

Heritability Estimate of Yield Related Traits in Mungbean at Two Locations

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Abstract

Performance of 17 mungbean genotypes was tested at two diverse environments (Swat and Peshawar) of Khyber Pakhtunkhwa, Pakistan during 2012 to study heritability estimate of yield related traits in mungbean. Data were taken on pods plant⁻¹, pod length, seeds pod⁻¹, 100-seed weight, seed yield. Pooled analysis of variance across locations revealed significant differences among the two locations and genotypes for all traits. Genotype × location interaction was also highly significant (P=0.01) for all traits demonstrating differential performance of mungbean genotypes over the two test locations. Means for pods plant⁻¹, pod length, seeds pod⁻¹, 100-seed weight, seed yield were 21.7 vs. 39.0, 9.2 vs. 8.5 cm, 11.3 vs. 10.2, 4.2 vs. 5.4 g, 1429 vs. 1828 kg ha⁻¹ at Peshawar and Swat, respectively. All mungbean genotypes produced more pods plant⁻¹ and heavier seeds resulting in more seed yield per unit area at Swat than Peshawar. Genotypes AUP1210-9, AUP1210-10 and AUP1410-5 were high yielding at Swat location as well as across the two locations. AUP1210-9 and AUP6310-4 were the high yielding genotypes at Peshawar location. Genetic variances at each location as well as across locations were greater in magnitude than environmental variances for most of the traits. Magnitude of heritability and selection response for most traits varied over two locations. Heritability and selection response across two locations were 0.67 and 4.33 for pods plant⁻¹, 0.65 and 0.70 cm for pod length, 0.55 and 0.67 for seeds pod⁻¹, 0.66 and 0.72 g for 100-seed weight, 0.68 and 328.4 kg ha⁻¹ for seed yield, respectively.

Keywords: Mungbean, genetic association, heritability .

INTRODUCTION

Mungbean is an important pulse crop of Pakistan and substantive research is underway for its genetic improvement. There is great potential to improve mungbean seed yield and nutritional quality for cultivation as sole crop or intercropping with maize and other crops. The most important feature of mungbean is its ability to fix atmospheric nitrogen through symbiosis with nodule bacteria and thus has great potential to reduce fertilizer requirements of the following crop (Bashir, 1994). Adding mungbean to the cereal cropping system has the potential to increase farm income, improve human health and soil productivity, save irrigation water, and promote long-term sustainability of agriculture.

About 20 million hectares are planted with various *Vigna* species worldwide annually and that too mostly in developing countries (Fery, 2002). Mungbean was grown as a supplemental and cash crop on 137.4 thousand hectares in Pakistan during 2011, with total production of 76.2 thousand tons and average yield of 555 kg ha⁻¹. In Khyber Pakhtunkhwa, mungbean was grown on 8.5 ha only during 2010-2011 compared to 9777051 ha in 2009. Total production in Khyber Pakhtunkhwa was 5.1 tons during 2010-2011 only against 4434 tons in 2009. Average mungbean yield in Khyber Pakhtunkhwa during 2011 was 600 kg ha⁻¹ (Pakistan Bureau of Statistics, 2011). Development of genotypes which are adapted to a wide range of diversified environments is ultimate goal of plant breeders in mungbean improvement programs. This goal becomes more important when one consider the increasing demand for high protein and energy crops. When mungbean genotypes are evaluated in different locations (environments), their performance relative to each other may not be the same. Such change in the relative performance of genotypes across different locations is known as genotype × location interaction. This genotype × location interaction may be either due to change in scale or rank of the genotype (Fehr, 1993). The study of different developmental and productive traits through the estimation of different genetic parameters like heritability among traits is useful for framing valuable breeding programs.

- Therefore, the objectives of this research were to evaluate performance of mungbean genotypes across two locations of Khyber Pakhtunkhwa viz. Peshawar and Swat.
- To estimate heritability and selection response of maturity and yield related traits of mungbean.

Table 1. List of 17 mungbean genotypes evaluated at Peshawar and Swat during 2012.

Serial Number	Genotype	Serial Number	Genotype
1.	AUP6310-4	10.	AUP1410-5
2.	AUP6310-13	11.	AUP1410-6
3.	AUP6310-34	12.	AUP1410-7
4.	AUP6310-35	13.	AUP710-13
5.	AUP1110-13	14.	NM-92
6.	AUP1210-4	15.	NM-98
7.	AUP1210-5	16.	NM-9
8.	AUP1210-9	17.	Swat Mung-1
9.	AUP1210-10		

MATERIALS AND METHODS

Experiment site

A set of seventeen mungbean genotypes was evaluated at two locations viz. The University of Agriculture, Peshawar and Agricultural Research Institute Swat, during 2012 kharif season. The experiment was laid out in a Randomized Complete Block (RCB) design using three replications at each location. Experiments at both locations were planted in the 1st week of July, 2012. There were three rows per plot of each genotype spaced 30 cm apart. Length of each row was 3 m, with plant to plant distance of 3 cm within a row. A single row between adjacent plots was kept fallow to facilitate data recording. Data were collected on ten randomly selected plants from each plot.

Plant material

Thirteen of these genotypes with AUP initials were in F5 generation and selected from the breeding material of a Ph.D scholar Dr. Hydaytullah in Department Plant Breeding and Genetics at The University of Agriculture Peshawar. Genotypes NM-9, NM-92 and NM-98 are approved varieties of NIAB, Faisalabad, while Swat Mung-1 is released by ARI, Swat.

Observations

Data on pods plant⁻¹, pod length, seeds pod⁻¹, 100-seed weight and seed yield were recorded using ten randomly selected plants in each replication at both locations. These plants were tagged in each plot for convenience in data recording.

Statistical method

Heritability and expected selection response for each trait across the two locations were estimated as under,

$$\begin{aligned} \text{Genetic variance} &= V_g = (\text{GMS} - \text{GLMS})/r \\ \text{Genotype} \times \text{location variance} &= V_{g1} = (\text{GLMS} - \text{EMS})/r \\ \text{Error variance} &= V_e = \text{EMS} \\ \text{Heritability} &= h^2_{Bs} = V_g / (V_g + V_{g1} + V_e) = V_g / V_p \\ \text{Expected selection response (Re)} &= i\sqrt{V_p} h^2 \end{aligned}$$

Genetic and phenotypic variances were calculated based on the analysis of variance (ANOVA) under each location to determine heritability of important traits at each location following the procedures of Rowe and Brink (1993) and Pixley and Frey (1991). A similar selection intensity of 20% was assumed in predicting expected selection response under each location as well as across two locations (Falconer and Mackay, 1996).

RESULTS AND DISCUSSION

Number of pods per plant

Highly significant variation was observed for pods plant⁻¹ among genotypes. The variance due to location and genotype × location interaction were also highly significant (Table 2). This shows that ranking of genotypes at test location was not stable and genotypes performed differently at both locations. Raturi *et al.* (2012) and Ullah *et al.* (2011) also obtained significant variation for pods plant⁻¹ among genotypes, environments and genotype × environment interaction in mungbean. Independent analysis at each test location also revealed highly significant differences among genotypes for pod plant⁻¹. Pods plant⁻¹ of mungbean genotypes was higher in Swat as compared to Peshawar.

Genetic variances for pods plant⁻¹ were greater than environmental variances at both locations. Like other traits genetic variance was greater at Swat than Peshawar for pods plant⁻¹. High heritability estimates of 0.95, 0.92 and 0.67 were computed for pods plant⁻¹ at Peshawar, Swat and across locations, respectively (Table 3). High heritability for pods plant⁻¹ showed that the trait was least affected by environmental conditions. Our results of high heritability estimates for pods plant⁻¹ are also confirmed by Singh *et al.* (2009). Maximum selection response of 4.33 pods plant⁻¹ was observed across locations.

Pod length

Combined analysis of variance for pod length revealed highly significant differences among locations (Table 2). Our findings are in agreement with that of Raturi *et al* (2012) and Ullah *et al.* (2011) who observed significant variation among genotypes, locations and genotype by location interaction for pod length in mungbean. Significant genotype \times location interaction represents change in ranking of mungbean genotypes over test locations. Abna *et al.* (2012) who also observed highly significant differences among mungbean genotypes for pod length.

Genetic variance for pod length was less than environmental variance at Peshawar as well as across location but it was greater than environmental variance at Swat. Heritability estimates for pod length were 0.75, 0.86 and 0.65 at Peshawar, Swat and across locations, respectively. Heritability estimates of 0.41 to 0.96 for pod length in mungbean were computed at different locations by Singh *et al.* (2009). Heritability recorded at Peshawar (0.75) was less in magnitude than Swat (0.86). Hence, pod length had diverse expression among genotypes and across the two locations. Considering 20% selection intensity, selection response at two locations and across locations was 0.59, 0.88, and 0.70 cm, respectively. The selection response at Swat was about 29 units greater than at Peshawar (Table 3).

Number of seeds per pod

The pooled ANOVA exhibited highly significant differences for locations, genotypes and genotype \times location interaction (Table 2). Similar results of genetic variability for seeds per pod were also reported by Raturi *et al* (2012) in stability study of mungbean genotypes for yield related attributes. Individual analysis of variance at each location revealed that genotypes significantly differed from each other in production of seeds per pod.

Heritability estimate are important for breeder to plan their breeding programs. Genetic variance for seeds per pod (0.20) was less than environmental variance (0.52) at Peshawar; however it was greater than environmental variance (0.38) at Swat. Heritability estimates of seeds per pod were 0.53, 0.76 and 0.55 at Peshawar, Swat and across locations, respectively (Table 3). Singh *et al.* (2009) also observed high heritability estimates of 0.99 and 0.97 for number of seeds per pod in mungbean at different locations.

100-seed weight

Analysis of variance across locations revealed highly significant differences among locations and genotypes for 100 seed weight. Genotype \times location interaction for 100-seed weight was also highly significant ($P=0.01$) indicating change in seed size of genotypes over the two locations used in the study (Table 2). Similar results were reported by Raturi *et al.* (2012) who also observed highly significant differences among mungbean genotypes, environments and genotype \times environment interaction for 100 seed weight. Individual analysis at each location also revealed significant differences among genotypes for 100-seed weight.

Genetic variance for 100-seed weight was 0.24 at Peshawar vs. 0.45 at Swat. Heritability estimates of 100-seed weight were 0.90, 0.76 and 0.66 at Peshawar, Swat and across locations, respectively. Maximum selection response (0.72 g) for seed weight was observed across location. Using 20 % selection intensity, selection response was 0.65 g, at Peshawar compared to 0.82 g at Swat (Table 3).

Seed yield

Combined analysis of variance for seed yield showed highly significant differences among mungbean genotypes and locations. Genotype \times location interaction was also highly significant for seed yield (Table 2). Hence, seed yield of genotypes varied across two locations used in the study (Figure 1, 2).

Individual analysis of variance at each location also exhibited highly significant genetic variation among mungbean genotype. Abna *et al.* (2012) reported highly significant differences among mungbean genotypes for seed yield in Malaysian Tropical environment. Genotypic variance was less than environmental variance at Peshawar and across locations. In contrast, genetic variance was greater than environmental variance at Swat. Genotypic, genotype \times location and environmental variances for seed yield across two locations were 38781, 286670, and 50325. High heritability estimate for seed yield of 0.88% was observed at Swat. Similarly, heritability estimates across two locations and at Peshawar were 0.68 and 0.55, respectively. Expected selection at 20% selection intensity for seed yield was 155.8, 440.5 and 328.4 kg ha⁻¹ at Peshawar, Swat and across two locations, respectively (Table 3). Khan *et al* (2004) also reported moderate to high heritability, while Sadiq *et al* (2006) observed high heritability for seed yield in mungbean.

Conclusion

Genotype AUP-1210-9 out yielded all other genotypes followed by AUP1210-4 AUP1210-10, AUP-1410-5 showed highest performance across location. It is therefore, recommended that these genotypes could be included in further breeding programmes. On the basis of high heritability pod plant⁻¹ and 100-grain weight could be used as selection criteria in future breeding programmes.

Table 2. Mean squares various traits of 17 mungbean genotypes across two locations of Khyber Pakhtunkhwa during 2012.

Source	Df	Pod Length	Pods plant ⁻¹	Seed Pod ⁻¹	100-Seed Weight	seed yield
Loc (L)	1	13.7**	7678.7**	29.7**	41.5**	4077555.2**
Reps w/n Loc	4	1.0	4.9	0.6	0.2	98988.7
Genotype (G)	16	1.8**	81.0**	1.8**	1.9**	369019.2**
G × L	16	0.8**	33.7**	0.9**	0.7**	136334.0**
Error	64	0.2	3.6	0.4	0.3	50325.4
CV (%)		5.5	6.2	6.2	10.4	13.8

Table . 3 Variance components, heritability (h^2_{BS}) and selection response (Re) for various traits of 17 mungbean genotypes at each location and across locations of Khyber Pakhtunkhwa during 2012.

Trait	Location	Vg	Vgl	Ve	h^2_{BS}	Re
Pod plant⁻¹	Peshawar	16.33	-	2.11	0.95	5.53
	Swat	19.53	-	4.99	0.92	5.93
	Across Locations	7.89	10.05	3.55	0.67	4.33
Pod length (cm)	Peshawar	0.24	-	0.25	0.75	0.59
	Swat	0.46	-	0.22	0.86	0.88
	Across Locations	0.18	0.17	0.23	0.65	0.70
Seed per pod(no)	Peshawar	0.2	-	0.52	0.53	0.45
	Swat	0.4	-	0.38	0.76	0.77
	Across Locations	0.15	0.15	0.45	0.55	0.67
100 seed weight(g)	Peshawar	0.24	-	0.08	0.90	0.65
	Swat	0.45	-	0.42	0.76	0.82
	Across Locations	0.19	0.16	0.26	0.66	0.72
Seed yield (kg ha⁻¹)	Peshawar	22481	-	55013	0.55	155.8
	Swat	112420	-	45638	0.88	440.5
	Across Locations	38781	28670	50325	0.68	328.4

Figure1= Seed Yield of 17 mungbean genotypes at Swat and Peshawar.

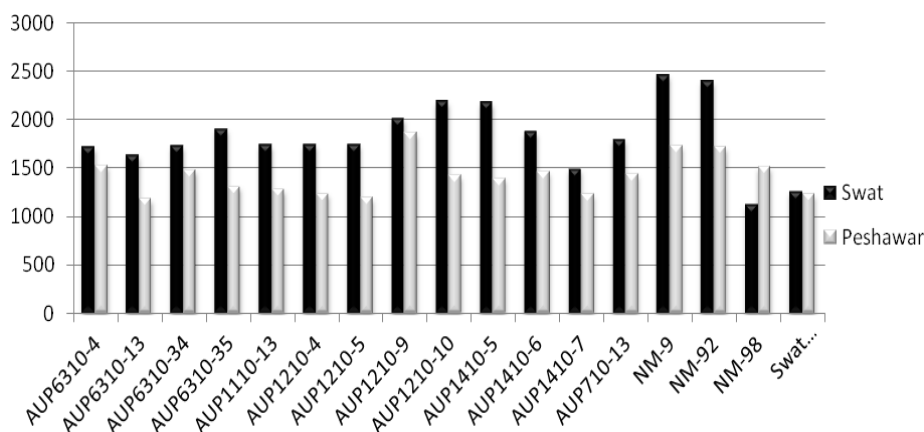
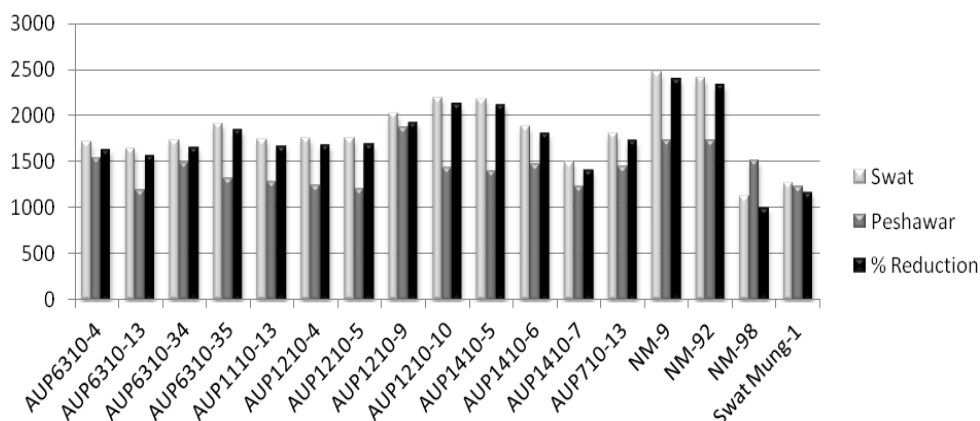


Figure 2= Seed Yield of 17 mungbean genotypes at each location and yield % reduction at Peshawar location.



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