



## Genetic variability, association and path analysis in mung bean (*Vigna radiata* L.)

Hafiz Bashir Ahmad<sup>1\*</sup>, Salsabeel Rauf<sup>2</sup>, Iqbal Hussain<sup>3</sup>, Chaudhry Muhammad Rafiq<sup>1</sup>, Aziz-u- Rehman<sup>1</sup>, Azhar Mehmood Aulakh<sup>4</sup>, Muhammad Afzal Zahid<sup>1</sup>

<sup>1</sup>Pulses Research Institute AARI Faisalabad, Pakistan

<sup>2</sup>Oil Seed Research Institute AARI Faisalabad, Pakistan

<sup>3</sup>Department of Agronomy, University College of Agriculture, University of Sargodha, Pakistan

<sup>4</sup>Arid Zone Research Institute, Bahkar, Pakistan

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### Abstract

Mung bean (*Vigna radiata* L.) germplasm comprising 84 genotypes was evaluated at Pulses Research Institute, Faisalabad (Pakistan) during summer 2013 in randomized complete block design with two replications. Variances due to genotypic and phenotypic expressions, heritability along with genetic advance exhibited in percentage of means for yield and its components were deliberated. High genotypic variance and high phenotypic variance for number of pods per plant (15 7.61, 169.14) and days to maturity (54.95, 119.79) were estimated. The Highest heritability was recorded for days to flowering (0.94) while the lowest was found to be associated with plant height (0.46). High heritability along with high genetic advance presented in percentage of mean for number of pods per plant and cluster per plant, depicted the additive gene effects. Correlation studies presented that Seed yield per plant possessed highly significant positive correlation with days to flowering, days to maturity, plant height, number of pods per plant, and number of clusters per plant. Path analysis studies showed that plant height and cluster per plant had maximum positive direct effects on seed yield.

\*Corresponding Author: Hafiz Bashir Ahmad ✉ [easahafiz@yahoo.com](mailto:easahafiz@yahoo.com)

## Introduction

Mung bean is the third major pulse crop in Pakistan. Its production was 89.3 thousand tonnes and area was 136.1 thousand hectares during 2012-13. It belongs to leguminous family and is native to Asiatic region. Mung bean possesses great diversity that can be used for the development of new high yielding varieties. Gupta *et al.* (1969) observed the genetic and heritable constituents of variation in 46 chickpea varieties and accentuated the selection based on 100 seed weight. Veeraswamy *et al.* (1973) studied variability in Mash (*Vigna mungo*) genotypes and made selection on the basis of various traits like number of pods per plant, plant height and per plant seed yield. Genetic variability and correlation between yield and its components in mung bean was studied by Islam *et al.* (1999) who observed significant differences among the various genotypes. High genetic variability, moderate to high heritability and genetic advance were found in yield contributing traits i.e., 100-seed weight, seed yield per plant and number of pods per plant whilst high heritability and genetic advance were estimated for plant height and low for days to flowering and days to maturity (Yimram *et al.*, 2009). Yield contributing traits

showed the significant variation studied by Gul *et al.* (2007). Similar findings were also observed by Hozyn *et al.* (2013). Phenotypic coefficient of variation was equal to the genotypic coefficient of variation for most of the traits studied (Hozyn *et al.*, 2013). The highest genotypic and phenotypic variances were studied for number of pods per plant, branches, harvest index and biological yield (Narasimhulu *et al.*, 2013). So, it is obvious that genetic variability is vital in breeding programs. Therefore, to evaluate the genetic variation for desired traits, current studies were carried out in mung bean germplasm which will be helpful in selection of high yielding lines to use them in next breeding program.

## Materials and methods

### Site, design and crop husbandry

The experiment was conducted at Pulses Research Institute, Faisalabad during summer 2013 in a randomized complete block design with two replications. Sowing was done in first week of July. Plant to plant and row to row distances were maintained at 15 cm and 30 cm respectively. Eighty four genotypes were evaluated for variation. These genotypes were:

1. L. X.-163	15. L. X-10-162	29. L X 10-101	43. 11-2	57. 97007	71. 6368-46-404
2. 6601-6	16. 6173-8-33	30. L X 10-7-1	44. ASTLIA-9	58. NM-1	72. 97-17
3. M-6	17. E-136	31. L X-10-3	45. L9-20-9	59. NM-2	73. L X-10-167
4. 98009	18. L. X-10-77	32. L X-10-10	46. RL-70	60. NM-14	74. R6-63
5. M-6-A	19. E-18-1	33. L X-10-29	47. L X-10-165	61. NM-6	75. E182-1
6. L. X.-10-11	20. L. X-1010-10	34. E-96	48. 4506-B	62. NM-12	76. L X-10-173
7. 6163-B4	21. L X -10-10-39	35. L X-10-162	49. DRM-311	63. NM-3	77. E332
8. E-89	22. E28-1	36. 230-27-680-4	50. NM-4	64. L X 10-7	78. E-1121
9. L. X-10-168	23. NM92-17	37. 6153--538-2FR	51. NO-303	65. ASTROL-3	79. 6144-A
10. NL-31	24. L X-10-54	38. L X-10-207	52. 98004	66. 1973-A	80. L X-10-137
11. 0173-B-10	25. 97019	39. L X-10-103	53. 97001	67. L X 10-107	81. L X-10-60
12. M-303	26. LA-10-127-1	40. S-907	54. NM-9	68. E-253	82. E-33
13. M-319	27. 97017	41. 637-72	55. NM-10	69. E-86	83. E-39
14. GP98-3-45	28. 6148-51-12	42. 166-L X-10	56. C99-3-115	70. L X -10-120	84. E-180

Data were collected on cluster per plant, pods per plant, plant height, days to flowering, days to maturity, number of seeds per pod, 1000-seed weight and seed yield per plant. Estimation of heritability

and expected genetic advance of various components were estimated according to the formula given by Singh and Chaudhary (1979). Correlation and path analysis were estimated according to Dewey and Lu

(1959).

$$\text{Heritability (h)} = \frac{\sigma^2 g}{\sigma^2 p}$$

Where  $\sigma^2 g$  and  $\sigma^2 p$  are genotypic and phenotypic variances, respectively.

$$\text{Genetic advance} = Kh^2\sigma p$$

Where,

K = selection differential at 5% selection intensity = 2.06

$h^2$  = heritability coefficient

$\sigma p$  = phenotypic standard deviation.

### Results and discussion

The results of analysis of variance for characters studied indicated that means sum of square owing to genotypes was significantly different. Highest significant differences were noted for pods per plant, plant height and 1000-seed weight. It means that performance of genotypes with respect to various traits was statistically different. Genotypic, phenotypic variance and their coefficient of variation, heritability along with genetic advance exhibited as percentage of means are shown in Table 1. Genotypic and phenotypic variation for number pods per plant (157.61 and 169.14), 1000-grain weight (71.36 and 79.90) and plant height (54.95 and 119.79) were observed to be high. Similar results were reported by Pande *et al.* (1975), Malik *et al.* (1983) and Yimram *et al.* (2009). The lowest genotypic variance and phenotypic variance showed by seeds per pods (1.22 and 1.42 respectively). Whereas seed yield, flowering

days, maturity days and cluster per plant showed 7.70 and 14.89, 7.04 and 7.51, 5.55 and 5.95, 3.47 and 3.79 genotypic and phenotypic variances respectively. Coefficients of variation due to genotype and phenotype were also high for number of pods per plant (33.73% and 34.94% respectively) followed by cluster per plant (25.75% and 26.89% respectively). While days to maturity exhibited the lowest GCV and PCV (2.51 and 2.60 respectively). The highest broad sense heritability was recorded for flowering days (0.94) followed by number of pods per plant and maturity days to with an equal magnitude (0.93). These results were found to be in accordance with Chowdhary *et al.* (1971) and Malik *et al.* (1983). The selection only on the heritable basis is not effective criteria for the best genotypes however the selection, heritability with genetic advance is more effective (Johnson *et al.*, 1955). Percentage of means of genetic advance showed that differences were observed among the characters studied. Number of pods number per plant followed by cluster per plant showed high genetic advance and high heritability, which indicated the predominant role of additive gene action and the selection will be rewarding based on these parameters. These findings are in accordance with Pande *et al.* (1975) and Malik *et al.* (1983). Selection methods such as mass selection, pedigree selection and pure line selection are effective for self-pollinated crops like mung bean. High heritability (0.936) with low genetic advance (11.59) for days to flowering indicated the non-additive gene action and the selection will not be rewarding. Similar findings were reported by Rahman and Hussain (2003).

**Table 1.** Mean sum of squares and genetic parameters for various quantitative traits in mungbean genotypes.

Characters	Mean sum of squares	Genotypic variance	Phenotypic variance	Genotypic coefficient of variance	Phenotypic coefficient of variance	Environmental variance	Environmental coefficient of variance	Heritability	Genetic advance	Genetic advance (%)
Cluster per plant	7.258**	3.47	3.79	25.75	26.89	7.26	37.24	0.917	3.68	50.80
Pod per plant	326.751**	157.61	169.14	33.73	34.94	326.75	48.56	0.932	24.96	67.07
Plant height (cm)	174.745**	54.95	119.79	16.89	24.94	174.75	30.12	0.459	10.34	23.57
Days to flowering	14.549**	7.04	7.51	5.81	6.01	14.55	8.36	0.936	5.29	11.59
Days to maturity	11.501**	5.55	5.95	2.51	2.60	11.50	3.61	0.932	4.68	4.99
Seed per pod	2.632**	1.22	1.42	13.41	14.46	2.63	19.72	0.860	2.11	25.61
1000-seed weight (g)	151.261**	71.36	79.90	17.99	19.04	151.26	26.20	0.893	16.45	35.03
Seed yield per plant (g)	22.59**	7.70	14.89	19.84	27.59	22.59	33.99	0.517	4.11	29.40

Results (Table 2) showed that genotypic correlations were greater than their corresponding phenotypic correlations signified characters are genetically controlled (Gill *et al.*, 1995 and Biradar *et al.*, 2007). Seed yield per plant possessed highly significant positive correlation with days to flowering, days to maturity, plant height, number of pods per plant, and number of clusters per plant but showed negative and non-significant correspondence with seeds per pod significant association with 1000 seed weight. Degefa *et al.* (2014) and Sadiq *et al.* (2005) reported that seed yield was negatively correlated with days to flowering, non-significant but positive with days to maturity, plant height, number of pods, seed per pod, and 100 seed weight and highly significant with cluster per plant. Days to flowering showed positive significant correlation with days to maturity, plant height, number of pods per plant, and number of clusters per plant but negatively significant association with number of seeds per pod and 1000 seed weight. Gul *et al.* (2008) found that days to flowering had positive association with days to maturity, plant height, number of pods but negative

with seed per pod. Days to maturity showed significant positive association with plant height, pods per plant and cluster per plant but significantly negative correlated with 1000 seed weight. Gul *et al.* (2008) observed that days to maturity were significantly positively correlated with plant height and negatively correlated number of pods, seed per pod and 100-seed weight. Plant height revealed significant correspondence with pods per plant and cluster per plant however seeds per pod and 1000 seed weight were in negative association. Suresh *et al.* (2013) indicated that plant height had significant and positive assimilation with number of pods per plant, number of seed per pod but negatively correlated with 100 seed weight. Similarly highly significant positive association was noted for pods per plant with cluster per plant but negative with seeds per pod and 1000 seed weight. Degefa *et al.* (2014) studied the positive association Seeds per pod showed highly negative significant relationship with cluster per plant. Srivastava *et al.* (2012) noted the negative correlation of seed per pod with cluster.

**Table 2.** Phenotypic and genotypic correlations.

	Df	Dm	ph	pp	sp	swt	cp	y.p
df	1	0.17109*	0.42809*	0.40973**	-0.14027	0.060316	0.25457**	0.15745*
dm	0.18204*	1	0.22847**	0.25394**	0.00934	-0.16988*	0.32553**	0.09756
Ph	0.61898**	0.37529**	1	0.53707**	-0.15546*	-0.1882*	0.26922**	0.21398**
Pp	0.42586**	0.27564**	0.81324**	1	-0.14672	-0.24261**	0.47292**	0.2463**
Sp	-0.15671*	0.01886	-0.16021*	-0.15872*	1	0.10992	-0.18975*	-0.04208
Swt	-0.19787*	-0.18548*	-0.2722**	-0.2483**	0.11651	1	-0.11084	-0.27792**
Cp	0.26197**	0.36401**	0.46803**	0.51448**	-0.22348**	-0.13516	1	0.30378**
y.p	0.22689**	0.17049*	0.39825**	0.27392**	-0.06814	-0.36299**	0.4972**	1

df = days to flowering, dm = days to maturity, ph = plant height, pp = pods per plant, sp = seed per pod, swt = seed weight, cp = cluster per plant, y.p = yield per plant.

Below Diagonal Genotypic Correlations

Above Diagonal Phenotypic Correlations.

#### Path analysis

Path analysis has been used in many crop species like cereals and legumes. This technique helps in the improvement of yield by the indirect selection. A good response in yield can be attained if indirect selected character has high heritability along with high correlation with yield. Path analysis studies showed (Table 3) that plant Height and cluster per plant had maximum positive direct effects on seed Yield .These

traits have strong correlation with yield. Results are in accordance with Degefa *et al.* (2014) and Sadiq *et al.* (2005). The residual effect was high it means that other trait should be included in the studies. Rohman and Hussain (2003) reported the high residual value in mungbean. The negative direct effect was observed for number of pods per plant followed by seed weight, days to maturity and days to flowering. Pods per plant, days to flowering and days

to maturity had positive indirect effects on seed yield via plant height. Similar results were also reported by srivastava and singh (2012) and Degefa *et al.* (2014). In path analysis, correlation of various traits with yield is divided into direct and indirect effects. If correlation and direct effects are positive and equal so, there may be true relationship and selection of that character will improve the yield. If direct effects are negligible or negative and correlation is positive the importance of indirect effect is increased, in these

situations, the indirect casual factors are measured instantaneously. However, in some situation correlation may be negative along with high positive direct effect then restricted instantaneous selection model can be followed. Hence the traits like plant height cluster per plant and pods per plant have highest positive direct effects along with correlation coefficient with seed yield so these characters may be used for yield improvement in seed yield in mungbean.

**Table 3.** Direct(Diagonal) and indirect effect path coefficients.

	Df	Dm	ph	pp	sp	swt	cp
Df	-0.07627	-0.02622	0.318155	-0.16892	-0.01443	0.060316	0.134254
Dm	-0.01388	-0.14402	0.192898	-0.10933	0.001736	0.056538	0.186547
Ph	-0.04721	-0.05405	0.514003	-0.32258	-0.01475	0.082974	0.239855
Pp	-0.03248	-0.0397	0.418009	-0.39665	-0.01461	0.075689	0.263661
Sp	0.011951	-0.00272	-0.08235	0.062955	0.092061	-0.03551	-0.11453
Swt	0.01509	0.026711	-0.13991	0.098489	0.010726	-0.30483	-0.06927
Cp	-0.01998	-0.05242	0.240569	-0.20407	-0.02057	0.041201	0.512479

df = days to flowering, dm = days to maturity, ph = plant height, pp = pods per plant, sp = seed per pod, swt = seed weight, cp = cluster per plant

Residual Effect<sup>2</sup> = 0.5866231.

### Conclusion

The current studies were carried out to evaluate the genetic variability among existing germplasm of mung bean in AARI Faisalabad. Significant differences among genotypes with respect to various traits confirmed the variability which is prerequisite for any breeding program. The estimated variability, heritability and genetic advance will be extremely helpful for exploitation and utilization of these genotypes in future breeding programs. Results from correlation and path analysis also concluded that character like plant height ,number of pods and cluster per plant have highest positive direct effects and correlation with seed yield. Therefor these characters can be used for the improvement in mungbean yield.

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