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Association and Variability of Morphological, Yield and Yield Attributing Traits in Mungbean [Vigna ridiata (L.) Wilezek]

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Abstract:

The efficacy of 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 fifty-one diverse genotypes of mungbean for the estimation of genetic variability, heritability & genetic advance, 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 offering an ample opportunity for selecting suitable genotypes with desired traits. Phenotypic coefficients of variation were greater in magnitude over the respective genotypic coefficient of variation. High to moderate estimates of heritability coupled with higher genetic advance as per cent of mean was observed for number of pods per plant, seeds per pod, biological yield per plant and seed yield per plant 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. 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, number of seeds per pod while the highest negative direct effect was recorded for harvest index.

Keywords: variability; correlation coefficient; path analysis; mungbean

Introduction

Pulses are excellent option of dietary protein. Pulses when used as food with other cereals they definitely meet the requirement of a balanced diet. Mungbean (*Vigna radiata* L.) is a vital and important pulse crop also known as greengram, 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 mungbean is a complex character like other crop determined by various components. A clear knowledge of variability in various quantitative characters existing in the breeding material helps plant breeder for selecting 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 characters and environmental conditions that exist during crop growth. It is, therefore, essential to study association of characters among themselves and with yield of crop. Genotypic correlation provides a measure of genotypic association between two characters and helps to identify more useful relationship between characters. Indirect association becomes complex and important when a number of variables are included in the study of correlation. In such cases more defined technique as path coefficient analysis helps to find out 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 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 indirect effect is exerted. Presence of high variability in this crop offers much scope for its improvement. Hence, an attempt was made to assess the genetic variability, heriabilty,

genetic advance, correlation and path analysis in respect to desirable traits in fifty one genotypes of mungbean which will help in the selection of promising lines for further breeding programme and to explore high yielding lines of mungbean.

Materials & Methods:

The experiment was under taken at 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 mungbean for genetic variability with respect to yield and yield contributing traits and maturity. The experiment was laid out in Randomized Block Design with 3 replications. 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. Uniform standard plant population was maintained throughout the experiment. 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 plot basis. The data of eleven morphological traits viz days to maturity, number of branches plant^{-1}, Plant height (cm), Pod length (cm), number of pods plant^{-1}, number of seeds pod^{-1},100-seed weight (g), Seed yield plant^{-1} (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 broad sense and Genetic advance were worked out as per the procedures of Burton and Dewane (1953), 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 & Discussion

Analysis of variance and mean performance

Since, yield is governed by polygenes with small, similar and cumulative effects and highly influenced by environment, selection based on yield alone is not effective. The breeders apply indirect selection on yield through selection of yield attributes with high heritability so that environmental influence can be minimized.

The mean sum of squares with respect morphological traits has been given in (Table-1).

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 (%),

Table-1: Analysis of variance(Mean Squares)for the eleven characters of Mungbean genotypes

The results revealed that the mungbean genotypes differed significantly for all the traits *viz* days to 50% flowering, days to maturity ,number of branches plant^{-1}, Plant height (cm), Pod length (cm),number of pods plant^{-1}, number of seeds pod^{-1},100-seed weight (g),Seed yield plant^{-1}(g),Biological yield plant^{-1} (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. Similar finding was also reported by Gul *et al.* (2007), Singh *et al*. (2012), Srivastava and Singh (2012), Javed *et al.* (2014) and Bisht *et al.* (2014).

The means performance of the genotypes showed a wide range of variability for all the parameters studied (Table-2).

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

Table-2: Range Mean and co-efficient of variability for different traits of Mungbean

The variation was highest for Plant height (cm) followed by biological yield per plant (g), number of pods per plant and the seed yield /plant(g). This may be due to the existence of diversity in genotypes evaluated. The range and coefficient of variation were higher for seed yield and number of branches/plant, and medium to low values were observed for biological yield per plant (g), Pod length (cm), number of pods plant-1, number of seeds pod-1, 100-seed weight (g), Harvest index (%), Plant height (cm) and days to flowering/ maturity. Coefficient of variation was low which indicated that most of the genotypes were having average height and mass selection would be effective for shorter height. Similar finding was also reported by Ahmad *et al.* (2015), Easwari and Rao (2006), 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 phenotypic coefficient of variation was observed higher than genotypic coefficient of variation for all characters indicated that environment had important role in 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 selection of these traits. Similar results were also reported by Panigrahi *et al* (2014), Konda *et al* (2009), Pervin *et al*. (2007), and Suresh *et al.* (2010), While as 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 genotypic coefficient of variation was close to that of phenotypic variation for days to 50% flowering, days to maturity and harvest index indicating that 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) Tabasum *et al.* (2010), More *et al.* (2016) and Usharani *et al.* (2016). However, considerable difference was observed between GCV and PCV value for primary branches per plant and seed yield per plant indicating role of environment in expression of these traits.

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 give the clear picture of the extent of genetic advances for selection. Johnson et al., (1955) had also suggested that high heritability coupled with high genetic advance could be helpful in establishing 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 Rohman and Hussain, 2003; Siddique *et al.,* 2006 and Suresh *et al.* (2010). 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 percent of 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 percent of mean indicated that 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 shows of non-additive gene action and selection may not be effective. These findings confirm the studies of Siddique *et al.,* 2006; Yaqoob *et al.,* 2010, Firoz *et al*., 2006 and Rahim *et al*., 2010.

Characters	$\sigma^2 g$	$\sigma^2 p$	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

$\sigma^2 g$ = Genotypic variance, $\sigma^2 p$ = 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 -3: Estimation of genetic variability parameters for eleven characters in Mungbean

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 (%).

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

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

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

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 (%)

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 (%).

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

Correlation studies

Yield is a complex polygenic trait 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 association of various traits would determine their relative significance to improve yield.

In the present study, correlation coefficient on genotypic and phenotypic levels between yield and its components traits have 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 significantly and positive phenotypic correlation with number of seeds per pod. Thus, number of pods per plant, primary branches per plant, biological yield per plant emerged as a significant and strong association with seed yield /plant while days to 50% flowering and harvest index were negatively associated with seed yield. At the genotypic level, the correlation coefficient (Table-) 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 Hakim 2008; Rahim *et al.,* 2010; Suresh *et al.* (2013, Chauhan *et al*. (2007), 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 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 selection of early flowering accessions would lead to simultaneous improvement in yield. These results are in agreement with the findings of Titumeer *et al.* (2014), Khaimichho *et al.* (2014), Patel *et al*. (2014), Primary branches per plant was positively and significantly associated with number of pods per plant, number of seeds per pod and biological yield per plant while as seeds per pod showed positive and significant correlation with primary branches per plant, number of pods per plant, pod length and seed yield per plant. (Chauhan *et al.,* 2007; Shivade *et al*., 2011; Ahmad *et al*., 2014).

Path coefficient analysis

The correlation values decide only the nature and degree of association existing between two characters. However, this may not give 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 provided 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 level respectively followed by biological yield per plant, number of seeds per plant, days to maturity, plant height and 100 seed weight (Table-5&6). Thus, these traits emerged as the most important direct yield component. So, these results clearly indicated the improvement for seed yield in mungben, major emphasis should be given on these traits. The findings are in accordance with findings of Tabasum *et al.* (2010), Prasanna *et al*. (2013), Gadakh *et al.* (2013), Rathor *et al*. (2015) and Raselmiah *et al*. (2016).

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 Singh *et al.* (2009) and Tabasum *et al.* (2010) who found maximum negative indirect contribution via., days to 50% flowering.

Conclusion

These results with the above information showed a good amount of variability available for all the agro-morphological traits studied and having considerable scope to select the superior moongbean genotypes. Further studies revealed the primary emphasis should be given for selection of characters like primary branches plant[-1], pods plant[-1], number of seeds pod[-1] and biological yield plant[-1] as these traits had a strong positive correlation with seed yield plant[-1] with high direct effects and also most important traits for their exploitation through selection for future yield improvement in moongbean.

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