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Location effect on heritability estimates of yield traits in mungbean derived from F_2 populations

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Heritability and genetic advance were estimated in four F_2 mungbean populations (Ramzan×ML-5, NM-92×NM-1919, NM-1919×ML-5 and ML-5×NM-51) at two locations (Peshawar and Swat) of Khyber Pakhtunkhwa province, Pakistan, during 2008. Combined analysis exhibited highly significant differences among the genotypes and locations for pods plant^{-1}, pod length, seeds pod^{-1}, 1000-seed weight and seed yield. Similarly, genotype-by-location interaction was highly significant for pods plant^{-1} and 1000-seed weight. Averaged over five parents and four F_2 populations, means for clusters plant^{-1}, pods plant^{-1}, pod length, seeds pod^{-1}, 1000-seed weight and seed yield plant^{-1} at Peshawar and Swat were 9.2 vs. 9.8, 28.7 vs. 35.3, 8.5 vs. 8.7 cm, 9.3 vs. 10.0, 50.4 vs. 56.5 g and 7.1 vs. 7.6 g, respectively. Broad-sense heritability estimates in four F_2 population of mungbean ranged from 0.22 to 0.70 and 0.34 to 0.58 for clusters plant^{-1}, 0.33 to 0.75 and 0.19 to 0.61 for pods plant^{-1}, 0.19 to 0.74 and 0.45 to 0.68 for pod length, 0.21 to 0.58 and 0.48 to 0.66 for seeds pod^{-1}, 0.34 to 0.63 and 0.58 to 0.89 for 1000-seed weight and 0.15 to 0.64 and 0.45 to 0.61 for seed yield at Peshawar and Swat, respectively. Genetic advance was greater at Swat than at Peshawar. Among the four F_2 populations, genetic improvement of yield-associated traits will be more effective in Ramzan×ML-5 and ML-5×NM-51. Moreover, among the parents, ML-5 showed good combination with Ramzan and NM-51.

Key words: Heritability, harvest traits, F_2 populations, mungbean.

INTRODUCTION

Mungbean production is adversely affected by number of factors including low genetic potential of existing cultivars, environmental stresses, diseases, pests and poor cultural management. The average yield of mungbean in Pakistan is less than that of the world average. The major reason for this low yield is the unavailability of genotypes with high yield potential and adaptability to different ecological zones. To meet the demands of an ever-increasing population, plant breeders are continuously engaged to improve the gene-tic level of mungbean. To make significant genetic

improvement in mungbean production, information is needed on nature and magnitude of genetic variation in quantitative characters and their inter-relationship in population comprising diverse genotypes. Several plant researchers have emphasized on the use of heritability and genetic advance in identification of desirable populations in legumes (Malik et al., 1988; Ghafoor et al., 1990, 2000; Ullah et al., 2011a).

Development of a new variety with high yield and stable performance is the target of all breeders. Earliest step in a successful crop breeding program is to select appropriate parents. The search of inherited variation following the cross between diverged genotypes has been an important tool in genetic research for decades (Falconer and MacKay, 1996). The success of most crop improvement programs largely depends upon the genetic

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Table 1. List of F_2 mungbean populations along with parents evaluated at Agricultural University Peshawar and Mingora, Swat during 2008.

Parents	Salient characteristics
Ramzan	Early maturing, resistant to Mungbean Yellow Mosaic Virus (MYMV), bold seeded
ML-5	Late maturing, indeterminate, small seed size, moderate resistant to MYMV
NM-92	Photo-insensitive, early flowering, and maturity, MYMV resistant
NM1919	Mutant line, early blooming and maturing
NM-51	Early, bold seeded, dull seed color, tolerant to *cercospora* leaf spot

variability and the heritability of desirable traits. The magnitude and type of genetic variability helps the breeders to determine the selection criteria and breeding schemes to be used for improvement purposes. For any planned mungbean breeding program to improve seed yield potential through important parameters of crops, it is necessary to obtain adequate information on the magnitude and type of genetic variability and their corresponding heritability (Ullah et al., 2010). This is because selection of superior genotypes is proportional to the amount of genetic variability present and the extent to which the characters are inherited. Heritability indicates the relative degree of a character transmitted from parents to progeny. The magnitude of such estimates also suggests the extent to which improvement is possible through selection. Brigges and Knowles (1967) forwarded the view that if the environmental variability is negligible compared to genetic variability, selection will be effective in improving the character if such character has high genetic variability and is also highly correlated with yield. Grafius et al. (1976, 1978) applied this concept to practical breeding by employing cultivar differences in morphological traits to select genetically diverse breeding parents.

In this study, four F_2 mungbean populations namely Ramzan×ML-5, NM-92×NM-1919, NM-1919×ML-5 and ML-5×NM-51 and the five parents were evaluated at two locations (Peshawar and Swat) of Khyber Pakhtunkhwa to determine broad-sense heritability and genetic advance for yield associated traits.

MATERIALS AND METHODS

Five diverse mungbean parents obtained from Nuclear Institute for Food and Agriculture, Peshawar, were crossed at Agricultural University Peshawar during spring 2007 and F_2 were obtained raising F_1 in summer 2007. The resultant four F_2 populations and parental lines were planted in RCB design using four replications at Agricultural University, Peshawar and Agricultural Research Institute, Mingora, Swat, during 2008 (Table 1). Plot size for F_2 mungbean populations and parents in each replication was 2.4 m^2. Each plot comprised two rows each with 4 m long with row-to-row and plant-to-plant distance of 0.30 and 0.10 m, respectively. A single row between adjacent plots was kept fallow to facilitate data recording on the following parameters: Harvest traits related to yield, which include clusters plant^{-1} (no.), pods plant^{-1} (no.), pod length (cm), seeds pod^{-1} (no.), 1000-seed weight (g) and seed yield plant^{-1} (g).

Broad-sense heritability on the basis of single plant was estimated using the following modified version of the formula proposed by Mahmud and Kramer (1951):

$h^2_{Bs} = (VF_2 - \sqrt{(VP_1 + VP_2)}/VF_2$

Where, h^2_{Bs} is the broad sense heritability for a specific trait at each location; VP_1, VP_2, and VF_2 are phenotypic variances among parent 1, parent 2 and F_2 plants for a specific trait at each location. The estimates of broad-sense heritability were used to predict effectiveness of selection as genetic advance at specific selection intensity (20%) in the four F_2 mungbean populations as follows (Falconer and Mackay, 1996):

$G_A = i_X \sigma_{PX} h^2_X$

Where, i_X is the selection intensity for trait x; h^2_X is the heritability for trait x in a specific F_2 population at each location and σ_{PX} is the square root of the phenotypic variance of trait x in a specific F_2 population at each location.

RESULTS AND DISCUSSION

Clusters and pods plant^{-1}

More number of clusters plant^{-1} is an important yield component in mungbean breeding program. Combined analysis exhibited highly significant (P≤0.01) differences among the genotypes and locations; however, G×L interaction was significant (P≤0.05) for clusters plant^{-1} (Table 2). Analysis of variance at each location also showed highly significant variation among the genotypes, parents and F_2 populations. Similarly, the contrast effect of parents vs. F_2 was also significant for clusters plant^{-1} at both locations. The coefficient of variation for clusters plant^{-1} was comparatively higher at Swat (5.8%) than at Peshawar (5.4%). Number of clusters bearing pods ranged from 6.4 to 10.7 at Peshawar vs. 8.3 to 11.0 at Swat (Table 3). Clusters plant^{-1} for parents averaged 8.8 at Peshawar and 9.5 at Swat. Similarly, averaged over four F_2 populations, clusters plant^{-1} at Peshawar were 9.7 vs. 10.2 at Swat. Averaged over five parents and four F_2 populations, clusters plant^{-1} were 9.2 vs. 9.8 at Peshawar and Swat, respectively. Among the parents, highest clusters plant^{-1} was recorded for ML-5 (10.1). Similarly, the highest clusters producing population was NM-92×NM-1919 (10.9 clusters plant^{-1}).

Magnitude of broad-sense heritability for clusters plant^{-1} among the four F_2 mungbean populations ranged from

Table 2. Mean squares for clusters and pods plant[-1] of parents and F_2 populations of mungbean evaluated at Peshawar and Swat during 2008.

Source	Degrees of freedom	Clusters plant[-1]			Pods plant[-1]		
		Pooled	Peshawar	Swat	Pooled	Peshawar	Swat
Location (L)	1	5.6*	-	-	774.2**	-	-
Reps (L)	6	0.9	-	-	55.8	-	-
Genotypes (G)	8	9.5**	6.6**	3.61**	48.7**	52.0*	59.5**
Parents	4	-	9.0**	3.3**	-	83.5**	14.2[NS]
F_2	3	-	3.4**	3.8**	-	21.1[NS]	114.2**
Parents vs. F_2	1	-	7.0**	13.7**	-	18.5[NS]	7.6**
G × L	8	0.7*	-	-	62.8**	-	-
Error	48(24)	0.3	0.3	0.3	14.7	19.2	10.2
CV (%)	-	5.6	5.4	5.8	12.0	15.2	9.0

*,** Significant at 5 and 1% probability level, respectively. [NS] Non-significant. Value in parenthesis refer to error df for individual location.

Table 3. Means for clusters and pods plant[-1] for parents and F_2 populations of mungbean evaluated at Peshawar and Swat during 2008.

Genotype	Clusters plant[-1] (no.)			Pods plant[-1] (no.)		
	Peshawar	Swat	Mean	Peshawar	Swat	Mean
Ramzan	6.4	8.3	7.4	29.5	32.4	31.0
ML-5	9.9	10.3	10.1	37.2	33.2	35.2
NM-92	8.4	8.8	8.6	25.8	33.0	29.4
NM-1919	9.9	9.7	9.8	26.9	37.2	32.1
NM-51	9.6	10.3	10.0	27.5	34.2	30.9
Ramzan×ML-5	8.5	8.8	8.7	25.0	31.6	28.3
NM-92×NM-1919	10.7	11.0	10.9	27.6	44.0	35.8
NM-1919×ML-5	10.1	10.4	10.3	28.7	37.8	33.3
ML-5×NM-51	9.6	10.5	10.1	30.5	34.3	32.4
LSD (0.05)	0.7	0.8	0.8	6.4	4.7	5.6
Parents mean	8.8	9.5	-	29.4	34.0	-
F_2 pop mean	9.7	10.2	-	27.9	36.9	-
Location mean	9.2	9.8	-	28.7	35.3	-

0.22 to 0.70 at Peshawar and 0.34 to 0.58 at Swat (Table 8). Maximum broad-sense heritability for clusters plant[-1] at both locations was recorded for ML-5×NM-51 (0.70 at Peshawar and 0.58 at Swat) followed by Ramzan×ML-5 (0.65 at Peshawar and 0.58 at Swat). Considering 20% selection intensity, genetic advance for clusters plant[-1] ranged from 1.0 to 4.0 units at Peshawar vs. 2.8 to 5.3 units at Swat. Although, the heritability of ML-5×NM-51 at Swat was moderate, however, the resultant genetic advance was greater in magnitude. Low to moderate broad-sense heritability of 15.7 to 33.3% and genetic advance of 24.8 to 68.7% for clusters plant[-1] in mungbean have been reported by Idress et al. (2006). Abbas et al. (2005) reported positive and significant correlation of seed yield with clusters plant[-1], pods plant[-1], pod length and seeds pod[-1] in mungbean. Sarwar et al. (2004) reported high heritability and genetic advance for

pods plant[-1] in F_3 populations of 6601×NM-92 and NM-92×Pusa Baisakhi and attributed it to additive gene action.

In addition, combined analysis of variance exhibited highly significant (P≤0.01) differences among mungbean genotypes, as well as two test locations for pods plant[-1]. G×L interaction effect was also highly significant for pods plant[-1]. The coefficient of variation for pods plant[-1] across the two locations was 12.0%. Analysis of variance at Peshawar showed significant (P≤0.05) differences among the genotypes for pods plant[-1]. Partitioning the genotypes into parents, F_2 and their contrast, pods plant[-1] were highly significant among the parents while non-significant for F_2 population and parents vs. F_2 contrast at Peshawar. Similarly, at Swat analysis showed that geno-types, F_2 and parents vs. F_2 contrast were highly significant for pods plant[-1]. However, the parents showed

Table 4. Mean squares for pod length and seeds pod^{-1} of parents and F_2 populations of mungbean evaluated at Peshawar and Swat during 2008.

Sources	Degree of freedom	Pod length			Seeds pod^{-1}		
		Pooled	Peshawar	Swat	Pooled	Peshawar	Swat
Location (L)	1	1.0**	-	-	8.1**	-	-
Reps (L)	6	0.01	-	-	0.2	-	-
Genotypes (G)	8	5.6**	2.8**	2.9**	11.2**	4.6**	7.2**
Parents	4	-	4.9**	5.1**	-	7.8**	13.9**
F_2	3	-	1.0*	6.1**	-	1.7*	0.1^{NS}
Parents vs. F_2	1	-	0.01^{NS}	0.1^{NS}	-	0.01^{NS}	1.4*
G × L	8	0.4^{NS}	-	-	0.6^{NS}	-	-
Error	48(24)	0.5	0.2	0.1	0.4	0.5	0.3
CV (%)	---	4.2	5.6	4.2	6.2	7.2	5.1

*,** = Significant at 5 and 1% probability level, respectively. ^{NS}Non-significant. Value in parenthesis refer to error df for individual location.

a non-significant variation at Swat for this particular trait (Table 2). Pods plant^{-1} ranged from 25.0 to 37.2 at Peshawar vs. 31.6 to 44.0 at Swat. Mean values of pods pant^{-1} for parents were 29.4 vs. 34.0 at Peshawar and Swat, respectively. Similarly, mean pods plant^{-1} for the F_2 population was 27.9 at Peshawar and 36.9 at Swat. Averaged over five parents and four F_2 populations mean at Peshawar (28.7) was comparatively less than at Swat (35.3) for pods plant^{-1}. Across two locations the lowest and highest number of pods plant^{-1} among the parents was recorded for ML-5 (35.2) and NM-92 (29.4). Among the F_2 populations highest pods plant^{-1} were produced by NM-92×NM-1919 (35.8) and lowest by Ramzan×ML-5 (28.3). Both of the F_2 populations also had highest and lowest clusters plant^{-1} respectively (Table 3).

Broad-sense heritability for pods plant^{-1} among the four F_2 populations ranged from 0.33 to 0.75 at Peshawar vs. 0.19 to 0.61 at Swat (Table 8). F_2 population Ramzan×ML-5 (0.75 and 0.57) and ML-5×NM-51 (0.73 and 0.61) had the highest heritability for pods plant^{-1} at both locations. Genetic advance for pods plant^{-1} ranged from 1.6 to 3.9 at Peshawar and 1.6 to 6.4 at Swat. The broad-sense heritability for seed yield, pods plant^{-1}, seeds pods^{-1} and seed weight in mungbean has been reported to be 89.4, 75.3, 66.8 and 76.2%, respectively (Ramana and Singh, 1987). Similarly, Kalia and Sood (2004) have reported that high heritability (97%) along with high genetic advance (126%) for pod yield indicated the additive gene action in broad bean. Idress et al. (2006) reported high broad-sense heritability of 90.8% and genetic advance (60.6%) for pods plant^{-1} in F_2 population of mungbean.

Pod length and seeds pod^{-1}

Pod length and more number of seeds are primary yield known parameters in mungbean. Of these, pod length is

an important yield contributing trait in mungbean. A long pod with compact seeds has positive impact on seed yield. The pooled analysis of variance revealed highly significant (P≤0.01) differences among mungbean genotypes and locations for pod length (Table 4). The G×L interaction effect was non-significant for pod length. The coefficient of variation across locations for pod length was 4.2%. Individual location mean squares for pod length exhibited highly significant differences for genotypes and parents. Similarly, F_2 populations were also highly significant for pod length at Swat but significant at Peshawar. The parents vs. F_2 contrast were non-significant for pod length at both locations. Length of pod ranged from 7.5 to 10.4 cm at Peshawar vs. 7.7 to 10.6 cm at Swat (Table 5). Mean pod length for parents (8.5 vs. 8.7 cm) and for F_2 populations (8.5 vs. 8.8 cm) was recorded at Peshawar and at Swat, respectively. Averaged over five parents and four F_2 populations, pod length was 8.5 and 8.7 cm at Peshawar and Swat, respectively. Averaged over two locations mungbean parents with longest and shortest pod was NM-92 (10.5 cm) and ML-5 (7.6 cm), respectively. Among the four F_2 populations, Ramzan×ML-5 had 1.3 and 1.7 cm long pod than Ramzan and ML-5 parents, respectively. Similarly, F_2 populations NM-1919×ML-5 and ML-5×NM-51 each had 8.6 cm long pod.

Broad-sense heritability for pod length among the four F_2 mungbean populations ranged from 0.19 to 0.74 at Peshawar and 0.45 to 0.68 at Swat (Table 8). Maximum broad-sense heritability for pod length was observed for ML-5×NM-51 (0.74 vs.68) and Ramzan×ML-5 (0.67 vs. 0.59) at Peshawar and Swat, respectively. Using 20% selection intensity, genetic advance for pod length ranged from 0.9 to 5.0 cm at Peshawar vs. 3.8 to 6.7 cm at Swat. Genotypes with high heritability produced more genetic advance. At both locations maximum genetic advance (5.0 vs. 6.7 cm) for pod length was recorded for ML-5×NM-51. Similarly, Ramzan×ML-5 had 4.0 and 5.1 cm

Table 5. Means for pod length and seeds pod[-1] for parents and F_2 populations of mungbean evaluated at Peshawar and Swat during 2008.

Genotype	Pod length (cm)			Seeds pod[-1] (no.)		
	Peshawar	Swat	Mean	Peshawar	Swat	Mean
Ramzan	8.0	8.0	8.0	8.5	8.7	8.6
ML-5	7.5	7.7	7.6	8.3	9.2	8.8
NM-92	10.4	10.6	10.5	11.8	13.4	12.6
NM-1919	8.3	8.7	8.5	9.0	10.1	9.6
NM-51	8.1	8.4	8.3	9.3	9.6	9.5
Ramzan×ML-5	9.2	9.3	9.3	10.3	10.0	10.2
NM-92×NM-1919	8.1	8.2	8.2	8.8	9.6	9.2
NM-1919×ML-5	8.4	8.7	8.6	9.0	9.7	9.4
ML-5×NM-51	8.3	8.9	8.6	9.3	9.8	9.6
LSD $_{(0.05)}$	0.7	0.5	0.6	0.9	0.7	0.8
Parents mean	8.5	8.7	-	9.4	10.2	-
F_2 pop mean	8.5	8.8	-	9.4	9.8	-
Location mean	8.5	8.7	-	9.3	10.0	-

genetic advance for pod length at Peshawar and Swat, respectively. The long pod showing a direct proportion with grain yield as it had the potential to accommodate more seeds in pod. The additive gene action was found significant for pod length in mungbean segregating populations (Aher et al., 2001; Khattak et al., 2001).

Combined analysis of variance exhibited highly significant (P≤0.01) differences among mungbean genotypes as well as two test locations for seeds pod[-1]. But, G×L interaction effect was non-significant for seeds pod[-1]. The coefficient of variation for seeds pod[-1] across the two locations was 6.2%. Analysis of variance at each location also showed highly significant (P≤0.01) differences among the genotypes for seeds pod[-1]. Partitioning the genotypes into parents, F_2 and parents vs. F_2 contrast seeds pod[-1] were highly significant among the parents at both locations, while significant for F_2 population at Peshawar. Similarly, parents vs. F_2 contrast were significant at Swat for seeds pod[-1] (Table 4). Seeds pod[-1] ranged from 8.3 to 11.8 at Peshawar vs. 8.7 to 13.4 at Swat. Mean values of seeds pod[-1] for parents was 9.4 vs. 10.2 at Peshawar and Swat, respectively (Table 5). In addition, mean seeds pod[-1] for the F_2 population was 9.4 at Peshawar and 9.8 at Swat. Averaged over five parents and four F_2 populations mean at Peshawar (9.3) was comparatively less than that at Swat (10.0) for seeds pod[-1]. Across two locations among the parents maximum seeds pod[-1] (12.6) was recorded for NM-92. Similarly, among the four F_2 populations Ramzan×ML-5 (10.2) had the highest number of seeds pod[-1]. Least number of seeds (9.2) pod[-1] was recorded for NM-92×NM-1919 across location.

More also, magnitude of broad-sense heritability for seeds pod[-1] among the four F_2 mungbean populations was moderate (0.21 to 0.58) at Peshawar and high (0.48 to 0.66) at Swat (Table 8). Maximum broad-sense herit-

ability (0.58 vs. 0.66) for seeds pod[-1] was recorded for Ramzan×ML-5 at Peshawar and Swat, respectively. In contrast, the least estimate of heritability (0.21 vs. 0.48) was recorded for NM-92×NM-1919 at Peshawar and Swat, respectively. Due to variation in the mean variance of parents used for the calculation of heritability and genetic advance the values for genetic advance scattered differently. Considering 20% selection intensity, genetic advance for seeds pod[-1] ranged from 1.4 to 3.5 at Peshawar vs. 3.1 to 5.0 at Swat. Genotypes with maximum heritability also coupled with maximum genetic advance Ramzan×ML-5 (3.5 vs. 4.9) and ML-5×NM-51 (3.0 vs. 5.0) for seeds pod[-1]. Idress et al. (2006) reported a low magnitude of broad-sense heritability (18.7%) and genetic advance (56.9%) for pod length in mungbean. Pod length and seeds pod[-1] showed very low genotypic and phenotypic variations resulting in less heritability and genetic advance values in almost all the cross combinations of mungbean (Sarwar et al., 2004). Positive association of pods plant[-1] and seeds pod[-1] with seed yield in mungbean genotypes of diverse origin have been reported (Aslam et al., 2002; Saifullah and Hassan, 2002). These results also confirmed the findings of Ram and Singh (1997) who reported high heritability for pod length and seed yield in cowpea.

1000-seed weight and seed yield

Selection based on yield components is advantageous if different yield related traits have been well documented. The knowledge of interrelationship among various developmental and productive traits is necessary for framing an effective breeding programme. Combined analysis of variance exhibited highly significant (P≤0.01) differences among mungbean genotypes as well as two test

Table 6. Mean squares for 1000-seed weight and seed yield of parents and F_2 populations of mungbean evaluated at Peshawar and Swat during 2008.

Sources	Degree of freedom	1000-seed weight			Seed yield plant^{-1}		
		Pooled	Peshawar	Swat	Pooled	Peshawar	Swat
Location (L)	1	665.5**	---	---	5.2**	---	---
Reps (L)	6	1.1	---	---	0.02	---	---
Genotypes (G)	8	399.9**	161.8**	248.6**	18.1**	9.8**	8.4**
Parents	4	---	261.9**	318.0**	---	13.9**	11.6**
F_2	3	---	21.5**	32.1**	---	7.1**	6.7**
Parents vs. F_2	1	---	181.9**	620.5**	---	0.9**	0.6**
G × L	8	10.5**	---	---	0.1^{NS}	---	---
Error	48(24)	3.1	2.7	3.6	0.08	0.1	0.1
CV (%)	---	3.3	3.2	3.3	3.9	4.1	3.7

** = Significant at 1% probability level; ^{NS}Non-significant. Value in parenthesis refer to error df for individual location.

Table 7. Means for 1000-seed weight and seed yield for parents and F_2 populations of mungbean evaluated at Peshawar and Swat during 2008.

Genotype	1000-seed weight (g)			Seed yield plant^{-1} (g)		
	Peshawar	Swat	Mean	Peshawar	Swat	Mean
Ramzan	45.8	49.2	47.5	8.8	9.0	8.9
ML-5	37.5	41.4	39.5	5.6	6.6	6.1
NM-92	59.7	65.1	62.4	8.5	8.9	8.7
NM-1919	51.4	57.4	54.4	4.8	5.3	5.1
NM-51	47.7	50.9	49.3	8.4	8.9	8.7
Ramzan×ML-5	53.6	62.7	58.2	7.4	8.0	7.7
NM-92×NM-1919	50.8	59.5	55.2	5.6	6.1	5.9
NM-1919×ML-5	55.9	64.3	60.1	8.5	9.0	8.8
ML-5×NM-51	51.4	58.1	54.8	6.1	6.8	6.5
LSD $_{(0.05)}$	2.4	2.8	2.6	0.42	0.41	0.42
Parents mean	48.4	52.8	-	7.2	7.7	---
F_2 mean	52.9	61.2	-	6.9	7.5	---
Location mean	50.4	56.5	---	7.1	7.6	---

locations for 1000-seed weight (Table 6). Similarly, G×L interaction effect was also highly significant for seed weight. The coefficient of variation for 1000-seed weight across the two locations was 3.3%. Analysis of variance at each location exhibited highly significant (P≤0.01) differences among the genotypes for 1000-seed weight. Partitioning of the genotypes into parents, F_2 and parents vs. F_2 contrast, seed weight was also highly significant among the parents, F_2, and parents vs. F_2 contrast at each location. Among the five parents and four F_2 populations, 1000-seed weight ranged from 37.5 to 59.7 g at Peshawar vs. 41.4 to 65.1 g at Swat (Table 7). Averaged over five parents and four F_2 population mean, 1000-seed weight at Peshawar was 50.4 and 56.5 g at Swat. Across two locations among the parents highest 1000-seed weight (62.4 g) was recorded for NM-92 which also showed maximum pod length and seeds pod^{-1}. Similarly, among the four F_2 populations, maximum 1000-

seed weight (60.1 g) was recorded for NM-1919×ML-5. ML-5×NM-51 had the minimum 1000-seed weight of 54.8 g because the involved parents also had least seed weight. Seed yield being a complex and multifaceted character, is an ultimate expression of different factors. Though not many reports demonstrated the effects of seed size on yield, small seeds of several crop species had little influence on final seed yield (LeRoy et al., 1991; Tinius et al., 1991). However, the effect of seed size on yield is associated with planting time and location (Sexton et al., 1994). Seed size also has an indirect effect on number of seeds pod^{-1} which is a known yield component (Board et al., 1999).

Magnitude of broad-sense heritability for 1000-seed weight among the four F_2 mungbean populations was (0.34 to 0.63) at Peshawar and (0.58 to 0.89) at Swat (Table 8). All the tested F_2 populations produced more heritability at Swat for 1000-seed weight. Among them

Table 8. Heritability ($h^2_{(BS)}$) and genetic advance (G_A) in four F_2 mungbean populations for yield and associated traits at Peshawar and Swat during 2008.

Trait	F_2 population	Peshawar		Swat	
		$h^2_{(BS)}$	G_A	$h^2_{(BS)}$	G_A
Clusters plant[-1]	Ramzan×ML-5	0.65	3.4	0.58	5.3
	NM-92×NM-1919	0.22	1.0	0.34	2.8
	NM-1919×ML-5	0.24	1.1	0.37	2.9
	ML-5×NM-51	0.70	4.0	0.58	5.0
Pods plant[-1]	Ramzan×ML-5	0.75	3.8	0.57	5.6
	NM-92×NM-1919	0.33	1.6	0.19	1.6
	NM-1919×ML-5	0.39	1.8	0.30	2.5
	ML-5×NM-51	0.73	3.9	0.61	6.4
Pod length (cm)	Ramzan×ML-5	0.67	4.0	0.59	5.1
	NM-92×NM-1919	0.27	1.4	0.45	3.8
	NM-1919×ML-5	0.19	0.9	0.56	5.0
	ML-5×NM-51	0.74	5.0	0.68	6.7
Seeds pod[-1]	Ramzan×ML-5	0.58	3.5	0.66	4.9
	NM-92×NM-1919	0.21	1.4	0.48	3.1
	NM-1919×ML-5	0.55	4.1	0.52	3.3
	ML-5×NM-51	0.48	3.0	0.63	5.0
1000-seed weight (g)	Ramzan×ML-5	0.53	3.0	0.89	7.5
	NM-92×NM-1919	0.47	2.4	0.58	2.8
	NM-1919×ML-5	0.34	1.6	0.68	3.4
	ML-5×NM-51	0.63	4.2	0.87	6.9
Seed yield (g)	Ramzan×ML-5	0.53	3.2	0.61	6.1
	NM-92×NM-1919	0.15	0.7	0.45	4.3
	NM-1919×ML-5	0.45	2.5	0.59	6.2
	ML-5×NM-51	0.64	4.0	0.58	5.4

ML-5×NM-51 and Ramzan×ML-5 had maximum heritability at both locations. In contrast, the minimum magnitude of heritability at Peshawar for 1000-seed weight was recorded for NM-1919×ML-5 (0.34). But at Swat the low heritability was recorded for NM-92×NM-1919 (0.58). At 20% selection intensity, genetic advance for 1000-seed weight ranged from 1.6 to 4.2 at Peshawar vs. 2.8 to 7.5 at Swat. At Peshawar maximum genetic advance (4.2 g) was recorded for F_2 population ML-5×NM-51. However, at Swat Ramzan×ML-5 excelled with 7.5 g genetic advance for 1000-seed weight. Idress et al. (2006) reported 50.1 and 68.5% of the broad-sense heritability and genetic advance respectively, in mungbean for 100-seed weight. Sarwar et al. (2004) reported that while making selection, pods plant[-1] should be given more emphasis followed by 100-seed weight, seeds pod[-1] and preference must be given to medium tall plant. Bravo et al. (1980) have reported that pod width is more effective than direct selection for seed weight per

se in bean. Similarly, indirect selection for seed weight should be carried out early when pod reach to maximum width and length, while seed weight obtained after harvesting.

Combined analysis for seed yield plant[-1] exhibited highly significant (P≤0.01) differences among the genotypes and test locations. The G×L interaction effect was non-significant across locations for seed yield. Coefficient of variation was 3.9% for seed yield across two locations (Table 6). Analysis of variance at each location also showed highly significant variation among the genotypes, parents, F_2 populations. Similarly, the contrast effect of parents vs. F_2 was also highly significant for seed yield plant[-1] at both locations. Seed yield plant[-1] ranged from 4.8 to 8.8 g at Peshawar vs. 5.3 to 9.0 g at Swat (Table 7). Mean seed yield for parents was 7.2 g at Peshawar and 7.7 g at Swat. Similarly, averaged four F_2 populations seed yield plant[-1] at Peshawar was 6.9 vs. 7.5 g at Swat. Averaged over five parents and four F_2 populations,

location mean for seed yield plant^{-1} was 7.1 vs. 7.6 g at Peshawar and Swat, respectively. Among the parents across two locations high and low yielding genotypes were Ramzan (8.9 g) and NM-1919 (5.1 g), respectively.

Similarly, among the four F_2 populations the low yielding population was NM-92×NM-1919 (5.9 g) and high yielding population was NM-1919×ML-5 (8.8 g).

Estimates of heritability showed that seed yield is under the influence of additive genes and environmental stresses have some remarkable effects on the expression of this character. Magnitude of broad-sense heritability for seed yield plant^{-1} among the four F_2 mungbean populations was low to high ranged from 0.15 to 0.64 at Peshawar and 0.45 to 0.61 at Swat (Table 8). Maximum broad-sense heritability was recorded for ML-5×NM-51 (0.64) and Ramzan×ML-5 (0.61) at Peshawar and Swat respectively. Considering 20% selection intensity, genetic advance for seed yield plant^{-1} ranged from 0.7 to 4.0 at Peshawar vs. 4.3 to 6.2 at Swat. The genetic advance for seed yield was high at Swat for all the F_2 populations than at Peshawar. The differences in the results might be due to experimental material and environments under which the experiment was conducted because polygenic characters are more influenced by the environmental fluctuation.

Additive type of genes may be exploited more efficiently by selecting genotypes on the basis of seed yield in all cross combinations as they all possessed very high degree of heritability and genetic advance. Idress et al. (2006) have reported high broad-sense heritability (68.4%) and genetic advance (87.6%) for seed yield in mungbean genotype VC1560D in M_4 generation. Selecting suitable genotypes and environment of interest for yield in mungbean is also reported using biplot methodology (Ullah et al., 2011b). High heritability for biological yield coupled with high genetic advance revealed that additive gene effects are important in determining these characters (Arshad et al., 2004). Sarwar et al. (2004) reported maximum heritability (92%) along with highest genetic advance of 70% for NM-92×NM-51 cross combination. These results are in accordance with the findings of Venkateswarlu (2001) who reported high heritability for seed yield in mungbean. Johnson et al. (1955) and Panse (1957) have also mentioned the importance of additive type of genes. Their study further stated that a high genetic advance accompanied with high heritability estimates offered a most effective criterion of selection from segregating populations.

Conclusion

Among the parental lines used in hybridization, exotic parent ML-5 was potentially good for traits as 1000-seed weight and seed yield. The cross involving exotic ML-5 also showed the highest magnitude of heritability and genetic advance for most of the post harvest traits. High heritability and genetic advance linked to these traits is an indication that they can easily be transferred to succeeding generations and will remain stable under specific environments. Genetic advance for most of the traits at both locations was high enough suggesting selection equally at both locations for the improvement of traits. Similarly low value of coefficient of variation for most of the parameters indicated experimental suitability that leads to high broad-sense heritability.

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