

Inheritance pattern of degree of indetermination in mungbean [*Vigna radiata* (L.) wilczek]

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Abstract

A complete diallel mating system involving eight divergent parents was used to work out the inheritance basis of degree of indetermination and its related parameters like plant height at flowering and maturity in mungbean. Eight parents, viz. 562-1, 56-2, NM-95, NM-92, L.No.1, L. No.21, 6601 and E32-1 were selected from 55 genotypes on the basis of variability for days to flowering and grain yield per plant. Briefly explain how study was conducted. Genotypic differences for male and female parents were significant for all the characters. The results (formal ANOVA and components of variation) advocated the importance of both additive (A) and dominance (D) effects for the all the traits in both generations. However, the value $H_1 > D$ for plant height at flowering in F_2 , plant height at maturity in F_1 and degree of indetermination in F_1 generation revealed the preponderance of dominant genes while $D > H_1$ demonstrated additive nature of height at flowering in F_1 , plant height at maturity in F_2 generation. Low to moderate estimates of narrow sense heritability indicated occurrence of dominance effects for all the characters. This study suggested the utilization of heterosis breeding for the improvement of indetermination in mungbean due to the involvement of dominance effects in its genetic control.

Keywords: Mungbean, inheritance pattern, maturity, degree of indetermination.

Abbreviations: DDh_degree of indetermination based on plant height, a_additive, b_ over all dominance effects, c_maternal effects, and d_reciprocal affects, b1_directional dominance effects, b2_ effects due to parents contributing varying degree of dominant alleles, b3_specific gene interaction, D_ estimate of additive effects, H1 and H2_variation due to dominance effects of genes, F_estimate of the relative frequency of dominant to recessive alleles in the parental lines, F_positive when-ever the dominant alleles are more frequent than the recessive alleles, h2_ direction of dominance, (H1/D) 0.5_mean degree of dominance, H2/4H1_ proportion of genes with positive and negative effects in the parents, [(4DH1)0.5+F]/[(4DH1)0.5-F]_ proportion of dominant and recessive genes in the parents.

Introduction

Mungbean (*Vigna radiata* (L.) Wilczek) has indeterminate growth habit with lengthy flowering period in consecutive flushes (Tah, 2009). This type of growth habit in grain legumes is a function of natural selection because in rainy season, due to high humidity, the flowering once continued goes right till harvesting and plants may flower even thereafter if left standing in the field (Tickoo et al., 1996). However, in spring/summer mungbean produces flowers in one flush. In summer season the newly developed dwarf and early varieties could be manipulated to a great extent to have synchronous flowering and maturity by controlled irrigation with no rainfall (Khattak et al., 2001b, c, 2002a, b). This result in lower grain yields of these new varieties in spring/summer as compared with those of kharif season because they developed pods only from a single flush.

In the past, several scientists concluded that synchronous pod maturity had positive effect on grain yield (Afzal et al., 2003; Pierre et al., 2003; Hamid et al., 2004; Chen et al., 2008). Synchronous conversion of vegetative phase into reproductive one and the time of pod maturation are important factors leading to synchronous pod maturity (Corbesier et al., 2003). Similarly, patchy pod maturity and

maturity leads to stumpy yield potential and low harvesting index in mungbean (Egli and Bruening 2002; Tah, 2009). These factors might be the function of variation in the degree of indetermination of growth duration (Khattak et al., 2001a; Khattak et al., 2004). The variability in time period from first flower opening to 90% pod maturity in mungbean has been expressed as degree of indetermination (DDd) of growth duration (Na Lampang et al., 1988). Breeding mungbean cultivars with determinate growth habit with synchronous pod maturity is critical for mungbean to survive as a kharif main pulse crop in Pakistan. Moreover, development of determinate varieties could help mungbean to be established as the key pulse crop in Asian countries in high fertile lands without competing directly with major crops.

The assessment of inheritance pattern of degree of indetermination and its related traits would lead the mungbean breeders to determine and adopt appropriate and proficient breeding techniques for the development of mungbean genotypes with uniform pod maturity. Up to the date very little information is available on the subject of the genetic architecture of degree of indetermination and its

Table 1. Number of days taken to maturity and grain yield per plant of mungbean accessions evaluated during spring (2005).

Sr. No	Lines/varieties	Days to maturity	Grain yield per plant (g)	Sr. #	Lines/varieties	Days to maturity	Grain yield per plant (g)
1	NM-51	72.00	5.54	29	97012	80.33	10.05
2	NM-54	79.33	5.99	30	97015	79.70	3.76
3	NM-89	80.00	4.41	31	97016	77.66	10.00
4	NM-92	63.00	9.77	32	97018	80.33	10.63
5	NM-95	70.33	3.29	33	97019	76.67	7.80
6	NM-98	75.66	10.83	34	98008	80.00	7.41
7	AUM-9	76.00	3.53	35	L. No. 1	75.33	7.40
8	AUM-13	75.66	7.22	36	L. No. 2	78.33	10.01
9	AUM-18	77.00	5.61	37	L. No. 9	80.00	9.22
10	AUM-19	78.66	4.20	38	L. No. 21	78.00	11.48
11	AUM-27	78.66	4.11	39	L. No. 23	69.00	6.38
12	AUM-28	79.00	7.22	40	L. No. 25	72.33	7.57
13	AUM-29	78.33	4.40	41	L. No. 32	74.33	8.13
14	AUM-31	77.33	5.27	42	L. No. 71	74.66	7.51
15	AUM-38	78.00	8.41	43	L. No. 74	72.33	7.90
16	6375	76.00	4.41	44	L. No. 103	72.66	8.53
17	56-2	88.33	6.33	45	L. No. 113	74.66	9.07
18	562-1	91.00	9.21	46	L. No. 122	74.66	8.72
19	96002	77.00	11.70	47	L. No. 158	74.66	7.61
20	96005	76.67	9.93	48	E22-2	69.00	7.71
21	96008	79.00	10.32	49	E32-1	75.00	9.87
22	96010	76.00	8.39	50	E44-2	77.00	8.10
23	96011	76.00	10.39	51	E101-1	75.33	8.03
24	96012	78.66	10.72	52	E195-1	75.33	8.45
25	96014	78.00	8.51	53	RC-68	73.00	8.85
26	97006	80.33	9.52	54	M20-21	70.33	5.54
27	97008	76.33	10.65	55	6601	82.00	5.28
28	970011	76.66	7.89				

related characters like plant height at flowering and maturity in mungbean. However, in past some scientists conducted experiments to work out genetic basis of degree of indetermination. The involvement of non-allelic interaction along with additive and dominance gene effects in the inheritance of plant height and indetermination in mungbean have been reported earlier by some workers (Singh & Singh, 1996; Ram, 1997; Khattak et al., 2001 a and c). The objective of this experiment was to investigate the inheritance of synchrony in mungbean pod maturity in terms of the degree of indetermination of plant height (DDh).

Results

Assessment of germplasm and selection of the parents

Fifty five genotypes of mungbean (Table 1) were evaluated for range of variability regarding days taken to maturity and yield per plant subsequently to earmark parents for hybridization. Analysis of variance showed significant diversity ($P < 0.01$) among the genotypes for both maturity duration and grain yield per plant with mean squares of 3041.48 and 14.71 respectively. For reliable selection scatter diagram was plotted by taking grain yield per plant along X-axis and days to maturity along Y-axis (Figure 1) (Rehman et al., 2009, 2010). It was observed that for maturity duration most of the genotypes scattered in the region belonging 70 to 80 days. However, for yield per plant the genotypes covered wider area i.e. from 4 to 11 g region. A horizontal line drawn from the point representing population mean for maturity duration (76.55

days) on Y axis and a vertical line drawn from the point of mean grain yield per plant (7.79g) on the X axis has divided the scatter diagram field in to four regions viz. a region representing early maturity low yield, a region for early maturity high yield, a region for late maturity high yield and a region for late maturity low yield combination. Twelve lines were positioned in early maturity low yield region, fifteen appeared to be in early maturity high yield region, sixteen were related to late maturity high yield group and twelve showed their relationship with late maturity low yield group. Eight lines/varieties viz. 562-1, 56-2, NM-95, NM-92, L. No. 1, L. No. 21, 6601 and E 32-1 i.e., two from each combination of grain yield and maturity duration were selected for use as parents in the hybridization program (Table 2).

Preliminary analysis of variance and adequacy tests for additive-dominance model

The analysis of variance (Table 3) showed highly significant differences for female and male parents and their interaction in F_1 and F_2 generations for the degree of indetermination and its related traits. Reciprocal effects were significant for both the generations.

Before performing genetic analysis (Hayman-Jinks approach), the adequacy of data to additive dominance model was tested through two tests i.e. joint regression analysis and analysis of variance for $Wr+Vr$ and $Wr-Vr$. The regression line deviated significantly from zero but not from unity in F_1 as well as in F_2 generation for plant height at flowering and plant height at maturity but for degree of indetermination only in F_1 generation (Table 4).

Table 2. Days taken to maturity and grain yield per plant recorded for the selected genotypes during spring-2005.

Sr. No.	Genotypes	Days to maturity	Grain yield per plant (g)
1	562-1	91.00a	9.21b
2	56-2	88.33b	6.33cd
3	NM-95	70.33d	3.29e
4	NM-92	63.00e	9.77b
5	L. No. 1	75.33c	7.40c
6	L. No. 21	78.00bc	11.48a
7	6601	82.00b	5.28d
8	E 32-1	75.00c	9.87b

Indicate by which multiple-comparison test and what p-level.

Table 3. Analysis of variance for 8× 8 diallel set of crosses in mungbean.

Characters	Height at flowering		Height at maturity		Degree of indetermination	
	F1	F2	F1	F2	F1	F2
Blocks	35.17ns	2.63ns	167.13**	559.68**	93.01*	560.70*
Female (F)	214.48**	140.79**	367.87**	261.06**	108.60**	108.52**
Male (M)	254.69**	358.73**	1319.53**	346.02**	129.94**	472.83**
FxM	90.67**	102.58*	541.59**	239.11**	110.19**	363.70**
Error	18.17	27.90	37.44	77.86	26.01	117.71
Total						
Reciprocal	42.70**	83.89**	486.89**	174.04**	40.34**	294.70**

However, opposite results were revealed in case of degree of indetermination in F₂ generation where regression line deviated significantly from unity but not from zero. Similarly, the values of Wr+Vr varied significantly from array to array which may be due to the involvement of dominance but the values of Wr-Vr did not change significantly from array to array in both F₁ and F₂ generations for plant height at flowering and plant height at maturity (Table 4). The data for plant height at flowering and plant height at maturity qualified both the tests, revealing its full adequacy for additive dominance model. Hence, further analysis was processed. On the other hand the analysis of variance of Wr and Vr for degree of indetermination showed that for F₁ as well as F₂ generations, values of Wr+Vr were constant (Table 4) from array to array but Wr-Vr values varied. The F₁ and F₂ data failed to qualify this test. Thus the data for F₁ were found partially adequate for further analysis as it qualified regression analysis test. But the data for F₂ generation were failed to qualify both the tests and hence were not subjected to further genetic analysis.

Formal analysis of variance and estimation of components of variation

Formal analysis of variance (Mather and Jinks, 1982) partitioned the genetic variance in to additive (a), overall dominance (b), reciprocal effects (c) and reciprocal effects other than c i.e. (d). Overall dominance (b) was further subdivided into directional dominance (b₁), asymmetrical gene distribution (b₂) and specific gene interaction (b₃). Before testing the significance of these mean squares against their own block interaction or pooled block interaction, Bartlett's test (Bartlett, 1937) was applied to see the homogeneity of means squares for individual block interaction (Table 5). For plant height at flowering in F₁, these error variances were homogenous as calculated chi square value ($\chi^2 = 11.83$) is less than tabulated value ($\chi^2=12.59$) and thus item mean squares were tested against pooled block interaction while for F₂ error variances were not homogenous ($\chi^2=14.31$) thus items were tested against their own block interactions.

Application of Bartlett's test for plant height at maturity ($\chi^2=24.06$) indicated that error mean squares for each item in F₁ were not homogenous over replications. Therefore each item was tested against its own block interaction for F₁ generation. In F₂ generation, for plant height at maturity, error variances were found homogenous after the application of Bartlett's test ($\chi^2 = 10.20$). Thus, each item was tested against pooled block interaction. Formal analysis of variance for the degree of indetermination in F₁ generation showed that all the error variances were heterogeneous when Bartlett's test was applied ($\chi^2=17.33$). Thus all the items were tested against their own block interaction.

For F₁ and F₂ generations the items a and b were significant (Table 5). Among components of b, b₁ was non-significant for plant height at flowering and at maturity; however b₁ for degree of indetermination in F₁ generation was significant. On the other hand b₂ and b₃ were significant for each generation for all the traits except for plant height at maturity in F₂ generation. Reciprocal effects c and d were also significant for both the generations for plant height at flowering as well as at maturity which necessitated the retesting of a against c; b and its components against d. This reduced the significance of all these components to non-significant level in each generation. However, testing against their individual block interaction was valid and therefore further analysis was proceeded with. For degree of indetermination, item c was non-significant showing absence of reciprocal effects. Reciprocal effects other than maternal effects (d) were significant. Hence b and its components were retested against d which reduced them to non-significant.

Components of variation (Table 6) revealed that additive component (D) and components due to dominance effects (H₁ and H₂) were significant all the characters in F₁ and F₂ generations. The value of H₂ was greater than H₁ for most of the parameters and value H₂/4H₁ was less than its minimum value (0.25) in case of each generation. The degree of dominance (H₁/D)^{0.5} for F₁ was almost one for plant height at flowering in F₂ generation, whereas its value was less than one for plant

Table 4. Adequacy tests for assessment of the data of degree of indetermination and its related traits in mungbean for additive-dominance model.

Characters	Height at flowering		Height at maturity		Degree of indetermination	
	F1	F2	F1	F2	F1	F2
Adequacy tests						
Joint regression coefficient (b)	1.10±0.23	0.86±0.18	0.93±0.16	0.85±0.31	1.201±0.49	0.24±0.26
t test for b=0	4.684*	4.78*	5.58*	2.72*	2.45*	0.92 ^{NS}
t test for b=1	-0.43 ^{NS}	0.73 ^{NS}	0.41 ^{NS}	0.44 ^{NS}	-0.41 ^{NS}	2.82*
Mean squares for Wr+Vr (between arrays)	Significant	Significant	Significant	Significant	Significant	Significant
Mean squares for Wr-Vr (between arrays)	Non-significant	Non-significant	Non-significant	Non-significant	Significant	Significant
Adequacy to AD-model	Full	Full	Full	Full	Partial	Inadequate

height at flowering in F₁ and plant height at maturity in F₂ generation. The component F was positive and significant for all the traits in both the generations. Similarly proportion of dominant to recessive genes in the parents $[(4DH_1)^{0.5}+F]/[(4DH_1)^{0.5}-F]$ was over unity for F₁ and F₂ generations for all the characters. The net dominance, h² was significant in both the generations for degree of indetermination and both of its related parameters. Environmental component of variation (E) was non-significant for plant height at flowering and degree of indetermination, whereas it was significant for F₁ but non-significant for F₂ generation for plant height at maturity. Heritability in narrow sense was low to moderate in both the generations for all the traits, however, plant height at flowering in F₁ and plant height at maturity in F₂ generation exhibited relatively high heritability in narrow sense.

Discussion

Considerable efforts have been made to improve the genetic architecture of mungbean plant, which resulted in the development of some improved mungbean cultivars with some desirable traits like early and uniform maturity, bold seed size and determinate growth habit but there is disagreement between researchers regarding the superiority of such cultivars against ancient late maturing, indeterminate types. Exploitation of genetic variability in the germplasm of any crop species is considered to be the key point for making further genetic improvement in yield as well as other economically important traits. In mungbean a large amount of genetic variability has been reported (Tickoo et al., 1988 and Sinha et al., 1996), which indicates the potential for genetic improvement. To tailor a plant genotype with desirable combination of traits, detailed information on the genetic mechanism controlling various characters is considered a pre-requisite to launch a breeding program.

For the initiation of such program, suitable parents (viz. 562-1, 56-2, NM-95, NM-92, L. No. 1, L. No. 21, 6601 and E 32-1) exhibiting maximum range of variability were selected for hybridization program from the available germplasm comprising 55 genotypes particularly for maturity duration and grain yield. The parents NM-95, NM-92, L. No. 1 and E 32-1 were early maturing genotypes while the remaining parents exhibited high number of days to maturity (Rehman et al., 2009, 2010). The crossing of this set of genotypes in all possible combinations resulted in maximum range of variability for maturity in mungbean. Genetic variability have been

reported by Byregowda et al. (1997), Chakraborty and Haque (1999) for grain yield while Tickoo et al. (1988) mentioned the presence of considerable variability for maturity duration and grain yield in mungbean. Full diallel mating system (Hayman, 1954a, b) was utilized to create and estimate the heritable variation among the parents and their crosses in which female and male parent's showed significant differences revealing additive gene action however, significant interaction indicated the involvement of non-additive genetic components involved in the genetics of degree of indetermination in mungbean. Significant reciprocal effects for both generations revealed the importance of cytoplasmic inheritance for the trait (Mather and Jinks, 1982).

Adequacy tests demonstrated no involvement of epistasis for plant height at flowering and at maturity in both the generations. On the other hand, significant mean squares between arrays for Wr + Vr as well as within arrays for degree of indetermination in F₁ generation suggested some dominance effects. Significance of mean squares at both the levels also revealed epistatic effects gripping the inheritance of this parameter. In F₂ generation coefficient of regression (b) did not depart significantly from zero but from unity, which indicated non-additive variation included epistasis or multiple allelism. Bartlett's test (Bartlett, 1937) displayed non-significant χ^2 values for plant height at flowering in F₁ and in F₂ generation, for plant height at maturity, suggested homogeneity in the error variances. However, in F₂ generation for plant height at flowering and in F₁ for plant height at maturity, error variances were not homogenous revealing the absence of non-allelic gene interaction for plant height at maturity. Similarly, for the degree of indetermination in F₁ generation showed that all the error variances were heterogeneous suggesting the lack of non-allelic interaction in the inheritance of this character.

The significance 'a' and 'b' components in the formal ANOVA revealed the importance of both additive and dominance effects for the all the traits in both generations. Plant height at flowering and at maturity demonstrated that dominance was ambidirectional as the value of b₁ was non-significant; however that of degree of indetermination in F₁ generation exposed directional dominance for this character. Similarly, significance of b₂ and b₃ for each generation for most of the traits exhibited asymmetrical distribution of dominant genes among the parents and importance of specific gene interactions. Significance of c and d for plant height at flowering and plant height at maturity advocated the presence of some maternal effects in their inheritance while absence of maternal effects was

Table 5. Formal analysis of variance for degree of indetermination and its related traits for 8×8 diallel cross in mungbean.

Item	Df	Height at flowering		Height at maturity		Degree of
		F1	F2	F1	F2	indetermination
a	7	257.06*	269.24*	1318.76*	344.24*	166.62*
b ₁	1	56.57ns	3.24ns	2.99ns	8.64ns	101.69*
b ₂	7	188.62*	183.90*	312.27*	186.16ns	129.34*
b ₃	20	75.42*	90.40*	595.46*	274.46*	60.26*
b	28	103.05*	110.66*	503.50*	242.89*	79.01*
c	7	128.69*	140.02*	713.14*	101.28*	67.41ns
d	21	105.80*	121.88*	477.54*	287.91*	165.85*
a × blocks	14	-	20.94	24.80	-	18.04
b ₁ × blocks	2	-	15.99	13.55	-	5.26
b ₂ × blocks	14	-	30.28	8.09	-	15.11
b ₃ × blocks	40	-	29.55	34.45	-	26.71
b × blocks	56	-	29.25	27.11	-	23.05
c × blocks	14	-	41.80	64.61	-	35.87
d × blocks	42	-	23.77	46.36	-	28.35
Block interaction	63	-	27.89	74.88	-	51.38

clear due to non-significance of c item. Significance of both D and H₁ & H₂ revealed the involvement of both additive and dominance effects controlling the inheritance plant height at flowering and plant height at maturity. But the value of H₁ was greater than additive component (D) for plant height at flowering in F₂, plant height at maturity in F₁ and degree of indetermination in F₁ generation which revealed the predominance of dominant genes while greater magnitude of additive component demonstrated additive nature of genes with incomplete dominance in the control of height at flowering in F₁ and plant height at maturity in F₂ generation. The degree of dominance (H₁/D)^{0.5} was in the range of additive gene action with partial dominance for plant height at flowering in F₁ while for plant height at maturity in F₂ generation. However, its values demonstrated complete dominance for plant height at flowering in F₂ generation. Over dominance was displayed by (H₁/D)^{0.5} value for plant height at maturity and degree of indetermination in F₁ generation. Naidu and Satyanarayana (1993) reported non-additive gene action for plant height at maturity. Joseph and Santhoshkumar (2000b) reported the presence of both additive and dominance gene effects and Loganathan et al. (2000) revealed the presence of over dominance type of gene action and preponderance of dominant genes for plant height at maturity in mungbean. The predominance of non-additive gene action has also been reported by Seenaiah et al. (1993) in urdbean and Dijee et al. (2000) in cowpea. The prevalence of non-additive gene effects for plant height has been reported by Loganathan (2000). Khattak et al. (2001c) reported that days to 90% maturity and the degree of indetermination were controlled both by additive and dominance gene effects with additive ones as major effects. Khattak et al. (2002a) reported the preponderance of additive genetic components for plant height at flowering and at 90% pod maturity in kharif season. Epistatic effects were found to be considerable for degree of indetermination and plant height at different growth stages during spring season (Khattak et al., 2002a). Khattak et al. (2004) working on generation mean analysis found that both additive (d) and dominant (h) gene effects were important in the inheritance of degree of indetermination. However, Tah (2009) concluded that only additive and dominance gene action was involved for days to first flower and degree of indetermination from first pod

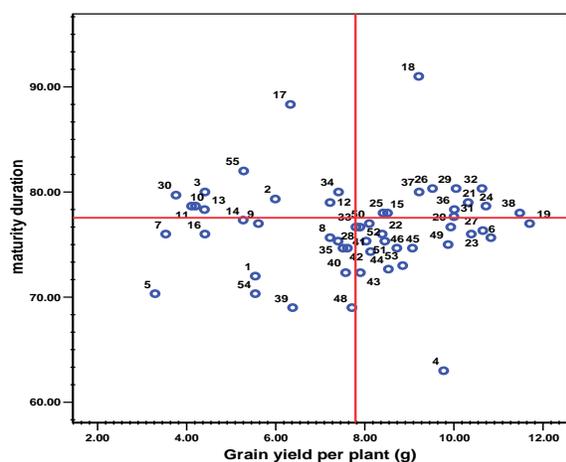
maturity to 90% pod maturity, respectively. Jana (1975) reported that gene action deviates with experimental material and environmental conditions under which the experiment was conducted. Khattak et al. (2002a, b) reported seasonal effects on gene action in mungbean.

The H₂ > H₁ for most of the parameters and value H₂/4H₁ > 0.25 indicated unequal frequencies negative versus positive alleles at loci showing dominance in the parents. Moreover, its value less than 0.25 indicated that the additive components did not contain all the dominance effects in all the traits. The significance for the component h² for all the characters in each generation confirmed that dominance was unidirectional. The positive and significant value of 'F' showed that dominant genes were more frequent in the parents than the recessives and this was strongly supported by the values [(4DH₁)^{0.5}+F]/[(4DH₁)^{0.5}-F] which also revealed high proportion of dominant to recessive genes in the parents. Environmental component (E) suggested that some blocking effects were prominent for plant height at maturity in F₁ generation.

Low to moderate estimates of narrow sense heritability indicated prevalence of dominance effects as compared to additive ones for plant height at flowering in F₂, plant height at maturity and degree of indetermination in F₁ generation. This suggested the utilization of over-dominance in heterosis breeding for improvement of these parameters. Plant height at maturity in F₂ generation exhibited relatively higher narrow sense heritability which suggested the hold of additive effects with partial dominance and this was soundly supported by the significant values of both additive and dominance components, degree of dominance and frequencies negative versus positive alleles at loci showing dominance in the parents. This advocated the use of simple selection procedure for the genetic improvement of these parameters in these generations. Dobhal and Rana (1997) also reported low heritability for plant height at maturity in mungbean, while Sinha et al. (1996), Tiwari et al. (1996) and Islam et al. (1999) demonstrated opposite conclusion. Khattak et al. (2001c) and Tah, (2009) reported low narrow sense heritability for degree of indetermination from first flower to 90% pod maturity.

Table 6. Components of variation involving 8×8 diallel cross for degree of indetermination and its related traits.

Components of variation	Height at flowering		Height at maturity		Degree of indetermination
	F ₁	F ₂	F ₁	F ₂	F ₁
E	4.062 ± 1.398*	4.220 ± 0.958*	13.155 ± 8.219	28.670 ± 7.055*	9.019 ± 4.66
D	46.255 ± 4.175*	22.230 ± 2.862*	288.631 ± 24.549*	273.946 ± 20.924*	93.779 ± 13.94*
F	50.438 ± 9.911*	26.344 ± 6.792*	535.811 ± 58.267*	259.847 ± 49.662*	123.109 ± 33.095*
H ₁	38.175 ± 9.642*	23.341 ± 6.608*	773.479 ± 56.687*	245.989 ± 48.315*	134.590 ± 32.197*
H ₂	23.776 ± 8.389*	13.999 ± 5.749*	443.661 ± 49.319*	117.742 ± 42.035*	91.303 ± 28.012*
h ²	7.222 ± 5.612	6.964 ± 3.846	128.221 ± 32.994*	-10.61 ± 28.121	1.218 ± 18.740
(H ₁ /D) ^{0.5}	0.908	1.02	1.63	0.94	1.19
H ₂ /4H ₁	0.15	0.14	0.14	0.12	0.16
(4DH ₁) ^{0.5} +F/(4DH ₁) ^{0.5} -F	4.00	3.74	3.61	3.00	3.42
h ² (n. s)	0.33	0.25	0.24	0.47	0.17

**Fig 1.** Scatter plot diagram for the assessment of diversity in 55 mungbean genotypes based on grain yield per plant and maturity duration.

Materials and Methods

Assessment of the germplasm accessions for genetic diversity

The research work presented in this manuscript was conducted in the experimental area of the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad during the year 2005 and 2006.

Fifty five diverse mungbean lines developed by the University of Agriculture, Faisalabad; Pulses Research Institute, Faisalabad and Nuclear Institute for Agriculture and Biology, Faisalabad were planted in the field during spring 2005. The experiment was planted in a triplicate randomized complete block design. Inter and intra row distance was maintained as 30 and 10 cm, respectively. Each genotype comprised a single row of 3m length thus accommodating 31 plants. At maturity, data regarding days taken to maturity and grain yield per plant were recorded. Days taken to maturity were counted from sowing to maturation of 90% pods in each entry. Data for grain yield per plant were recorded from 10 equally competent guarded plants in each entry. The data were

analyzed using MSTAT-C (version 1.3) computer programme. Eight genotypes exhibiting a range of variability for maturity duration and grain yield per plant were selected for hybridization.

Hybridization and evaluation of crosses

Eight lines/varieties viz. 562-1, 56-2, NM-95, NM-92, L.No.1, L. No.21, 6601 and E32-1 were sown during July, 2005 (kharif season) in the field and all possible crosses, including reciprocals were made. Sixty four entries (56 F₁'s and 8 parents) were planted in the field during March 2006 (spring season). The experiment was conducted using a randomized complete block design with three replications. Row to row and plant to plant spacing was kept 30 cm and 10 cm, respectively. Seeds were dibbled at the rate of two seeds per hole, which were later thinned to single healthy seedling per hole after germination. Each treatment comprised single row of 2.5 m length with 26 plants. Twenty equally competent guarded plants were selected for data recording.

The seed obtained from the F₁ plants was used to grow the F₂ generation during kharif 2006 in a randomized complete block design replicated thrice. The plot size was 5 x 1.2 m thus accommodating 204 plants per cross. Crop was raised following standard agronomic practices in each season. All the cultural operations including hoeing, weeding, irrigation, fertilizer etc were carried out identically to reduce experimental error. Observations were recorded from all the plants by leaving one plant on each side of the row. The data regarding the following parameters from F₁ and F₂ generations on individual plant basis were recorded for different morphological traits.

Measurements of morphological traits

Height of the plants was recorded in cm from base of the plant to the top 50% flowering and 90% pods maturity. Variation in growth habit i.e., determinate vs indeterminate was described as degree of indetermination (DDh) and quantified its relationship by the ratio of plant height increase after flowering (H₂-H₁) to the plant height at maturity (Na Lampang et al., 1988).

$$DDh = [(H_2 - H_1) / H_2] \times 100$$

Where, H_1 is height at 50% flowering and H_2 is height at 90% pod maturity.

Statistical analysis

The data were analyzed by standard analysis of variance (Steel et al., 1997). The diallel technique used here in this experiment was developed by Hayman (1954a,b) and Jinks (1954,1955,1956). Mather and Jinks (1971, 1977 and 1982) suggested some improvement for the genetic analysis of undefined diallel cross experiment. The assumptions of the model such as independent action of non-allelic genes, no multiple allelism and independent distribution of genes were tested by subjecting the data to two scaling tests. The first test was carried out by joint regression analysis of variance (Vr) and covariance (Wr) according to Mather and Jinks (1982). The regression coefficient (b) must deviate significantly from zero but not from unity, if all the assumptions underlying the genetic model were met. The second test for the adequacy of the model was made by conducting analysis of variance for (Wr+Vr) and (Wr-Vr). In the presence of dominance, Wr+Vr may change from array to array and if there is absence of non-allelic interactions Wr-Vr will not vary between arrays, if an additive-dominance model with independent gene distribution is adequate.

The characters qualifying both the tests were fully adequate for additive dominance model and those qualifying only one test were considered partially adequate (Azhar and McNeilly, 1988; Ali et al., 2008; Ali et al., 2009, Ali and Awan, 2009). The characters showing full or partial adequacy were subjected to diallel analysis with the following distinct steps.

Formal analysis of variance

The data were subjected to formal analysis of variance according to Mather and Jinks (1982). This partitioned the family means in to additive (a), dominance (b), maternal (c) and reciprocal affects (d). The b item is further partitioned in to directional dominance effects (b_1), effects due to parents contributing varying degree of dominant alleles i.e. asymmetrical gene distribution among the parents (b_2) and specific gene interaction (b_3) i.e. specific combining ability. Mather and Jinks (1982) further elaborated this method and demonstrated the testing of a, b, c and d items against their individual interaction with the blocks. However, if error variances are homogenous they may be pooled to give block interaction mean square as a common error variance. Homogeneity was tested by Bartlett's test (Bartlett, 1937). If items c and d are significant, they become appropriate error for the a and b mean squares, respectively and therefore must be tested against their error variances i.e., against items c and d.

Estimation of genetic components of variation

The variance of the components of each array (Vr), the covariance of all off- spring included in each parental array with the non-recurrent parents (W_r) and variance of the parental means ($V_0L_0 = V_p$) were computed. In addition, the means of array variances (V_1L_1), the variance of mean of arrays (V_0L_1) and the means of array

covariances (W_0L_0) were calculated. These statistics were used for the estimation of genetic components of variation. D, F, H_1 , H_2 h^2 . The statistic D, is an estimate of additive effects; H_1 and H_2 , variation due to dominance effects of genes, F provides an estimate of the relative frequency of dominant to recessive alleles in the parental lines and the variation in dominance over loci. Hence F will be positive when-ever the dominant alleles are more frequent than the recessive alleles, irrespective of the fact that dominant alleles have decreasing or increasing effects. Statistic h^2 (F_1 mean-parental mean) provides direction of dominance i.e. positive sign shows increasing gene's dominance at most of loci and negative sign shows decreasing gene's dominance. These components are used to compute further information as $(H_1/D)^{0.5}$, mean degree of dominance; $H_2/4H_1$, proportion of genes with positive and negative effects in the parents and $[(4DH1)^{0.5}+F]/[(4DH1)^{0.5}-F]$ provides the proportion of dominant and recessive genes in the parents. Narrow sense heritability and broad sense heritability are also based on these parameters that reflect the amount of additive and total genetic variation in parents. All these components were calculated following Mather and Jinks (1982) and Singh and Chowdhary (1985). In F_2 generation these formulae have been modified as proposed by Verhalen and Murray (1969) and Verhalen et al. (1971). Heritabilities were rated as low, medium and high following Stansfield (1986).

Conclusion

The germplasm revealed significant magnitude of diversity for selection of different parents for hybridization program. The inheritance of degree of indetermination was controlled by over-dominant genes with some proportion of additive effects. This advocated that utilization of heterosis might be helpful for selecting desirable plant type with maximum degree of indetermination which obviously will lead to the synchronous maturity in mungbean. This in turn would direct the breeder to understand the genetic control of synchronous maturity which is of utmost importance as whole crop will be ready and mechanical harvesting will be possible.

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