.37	1.14	2.42	-0.64	0.89
SE (g_i)	0.47	0.43	0.46	0.42	0.32
SE (g_i-g_j)	0.73	0.66	0.71	0.62	0.50

Table 4 Specific combining ability effects of days to flower and maturity, and degree of indetermination of maturity (DDd).

F_1cross combination	Days taken to			DDd	
	First flower	First pod maturity	90% pods maturity	DDd_1	DDd_2
NM 92 x 6601	0.51	2.11	0.88	2.50	-3.47
NM 92 x NM 89	-3.78	-2.89	-2.22	3.60	1.92
NM 92 x VC 1560D	2.04	0.76	-0.97	-2.54	-2.69
NM 92 x VC 3902A	-1.61	-0.96	-2.11	2.38	-0.54
NM 92 x ML-5	0.89	1.94	5.92	-5.92	4.37
6601 x NM 89	0.09	0.71	2.55	0.25	-0.76
6601 x VC 1560D	-0.30	1.88	4.20	-1.39	0.63
6601 x VC 3902A	0.66	-1.64	0.72	-2.44	0.98
6601 x ML-5	-1.17	-2.34	1.02	1.99	2.26
NM 89 x VC 1560D	-0.52	-0.52	-1.37	-0.49	-0.28
NM 89 x VC 3902A	0.24	0.16	-0.31	0.59	-0.43
NM 89 x ML-5	0.80	1.66	0.25	0.16	-1.38
VC 1560D x VC 3902A	-1.95	-0.46	-0.46	3.72	0.26
VC 1560D x ML-5	-0.52	2.77	2.30	3.96	-0.46
VC 3902A x ML-5	1.04	-0.48	-1.98	-0.26	-1.48
SE (S_{ij})	1.30	1.17	1.26	1.16	0.89
SE (S_{ij}-S_{ik})	1.94	1.75	1.89	1.73	1.32
SE (S_{ij}-S_{kl})	1.80	1.62	1.75	1.60	1.23

x 6601 for DDd_1 and DDd_2, respectively with higher negative *SCA* value. The cross NM 92 x ML-5 may be used directly for exploitation of its heterosis to get desirable segregates with more synchrony in maturity from first flower to 90% pod maturity.

The test of adequacy of additive-dominance model (Table 5) showed that days to first flower, days to 90% pod maturity, DDd_1 and DDd_2 were partially adequate while days to first pod maturity was adequate for additive dominance model through both tests.

The genetic components of variation (Table 6) revealed that both additive (*D*) and dominance (*H*) effects were significant for days to first pod maturity, days to 90% pod maturity and DDd_1 whereas only additive and dominance effects were significant for days to first flower and DDd_2, respectively. Estimates of H_1 and H_2 were unequal for days to first pod and 90% pod maturity indicating unequal distribution of positive and negative alleles among the parents. The ratios of $H_2/4H_1$ (0.182 and 0.171 for days to first pod and 90% pod maturity, respectively) also indicated the unequal distribution of positive and negative alleles among the parents. The H_1 and H_2 values were about equal for days to first flower, DDd_1 and DDd_2 showing equal distribution of positive and negative alleles among the parents for these traits. This was also confirmed by the ratios of $H_2/4H_1$ (0.277, 0.244 and 0.230, for days to first flower,DDd_1 and DDd_2, respectively), which were close to 0.25 (the $H_2/4H_1$ ratio where dominant and recessive alleles of a character equal

Table 5 Test of adequacy of additive-dominance model for days to flower and maturity, and degree of indetermination of maturity (DDd).

Traits	Uniformity of *W*r and *V*r	Regression analysis		Remarks
	(t^2)	b=0	b=1	
Days to first flower	*	NS	*	Uniformity of *W*r and *V*r invalidated the model but regression analysis suggested the model was adequate, thus it was considered that partially adequate.
Days to first pod maturity	NS	*	NS	Both tests suggested the adequacy of the model.
Days to 90% pod maturity	NS	NS	NS	Uniformity of *W*r and *V*r indicated the adequacy of the model but regression analysis invalidated the model, thus it was considered partially adequate.
DDd1	NS	NS	*	Uniformity of *W*r and *V*r indicated the adequacy of the model but regression analysis in validated the model, thus it was considered partially adequate.
DDd2	NS	NS	NS	Uniformity of *W*r and *V*r indicated the adequacy of the model but regression analysis invalidated the model, thus it was considered partially adequate.

* = Significant at 0.05 level NS = Non-significant

Table 6 The components of variation for days to flower and maturity, and degree of indetermination for maturity (Ddd).

Parameters and ratios	Days taken to			DDd	
	First flower	First pod maturity	90% pod maturity	DDd_1	DDd_2
D	28.491*	22.995*	43.554	11.386*	2.445
H_1	4.011	9.543*	32.962*	27.205*	13.704*
H_2	4.438	6.944*	22.538*	26.559*	12.691
F	-4.569	5.437	22.498*	4.426	-0.832
H^2	1.061	-0.433	9.821	4.622	-0.430
E	2.096*	1.786	1.958	1.669	1.055
$H_2/4H_1$	0.277	0.182	0.171	0.244	0.232
KD/KR	0.648	1.449	1.844	1.288	0.866
Heritability (*ns*)	0.836	0.741	0.675	0.314	0.069
Heritability (*bs*)	0.863	0.873	0.926	0.867	0.229

* = Significant at 0.05 level

distributed among parents). The negative and non-significant *F* component for days to first flower and DDd_1 signified the importance of dominant genes. The non-significance of h^2 component for these five traits indicated the absence of overall dominance effect due to heterozygous loci. The environmental (*E*) effect was significant only for days to first flower. Average degree of dominance showed over-dominance for DDd_1 and DDd_2 while partial dominance for days to first flower, days to first pod maturity and days to 90% pod maturity. High broad sense and narrow sense heritability estimates were found for days to first flower, days to first pod and 90% pod maturity. This indicated that an greater proportion of genetic variation was of additive nature. Poehlman (1991) has also reported high broad sense heritability for days to flowering and maturity in mungbean. The DDd_1 showed high broad sense heritability but very low narrow sense heritability, whereas DDd_2 showed very low estimates for both narrow-and broad-sense heritabilities. The low heritability estimates of DDd_1 and DDd_2 indicate the low success in selection for uniform pods maturing mungbean genotypes. To our knowledge, the inheritance of synchrony in pods maturity is the first ever report in mungbean.

The present study suggests multiple crossing to develop early flowering and pods maturing genotypes in mungbean. The segregates with synchrony in maturity may be selected in advanced generations.

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