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RESEARCH ARTICLE

Association and Variability of Morphological, Yield and Yield Attributing Traits in Mung Bean [*Vigna radiata* (L.) Wilezek]

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Abstract

The efficacy of the selection process is greatly enhanced by using appropriate selection indices. The knowledge of the genetic variability and relationship among various traits affecting seed yield is essential for crop improvement. The present study was undertaken to evaluate 51 diverse genotypes of mungbean for the estimation of genetic variability, heritability & genetic advance, the correlation coefficient for eleven traits and their association level with yield. Results of the analysis of variance revealed significant differences for all the characters studied and, thereby offered an ample opportunity for selecting suitable genotypes with desired traits. High PCV and GCV were observed for seed yield per plant (56.05/47.60), primary branches per plant (40.27/32.38), pods per plant (36.31/32.93) and biological yield per plant (38.46/33.17) indicating the role of additive gene action in the expression of these characters. Analysis of correlation revealed that the magnitude of genotypic correlation coefficients was higher than the phenotypic correlation coefficients suggesting the existence of inherent association among the traits studied. High heritability was observed for plant height (0.89) followed by pods per plant (0.82) and seeds per pod ((0.81), indicating the less influence of environment on these characters. Seed yield was found to be positively correlated with primary branches per plant, number of pods per plant, number of seeds per pod and biological yield per plant. Path coefficient analysis revealed the importance of pods per plant and, the number of seeds per pod, while the highest negative direct effect was recorded for the harvest index.

Keywords: - Correlation coefficient, Mung bean, Path analysis, Variability.

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Introduction

Pulses are an excellent option for dietary protein. Pulses, when used as food with other cereals, definitely meet the requirement of a balanced diet. Mung bean (*Vigna radiata* L.) is a vital and important pulse crop, also known as green gram, and is an excellent source of easily digestible proteins with low flatulence, which complements the staple rice diet in Asia. In India, it is the third most important pulse crop after chickpea and pigeonpea. It is grown mainly as a *kharif* season crop. However, its cultivation in rabi season is restricted to the eastern and southern parts of the country.

Seed yield in mung bean is a complex character like other crops, determined by various components. A clear knowledge of variability in various quantitative characters existing in the breeding material helps plant breeders select superior genotypes on the basis of different genetic parameters such as genotypic variation, heritability, genetic gain, etc, to understand the nature and magnitude of variation for the available plant characters. Hence it is necessary to estimate the relative amount of genetic and non-genetic variability exhibited by the traits under the study (Moose and Mumm, 2008). Yield is dependent on various characteristics and environmental conditions that exist during crop growth. It is, therefore, essential to study the association of characters among themselves and with the yield of crops. Genotypic correlation provides a measure of genotypic association between two characters and helps to identify more useful relationships between characters. Indirect association becomes complex and important when a number of variables are included in the study of correlation. In such cases, a more defined technique as, path coefficient analysis, helps to find out the direct and indirect causes of character association. Every component character has a direct and indirect effect on yield. If correlation is due to direct effect, it reflects a true relationship and selection is practiced for such a character for improving the yield. In case if the effect is indirect through another component trait, the breeder has to select the latter trait through which the indirect effect is exerted. The presence of high variability in this crop offers much scope for its improvement. Hence, an attempt was made to assess the genetic variability, heritability, genetic advance, correlation and path analysis in respect to desirable traits in 51 genotypes of mung bean, which will help in the selection of promising lines for the further breeding program and to explore high yielding lines of mung bean.

Materials and Methods

The experiment was undertaken at the Research Farm of Division of Genetics and Plant Breeding (GPB), Faculty of Agriculture (FoA), Wadura, Sopore, Sher-e-Kashmir University of Agricultural Sciences and Technology Kashmir (SKUAST-K), to evaluate the 51 genotypes of mung bean for genetic variability with respect to yield and yield contributing traits (Table 1a) The experiment was laid out in randomized block design with three replications during 2021-22. Each genotype was sown at the spacing of 30 cm between rows and 10 cm between plants and about two seeds were dibbled at each hill to assure germination. A uniform standard plant population was maintained throughout the experiment. A standard recommended package of practices was followed to raise a good crop. Observations for all the traits (except days to 50% flowering and days to maturity) were recorded by taking ten randomly selected plants from each replication. Days to 50% flowering and days to maturity were computed on a plot basis. The data of 11 morphological traits *viz* days to maturity, number of branches per plant, plant height (cm), pod length (cm), number of pods per plant, number of seeds per pod, 100-seed weight (g), seed yield per plant (g), biological yield per plant (g) and harvest index (%) were recorded at the time of maturity, whereas observation on days to 50% flowering was recorded for different genotypes when they attained 50% flowering stage. Analysis of variance for the observations recorded on different traits was carried out as per the standard procedure of Box *et al.* (1978). Genotypic and phenotypic coefficients of variability were estimated according to Johnson *et al.* (1955). Heritability in a broad sense and Genetic advance were worked out as per the procedures of Burton and Dewane (1953) and Johnson *et al.* (1955), respectively. Estimation of phenotypic and genotypic correlation suggested by Fisher (1954) and Al-Jibouri *et al.* (1958). Path coefficient of variation was computed as per the method given by Dewey and Lu (1959).

Results and Discussion

Analysis of Variance and Mean Performance

Since, yield is governed by polygenes with small, similar and cumulative effects and highly influenced by the environment, selection based on yield alone is ineffective. The breeders apply indirect selection on yield through a selection of yield attributes with high heritability so that environmental influence can be minimized.

The mean sum of squares with respect to morphological traits has been given in (Table 1b). The results revealed that the mung bean genotypes differed significantly for all the traits *viz* days to 50% flowering, days to maturity, number of branches per plant, plant height (cm), pod length (cm), number of pods plant^{-1}, number of seeds per pod, 100-seed weight (g), seed yield per plant (g), biological yield per plant (g) and harvest index (%) indicating the presence of sufficient variability and all the genotypes differed from each other in respect of characters, which open a way for improvement in the material through selection. A similar finding was also reported by Bisht *et al.* (2014), Javed *et al.* (2014), Singh *et al.* (2012) and Srivastava and Singh (2012).

The mean performance of the genotypes showed a wide range of variability for all the parameters studied (Table 2). The range of variation was highest for plant height (cm) followed by biological yield per plant (g), number of pods per plant and the seed yield per plant (g). This may be due to the existence of diversity in genotypes evaluated, while the coefficient of variation was higher for seed yield and number of branches per plant, and medium to low values were observed for biological yield per plant (g), pod length (cm), number of pods per plant, number of seeds per pod, 100-seed weight (g), harvest index (%), plant height (cm) and days to flowering and maturity. The coefficient of variation was low which indicated that most of the genotypes had average height and mass selection would be effective for shorter height. Similar finding was also reported by Ahmad *et al.* (2015), and Payasi (2015).

Coefficients of Variability

Genotypic and phenotypic coefficients of variability are of greater importance in determining the extent of variability present within germplasm. The value of the phenotypic coefficient of variation was observed to be higher than the genotypic coefficient of variation for all characters, indicating that the environment had an important role in

Table 1a: Passport information and pedigree of mung bean genotypes

S. No.	*Genotype*	*Pedigree*	*Originating centre*	*Area of adoption*
1	IPM 02-3	IPM 99-125×Pusa Bold 2	IIPR, Kanpur	NWPZ (DL, HR, HP, J&K, PN, RJ)
2	IPM 205-7	IPM02-1×EC398899	IIPR, Kanpur	SZ (AP, TN) CZ (MP, & GJ)
3	IPM-410-3	IPM03-1×NM1	IIPR, Kanpur	NWPZ/CZ (RJ, PN, HR, DL, HP, UK, J&K, MP, MH & GJ
4	PKV-AKM-4	BM 4×PS 7	PKV, Akola	CZ (MH, MP) SZ (KA, OD, TN)
5	Pat-Mung-5	Selection from VC 6368	GBPUA& T, Pantnagar	Uttar Pradesh
6	SML 832	SML 302 × Pusa Vishal	PAU, Ludhiana	Punjab
7	TMB 136	TM 98-80 × SML 668	BARC, Trombey	West Bengal
8	IPM-99-125 (Meha)	PM 3× AMP 36	IIPR, Kanpur	NWPZ (DL, HR, HP, J&K, PN, RJ)
9	RMG 268	R 288-8 × J 780	RARI, Dugapura	Rajasthan
10	ML 818	5145/87 × ML 267	PAU, Ludhiana	NWPZ (HR, PN, UP, UK)
11	PM 14-3	PM 6 × Pusa Ratna	GBPUAT, Pant Nagar	Uttarakhand
12	Samrat	ML 20/19 × ML 5	IIPR, Kanpur	NWPZ/CZ (RJ, PN, HR, DL, HP, UK, J&K, MP, MH & GJ
13	COGG-8	COGG 923 × VC6040	TNAU, Coimbatore	Tamil Nadu
14	EC581523 B	Exotic collection	-	-
15	HUM 16	Pusa Bold 1 × HUM 8	IARI, New Delhi	Uttar Pradesh, Bihar, West Bengal and Assam
16	EC581523	Exotic collection	-	-
17	IPM 02-14	IPM 99-125 × Pusa Bold 2	IIPR, Kanpur	SZ (AP, KN, TN, OD)
18	MH 421	Muskan × BDYR 2	CCSHAU, Hissar	NWPZ/CZ (DL, HR, RJ, W. UP)
19	MH 1-25	Asha × PDM 90-1	CCSHAU, Hissar	Haryana
20	SML 1817	PAU 911 × Mash 114	PAU, Ludhiana	Punjab
21	NDMZ 15-2	NDM 1 × Pant Mung -5	NDUAT, Kumarganj	UP, Uttrakhand
22	MH-1010	MH 98-1 × PDM 96-262	CCSHAU, Hissar	NEPZ & NWPZ (BH, HA, DL, JH, PB, RJ, UP, WB)
23	ML 2037	ML 818 × VC 6372-45-8-1	PAU, Ludhiana.	Punjab
24	MH 534	ASHAXBDYR-2	CCSHAU, Hissar	Haryana
25	KM 2241	Samrat × PDM 54	CSAU, Kanpur	NHZ (TR, MN, J&K, HP)
26	TMB 37	Kopergaon ×TARM 2	BARC, Trombey	West Bengal
27	Pusa Vishal	Selection from NK 92	IARI, New Delhi	NHZ (J&K, MN, TR)
28	MH 2-15	PDM116×Gujarat-1	CCSHAU, Hissar	NWPZ/CZ (DL, HR, RJ, W. UP)
29	SML 668	Selection from AVROC line NM 94	PAU, Ludhiana	Punjab
30	SML 1018	ML 613×BDYR-2	PAU, Ludhiana	Punjab
31	MH 929	RMG 268×UPM 98 1	CCSHAU, Hissar	Haryana
32	MH 925	PUSA VISHAL × ML 682	CCSHAU, Hissar	Haryana
33	MH 934	MH 96-1× 2KM 117	CCSHAU, Hissar	Haryana
34	MH 926	Rice bean × ML 1108/682	CCSHAU, Hissar	Haryana
35	MH 921	MH 96-1× 2KM 114	CCSHAU, Hissar	Haryana
36	MH 919	RMG-62 × UPM 98-1	CCSHAU, Hissar	Haryana
37	MH 539	MH 96-1×BDYR-1	CCSHAU, Hissar	Haryana
38	EC 30400	Exotic collection	-	-
39	EC 399223	Exotic collection	-	-

40	EC 470095	Exotic collection	-	-
41	EC 581523	Exotic collection	-	-
42	IPM 06-5	Mutant of EC 369223	IIPR, Kanpur	NWPZ (DL, HR, HP, J&K, PN, RJ)
43	TMB 131	Samrat × Kopergoan	BARC, Trombey	-
44	EC 393410	Exotic collection	-	-
45	GM 11-02	GM 9910 × Pusa Vishal	SDAU, S.K. Nagar	Gujarat
46	Pusa Ratna	VC 6368 × ML 267	IARI, New Delhi	NHZ (J&K, MN, TR)
47	Pusa 251552	Exotic collection	-	-
48	MH 560	ASHAXBDYR-1	CCSHAU, Hissar	Haryana
49	LGG 460	Lam M2× ML 267	ARS, Lam	Andhra Pradesh, Tamil Nadu, Eastern Uttar Pradesh
50	Pusa 9531	Selection from NM 9473	IARI, New Delhi	NHZ (J&K, MN, TR)

Table 1b: Analysis of variance (Mean Squares) for the eleven characters of mung bean genotypes

Source of variation	*df*	*Mean squares*										
		DFF	*DM*	*PH (cm)*	*PBPP*	*NPPP*	*PL*	*NSPP*	*100-SW*	*SYPP*	*BYPP*	*HI*
Replications	2	260.784	731.314	1730.693	3.549	117.849	12.414	8.471	0.042	41.700	228.629	29.166
Treatment	50	19.071**	23.038**	343.284**	1.985*	49.971**	13.223**	14.957**	2.033**	36.756**	137.251**	43.756**
Error	100	3.104	2.694	13.579	0.306	3.356	2.027	1.031	0.166	4.194	14.121	4.973

**Significant at 1% level
*Significant at 5% level
DFF - Days to 50% flowering (days), DM - Days to maturity (days), PH - Plant height (cm), PBPP – number of Primary branches per plant, NPPP – Number of Pods per plant, PL - Pod length (cm), NSPP - Number of seeds per pod,100-SW - 100 seed weight (g), SYPP - Seed yield per plant (g), BYPP - Biological yield per plant (g), HI - Harvest index (%),

influencing the expression of these characters (Table 3). High PCV and GCV were observed for seed yield per plant (56.05/47.60), primary branches per plant (40.27/32.38), pods per plant (36.31/32.93) and biological yield per plant (38.46/33.17) indicating that improvement could be possible through the selection of these traits. Similar results were also reported by Panigrahi *et al.* (2014), and Suresh *et al.* (2010), while moderate PCV and GCV were recorded for pod length (28.98/23.33), seeds per pod (20.62/18.65) and 100-seed weight (17.75/15.77). The low PCV and GCV were recorded for days to 50% flowering (6.78/5.39) and days to maturity (4.34/3.67). Low to moderate GCV and PCV values indicated the influence of the environment on these traits and limited scope for improvement by selection. The results revealed that the genotypic coefficient of variation was close to that of phenotypic variation for days to 50% flowering, days to maturity and harvest index, indicating that the phenotypic coefficient of variation was largely due to genetic differences and less environmental influence. Similar results were also reported by Das and Baru (2015), (Raselmiah *et al.* (2016), More *et al.* (2016), Usharani *et al.* (2016) and Tabasum *et al.* (2010). However, a considerable difference was observed between GCV and PCV values for primary branches per plant and seed yield per plant, indicating a role of the environment in the expression of these traits.

Table 2: Range mean and co-efficient of variability for different traits of mung bean

Characters	Mean ± SE	Range	CV (%)
Days to 50% flowering	42.76 ± 0.19	38.00-47.00	4.12
Days to maturity	70.78 ± 0.18	65.67-75.66	2.32
Plant height (cm)	78.26 ± 0.44	61.00-114.00	4.71
Primary branches per plant	2.31 ± 0.47	1.33-3.66	23.95
Number of pods per plant	11.97 ± 1.06	6.67-23.00	15.30
Pod length (cm)	8.28 ± 0.06	5.97-11.70	17.19
Number of seeds per pod	11.55 ± 0.76	8.00-15.67	8.79
100 seed weight (g)	5.00 ± 0.15	4.17-6.83	8.15
Seed yield per plant (g)	6.92 ± 0.75	3.34-18.08	29.59
Biological yield per plant (g)	19.31 ± 2.25	9.63-40.33	19.46
Harvest index (%)	35.60 ± 2.42	30.95-45.99	6.26

Heritability and Genetic Gain

Heritability, in a broad sense, includes additive and epistatic effects; it is realized only when accompanied by genetic advances. However, GCV with heritability estimates would

Table 3: Estimation of genetic variability parameters for eleven characters in mung bean

Characters	*σ^2g*	*σ^2p*	*GCV (%)*	*PCV (%)*	*$h^2_{(b)}$*	*GA*	*GA as % of mean*
Days to 50% flowering	5.322	8.426	5.395	6.789	63.16	3.78	8.83
Days to maturity	6.781	9.475	3.679	4.349	71.57	4.54	6.41
Plant height (cm)	109.902	123.481	13.396	14.199	89.00	20.37	26.03
Primary branches per plant	0.560	0.866	32.386	40.278	64.65	1.24	53.64
Pods per plant	15.538	18.894	32.931	36.314	82.24	7.36	61.52
Pod length (cm)	3.732	5.759	23.331	28.983	64.80	3.20	38.69
Seeds per pod	4.642	5.673	18.654	20.622	81.83	4.01	34.76
100 seed weight (g)	0.622	0.788	15.778	17.758	78.94	1.44	28.88
Seed yield per plant (g)	10.854	15.048	47.609	56.057	72.13	5.76	83.29
Biological yield per plant (g)	41.043	55.164	33.177	38.463	74.40	11.38	58.95
Harvest index (%)	12.928	17.901	10.100	11.885	72.22	6.29	17.68

σ^2g = Genotypic variance, σ^2p = Phenotypic variance, GCV = Genotypic coefficient of variance, PCV = Phenotypic coefficient of variance, $h^2_{(b)}$ = Heritability (Broad sense), GA = Genetic advance, GAM = Genetic advance as per cent mean.

Table 4: Phenotypic (above diagonal) and genotypic (below diagonal) correlation among various characters in mung bean

Character	*DFF*	*DM*	*PH*	*PBPP*	*NPPP*	*PL*	*NSPP*	*100-SW*	*BYPP*	*HI*	*GYPP*
DFF	1.000	0.405**	0.067	-0.026	0.124	-0.175	-0.011	-0.16	-0.364**	0.0494	-0.067
DM	0.544**	1.000	0.168*	-0.038	0.323	-0.144	-0.061	-0.026	-0.27**	0.196*	0.103
PH	-0.004	0.190*	1.000	-0.002	0.038	0.348**	0.005	-0.437**	-0.196*	0.406**	-0.051
PBPP	-0.075	-0.074	-0.009	1.000	0.209**	0.126	0.243**	0.077	0.164*	-0.021	0.290**
NPPP	0.198*	0.386**	0.051	0.270**	1.000	-0.0118	0.162*	-0.112	0.013	0.040	0.629**
PL	-0.246**	-0.13	-0.457**	0.153	0.050	1.000	0.248**	0.347**	0.054	-0.064	0.053
NSPP	0.016	0.048	0.046	0.364**	0.162*	0.308**	1.000	-0.135	-0.019	0.091	0.171*
100-SW	-0.233*	-0.026	-0.505**	0.078	-0.128	0.648**	-0.157	1.000	0.297**	-0.107	0.108
BYPP	-0.424**	-0.295**	-0.231**	0.248**	-0.015	0.07	-0.044	0.460**	1.000	0.012	0.287**
HI	0.040	0.328**	0.65**	-0.064	0.070	-0.040	0.114	-0.162*	0.038	1.000	-0.031
GYPP	-0.068	0.128	-0.085	0.296**	0.694**	0.057	0.171*	0.112	0.428**	-0.063	1.000

**Significant at 1% level
*Significant at 5% level
DFF - Days to 50% flowering (days), DM - Days to maturity (days), PH - Plant height (cm), PBPP - Primary branches per plant (No.), NPPP - Pods per plant (No.), PL - Pod length (cm), NSPP - Number of seeds per pod (No.), 100-SW - 100 seed weight (g), SYPP - Seed yield per plant (g), BYPP - Biological yield per plant (g), HI - Harvest index (%).

give a clear picture of the extent of genetic advances for selection. Johnson *et al.*, (1955) also suggested that high heritability coupled with high genetic advance could be helpful in establishing a close relationship between genotype and phenotype.

In the present study, results revealed that the high heritability (bs) was observed for plant height (0.89) followed by pods per plant (0.82) and seeds per pod (0.81), indicating the less influence of environment on these characters (Table 3). These findings confirm the studies of Suresh *et al.* (2010) and Siddique *et al.* (2006). The heritability is not sufficient to select the best individual. However, heritability associated with genetic advance is more reliable as compared to only heritability. The high genetic advance as a percent of the mean was recorded for primary branches per plant (20.37) and biological yield per plant (11.38). Tabasum *et al.* (2010) and Yaqoob *et al.,* 2010. High heritability coupled with high genetic advance as a percent of the mean indicated the presence of additive genes for better selection plant height, pods per plant, seed yield per plant, primary branches per plant, 100-seed weight and biological yield per plant. Moderate to high heritability and low genetic advance were recorded for primary branches per plant, days to 50% flowering, seeds per pod and 100-seed weight,

Table 5: Estimates of direct (bold values) and indirect effects at genotypic level between yield and its components in mung bean

Characters	*DFF*	*DM*	*PH*	*PBPP*	*NCPP*	*NPPP*	*PL*	*NSPP*	*100-SW*	*PC*	*BYPP*	*HI*	*Correlation with SY*
DFF	-0.163	0.195	-0.001	0.016	-0.143	0.196	0.068	0.006	-0.030	-0.006	-0.240	-0.020	-0.068
DM	-0.089	0.359	0.028	0.016	-0.265	0.383	0.036	-0.017	-0.003	0.013	-0.167	-0.164	0.128
PH	0.007	0.068	0.146	0.002	0.020	0.051	0.127	0.017	-0.065	0.004	-0.131	-0.325	-0.085
PBPP	0.012	-0.027	0.013	-0.214	0.028	0.267	-0.043	0.132	0.009	-0.041	0.140	0.040	0.296**
NPPP	-0.032	0.138	0.007	-0.058	-0.380	0.992	0.014	0.059	-0.017	0.017	-0.009	-0.035	0.654**
PL	0.040	-0.047	-0.066	-0.033	0.103	-0.049	-0.278	0.112	0.083	0.019	0.153	0.021	0.057
NSPP	-0.003	-0.017	0.007	-0.078	-0.014	0.161	-0.086	0.363	-0.020	-0.009	-0.025	-0.107	0.171*
100-SW	0.004	-0.009	-0.073	-0.105	0.087	-0.127	-0.180	-0.057	0.129	-0.020	0.260	0.081	0.112
BYPP	0.069	-0.106	-0.034	-0.053	0.049	-0.015	-0.075	0.016	0.059	0.003	0.566	-0.019	0.428**
HI	-0.007	0.118	0.094	0.014	0.028	0.069	0.011	0.077	-0.020	0.032	0.021	-0.501	-0.063

**Significant at 1% level
*Significant at 5% level
DFF - Days to 50% flowering (days), DM - Days to maturity (days), PH - Plant height (cm), PBPP - Primary branches per plant (No.), NCPP - Clusters per plant (No.), NPPP - Pods per plant (No.), PL - Pod length (cm), NSPP - Number of seeds per pod (No.), 100-SW - 100 seed weight (g), SYPP - Seed yield per plant (g), BYPP - Biological yield per plant (g), HI - Harvest index (%), PC - Protein content (%)

Table 6: Estimates of direct (bold values) and indirect effects at phenotypic level between yield and its components in mung bean

Characters	*DFF*	*DM*	*PH*	*PBPP*	*NCPP*	*NPPP*	*PL*	*NSPP*	*100-SW*	*PC*	*BYPP*	*HI*	*Correlation with SY*
DFF	-0.064	-0.017	-0.003	-0.003	0.021	0.070	0.016	0.001	-0.029	0.000	-0.071	-0.002	-0.067
DM	-0.026	-0.043	0.007	0.005	-0.040	0.183	0.013	-0.003	-0.005	0.001	-0.053	-0.006	0.103
PH	0.004	0.007	0.041	0.000	-0.005	0.022	0.031	0.000	-0.079	0.000	-0.380	-0.012	-0.051
PBPP	0.002	0.002	0.000	0.132	-0.004	0.118	0.011	-0.010	0.014	-0.005	0.032	0.001	0.290*
NPPP	-0.008	-0.014	0.002	0.028	0.065	0.565	0.001	0.007	0.020	0.002	0.003	-0.001	0.629**
PL	0.011	-0.047	-0.066	0.033	0.103	-0.049	-0.278	0.112	0.083	0.018	0.153	0.021	0.053
NSPP	-0.003	-0.017	0.007	-0.078	-0.014	0.161	-0.085	0.363	-0.020	-0.009	-0.025	-0.107	0.171**
100-SW	0.010	0.001	-0.018	-0.010	-0.015	-0.063	-0.049	-0.005	0.180	-0.002	0.058	0.003	0.108
BYPP	0.023	0.012	-0.008	0.022	-0.002	0.007	-0.014	-0.001	0.005	-0.001	0.195	0.000	0.287*
HI	-0.064	-0.017	-0.003	-0.003	0.021	0.070	0.016	0.001	-0.029	0.000	-0.071	-0.002	-0.031

**Significant at 1% level
*Significant at 5% level
DFF - Days to 50% flowering (days), DM - Days to maturity (days), PH - Plant height (cm), PBPP - Primary branches per plant (No.), NPPP - Pods per plant (No.), PL - Pod length (cm), NSPP - Number of seeds per pod (No.), 100-SW - 100 seed weight (g), SYPP - Seed yield per plant (g), BYPP - Biological yield per plant (g), HI - Harvest index (%), PC - Protein content (%).

showing non-additive gene action and selection may not be effective. These findings confirm the studies of Yaqoob *et al.,* (2010) and Rahim *et al.* (2010).

Correlation Studies

Yield is a complex polygenic trait that has a large number of other contributing component traits. Correlation analysis reveals the information on the relationship of dependent variable yield with its independent variables, thus, an association of various traits would determine their relative significance to improve yield.

In the present study, the correlation coefficient on genotypic and phenotypic levels between yield and its component traits has been worked out and the results revealed that there is a strong inherent association between the various traits (Table 4). Seed yield per plant exhibited a highly significant and positive phenotypic correlation with number of seeds per pod. Thus, the number of pods per plant, primary branches per plant, and biological yield per plant emerged as a significant and strong association with seed yield per plant, while days to 50% flowering and harvest index were negatively associated with seed yield. At the genotypic level, the correlation coefficient (Table 4) for these traits was the same in direction but higher in magnitude with seed yield, indicating that these traits could be helpful for the improvement of seed yield/plant through improving these traits. Similar results were reported by Rahim *et al.* (2010), Suresh *et al.* (2013) and Pushpa Reni *et al.* (2013).

Among other traits, days to 50% flowering exhibited positive and significant genotypic correlation with days to maturity, number of pods per plant and positive and non-significant correlation with harvest index. It showed a negative and significant correlation with 100-seed weight, pod length and biological yield per plant. The high association of days to 50% flowering with these important yield components revealed that the selection of early flowering genotypes would lead to simultaneous improvement in yield. These results are in agreement with the findings of Khaimichho *et al.* (2014), Patel *et al.* (2014) and Titumeer *et al.* (2014). Primary branches per plant were positively and significantly associated with the number of pods per plant, number of seeds per pod and biological yield per plant, while seeds per pod showed a positive and significant correlation with primary branches per plant, number of pods per plant, pod length and seed yield per plant (Shivade *et al.* 2011; Ahmad *et al.* 2014).

Path Coefficient Analysis

The correlation values decide only the nature and degree of association existing between the two characters. However, this may not give a true picture and this might affect the true association of component characters, both in magnitude and direction. Hence it is necessary to partition the correlation coefficient into direct and indirect effects of yield components on seed yield, which provides a better index for selection.

The estimate of direct effects revealed that the number of pods per plant depicted maximum positive direct effects on seed yield at phenotypic as well as genotypic levels, respectively, followed by biological yield per plant, number of seeds per plant, days to maturity, plant height and 100 seed weight (Tables 5 & 6). Thus, these traits emerged as the most important direct yield component. So, these results clearly indicated the improvement in seed yield in mung bean, and major emphasis should be given to these traits. The findings are in accordance with the findings of Raselmiah *et al.* (2016), Rathor *et al.* (2015), Gadakh *et al.* (2013), Prasanna *et al.* (2013) and Tabasum *et al.* (2010).

Biological yield per plant showed maximum positive indirect effect *via* days to 50% flowering while it exhibited maximum negative indirect effect via pod length both at phenotypic and genotypic levels. These results are in contrast with the earlier reports of Tabasum *et al.* (2010) and Singh *et al.* (2009), who found maximum negative indirect contribution *via*., days to 50% flowering.

Conclusion

The present results confirmed that geographical background plays an important role in creating variations among the morphological traits and thus, these traits can be considered as favorable attributes for improvement through various breeding programs.

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References

Ahmad HB, S Rauf, CM Rafiq, AU Mohsin, U Shahbaz and M Sajjad (2014) Genetic variability for yield contributing traits in mung bean (*Vigna radiate* L.). *J. Glob. Agric. Soc. Sci*. 2(2): 52-54.

Ahmad HF, F Rauf, I Hussain, CM Rafiq, A Rehman, AM Aulakh and MA Zahid (2015) Genetic variability, association and path analysis in mung bean (*Vigna radiata* L.). *Int. J. Adv. App. Res.* 6(6): 75-81.

Al-Jibouri KA, RA Mider and HF Rdoinson (1958) Genotype and environmental variances and covariance in upland cotton crosses of interspecific origin. *J. Agron*. 50: 633-637.

Bisht N, DP Singh and RK Khulbe (2014) Genetic variability and correlation studies in advance inter-specific and inter-varietal lines and cultivars of mung bean *(Vigna radiata*). *J. Food. Legume* 27(2): 155-157.

Box GE, WG Hunter and JS Hunter (1978) Statistics for Experimenters. New York: John Wiley.

Burton GW and CH Devane (1953). Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. *J. Agron*. 45: 478-481.

Das RT and PK Barua (2015) Association studies for yield and its components in green gram. *Inter. J. Agri. Environ. Biotech*. 8(3): 561-565.

Dewey DR and Lu KH (1959) A correlation and path analysis of crested wheat grass and seed production. *J. Agron.* 51:315-318.

Fisher RA (1954) Statistical methods for research workers (12thEdn). *Bio. Mono. Man*. 5: 130-131.

Gadakh SS, AM Dethe and MN Kathale (2013) Genetic variability, correlations and path analysis studies on yield and its components in mung bean (*Vigna radiata* (L.) Wilczek). *Bioinfolet* 10(2A): 441-447.

Javed I, HM Ahmad, M Ahsan, Q Ali, MU, MS Ghani Iqbal, M Rashid and HN Akram (2014). Induced genetic variability by gamma radiation and traits association study in mung bean (*Vigna radiata* L.). *Life Sci. J.* 11(8s): 530-539.

Johnson HW, HF Robinson and RE Comstock (1955) Genotypic and phenotypic correlation in soybean and their implications in selection. *J. Agron*. 47: 477-483.

Khaimichho EB, L Hijam, KK Sarkar, and S Mukherjee (2014) Genetic control and character association estimates of yield and yield attributing traits in some mung bean genotypes. *J. Crop Weed* 10(2): 82-88.

Mooose SP and RH Mumm (2008) Molecular plant breeding as the foundation for 21st century crop improvement. *Plant*

Physiology 147(3): 969-977.

More AD and AT Borkar (2016) Analysis of genetic variability, heritability and genetic advance in *Phaseolus vulgaris* L. *Int. J. Curr. Microbiol. Appl. Sci*. 5(10): 494-503.

Panigrahi KK and B Baisakh (2014) Genetic diversity assessment for yield contributing characters of green gram [*Vigna radiata* (L.) Wilczek]. *J. Ecol. Environ.*32 (1a) pp: 294-297.

Payasi DK (2015) Genetic variability analysis for seed yield and its components in mung bean (*Vigna radiata* L. Wilczek). *Int. J. Plant Breed. Genet.* 9(3):177-188.

Prasanna BL, PJM Rao, KGK Murthy and KK Prakash (2013) Genetic variability, correlation and path coefficient analysis in mungbean. *J. Ecol. Environ.* 31(4): 1782-1788.

Pushpa Reni Y, Y Rao Koteswara, Y Satish and J Sateesh Babu (2013) Estimates of genetic parameters and path analysis in blackgram (*Vigna mungo* (L.) Hepper). *Int. J. Plant Animal Environ. Sci.* 3(4): 231-234.

Rahim MA, AA Mia, F Mahmud, N Zeba and KS Afrin (2010) Genetic variability, character association and genetic divergence in Mung bean [*Vigna radiate* (L.) Wilczek]. *Plant Omics J*. 3(1): 1-6.

Raselmiah MD, MM Rob, U Habiba, KR Das and MS Islam (2016) Correlation and path coefficients analysis of black gram (*Vigna mungo* L). *Eur. J. Acad. Res.* 3(5): 2286-4822.

Rathor P, A Singh, M Imran, K Ali and R Fatma (2015) Character association and path analysis for yield and yield component traits in mung bean [*Vigna radiata* (L.) Wilczek]. *Indian Res. J. Genet. Biotech*. 7(1): 93-97.

Shivade HA, AP Rewale and SB Patil (2011) Correlation and path analysis for yield and yield components in blackgram [*Vigna mungo* (L.) Hepper]. *Leg. Res*. 34 (3): 178 - 183.

Siddique M, M Faisal, M Anwar and IA Shahid (2006) Genetic divergence, association and performance evaluation of different genotypes of mungbean (*Vigna radiate* L.). *Int. J. Agri. Biol*. 6: 793-795.

Singh SK, GR Lavanya, A Krupakar and GS Babu (2012) Selection of diverse mung bean genotypes for seed yield improvement. *New Agriculturist* 23(1): 5-9.

Singh SK, IP Singh, BB Singh and O Singh (2009) Correlation and path coefficient studies for yield and its components in mungbean (*Vigna radiata* (L.) wilczek). *Leg. Res*. 32 (3):180-185.

Srivastava RL and G Singh (2012) Genetic variability, correlation and path analysis in mung bean [*Vigna radiata* (L.) Wilczek]. *Ind. J. Life Sci*. 2(1): 61-65.

Suresh S, S Jebaraj and S Arulselvi (2013) Genetic variability, correlation and path analysis for yield and yield attributing traits in mutant populations of mungbean (*Vigna radiata* (L.) Wilczek). *Int. J. Sci. Res.* 2 (10): 1- 3.

Suresh S, S Jebaraj, J Hepziba and M Theradimani (2010) Genetic studies in mung bean (*Vigna radiata* (L). Wilczek). *Electron. J. Plant Breed*. 1(6): 1480-1482.

Tabasum Aqsa, Saleem Muhammad and Aziz Irum (2010) Genetic variability, trait association and path analysis of yield and yield components in mungbean (*Vigna radiata* (L.) Wilczek). *Pak. J. Bot*. 42(6): 3915-3924.

Titumeer SM, MA Rahim and N Zeba (2014) Genetic variability, character association and genetic divergence in mungbean (*Vigna radiate* L. Wilczek*). Agronomski Glasnik* 6:305-326.

Usharani KS and CRA Kumar (2016) Estimation of variability, heritability and genetic advance in mutant populations of black gram (*Vigna mungo* L. Hepper*). SABRAO J. Breed. Genet.* 48(3): 258-265.

Yaqoob M, B Ahmad, N Khan, ZM Ashraf and HA Lal (2010) Studies on heritability and genetic advance in chickpea (*Cicer arietinum* L.). *Sci. Tech. Develop.* 29(3): 10-13.