



Evaluation of Genetic Parameters for Yield and Related Traits in new Recombinants interspecific Mungbean × Mashbean Genotypes

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SEVENTY TWO Mungbean × Mashbean recombinant genotypes were evaluated in the field for seed yield and its components traits. Highly significant differences were observed among the genotypes. The magnitudes of genotypic and phenotypic coefficients of variability ranged from 2.73% to 28.97% and 3.46% to 31.95%, respectively. Pods per plant exhibited maximum amount of genetic variability followed by clusters per plant and seed yield per plant. 100-seed weight was observed to be the most heritable trait with greatest magnitude ($h^2 = 99\%$). Pods per plant had maximum positive and significant genotypic ($r_g = 0.90$) and phenotypic ($r_p = 0.86$) correlations with clusters per plant. Both traits were identified as the most important characters as they had strong genetic and phenotypic relationships with seed yield. Selection for number of pods per plant among different agronomic traits showed greatest improvement in seed yield that was 54% of the improvement possible through direct selection for seed yield. Likewise, clusters per plant and plant height also showed higher improvement in seed yield through indirect selection which was 29% and 20% of the improvement possible by direct selection for yield. Days to flowering also showed promise for 8% of the improvement in seed yield possible through direct selection for seed yield. Thirty six promising recombinants were selected on the basis of desirability index. On the basis of overall performance seven recombinant genotypes, viz; MMH 1115, MMH 4224, MMH 4255, MMH 7124, MMH 2112, MMH 4295 and MMH 2225 were selected as elite lines.

Keywords: Character association desirability index, Indirect selection, Inter-specific recombinants, Mashbean, Mungbean.

Introduction

Both Mungbean (*Vigna radiata* L. Wilzeck) and Mashbean (*Vigna mungo* L. Happer) belong to family Fabaceae and are considered as highly valuable short duration pulse crops. These have many common desirable traits such as high protein contents, wider adaptability, low input requirements and ability to improve soil fertility through biological nitrogen fixation (Makeen et al., 2007) and can be grown in crop rotation practices to restore soil fertility by fixing atmospheric nitrogen (Somta & Srinives, 2007). In Pakistan, mungbean is the second major pulse crop after chickpea and grown for its edible seeds.

It is grown on an area of 162.4 thousand hectares with an annual production of 122 thousand tons whereas mashbean which is less in area and production occupies 15.5 thousand hectares with annual production of 7.3 thousand tons. Average yield per hectare of both crops is low due to less genetic potential and poor management practices (Anonymous, 2017-18). Most mungbean improvement programmes aimed to enhance productivity per unit area.

The study of different genetic parameters such as variance components, co-efficient of variations and heritability estimates of different morphological and economic traits helps in

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understanding the nature of inheritance patterns of these traits, the amount of genetic variability present and the extent the progress can be achieved by the selection of a particular trait. Inability to visually recognize small differences in quantitative traits have led to frequent attempts to find associated traits more amenable to visual selection. The understanding of interrelationship among various morphological and economic traits is very necessary for framing of an effective breeding programme. Correlation coefficient gives a measure of the relationship between traits and provides the degree to which various characters of a crop are associated with economic productivity. Seed yield being a complex trait, is ultimately the aggregate outcome of different yield contributing traits. Selection based on ideotype concept can be carried out if the genetic behavior of different traits is well understood (Singh & Singh, 1995). Keeping these facts in view, the present study was planned to evaluate the extent of genetic improvement in mungbean through hybridization with mashbean by determining the nature and extent of genetic variability among new recombinants and estimating the correlation coefficients both at genetic and phenotypic levels among various agronomic traits. Further, the objective was to determine the response of various traits to selection, effectiveness of indirect selection for grain yield and identification/selection of Mung × Mash recombinants with desirable features.

Materials and Methods

Present investigation was carried out at Nuclear Institute for Agriculture and Biology (NIAB), Faisalabad (31.26 °N, Longitude 73.06 °E and Altitude 184m) during summer in 2016. The climate of the study region is semi-arid with summer maximum temperature of 46°C. Soil type is predominately clay loam, which varies spatially from clay loam to loam horizontally and is silt clay loam at lower depths. Seventy two Mungbean × Mashbean inter-specific true breeding genotypes selected from F₈ generation were developed at NIAB through inter-specific hybridization between mungbean and mashbean parents (Table 1) and evaluated in field experiment for different agronomic traits in randomized complete block design (RCBD) with three replications. Two rows of each entry were sown in a row

plot of 2.4m², distances between rows 30cm apart and 10cm between plants within rows. Uniform agronomic practices were followed for maintenance of crop. Five randomly selected guarded plants were used for recording data on different traits like plant height (cm), number of clusters and pods per plant, pod length, seeds per pod, 100-seed weight (g) and seed yield per plant (g). Days to flowering was determined by counting the number of days taken from the date of sowing to the time when 50% of the plants in a genotype exhibited flowering. Days to maturity were determined by counting the number of days taken from the date of sowing to the time when 90% of the plant in a genotype had mature pods.

TABLE 1. Mung × Mash recombinant genotypes in different inter-specific crosses and number of genotypes developed in each cross in F₈ generation and used in present study

Set #	♀ Parent (Mungbean)	♂ Parent (Mashbean)	Recombinant genotypes
1	NIAB MUNG 92	Mash-97	12
2	NIAB MUNG 2006	Mash-88	32
3	VAR. 6601	Mash 3-156-1	28
		Total	72

The data recorded for different plant traits were subjected to the statistical analysis following Steel et al. (1997) and Singh & Chaudhry (1985). Statistical analysis was performed using Statistical package MSTATC and all biometrical parameters were computed using Microsoft Excel 2007. The mean squares from the analysis of variance were equated to their expected values to obtain the estimates of different genetic parameters as outlined by Robinson et al. (1951). Different genetic parameters like coefficients of variation (phenotypic and genotypic), components of variance, heritability and genetic advance were estimated using expected mean squares. Significance of heritability was tested following Lothrop et al. (1985). Genetic and phenotypic correlations were computed following Kown & Torrie (1964). Significance of genetic correlation was tested as demonstrated by Reeve (1955) and Robertson (1959). The estimates of expected correlated responses in primary trait,

i.e., 'y' (seed yield per plant) when selection was practiced for secondary traits, i.e., 'x' (remaining traits) were computed as outlined by Falconer (1989) in the following way:

$$CR_y = i_{(x)} \cdot h_{(x)} \cdot h_{(y)} \cdot \hat{r}_{g(x,y)} \cdot \hat{\sigma}_{p(y)}$$

where:

$CR_y(x)$ = Expected correlated response in trait 'y' when selection is for trait 'x',

$i_{(x)}$ = Selection intensity at 10%, i.e.; 1.755 (Falconer, 1989),

$h_{(x)}$ = Square root of broad-sense heritability for trait x,

$h_{(y)}$ = Square root of broad-sense heritability for trait y,

$\hat{r}_{g(x,y)}$ = Estimate of genetic correlation coefficient between traits x and y,

$\hat{\sigma}_{p(y)}$ = Estimate of phenotypic standard deviation for trait y.

Percent improvement in seed yield was estimated as percent increase in mean seed yield as follows:

$$\% \text{ improvement in yield} = (\text{Gain from CR of a secondary trait on yield}) / (\text{mean seed yield}) \times 100$$

Similarly, percent increase over direct selection was computed as a ratio of expected gains from indirect selection (correlated response) and direct selection (genetic advance) expressed as percentage following Lothrop et al. (1985) as under:

$$\% \text{ increase over direct selection} = (\text{Gain from CR of a secondary trait on yield}) / (\text{Gain from direct selection of a secondary trait}) \times 100$$

Mean phenotypic values of different yield components were used for calculating the Desirability index as described by Asghar et al. (2010). The mean phenotypic values of all the traits were classified into three categories using grand mean and standard deviation. Maximum score for each trait was allotted to the genotypes falling in extreme desirable category and vice versa. The scores of all traits were then summed to find the aggregate score of each genotype. Desirability scores were assigned for all traits and the index values of genotypes were set for that trait (2 for high desirability, 1 for medium desirability and 0 for low desirability). The performance of a genotype was judged by its total index score,

which was the sum of the index values with regard to all characters. The index values (0, 1, and 2) meant lower to higher value of worth of a genotype/variety. For days to flower, days to maturity and percent disease index for mungbean yellow mosaic disease (MYMD), desirability was in lower magnitude; therefore higher index value (2) was given to the genotypes showing high resistance. For all other traits desirability was linked with higher magnitude, so high index value was given to the genotypes exhibiting greater mean values of these traits. Desirability index of Mung × Mash recombinant genotypes was constructed to assess the worth of a particular genotype for different traits. Different groups of genotypes were formed and the genotypes with same index score were kept in one group. Selection of top scoring promising genotypes was done on the basis of aggregate index scores of all genotypes.

Results

Analysis of variance revealed useful information about the variation present among treatment means. Mean squares from the analysis of variance of different traits under study are presented in Table-2. Highly significant differences were observed among the recombinant genotypes for all traits except seeds per pod which indicated the existence of variation among these genotypes.

Coefficients of variation

Phenotypic coefficients of variability (PCV) were generally observed to be greater as compared to their corresponding genotypic coefficients of variability (GCV) for all the traits (Table-3). However, 100-seed weight had same magnitudes of both GCV and PCV, likewise, less the close magnitudes of GCV and PCV for days to maturity, days to flowering and plant height also depicted that there was less influence of environment on these traits and thus greater contribution of genetic makeup of plants in the development of phenotype. Seeds per pod had lower estimate of genotypic coefficient of variability (2.73%) followed by days to maturity (3.36%). Similarly, phenotypic coefficient of variability was observed to be the lowest for days to maturity (3.46%) followed by seeds per pod (4.66%). The higher estimates of both genotypic and phenotypic coefficients of variability for pods per plant and clusters per plant implied that these two traits can be exploited as selection indices for further improvement in mungbean.

TABLE 2. Mean squares from the analysis of variance of different traits among Mung × Mash recombinant genotypes

SOV	Df	Days to flower	Days to maturity	Plant height (cm)	Clusters/plant	Pods/plant	Pod length (cm)	Seeds/pod	100-seed weight (g)	Seed yield (g/plant)
Replications	2	3.24	0.03	11.46	1.13	14.51	0.86	1.37	0.04	4.43
Genotypes	71	29.58**	16.32**	142.64**	14.50**	35.12**	0.70**	0.84*	1.02**	27.60**
Error	142	0.89	0.98	17.80	2.39	23.97	0.30	0.55	0.00	4.92
Total	215									

*, ** = Significant at 0.05 and 0.01 probability levels, respectively.

Components of variance

The estimates of components of variance for different traits among genotypes are given in Table-3. In general, the magnitudes of phenotypic variance were observed to be greater as compared to their respective genotypic and environmental variances for all the traits under study. The estimates of environmental variance were observed to be smaller than their respective genotypic variances for most of the traits which indicated greater contribution of genetic component to the total variance. However, in case of seeds per pod, the influence of environment was more as compared to genotype and thus the resultant phenotype seems to be more prone to environment.

The estimates of genetic variance were found to be mostly significant as their absolute magnitude exceeded twice their respective standard errors which indicated the presence of sufficient exploitable genetic variability for all the traits under study except seeds per pod among different recombinant genotypes. The estimates of genetic variance for 100-seed weight, clusters per plant, days to flower and maturity (0.34, 4.03, 9.56 and 5.11) were close to their respective estimates of phenotypic variance (0.34, 4.83, 9.86 and 5.44) indicating that genotype determined the expression of phenotype and there is no influence of environment on these traits. These results suggested that genetic variability for the above mentioned traits may be exploited in breeding program for the improvement of these traits. However, non-significant estimate for seeds per pod implied that there was no genetic variation for this trait among recombinants.

Heritability estimates

Broad sense heritability estimates presented in Table 3 were observed to be significant for all the traits since their absolute magnitudes exceeded twice of their respective standard errors except number of seeds per pod. It implied that heritable genetic variation existed for these traits. Greatest heritability magnitudes were found for 100-seed weight ($h^2= 99\%$) followed by days to flower ($h^2= 97\%$) and days to maturity ($h^2= 94\%$) which revealed that selection of desirable plants based on phenotypic observations can be made directly for these traits. Plant height, clusters per plant, pods per plant and seed yield per plant also exhibited higher estimates of broad sense

heritability. Moderate heritability estimate ($h^2=59\%$) were noted for pod length whereas seeds per pod had lowest magnitude of broad sense heritability ($h^2=34\%$). These results showed that contribution of genetic component of variation was maximum for 100- seed weight, days to flower and days to maturity. Such heritable genetic variation can be exploited for further improvement in mungbean. It also indicated the presence of additive gene effects in the genetic makeup of these traits which are likely to respond to direct selection. Similarly higher heritable genetic variation for traits like plant height, clusters per plant, pods per plant and seed yield per plant also suggested that these traits can be improved through simple selection procedure. Non-significant and lowest magnitude of heritability for seeds per pod implied that no heritable genetic variation exists for this trait. Therefore, selection for this trait would not be feasible.

Correlation coefficients

The magnitudes of genotypic correlation coefficients were found to be greater than their respective phenotypic correlation coefficients for most of the trait pairs among Mung \times Mash recombinant genotypes (Table 4). In general, out of thirty six trait pairs, twenty three showed positive relationships and the remaining thirteen had negative relationships. Positive and significant genetic correlations were found for pods per plant with clusters per plant ($r_g = 0.90$), pod length with seeds per pod ($r_g = 0.86$) and pod length with 100-seed weight ($r_g = 0.79$). These three traits also exhibited highly significant correlations among themselves at phenotypic level. Negative and significant genetic correlations were observed for pods per plant with pod length ($r_g = -0.75$), seeds per pod ($r_g = -0.79$) and 100-seed weight ($r_g = -0.76$). These traits also had negative and highly significant phenotypic correlations. Positive but non-significant genetic correlations fairly high in magnitude ($>\pm 0.50$) were noticed for days to maturity with days to flower and plant height; seeds per pod with 100-seed weight; and pods per plant with seed yield per plant. Similarly, insignificant negative genetic correlations were found for clusters per plant with pod length and 100-seed weight.

Seed yield per plant exhibited positive genetic association with days to flower, plant height, clusters per plant and pods per plant.

Strong linear genetic relationship of clusters per plant with pods per plant ($r_g = 0.90$) and their positive associations with days to flower, days to maturity, plant height and seed yield revealed the importance of vegetative growth of the plant in increasing seed yield through the development of optimum biomass required for high seed yield. Positive and significant genetic relationships of pod length with seeds per pod and 100-seed weight were observed. Negative genetic associations with seed yield indicated that by increasing any of these traits would lead to a decrease in seed yield. Negative and significant genetic relationships of pods per plant with pod length, seeds per pod and 100-seed weight were also observed.

Positive and highly significant ($P \leq 0.01$) phenotypic correlations were observed for days to flower with days to maturity, plant height and clusters per plant; days to maturity with plant height and clusters per plant; plant height with clusters per plant, pod length and seeds per pod; clusters per plant with pods per plant and seed yield per plant; pods per plant with seed yield per plant; pod length with seeds per pod and 100-seed weight; and seeds per pod with 100-seed weight. However, days to flowering with pods per plant and days to maturity with pods per plant showed positive and significant phenotypic correlations. Negative and highly significant ($P \leq 0.01$) phenotypic correlations were noted for clusters per plant with pod length and 100-seed weight; pods per plant with pod length, seeds per pod and 100-seed weight; and seeds per pod with seed yield per plant. Two trait pairs, viz; clusters per plant with seeds per pod; and pod length with seed yield per plant exhibited negative and significant phenotypic correlations. Rest of the trait pairs had non-significant phenotypic correlations.

Correlated responses

The estimates of correlated response to indirect selection and percent improvement in mean seed yield when selection was for other related traits of genotypes studied are given in Table 5. The magnitudes of correlated responses to indirect selection ranged from -1.2803g for seeds per pod to 2.3425g for pods per plant. The traits like days to flower, plant height, and clusters per plant and pods per plant exhibited positive response to indirect selection for seed yield, whereas the remaining traits responded negatively towards indirect selection.

TABLE 3. Mean, coefficients of variability, components of variance and broad-sense heritability of different traits of Mung × Mash recombinant genotypes

	Days to flower	Days to maturity	Plant height (cm)	Clusters/plant	Pods/plant	Pod length (cm)	Seeds/pod	100-seed weight (g)	Seed yield (g/plant)
Range	39.0-55.0	63.0-74.0	54.89-90.56	5.44-15.33	12.22-43.0	7.89-10.11	9.89-12.56	4.0-6.33	9.56-21.07
Mean ± σ	45.65 ± 3.13	67.36 ± 2.38	69.50 ± 6.90	8.49 ± 2.16	21.01 ± 7.02	8.88 ± 0.48	11.35 ± 0.53	5.49 ± 0.58	14.20 ± 3.03
GCV%	6.77	3.36	9.28	23.74	28.97	4.12	2.73	10.64	19.37
PCV%	6.87	3.46	9.92	25.98	31.95	5.43	4.66	10.64	21.37
$\sigma^2_g \pm SE(\sigma^2_g)$	9.56 ± 1.62	5.12 ± 0.89	41.61 ± 7.86	4.03 ± 0.80	37.05 ± 7.48	0.13 ± 0.04	0.09 ± 0.05	0.34 ± 0.06	7.56 ± 1.53
σ^2_e	0.2962	0.3254	5.9324	0.7980	7.9909	0.0985	0.1840	0.0004	1.6387
σ^2_p	9.8588	5.4408	47.5454	4.8320	45.0414	0.2326	0.2799	0.3409	9.2005
$h^2 \pm SE(h^2)$	0.97 ± 0.17	0.94 ± 0.17	0.88 ± 0.17	0.83 ± 0.17	0.82 ± 0.17	0.59 ± 0.17	0.34 ± 0.18	0.99 ± 0.16	0.82 ± 0.16

GCV% = Genetic coefficient of variation, PCV% = Phenotypic coefficient of variation, σ = Standard deviation, ± = Standard error value.

TABLE 4. Genetic (above diagonal) and phenotypic (below diagonal) correlation coefficients for various traits among Mung × Mash recombinant genotypes

Trait #	Days to flower	Days to maturity	Plant height (cm)	Clusters/Plant	Pods/plant	Pod length (cm)	Seeds/pod	100-seed weight (g/plant)	Seed Yield (g/plant)
Days to flower		0.6403	0.3195	0.3449	0.1909	0.0695	-0.1497	0.0680	0.0714
Days to maturity	0.6126**		0.5976	0.4756	0.2157	0.0705	0.1739	-0.0265	-0.0851
Plant Height (cm)	0.2928**	0.5323**		0.3457	0.2409	0.3134	0.4850	-0.0655	0.1906
Clusters/plant	0.3183**	0.4123**	0.2690**		0.9030*	-0.5094	-0.4736	-0.6242	0.2903
Pods/plant	0.1750*	0.1870*	0.1480	0.8598**		-0.7514*	-0.7945*	-0.7588*	0.5352
Pod length (cm)	0.0458	0.0345	0.2233**	-0.3393**	-0.5016**		0.8586*	0.7931*	-0.2353
Seeds/pod	-0.0942	0.0695	0.2622**	-0.2003*	-0.3656**	0.7757**		0.6163	-0.4533
100-seed weight (g/plant)	0.0704	-0.0254	-0.0547	-0.5741**	-0.6907**	0.6061**	0.3635**		-0.0992
Seed Yield (g/plant)	0.0731	-0.0780	0.1361	0.2929**	0.5066**	-0.1829*	-0.2379**	-0.0963	

+ = The estimate of genetic correlation coefficient differs significantly from zero as its absolute magnitude exceeded twice its respective standard error.

*, ** = Significant at 0.05 and 0.01 probability levels, respectively

It is evident from Table 5, that the pods per plant showed extreme potential for improving seed yield per plant with maximum gain (2.3425g) for grain yield per plant followed by the correlated responses of clusters per plant (1.2802g), plant height (0.8608g) and days to flower (0.3395g). Pods per plant appeared to be the most important secondary trait suggesting greatest improvement in mean seed yield (31%) followed by plant height (24%) and clusters per plant (5%) expressed in terms of percent increase over mean of seed yield. Every additional increment of pods per plant may increase seed yield by 2.3425g. Selection for number of pods per plant among different agronomic traits showed greatest improvement in seed yield that was 54% of the improvement possible through direct selection for seed yield. Likewise, clusters per plant and plant height followed pods per plant and also showed higher improvement in seed yield through indirect selection which was 29% and 20% of the improvement possible by direct selection for yield, respectively. Days to flowering also showed promise for 8% of the improvement in seed yield possible through direct selection for seed yield. Rest of the traits, namely, days to maturity, pod length, seeds per pod and 100-seed weight expressed negative responses to indirect selection for seed yield per plant.

Diversity analysis and selection of promising genotypes

Seed yield and its component traits like clusters per plant, pod length, pods per plant, seeds per pod, 100-seed weight and seed yield per plant and disease index for MYMD were used to construct desirability index. Aggregate desirability index scores of new interspecific recombinant genotypes for different yield components determined

from mean phenotypic values of different yield components are given in Table 6. The aggregate index score ranged from 4 to 13 showing diversity among genotypes. All the genotypes formed eight distinct groups (Table 7). The genotype, MMH 11534 was at the top securing maximum index score (13) followed by MMH 53105 (11). Nine genotypes possessed index score value of 9, eighteen genotypes were found to have index score of 8, eighteen genotypes exhibited 7, thirteen genotypes had 6, 11 genotypes got 5 and one had 4 (Table 7).

Out of seventy two Mung × Mash inter-specific genotypes, thirty six promising genotypes having high yield potential and resistance against mungbean yellow mosaic virus were selected on the basis of aggregate desirability index scores. The genotypes, viz; MMH 11534 (DIS= 13), MMH 53105 (DIS= 11), MMH 210115, MMH 3615, MMH 4335, MMH 5615, MMH 2131, MMH 4255, MMH 16111, MMH 7124 and MMH 16425 (DIS= 9), MMH 1125, MMH 356, MMH 4615, MMH 2112, MMH 2121, MMH 2133, MMH 2225, MMH 4211, MMH 4295, MMH 7111, MMH 7112, MMH 9125, MMH 10212, MMH 15135, MMH 15334, MMH 6235, MMH 1115, MMH 37414 (DIS= 8) and MMH 1312, MMH 3132, MMH 7142, MMH 13115, MMH 4224, MMH 24425, MMH 2333 (DIS= 7) secured highest aggregate index scores and were selected (Tables 6 and 7). Some genotypes also secured desirability index score of 7 but were not selected, since their mean performance (Table 8) in terms of important yield components (clusters per plant and pods per plant) and disease index was lower than selected genotypes.

TABLE 5. Correlated responses and percent improvement in grain yield when selection was for other yield related traits determined from Mung × Mash recombinant genotypes

Secondary traits selected (x)	Primary trait unselected (y)		
	Grain yield per plant (g)		
	Correlated response (g)	Improvement in yield (%)	% of direct selection
Days to flower	0.3395	2	8
Days to maturity	-0.3984	-3	-9
Plant height (cm)	0.8608	6	20
Clusters/plant	1.2802	9	29
Pods/plant	2.3425	17	54
Pod length (cm)	-0.8625	-6	-20
Seeds/pod	-1.2803	-9	-29
100-seed wt. (g/plant)	-0.4783	-3	-11
Seed yield (g/plant)	0	0	0

TABLE 6. Index scores of desirability for grain yield, its components and disease index of Mung × Mash inter-specific recombinant genotypes and aggregate genotype

Sr#	Genotype	CLUS	PODS	PODL	SPOD	100SW	SYLD/P	DI	Aggregate genotype
1	*MMH 1125	1	2	1	1	0	1	2	8
2	MMH 1312	2	2	0	0	0	1	2	7
3	MMH 210115	2	2	1	1	1	1	1	9
4	MMH 3132	2	2	0	0	0	1	2	7
5	MMH 3145	2	2	0	0	0	1	1	6
6	MMH 3563	2	2	0	0	0	2	2	8
7	MMH 3615	2	2	1	1	0	1	2	9
8	MMH 4335	2	1	1	1	1	1	2	9
9	MMH 4615	2	2	0	1	0	1	2	8
10	MMH 7142	1	1	1	1	2	0	1	7
11	MMH 53105	2	1	2	2	1	1	2	11
12	MMH 5615	2	2	0	1	1	1	2	9
13	MMH 28435	1	1	1	1	0	1	0	5
14	MMH 1143	1	1	1	1	0	1	0	5
15	MMH 1151	1	1	0	1	1	1	0	5
16	MMH 13115	1	1	1	1	1	1	1	7
17	MMH 2112	1	1	2	2	1	0	1	8
18	MMH 2121	1	1	2	2	1	1	0	8
19	MMH 2122	1	1	1	1	1	0	0	5
20	MMH 2131	1	1	2	2	1	1	1	9
21	MMH 2133	1	1	1	2	2	1	0	8
22	MMH 4224	1	1	1	1	1	1	1	7
23	MMH 2225	1	1	1	2	1	1	1	8
24	MMH 24425	1	1	1	1	1	1	1	7
25	MMH 2333	1	1	2	2	1	0	0	7
26	MMH 2413	1	1	0	1	1	0	1	5
27	MMH 2424	1	0	1	1	1	0	1	5
28	MMH 2435	1	1	1	1	1	0	1	6
29	MMH 4135	0	0	2	2	1	0	1	6
30	MMH 4174	1	1	1	1	1	0	1	6
31	MMH 4215	1	1	1	1	1	0	1	6
32	MMH 4211	1	1	1	1	2	1	1	8
33	MMH 2212	1	2	1	1	1	1	0	7
34	MMH 4255	1	1	2	1	2	1	1	9
35	MMH 4282	0	1	1	0	1	1	1	5
36	MMH 4295	1	1	1	2	1	1	1	8
37	MMH 4381	1	1	2	1	1	0	1	7
38	MMH 16211	1	0	1	1	1	1	1	6

TABLE 6. Cont.

Sr#	Genotype	CLUS	PODS	PODL	SPOD	100SW	SYLD/P	DI	Aggregate genotype
39	MMH 7111	1	1	1	1	2	1	1	8
40	MMH 16321	1	1	1	1	1	0	0	5
41	MMH 7131	1	1	1	1	1	1	1	7
42	MMH 5153	1	1	1	1	1	1	1	7
43	MMH 7252	1	0	1	1	1	0	0	4
44	MMH 8142	1	0	1	1	1	0	1	5
45	MMH 8231	0	1	1	1	1	0	1	5
46	MMH 7112	2	2	0	1	1	1	1	8
47	MMH 9111	1	1	1	0	1	1	1	6
48	MMH 9125	1	1	1	2	1	1	1	8
49	MMH 10212	1	1	1	1	2	1	1	8
50	MMH 12133	1	2	0	1	0	1	1	6
51	MMH 1171	1	1	2	2	1	0	0	7
52	MMH 15135	1	1	1	1	2	1	1	8
53	MMH 15334	1	1	1	1	2	1	1	8
54	MMH 6235	1	1	1	1	2	1	1	8
55	MMH 23413	0	1	1	1	1	2	1	7
56	MMH 2234	0	1	0	1	1	2	1	6
57	MMH 28415	0	0	1	2	1	2	1	7
58	MMH 1115	1	1	1	1	2	1	1	8
59	MMH 3221	1	1	1	1	1	1	1	7
60	MMH 15521	0	0	1	1	1	0	2	5
61	MMH 8625	1	2	0	0	0	2	1	6
62	MMH 11315	1	1	1	1	1	1	1	7
63	MMH 11534	1	2	2	2	2	2	2	13
64	MMH 11543	1	1	1	0	1	1	1	6
65	MMH 37414	1	1	1	1	1	2	1	8
66	MMH 16111	1	1	1	1	2	2	1	9
67	MMH 16311	0	1	1	1	1	2	1	7
68	MMH 7124	1	1	2	1	1	2	1	9
69	MMH 16425	1	1	1	1	2	2	1	9
70	MMH 16435	1	1	1	1	1	1	0	6
71	MMH 21235	1	1	1	1	1	2	0	7
72	MMH 23422	1	1	0	0	1	2	1	6

*MMH= Mung × Mash Hybrid

DF = Days to flower, DM = Days to maturity, PLHT = Plant height (cm), CLUS = Clusters/plant, PODS = Pods/plant, PODL = Pod length (cm), SPOD = Seeds/pod, 100SW = 100-Seed weight (g), SYLD = Seed yield/plant (g), DI= Disease index.

§ Desirability scores, i.e. High desirability = 2, Medium desirability = 1 and Low desirability = 0.

(Aggregate genotype was calculated as sum of index scores for different traits).

TABLE 7. Different groups of Mung × Mash inter-specific recombinant genotypes formed from desirability index scores and the number of genotypes included in each group

Sr. #	Index score	Genotypes	Number of genotypes
1	13	MMH 11534	1
2	11	MMH 53105	1
3	9	MMH 210115, MMH 3615, MMH 4335, MMH 5615, MMH 2131, MMH 4255, MMH 16111, MMH 7124, MMH 16425	9
4	8	MMH 1125, MMH 356, MMH 4615, MMH 2112, MMH 2121, MMH 2133, MMH 2225, MMH 4211, MMH 4295, MMH 7111, MMH 7112, MMH 9125, MMH 10212, MMH 15135, MMH 15334, MMH 6235, MMH 1115, MMH 37414	18
5	7	MMH 1312, MMH 3132, MMH 7142, MMH 13115, MMH 4224, MMH 24425, MMH 2333, MMH 2212, MMH 4381, MMH 7131, MMH 5153, MMH 1171, MMH 23413, MMH 28415, MMH 3221, MMH 11315, MMH 16311, MMH 21235	18
6	6	MMH 3145, MMH 2435, MMH 4135, MMH 4174, MMH 4215, MMH 16211, MMH 9111, MMH 12133, MMH 2234, MMH 8625, MMH 11543, MMH 16435, MMH 23422	13
7	5	MMH 28435, MMH 1143, MMH 1151, MMH 2122, MMH 2413, MMH 2424, MMH 4282, MMH 16321, MMH 8142, MMH 8231, MMH 15521	11
8	4	MMH 7252	1
		Total	72

Discussion

Variation for different traits has been previously reported in mungbean (Tabassum et al., 2010) and mashbean (Sharma et al., 2012). But no such evidence for Mung × Mash recombinants is readily available in literature. Yirman et al. (2009) reported that selection efficiency for yield improvement mainly depends upon the amount of genetic variability present for different yield contributing traits and selection based on these traits would be beneficial.

Phenotypic coefficients of variability (PCV) are generally observed to be greater as compared to their corresponding genotypic coefficients of variability (GCV) which indicates the role of environment in the expression of traits as mentioned by Dodake & Dahat (2011). Similar findings have also been reported by Abbas et al. (2005) and Makeen et al. (2007). Whereas, Biradar et al. (2007) reported lesser phenotypic coefficients of variability than their corresponding genotypic coefficients of variability. Our results were also in conformity with the finding of Dodake & Dahat

(2011). Kumar et al. (2010) found similar trend in genetic variation for these traits. Our results were also supported by the findings of Dhananjay et al. (2009) who found considerable range of genetic variability for pods per clusters and pods per plant. Dodake & Dahat (2011) also found lowest genotypic and phenotypic coefficients of variation for days to mature in rice bean.

According to our results, the magnitudes of phenotypic variance were observed to be greater as compared to their respective genotypic and environmental variances for all the traits under study. Ali et al. (2005) also found higher values of phenotypic variance as compared to the corresponding genotypic variance. The estimates of environmental variance were observed to be smaller than their respective genotypic variances for most of the traits which indicated greater contribution of genetic component to the total variance. It seems that genetic variation had the key role in determining the expression of these traits. Similar findings have been reported by Manggoel et al. (2012).

TABLE 8. Mean phenotypic values for various agronomic traits and disease index of Mung × Mash inter-specific recombinant genotypes along with parents

Sr#	Genotype	DF	DM	PLHT	CLUS	PODS	PODL	SPOD	100SW	SYLD/P	%DI
P1	NM 92	40	62	50.33	8.00	34.56	8.44	10.67	5.13	17.21	13.91
P2	NM 2006	40	63	61.22	7.56	20.00	8.44	11.22	5.27	12.23	10.26
P3	Var 6601	57	76	94.11	12.67	32.56	7.78	11.11	3.90	13.96	16.90
1	MMH 1125	45	68	76.67	10.22	40.56	8.44	11.11	4.27	16.53	2.76
2	MMH 1312	46	69	77.00	11.44	35.44	7.89	10.78	4.07	15.44	4.00
3	MMH 210115	51	74	78.56	10.89	29.00	9.00	11.33	5.30	15.56	6.84
4	MMH 3132	48	67	72.44	11.56	30.11	8.22	10.56	4.30	15.14	2.27
5	MMH 3145	49	69	67.67	13.44	30.78	8.11	9.89	4.53	15.84	8.95
6	MMH 3563	45	67	65.56	13.22	43.00	7.89	10.44	4.40	19.02	2.59
7	MMH 3615	46	68	69.22	12.22	34.33	8.56	11.11	4.13	15.69	2.08
8	MMH 4335	46	74	81.22	11.22	23.67	8.56	11.67	5.33	14.14	3.03
9	MMH 4615	50	69	69.56	15.33	31.89	8.33	11.00	4.60	15.60	2.79
10	MMH 7142	46	67	61.22	6.56	14.22	9.11	11.22	6.07	10.97	13.33
11	MMH 53105	55	74	80.22	14.00	24.11	9.44	11.89	5.30	14.01	1.46
12	MMH 5615	55	74	85.67	11.89	29.78	8.33	11.22	5.23	16.81	1.91
13	MMH 28435	42	67	70.44	10.67	26.67	9.00	11.44	4.47	15.63	15.68
14	MMH 1143	39	66	71.56	10.22	25.22	8.56	11.44	4.80	11.96	24.85
15	MMH 1151	39	67	74.22	10.56	19.78	8.22	11.33	5.17	11.73	15.61
16	MMH 13115	44	63	62.33	8.11	19.89	8.78	11.33	5.37	15.50	12.89
17	MMH 2112	42	67	68.56	7.67	15.56	9.44	12.22	5.37	11.07	10.95
18	MMH 2121	49	69	76.00	9.89	19.22	10.11	12.56	5.93	11.70	14.71
19	MMH 2122	46	67	66.67	7.44	17.33	8.78	11.00	5.13	10.52	15.26
20	MMH 2131	44	66	65.89	7.11	16.67	9.33	12.44	5.27	12.31	13.33
21	MMH 2133	51	69	72.56	10.33	22.78	9.22	12.00	6.33	14.50	19.20
22	MMH 4224	45	66	62.11	6.89	16.89	8.78	11.67	5.50	11.39	10.00
23	MMH 2225	41	63	63.00	9.22	27.11	8.89	12.00	5.30	15.13	6.67
24	MMH 24425	41	65	69.89	7.22	18.11	8.89	11.78	5.17	16.30	8.18
25	MMH 2333	46	69	90.56	6.67	14.22	10.00	12.33	5.73	10.47	14.63
26	MMH 2413	43	66	66.33	7.22	17.89	7.89	10.89	5.27	10.98	8.00
27	MMH 2424	42	65	64.22	6.89	14.00	8.56	11.67	5.27	10.74	7.50
28	MMH 2435	44	67	72.33	6.67	14.33	9.11	11.56	5.43	10.79	6.47
29	MMH 4135	45	67	68.22	6.22	12.33	9.56	12.33	5.53	9.69	8.89
30	MMH 4174	46	69	67.44	7.33	14.67	9.00	11.67	5.97	10.90	8.00
31	MMH 4215	51	66	59.33	6.89	16.89	8.78	11.11	5.37	10.89	10.00
32	MMH 4211	50	74	64.00	7.78	17.67	8.78	11.44	6.07	11.31	11.25
33	MMH 2212	45	65	65.00	10.11	30.44	9.11	11.78	5.67	14.47	21.67
34	MMH 4255	43	68	72.67	6.56	15.78	9.56	11.78	6.07	12.21	4.65
35	MMH 4282	46	69	71.67	6.33	15.89	8.56	10.78	6.05	12.68	8.29
36	MMH 4295	43	67	77.44	6.67	19.00	9.56	12.11	5.93	12.92	6.84
37	MMH 4381	49	67	73.22	6.89	16.11	8.78	10.89	5.93	10.42	10.95
38	MMH 16211	45	65	55.22	6.44	14.11	9.11	11.22	5.73	12.22	7.88
39	MMH 7111	45	66	60.67	6.78	16.00	9.11	11.00	6.13	12.64	10.30
40	MMH 16321	45	67	61.89	7.22	15.78	8.89	11.22	5.87	11.04	15.10

TABLE 8. Cont.

Sr#	Genotype	DF	DM	PLHT	CLUS	PODS	PODL	SPOD	100SW	SYLD/P	%DI
41	MMH 7131	43	67	66.44	8.67	20.11	8.67	11.00	5.33	12.39	12.09
42	MMH 5153	45	70	68.67	7.67	16.56	9.22	11.33	5.40	11.43	6.06
43	MMH 7252	45	67	59.44	7.22	14.00	9.22	11.56	5.73	10.72	21.08
44	MMH 8142	45	67	63.44	7.00	13.89	8.67	11.11	5.30	10.03	4.89
45	MMH 8231	46	69	60.89	6.22	14.89	8.44	11.00	6.00	9.56	11.67
46	MMH 7112	44	67	65.44	11.56	30.78	8.33	10.89	5.07	14.47	9.78
47	MMH 9111	44	66	66.11	7.33	19.33	8.67	10.78	5.87	14.81	5.50
48	MMH 9125	44	67	72.33	7.44	18.00	9.33	12.11	5.97	14.89	5.60
49	MMH 10212	50	68	68.33	8.00	16.22	9.11	10.89	6.13	11.68	5.53
50	MMH 12133	52	68	74.00	10.11	29.67	8.11	10.89	4.00	16.96	6.07
51	MMH 1171	45	69	82.44	8.22	17.78	9.56	12.22	5.37	11.06	16.50
52	MMH 15135	45	69	73.22	9.22	20.22	9.11	11.56	6.07	15.22	6.34
53	MMH 15334	49	66	76.89	8.22	20.56	9.22	11.44	6.30	16.16	10.87
54	MMH 6235	49	67	68.78	7.67	23.33	9.22	11.78	6.10	14.19	7.73
55	MMH 23413	45	67	76.56	6.33	16.33	9.22	11.11	5.73	17.77	10.46
56	MMH 2234	42	63	54.89	6.11	15.56	8.33	11.00	5.50	17.76	8.26
57	MMH 28415	45	65	71.67	5.44	12.22	9.33	12.00	6.03	17.32	6.40
58	MMH 1115	46	66	76.11	8.89	22.44	9.22	11.00	6.07	13.63	12.50
59	MMH 3221	43	65	70.89	8.44	20.33	9.22	11.44	5.13	13.94	6.22
60	MMH 15521	43	63	59.33	6.33	14.11	8.56	10.89	5.40	10.21	1.18
61	MMH 8625	43	65	57.56	9.67	37.78	8.22	10.33	4.73	17.96	8.29
62	MMH 11315	46	67	72.22	9.00	20.89	8.78	11.33	5.73	15.74	13.14
63	MMH 11534	46	67	59.89	10.56	30.44	9.56	11.89	6.07	19.98	3.26
64	MMH 11543	46	69	68.33	8.22	18.89	8.56	10.56	5.63	14.71	7.50
65	MMH 37414	45	66	74.33	7.56	19.00	9.00	11.44	6.03	18.38	10.24
66	MMH 16111	45	67	70.11	8.44	21.33	9.11	11.56	6.17	20.09	9.47
67	MMH 16311	49	67	70.67	6.33	19.11	8.89	11.11	5.77	19.13	5.64
68	MMH 7124	45	67	68.67	7.22	17.11	9.44	11.33	5.97	19.08	6.25
69	MMH 16425	45	67	69.00	7.56	18.89	8.78	11.22	6.20	21.07	12.86
70	MMH 16435	45	67	71.33	7.22	16.89	9.11	11.44	5.83	16.27	20.89
71	MMH 21235	45	66	75.11	6.67	16.56	9.00	11.00	5.90	18.86	16.60
72	MMH 23422	44	67	72.44	7.00	22.11	8.22	10.67	5.13	19.79	11.36

MMH= Mung × Mash Hybrid, P1= Parent-1 (NIAB Mung 92), P2= Parent-2 (NIAB Mung 2006), P3= Parent-3 (Variety 6601).

DF = Days to flower, DM = Days to maturity, PLHT = Plant height (cm), CLUS = Clusters/plant, PODS = Pods/Plant, PODL = Pod length (cm), SPOD = seeds/Pod, 100SW = 100-Seed weight (g), SYLD = Seed yield/Plant (g), DI= Disease index.

The estimates of genetic variance were found to be mostly significant as their absolute magnitude exceeded twice their respective standard errors which indicated the presence of sufficient exploitable genetic variability. The presence of available genetic variability for seed yield is crucial (Tabassum et al., 2010). The estimates of genetic variance were close to their respective estimates of phenotypic variance indicating that genotype determined the expression of phenotype

and there is no influence of environment on these traits. Our findings are in conformity with those of Rohman et al. (2003). Abbas & Sadiq (2008) also reported less genetic variability for seeds per pod in mungbean germplasm.

Heritable genetic variation existed which revealed that selection of desirable plants based on phenotypic observations can be made directly for the studied traits. It has been reported that for a population having high heritability values,

selection will be effective (Omoigui et al., 2006). Higher estimates of broad sense heritability for seed yield (Venkateswarlu, 2001), harvest index (Sadiq et al., 2000) and different other traits (Begum et al., 2013; Dhananjay et al., 2009) have also been previously reported in mungbean. Dhananjay et al. (2009) suggested that improvement in mungbean can be made through selection for pods per plant.

The magnitudes of genotypic correlation coefficients were found to be greater than their respective phenotypic correlation coefficients for most of the trait pairs among Mung × Mash recombinant genotypes. The reason might be that the genotypic variances were lower than their corresponding phenotypic variances and it indicated strong association between the traits studied as reported by Rohman et al. (2003). Ali et al. (2005) also observed similar trend for most of the traits. Both genetic and phenotypic correlations showed consistency in their direction of sign (either positive or negative) as observed by Asghar & Khan (2005). Our results are in accordance with the finding of Begum et al. (2013) who reported positive correlation of seed yield with number of pods per plant. Similarly, Srivastava & Singh (2012) noted positive phenotypic association of pod length with 100-seed weight. Negative genotypic and phenotypic correlations of pods plant⁻¹ with pod length and seeds per pod have been previously reported (Abbas & Sadiq, 2008). Ahmad et al. (2013) observed positive significant correlations of seed yield per plant with clusters per plant and pods per plant which is confirmation of our results. Likewise, other workers also noted positive associations of seed yield per plant with clusters per plant (Ali et al., 2005) and pods per plant (Makeen et al., 2007; Srivastava & Singh, 2012). Strong linear genetic relationship of clusters per plant with pods per plant and their positive associations with days to flower, days to maturity, plant height and seed yield revealed the importance of vegetative growth of the plant in increasing seed yield through the development of optimum biomass required for high seed yield. Good vegetative growth of the plant allows for the development of optimum canopy necessary for high yield (Ishiyaku et al., 2005). This is due to the fact that late flowering would provide extra time for vegetative growth of the plant leading to increase in plant height coupled with the production of more number of clusters bearing more pods. It has been reported in a recent study that increases in days to flower

leads to the production of more yields. Similar results were earlier reported by Manggoel et al. (2012). Positive and significant genetic relationships of pod length with seeds per pod and 100-seed weight depicted that long pods would bear more number of seeds with increased seed size. But their negative genetic associations with seed yield indicated that by increasing any of these traits would lead to a decrease in seed yield.

Contrary to the above facts, negative and significant genetic relationships of pods per plant with pod length, seeds per pod and 100-seed weight suggested that increased number of pods would reduce pod size, and number and size of grains. In view of these facts it may be suggested that such traits may be sacrificed, since the vegetative phase is more important and the worth of large number of clusters and pods may not be ignored in increasing the seed yield. However, the genetic relationships among pod size, and number and size of grains generated useful information about their genetic makeup.

Positive and highly significant phenotypic correlations were observed among studied traits. Similar results have also been reported in literature (Sadiq et al., 2000; Biradar et al., 2007; Makeen et al., 2007). Negative and highly significant phenotypic correlations were also noted for among some trait pairs which is in line with the findings of Dhananjay et al. (2009). On the basis of results, it has been concluded that the traits, viz; pod length, seeds per pod and 100-seed weight showed positive associations with each other but they had negative effects on seed yield per plant. Hence, clusters per plant and pods per plant may be included in selection criteria for the improvement of seed yield in mungbean.

Estimates of correlated response can be exploited to increase the expression of a primary trait if selection for a secondary trait produces greater genetic gain in the primary trait than direct selection (Hallauer & Miranda, 1998).

It is evident from results that the pods per plant showed extreme potential for improving seed yield per plant. Pods per plant appeared to be the most important secondary trait for improving seed yield. The results are in accordance with the findings of Chaudhary & Joshi (1992). Therefore, indirect selection for seed yield per plant through selection for pods per plant and clusters per plant may improve mean seed yield. Peng & Lu (1995) reported the effectiveness of indirect selection over

direct selection. Some traits expressed negative responses to indirect selection for seed yield per plant. These traits did not express any potential to improve yield rather they may tend to cause decline in yield. Therefore, selection cannot be based on such traits. However, direct selection is feasible for the improvement of these traits. It has been noted that correlated responses may cause changes in favorable or unfavorable directions in agronomically important traits when direct selection for a single trait is practiced (Cervantes-Martinez, 2002). Over all, the results suggested that healthy tall plants with increased number of clusters and pods had the potential to increase seed yield. Moreover, in such plants flowering would be initiated later which may be due to increased vegetative phase. As a result, the reproductive phase would be reduced. Negative correlated response of days to mature to selection for seed yield exhibited positive association of seed yield with earliness thereby indicating that reproductive phase would be comparatively shorter. Therefore, it may be suggested that the selection of genotypes with early maturing healthy tall plants would be beneficial to increase yield potential. Malik et al. (1988) suggested that early maturity makes the genotypes more suitable for intercropping practices and they possess greater degree of tolerance to yellow mosaic disease.

The results of present study seemed that the feasibility of indirect selection for some yield components showing promise for greatest improvement in seed yield made it mandatory to give due importance to all such traits in the improvement of mungbean. Combined with these traits is the resistance to diseases which may not be ignored. Therefore, selection of promising high yielding and disease resistant mung × mash recombinant genotypes on the basis of above mentioned traits will not only lead to the strengthening of future breeding programme but will also help in the evolution of high yielding varieties. Amin et al. (2014) found that the most effective means of increasing yield was by selecting for different important yield related traits. It has been found that index scores of individual traits based on metroglyph analysis are helpful in identifying the undesirable traits (Abbas et al., 2010). Similarly, Asghar et al. (2010) suggested the selection of superior genotypes through desirability index. Such genotypes may be used in hybridization programme as parents for the development of future varieties as suggested by Sultana et al. (2010). Overall, the studied genotypes exhibited high

yield potential coupled with disease resistance. Considering the worth of these genotypes, it is suggested that these may be selected as promising genotypes for further evaluation.

Conclusion

The traits clusters per plant, pods per plant and 100-seed weight were identified as important characters and may be used as selection criteria for the improvement of mungbean × mashbean recombinants. Selection for number of pods per plant among different agronomic traits showed greatest improvement in seed yield. The studies showed that seven recombinant genotypes, viz; MMH 1115, MMH 4224, MMH 4255, MMH 7124, MMH 2112, MMH 4295 and MMH 2225 were superior in overall performance and selected as elite lines.

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