Genetic studies of yield related traits in mungbean (*Vigna radiata* L. Wilczek)

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Abstract

A full diallel mating system involving eight divergent parents selected from a germplasm pool of 55 mungbean genotypes was used to determine the inheritance of yield related traits such as grain yield per plant, total dry matter, and harvest index. All traits displayed significant (P<0.01) genotypic differences. Adequacy tests founded on joint regression analysis and analysis of variance for Wr+Vr and Wr-Vr between arrays revealed the full fitness of the data and absence of epistatic effects for grain yield in F_1 and total dry matter for both generations. The data for grain yield in F_2 and harvest index in both generations were partially adequate for genetic analysis due to the presence of non-allelic interactions. The significance of 'a' & 'b', D, H_1 and H_2 components demonstrated the importance of both additive and dominance effects for all traits in both generations. However, the value $H_1 > D$ for grain yield in F_1 and harvest index in F_2 generation depicted the preponderance of dominant genes in their genetic control which, thus it was recommended that selection followed by hybridization in early generations was a suitable breeding method for progress in these traits. Conversely, greater value of D over H_1 demonstrated additive nature of genes for grain yield in F_2, harvest index in F_1 and total dry matter in both generations, which advocated the utilization of pedigree and full/half sib selection for improvement of these parameters. Grain yield in F_1 and harvest index in F_2 generation exhibited moderate narrow sense heritability, while grain yield in F_2, harvest index in F_1 and total dry matter in both generations had higher heritability (h^2 n. s. >0.60).

Key words: *Vigna radiata* L. Wilczek; inheritance mode; grain yield; harvest index

Introduction

Vigna, a pantropical genus, comprises about 150 species, most of which are found in Asia and Africa. Only seven species of *Vigna* are cultivated as pulse crops, of which two are of African and five have Asiatic origin. The African group constitutes cowpea (*V. unguiculata*) and Bambara groundnut (*V. subterranea*); the Asiatic group consists of mungbean/ greengram (*V. radiata*), blackgram/ urdbean (*V. mungo*), moth bean (*V. aconitifolia*), adzuki bean (*V. angularis*), and rice bean (*V. umbellata*). The *Vigna*, species are adapted to a range of agroclimatic conditions and their growth on marginal lands without supplementing nitrogen is particularly an added advantage for subsistence agriculture. Mungbean (*Vigna radiata* (L.) Wilczek)

is an ancient and well-known crop in Asia, particularly in the Indian subcontinent, and is now becoming popular in other continents. It is an excellent source of easily digestible protein, which causes low flatulence, and complements the staple rice/ wheat diet in Asia. Mungbean is consumed as split (dhal), bean sprouts, noodles, green beans and boiled dry beans. In Pakistan, mungbean is grown on about 247.4 thousand ha with an annual production of about 177.7 thousand tones (Anonymous, 2007-08) but the average yield is very low that is largely due to poor genetic make up of mungbean cultivars. Since it is a short duration legume, it fits well in to many cropping systems under rainfed and irrigated conditions and increases small farmer's income and

improves soil condition. In Pakistan, mungbean production has increased tremendously from 31.80 thousand tones in 1980-81 to 177.7 thousand tones in 2007-08. This increase in total production is attributed to increase in area under mungbean production that expanded from 67.0 to 247.4 thousand ha, whereas, the average yield remained more or less static (Anonymous, 2007-08). In contrast, the average yield of other major pulse crops of the country has significantly increased, which is mainly due to the genetic improvement in the yield potential of these species. Considerable efforts have been made to improve the genetic architecture of mungbean plant, which resulted in the development of some improved mungbean cultivars with desirable yield related traits like total dry matter and harvest index. These parameters were given utmost importance in the improving per unit area yield in mungbean as these were found to be positively associated with grain yield per plant (Rehman et al., 1998; Sadiq et al., 2000). Exploitation of genetic variability in the germplasm of any crop species is considered to be critical 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 provides potential for genetic improvement. To develop a plant genotype with desirable combination of traits, comprehensive information regarding the association of these traits with yield as well as detailed information on the genetic mechanism controlling various traits is considered a pre-requisite to launch a breeding programme. In past, Khattak et al. (2002 a, b), Joseph and Santhoshkumar (2000) found that additive gene action was controlling the heritage of these yield contributing traits in mungbean. In the case of mungbean, this type of information is scarce, which of course, is main reason for the poor yield potential of mungbean cultivars. Therefore, the present study was conducted to derive such information from a set of complete diallel crosses involving eight advanced lines of mungbean.

Materials and methods

Selection of parents and hybridization

The investigation regarding the inheritance mode of grain yield and its components was carried out in the experimental area of the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad, Pakistan during 2005-2006. A germplasm pool comprising of 55 diverse mungbean lines acquired from the University of Agriculture, Faisala-

bad; Pulses Research Institute, Faisalabad; and Nuclear Institute for Agriculture and Biology (NIAB), Faisalabad were planted in the field during spring 2005. Randomized complete block design with three replications was used for the execution of this experiment with a 30 and 10 cm row-to-row and plant-to-plant space, respectively. Each plot was planted as a single row of 3m in length thus accommodating 31 plants. At maturity, data regarding days taken to 90% maturity and grain yield per plant were recorded from 10 randomly selected guarded plants on a plot basis. Eight genotypes (viz. 562-1, 56-2, NM-95, NM-92, L.No.1, L. No.21, 6601 and E32-1) with a range of divergence for earliness and grain yield per plant (Fig 1) were finally selected and planted in July 2005 (kharif season) in the field and complete diallel mating was carried out for all possible combinations.

Field experiment and recording of the data

The F_0 seeds of 56 crosses and those of parents were sown in the field during March 2006 (spring season). A randomized complete block design (RCBD) with three replications was applied. Row to row and plant-to-plant spacing was kept 30 cm and 10 cm, respectively through seed dibbling method 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 seeds harvested from F_1 plants were used to raise F_2 populations during kharif 2006 along with eight parents. A RCBD with three replications was used and the plot size was 5 x 1.2 m thus accommodating 204 plants per population. Standard agronomic practices were followed from sowing till harvest in each season. The same cultural operations including hoeing, weeding, irrigation, fertilizer were carried out to reduce experimental error. Observations were recorded from all the plants by leaving one plant on each side of the row on the following traits.

1) Total plant dry matter (g)

At maturity, each plant was harvested just above the ground level. After harvest each plant was sun dried and weighed at regular intervals of one week. At the stage when further loss in the plant weight had ceased, dry weight of each plant was recorded in grams on an electronic balance and average dry weight was computed and taken as total plant dry matter.

Table 1. 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

Table 2. Analysis of variance for different characters in mungbean generations

Characters	Mean squares	
	F_1 generation	F_2 generation
Grain yield per plant	13.99**	18.26**
Total plant dry matter	298.40**	381.50**
Harvest index	87.06**	197.26**

** = P<0.01

2. Grain yield per plant (g)

After threshing, the produce obtained from each plant was cleaned and weighed in grams on electronic balance and average grain weight for each treatment was taken as grain yield per plant.

3. Harvest index (%)

Harvest index (HI) is the ratio of economic yield to total biological yield (Donald, 1965) as given HI = (Y/TDM) ×100, Where Y is grain yield and TDM is total plant dry matter.

The data were subjected to standard analysis of variance (Steel et al., 1997) using MSTATC computer program (M-STAT-C Development Team, 1989) to determine variation among the genotypes for the traits studied. Only significant genotypic differences allowed further analysis of the data.

Genetic Analysis

The diallel technique developed by Hayman (1954a, b) and Jinks (1954, 1955 and 1956) modified by Mather and Jinks (1971, 1977 and 1982) was used in this experiment. According to assumptions of the model such as multiple allelism and independent action and distribution of non-allelic genes were tested by subjecting the data against two adequacy tests. First, joint regression analysis, which is the regression coefficient (b) must deviate significantly from zero but not from unity, if all the assumptions underlying the genetic model were met. And the second adequacy test which was analysis of variance of (Wr+Vr) and (Wr-Vr) values which shows that the presence of dominance if there are significant differences among the values on Wr+Vr from array to array and if there is absence of non-allelic interactions, Wr-Vr will not vary between arrays. The traits 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, and Ali and Awan, 2009). The traits showing full or partial adequacy were subjected to diallel analysis by following distinctive steps according to Mather and Jinks (1982).

a) Formal analysis of variance

Through formal analysis of variance, the family means were partitioned into additive (a), dominance (b), maternal (c), and reciprocal affects (d). The b item was further separated into 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.

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Table 3. Adequacy tests for assessment of the data of yield related traits in mungbean for additive-dominance (AD) model

Characters	Grain yield per plant		Total plant dry matter		Harvest index	
	F_1	F_2	F_1	F_2	F_1	F_2
Adequacy tests						
Joint regression coefficient (b)	0.73 ± 0.25	0.99 ± 0.20	0.99 ± 0.11	0.86 ± 0.33	1.07 ± 0.18	0.41 ± 0.13
t test for b=0	2.91^*	4.78^*	8.85^*	2.57^*	5.72^*	2.96^*
t test for b=1	1.04^{NS}	0.02^{NS}	0.006^{NS}	0.39^{NS}	-0.40^{NS}	4.24^*
Mean squares for Wr+Vr (between arrays)	5.28^{**}	5.59^{**}	18.18^{**}	3.20^*	6.37^{**}	3.50^*
Mean squares for Wr-Vr (between arrays)	1.78^{NS}	4.22^{**}	1.38^{NS}	0.93^{NS}	3.51^*	0.92^{NS}
Adequacy to AD-model	Full	Partial	Full	Full	Partial	Partial

NS = Non-significant , * = P<0.05, ** = P<0.01

Homogeneity was tested by Bartlett,s test (Bartlett, 1937). If items c and d are significant, they become appropriate error for a and b mean square, respectively, therefore a and b must be tested against the error variances of c and d.

b) Estimation of genetic components of variation.

Among the genetic components of variation (D, F, H_1, H_2, h^2), the statistic D, was an estimate of additive effects; H_1 and H_2, variation due to dominance effects of genes, F provided an estimate of the relative frequency of dominant to recessive alleles in the parental lines and the variation in dominance over loci. The statistic h^2 provided 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 were used to compute further information as $(H_1/D)^{0.05}$, mean degree of dominance; $H_2/4H_1$, proportion of genes with positive and negative effects in the parents and $[(4DH_1)^{0.05}+F]/[(4DH_1)^{0.05} F]$ provides the proportion of dominant and recessive genes in the parents. Narrow sense heritability (h^2 n.s.) and broad sense heritability (h^2 b.s.) were also based on these parameters that reflect the amount of additive and total genetic variation in parents.

Results

Selection of the parents and preliminary analysis of variance

Fifty-five genotypes of mungbean 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 among the genotypes for both maturity duration and grain yield per plant.

For reliable selection, scatter diagram was plotted, taking grain yield per plant along X-axis and days to maturity along Y-axis (Figure 1). 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 1). Analysis of variance for grain yield and its attributes like total dry matter and harvest index revealed significant differences in both F_1 and F_2 generations (Table 2)

Adequacy tests for additive-dominance (AD) model

The adequacy of data to additive dominance (AD) model was tested by two scaling tests i.e. joint regression analysis and analysis of variance for Wr+Vr and Wr-Vr (Table 3). The regression line departed significantly from zero but not from unity for all the traits in both generations except for harvest index for which regression line deviated significantly from both the unity and zero in F_2 generation.
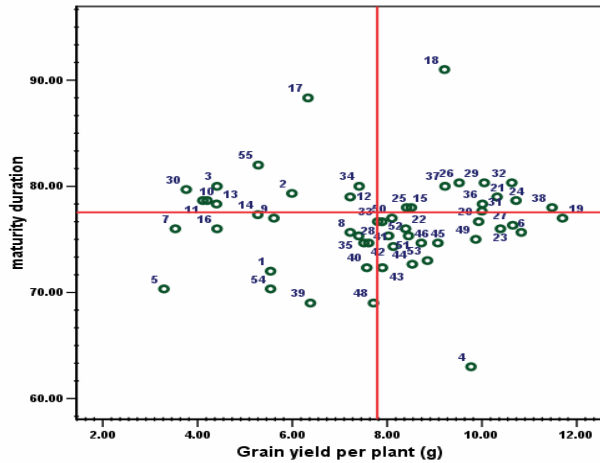
Fig 1. Scatter plot diagram for the assessment of diversity in 55 mungbean genotypes based on grain yield per plant (g) and maturity duration

In the second test, the values of Wr+Vr between arrays fluctuated significantly for all the characters in both generations, however, the values of Wr-Vr between arrays were not significantly different for grain yield in F_1, total dry matter in both generations, and for harvest index in F_2 generation. Both tests confirmed that the data of grain yield in F_1 and total dry matter in both generations fit the AD model. Conversely, the data for grain yield in F_2 and harvest index in both generations were partially adequate for AD model.

Formal analysis of variance

Bartlett's test (Bartlett, 1937) was applied to see the homogeneity of means squares for individual block interaction i.e. error variances (Table 4) which showed that the error variances were not homogeneous for grain yield per plant (χ^2 =19.65 and χ^2 =20.64) and total dry matter (χ^2 =17.43 and χ^2 =22.05) in both generations respectively. However, the error variances for harvest index were homogenous in both generations (χ^2 =10.50 and χ^2 =2.31 respectively). Thus, mean squares for grain yield per plant and total dry matter in both generations were tested against individual block interaction whereas for harvest index were tested against pooled block interaction. Among the components of formal ANOVA, both the items 'a' and 'b' were significant (Table 4) for all the yield related parameters. Amongst the components of b, b_1 was non-significant for grain yield per plant and harvest index in F_1 generation and for total dry matter in both generations but it was significant for grain yield per plant and harvest index in F_2 generation. On the other hand, b_2

and b_3 were significant for all the parameters in both generations. Reciprocal effects c and d were also significant for both the generations for all the yield associated traits except for harvest index in F_2 generation which imposed the retesting of the error variances of a against c; b and its components against d.

Estimates of components of variation

Components of variation revealed significance of both additive (D) and dominance components (H_1 and H_2) for all the traits in both the generations (Table 5). However the additive component (D) was exceeding than dominance counterpart H_1 for grain yield per plant and harvest index in F_1 and F_2 generation, respectively. In contrast, the dominance component (H_1) was greater than the additive component (D) for total dry matter in both generations, for grain yield per plant and harvest index in F_2 and F_1 generation respectively. Similarly, the value of average degree of dominance (H_1/D) 0.5 was less than unity for total dry matter in both generations, for grain yield per plant in F2, and for harvest index in F_1 generation. The value of H_1- H_2 for all the parameters was not equal to zero, and $H_2/4H_1$ value was less than its minimum value (0.25) in each generation. The component F, the frequency of dominant and recessive alleles in the genetic material, was positive for all the traits but significant only for harvest index in F_2 and total dry matter in F_1 generation. Correspondingly the proportion of dominant to recessive genes in the parents calculated by the formula $[(4DH_1)^{0.05}+F]/[(4DH_1)^{0.05}F]$ (Ali et al., 2008) was over unity for all the traits in both generations. The net dominance, h2 was only significant for total dry matter in both generations and grain yield in F_1 generation. Environmental constituent (E) was significant for only harvest index in F_2 generation. Heritability in broad sense was greater than narrow sense heritability for all the traits. All the parameters exhibited high narrow sense heritability (more the 0.60) except harvest index in F_2 and total dry matter in F_1 generation.

Discussion

In order to develop high yielding varieties of mungbean, information regarding inheritance pattern of yield related traits might facilitate breeders in improving genetic architecture of the plant in particular direction for maintaining and improving the proper crop production level (Ali and Khan 2007, Abbas et al., 2008). The exploitation of previously existing genetic variability in the breeding material as well as the creation of new variation in conjunction

Table 4. Formal analysis of variance for grain yield and its components for 8×8 diallel cross in mungbean

Item	Grain yield per plant		Total plant dry matter		Harvest index	
	F_1	F_2	F_1	F_2	F_1	F_2
a	13.93*	62.71*	1374.44*	1144.15*	211.01*	304.69*
b_1	0.72 NS	15.05*	187.94 NS	0.04 NS	29.43 NS	126.76*
b_2	18.90*	12.06*	255.18*	203.08*	138.15*	193.10*
b_3	7.37*	17.56*	100.93*	354.68*	57.68*	188.56*
b	10.02*	16.09*	142.60*	304.11*	76.79*	187.48*
c	43.30*	18.21*	312.00*	336.49*	132.37*	374.28*
d	9.53*	6.35*	142.94*	245.47*	44.33*	115.48 NS
a × blocks	1.33	0.75	19.39	151.72	-	-
b_1 × blocks	0.93	0.76	48.19	20.26	-	-
b_2 × blocks	0.86	0.62	20.26	42.81	-	-
b_3 × blocks	0.92	0.78	2.32	84.37	-	-
b × blocks	0.91	0.74	8.44	71.69	-	-
c × blocks	0.41	1.32	2.09	28.64	-	-
d × blocks	0.96	0.64	4.07	55.00	-	-
Block interaction	1.84	1.55	14.99	140.48	9.99	80.21

NS = Non-significant , * = P<0.05, ** = P<0.01

with its genetic knowledge is of fundamental significance for initiation of a breeding program aimed at improved yield (Khattak et al., 2004, Ali et al. 2008). Full diallel mating system was employed to create and evaluate heritable variation (Hayman, 1954a, 1954b). The crossing of the selected eight genotypes in all possible combinations concluded in maximum variability for grain yield in mungbean. The analysis of variance revealed significant differences for yield and its related traits among the hybrids and their parents in both the generations. Similar findings were reported by earlier scientists for grain yield in mungbean (Tickoo et al., 1988, Byregowda et al., 1997, Chakraborty and Haque, 1999, Ghaviami and Rezai, 2000).

The fitness tests authenticated absence of non-allelic interaction for grain yield per plant in F_1 generation and total dry matter in both generations. However, for harvest index in F_2 generation regression line significantly deviated from both zero and unity suggesting the involvement of some traces of epistatic effects. But the second adequacy tests recommended this trait for further genetic analysis. Similarly, the values of Wr-Vr varied significantly between arrays for grain yield in F_2 and harvest index in F_1 generation with independent gene distribution, which confirmed the participation of some non-allelic interactions in their genetic control. Hence, the data of these traits in respective generations were partially adequate for genetic analysis.

Bartlett's test was employed for the assessment of homogeneity in error variances in the components of formal ANOVA (Bartlett 1937) which demonstrated significant value of χ^2 for grain yield and total dry matter in both generations signifying the absence of non-allelic gene interaction in the inheritance of these traits. Conversely, non-significant Chi square values

for harvest in both generations suggested that error variances were homogeneous revealing the presence of epistatic effects in its inheritance. Aher and Dahat (1999) confirmed that epistatic component was involved in the expression of grain yield per plant in mungbean. Chand and Dawa (1996) reported contribution of non-allelic effects in the genetic control of harvest index in wheat. Khattak et al. (2002b) worked on triple test cross analysis in mungbean in two seasons (kharif and spring) for total dry matter and harvest index and reported interestingly the absence of epistasis during kharif season and presence of epistasis for biomass in spring season.

Formal analysis of variance displayed the significance of 'a' and 'b' components for all the traits in both generations suggestive of the implication of both additive and dominance effects. Ambidirectional dominance was demonstrated by the value of b_1 which was non-significant for all the traits except that of grain yield per plant and harvest index in F_2 generation for which directional dominance was operating. The significant values of items b_2 and b_3 for each generation for all the yield parameters proposed asymmetrical allocation of dominant genes among the parents and importance of specific gene interactions. Similarly, the significance of c and d components for all the traits supported the incidence of maternal effects in their inheritance while absence of maternal effects was clear due to non-significance of c item for harvest index in F_2 generation. Similar to the results of formal analysis of variance, significance of both D and H_1 & H_2 exposed the influence of both additive and dominant genes in the inheritance of all yield related traits in mungbean. However, the exceeding value of H_1 component over D component for grain yield in F_1 and harvest index

Table 5. Components of variation for grain yield and its attributes for 8×8 diallel cross in *Vigna radiata* L

Components of variation	Grain yield per plant		Total plant dry matter		Harvest index	
	F_1	F_2	F_1	F_2	F_1	F_2
E	0.304 ± 0.34	0.269 ± 0.156	2.464 ± 2.222	23.167 ± 9.235	1.652 ± 1.618	$13.692 \pm 4.925*$
D	$4.968 \pm 1.027*$	$7.620 \pm 0.468*$	$194.162 \pm 15.753*$	$196.772 \pm 27.58*$	$75.153 \pm 4.833*$	$64.025 \pm 14.709*$
F	1.902 ± 2.438	2.134 ± 1.110	21.250 ± 15.753	$158.567 \pm 65.464*$	$56.288 \pm 11.472*$	$37.25\ 0\pm 34.912$
H_1	$9.928 \pm 2.372*$	$5.120 \pm 1.082*$	$66.887 \pm 15.326*$	$162.494 \pm 63.68*$	$59.778 \pm 11.161*$	$89.257 \pm 33.960*$
H_2	$8.393 \pm 2.064*$	$3.988 \pm 0.941*$	$57.825 \pm 13.334*$	$118.420 \pm 55.411*$	$39.00 \pm 9.710*$	$72.163 \pm 29.551*$
h^2	$13.09 \pm 1.38*$	-0.111 ± 0.629	$109.220 \pm 8.920*$	$-9.473 \pm 37.070*$	0.601 ± 6.49	-5.610 ± 19.769
$(H_1/D)^{0.5}$	1.41	0.81	0.58	0.90	0.89	1.18
$H_2/4H_1$	0.21	0.19	0.21	0.18	0.16	0.20
H_1- H_2 $(4DH_1)^{0.5}+F/(4DH_1)^{0.5}$-F	1.31	1.41	1.20	2.59	2.44	1.65
h^2 (n. s)	0.48	0.72	0.84	0.43	0.63	0.40
h^2 (b. s)	0.93	0.94	0.97	0.75	0.94	0.77

in F_2 generation uncovered the prevalence of dominant genes in the genetics of these parameters. This supported the hypothesis that the exploitation of heterosis could be the suitable method for the improvement of these traits. This was soundly sustained by the values of degree of dominance $(H_1/D)^{0.5}$ that was over unity suggested the over-dominance nature of genes controlling these parameters in both F_1 and F_2 generations. Nevertheless, total dry matter in both generations, for grain yield in F_2 and for harvest index in F_1 generation was predominantly depicted by additive genetic effects, which were below unity value of $(H_1/D)^{0.05}$. This suggested that simple selection in early generations would be fruitful in improving harvest index in mungbean. Khattak et al. (2002a, b) concluded that seasonal effects had great influence on gene action in mungbean. Joseph and Santhoshkumar (2000) reported additive genetic effects for grain yield per plant in mungbean while Loganathan et al. (2000) reported over dominance for this trait in green gram. Paralkar et al. (1997) reported the presence of additive, dominance as well as epistasis for grain yield in blackgram. Khattak et al. (2002b) reported the preponderance of both additive as well as non-additive genetic components for total plant dry matter. However, Dijee et al. (2000) showed that gene action was predominantly non-additive for seed yield, dry matter production and harvest index in cowpea. Dana and Dasgupta (2001) reported the preponderance of additive gene action for seed yield per plant in black gram.

The unequal values of H_1 and H_2 as well as lower values of $H_2/4H_1$ than 0.25 for all the parameters signified uneven proportion of dominant genes and unequal frequencies of negative versus positive alleles at different loci showing dominance in the parents. The net dominance (h^2) suggested that dominance was not unidirectional for grain yield in F_2 and harvest index in both generations while it was directional for grain yield in F_1 and total dry matter in both generations. The positive value of 'F' illustrated that frequency of dominant genes were more in the parents than the recessives ones for all the parameters which was impressively sustained by the values $[(4DH_1)^{0.05}+F]/[(4DH_1)^{0.05} F]$ that revealed high proportion of dominant to recessive genes in the parents. Blocking effects were absent for all the yield related parameters except harvest index in F_2 generation.

The magnitude of broad sense heritability exceeded that of narrow sense heritability that signified the pervasiveness of phenotypic effects in the heritage of yield related characters. All the parameters exhibited additive nature of genetic control as demonstrated by D values and high narrow sense heritability with the exception of grain yield in F_1 and harvest index in F_2 for which heritability in narrow sense was moderate with increasing trend towards over dominance genetic behavior of these traits in respective generations. Sadiq et al. (2000) also reported broad sense heritability for harvest index while Islam et al. (1999) and Sharma (1999) found high heritability for seed yield in mungbean. Gowda et al. (1997) estimated high heritability for grain yield per plant in black gram while Dobhal and Rana (1997) reported high heritability for grain yield in adzuki bean.

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