

Genetic variability, character association and genetic divergence in Mungbean (*Vigna radiata* L. Wilczek)

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Abstract

Genotypic and phenotypic variance, coefficient of variance, heritability, genetic advance, correlation and path coefficient were evaluated for yield and its contributing characters in 26 Mungbean genotypes. Significant variations among the genotypes were observed for all the characters. High heritability (broad) along with high genetic advance in percent of mean was observed for plant height, number of pods per plant, number of seeds per pod, 1000-grain weight and grain yield per plant indicating these characters would be best for phenotypic selection. The number of pods per plant, panicle length and number of seeds per pod are positively correlated with grain yield. Based on path coefficient parameter, the number of pods per plant and number of seeds per pod are the important characters. Twenty six genotypes were grouped into 3 clusters. Maximum number of genotypes (12) was grouped into cluster II. The maximum range of variability was observed for number of pods per plant (12.22 - 20.55) among all the characters in 3 clusters. Crosses involving cluster I and III may exhibit high heterosis for yield as well as earliness.

Key words: Genetic variability; character association; genetic divergence; Mungbean

Introduction

Mungbean (*Vigna radiata* L. Wilczek) is an important pulse crop which is annual legume. It is well suited to dry areas, mainly under irrigated conditions. It has the diploid chromosome number $2n = 2x = 22$ (Karpechenko, 1925). Mungbean is cultivated in tropical, subtropical and temperate zones of Asia including Bangladesh, India, Pakistan, Myanmar, Indonesia, Philippines, Sri Lanka, Nepal, China, Korea and Japan. It is also cultivated in Australia, East Africa and United States of America (Chopra, 2001). It is a short duration crop and grown as sole as well as inter and multiple cropping system, hence it contributes to increase the income of marginal farmers. Mungbean is a source of digestible protein. In Bangladesh, dehulled grain is mainly used to make Daal. Besides, this it is used to prepare various delicious sweet items and salad (soaked and sprouted grains). It improves the nutrient status of soil through atmospheric nitrogen fixation and adds humus to the soil. It is also useful to cattle as it is a fodder and concentrate. In Bangladesh, the area under Mungbean is declining day by day due to replacement of land by high yielding winter vegetable and Boro rice. Therefore, it is very much essential to improve its yield. For yield improvement, it is essential to have knowledge on variability of different characters. The variability of a biological population is an outcome of genetic constitution of individuals making up that

population in relation to prevailing environment. A survey of genetic variability with the help of suitable parameters such as genotypic coefficient of variation, heritability and genetic advance are absolutely necessary to start an efficient breeding program (Mishra et al. 1988). The coefficient of correlation between yield and its contributing traits show a complex relationship. Path coefficient analysis partitions the components of correlation coefficient into direct and indirect effects and visualizes the relationship in more meaningful way. Genetic diversity is one of the criteria of parent selection in the hybridization program. The availability of transgressive segregant in any breeding program depends upon the diversity between the parents involves. The quantification of genetic diversity through biometrical procedures such as Mahalanobis's D^2 -statistic and Canonical Variate Analysis (CVA) has made possible to choose genetically diverged parents. Recent works indicated that the Mahalanobis generalized distance (D^2 -statistic) may be an efficient tool in the quantitative estimation of genetic diversity (Mahalanobis, 1936). The divergence analysis has a definite role to play in an efficient choice of divergent parents for hybridization to exploit maximum heterosis. The present study was undertaken to select the divergent parent for future hybridization program.

Table 1. Designation of Mungbean germplasms

Genotype	Name/ Accession No.	Source
1.	BARI Mung-2	BARI
2.	BARI Mung-3	BARI
3.	BARI Mung-4	BARI
4.	BARI Mung-5	BARI
5.	BARI Mung-6	BARI
6.	BD-6904	BARI
7.	BD-6907	BARI
8.	BD-6908	BARI
9.	BD-6909	BARI
10.	BD-6910	BARI
11.	BD-6911	BARI
12.	BD-6912	BARI
13.	BD-6913	BARI
14.	BD-6914	BARI
15.	BD-6915	BARI
16.	BD-6916	BARI
17.	BD-6918	BARI
18.	BD-6920	BARI
19.	BD-6921	BARI
20.	BD-6922	BARI
21.	BD-6923	BARI
22.	BD-6924	BARI
23.	BD-6925	BARI
24.	BD-6926	BARI
25.	BD-6927	BARI
26.	BD-6928	BARI

Materials and methods

The experiment was carried out at the experimental farm of Sher-e-Bangla Agricultural University, Dhaka, Bangladesh during March, 2005 to August, 2008. Twenty six genotypes (varieties/lines) of Mungbean (Table 1) were used in this experiment and were collected from Bangladesh Agricultural Research Institute (BARI), Gazipur. A Randomized Complete Block Design (RCBD) with three replications was used in the experiment. The individual plot was of 3m long with three rows. The seeds were sown on March 10th, 2008 with a spacing 30cm row to row and 10cm plant to plant. N, P and K fertilizers @ 40-60-20kg/ha were applied as a basal dose (Rohman et al., 2003) during final land preparation. The standard agronomic practices were maintained to raise a good crop. Data on 10 randomly selected plant from each plot were recorded on 8 characters viz., days to 50% flowering (days), days to 80% maturity (days), plant height (cm), number of pods per plant, pod length (cm), number of seeds per pod, 1000-grain weight (g) and grain yield per plant (g). Genotypic and phenotypic coefficient of variations, heritability and genetic advance were estimated as per Singh and Chowdhury (1985) and Johnson et al. (1955). Correlation coefficients were calculated as according to Miller et al. (1958) and path coefficient analysis was done following to the method suggested by Dewey and Lu (1959). Genetic diversity was found through cluster analysis, principal component analysis and D²-statistic, using Genstat software program (Digby et al., 1989).

Results and discussion

Genetic variability analysis

The estimate of genotypic variance (σ_g^2), phenotypic variance (σ_p^2), genotypic coefficient of variation (CVg) and phenotypic coefficient of variation (CVp), heritability (h^2_b), genetic advance (GA), genetic advance in percent of mean and coefficient of variation (CV%) for 8 different characters are presented in Table 2. The coefficient of variation indicated that there were significant differences among the genotypes for measured characters. The phenotypic variance (σ_p^2) and phenotypic coefficient of variation (CVp) was slightly higher than the genotypic variance (σ_g^2) or genotypic coefficient of variation (CVg) for all the characters suggesting the presence of environmental influence to some extent in the expression of these characters. Relatively higher value of genotypic variance and phenotypic variances were found for number of pods per plant, 1000-grain weight, plant height and grain yield per plant. The highest genotypic coefficient of variation was found for number of pods per plant followed by 1000-grain weight and plant height and the lowest for pod length indicating higher degree of genetic variability for these characters. A higher heritability (broad sense) estimate associated with good estimates of genetic advance expected in the next generation for grain yield per plant, number of pods per plant, plant height, number of seeds per pod and 1000-grain weight suggesting these characters are governed by additive genetic effect to a great extent and improvement of these characters would be effective through phenotypic selection. Similar results were found by Vikas et al. (1998) for plant height and number of pods per plant, Sharma (1999) for the number of pods per plant, number of seeds per plant, 100-seed weight and seed yield per plant. High heritability estimates has been found to be helpful in making selection of superior genotypes on the basis of phenotypic performance. Jonson et al., (1955) suggested that heritability estimates along with genetic gain were more useful in predicting the selection of best individual.

Character association

Correlation coefficient analysis

Correlation coefficient analysis among grain yield and its contributing characters are shown in Table 3. Grain yield was positively correlated with number of pods per plant, panicle length and number of seeds per pod. Similar results were reported by Sharma (1999) and Gill et al. (1995). Positive correlation was found only between days to 50% flowering and days to 80% maturity. Days to 50% flowering are positively associated with plant height and number of seeds per pod and negatively correlated with 1000-grain weight. Days to 80% maturity showed strong positive correlation with pod length. Plant height had no significant correlation but it show positive correlation with number of pods per plant, pod length and number

Table 2. Genetic variability, genetic parameter, heritability (h_b^2), GA and GA in percent of mean for nine yield contributing characters of 26 Mungbean genotypes

Characters	Grand Mean	Mean sum of square	σ_g^2	σ_p^2	GCV (%)	PCV (%)	h_b^2	GA (5%)	GA(5%) of mean	CV%
DFF	39.53	34.33**	8.75	16.84	7.48	10.38	51.94	4.39	11.11	7.20
DM	64.77	12.15**	2.41	7.32	2.40	4.18	32.95	1.84	2.84	3.42
PH	37.69	82.47**	24.65	33.16	13.17	15.28	74.34	8.82	23.40	7.74
NPP	20.83	115.02**	37.68	39.66	29.47	30.23	95.01	12.33	59.17	6.75
PL	6.87	1.62	0.13	1.35	5.32	16.93	9.85	0.24	3.44	16.05
NSP	10.76	7.83**	2.34	3.16	14.21	16.51	74.02	2.71	25.18	8.43
TSW	27.42	95.93**	25.09	45.75	18.27	24.67	54.84	7.64	27.87	16.58
YPP	8.47	32.56**	10.77	11.02	38.74	39.18	97.75	6.68	78.89	5.88

** Significant in 1% level of significance.

DFF = Day to 50% flowering, DM = Day to 80% maturity, PH = Plant height (cm), NPP = Number of pods per plant, PL = Pod length (cm), NSP = Number of seeds per pod, TGW = 1000-grain weight (g) and YPP = Grain yield per plant (g), σ_g^2 = Genotypic variance, σ_e^2 = Environmental variance, σ_p^2 = Phenotypic variance, GCV (%) = Genotypic co-efficient of variation, PCV (%) = Phenotypic co-efficient of variation, GA (5%) = Genetic advance in 5% and GA (5%) of mean = Genetic advance in 5 percent of mean.

Table 3. Genotypic and phenotypic correlation coefficient between yield and its component characters in 26 Mungbean genotypes

Characters	DM	PH	NPP	PL	NSP	TSW	YPP
DFF	-0.165	0.513**	0.351	0.344	0.471*	-0.467*	0.292
DM		-0.267	0.200	0.556**	-0.163	-0.109	0.144
PH			0.106	0.119	0.195	-0.145	-0.024
NPP				0.445*	0.538**	-0.197	0.785**
PL					0.267	-0.261	0.394*
NSP						-0.496**	0.455*
TGW							-0.303

* Significant in 5% and ** Significant in 1% level.

of seeds per pod and also negative correlation with 1000-grain weight and grain yield per plant. Rahman et al. (2002) reported that plant height is negatively correlation with 100-grain weight. Number of pods per plant showed positive correlation with pod length, number of seeds per pod and grain yield. Hakim (2008) mentioned that yield had significant positive correlation with number of pods per plant. Strong negative association was observed between number of seeds per pod and 1000-grain weight.

Path analysis

Path coefficient analysis (Table 4) revealed that days to 50% flowering showed negative direct effect on grain yield and positive indirect effect via days to 80% maturity, numbers of pods per plant, pod length and 1000-grain weight. It is mainly due to negative indirect effect via plant height and number of seeds per pod and finally contributed to positive correlation with grain yield. Upendra et al. (2005) reported very low positive direct effect of days to 50% flowering on grain yield. Days to 80% maturity had negative direct effect on grain yield but it had positive indirect effect on grain yield via days to 50% flowering, plant height, numbers of pods per plant, pod length and 1000-grain weight

and it also finally made positive correlation with yield. Plant height had negative direct effect on grain yield although it had positive indirect effect on grain yield via days to 80% maturity, numbers of pods per plant, pod length and 1000-grain weight. Numbers of pods per plant had positive direct effect on grain yield and it had positive indirect effect on grain yield via pod length and 1000-grain weight which finally made significant positive correlation with grain yield. Sharma (1999) reported positive direct effect for number of pods per plant. Gill et al. (1995) also mentioned that the direct effect of pod number per plant accounted for its high correlations with yield per plant. Pod length had also positive direct effect on grain yield while correlation was positive and significant. The indirect effect of this character via other characters like number of pods per plant and 1000-grain weight were positive and some other characters like days to 50% flowering, days to 80% maturity, plant height and number of seeds per pod were negative. Number of seeds per pod showed negative direct effect and significant positive correlation with yield. The highest positive direct effect was found for number of pods and the highest negative direct effect was found for days to 80% maturity. The residual effect was found 0.328 which

Table 4. Direct (Diagonal) and indirect effect of some yield contributing characters on grain yield in 26 Mungbean genotypes

Characters	DFE	DM	PH	NPP	PL	NSP	TGW	YPP(r)
DFE	-0.039	0.032	-0.088	0.282	0.051	-0.050	0.104	0.292
DM	0.006	-0.192	0.046	0.161	0.082	0.017	0.024	0.144
PH	-0.020	0.051	-0.169	0.085	0.018	-0.021	0.032	-0.024
NPP	-0.014	-0.038	-0.018	0.803	0.065	-0.057	0.044	0.785**
PL	-0.014	-0.107	-0.020	0.358	0.147	-0.028	0.058	0.394*
NSP	-0.018	0.031	-0.033	0.432	0.039	-0.107	0.111	0.455*
TGW	0.018	0.021	0.025	-0.158	-0.038	0.052	-0.223	-0.303

Residual effect, R = 0.328.

Table 5. Distribution of 26 genotypes of Mungbean in five clusters

Cluster	Number of genotypes	Name of genotypes
I	3	1 (BARI Mung-2), 2 (BARI Mung-3) and 10 (BD-6910).
II	12	3 (BARI Mung-4), 7 (BD-6907), 12 (BD-6912), 13 (BD-6913), 14 (BD-6914), 15 (BD-6915), 16 (BD-6916), 18 (BD-6920), 20 (BD-6922), 21 (BD-6923), 22 (BD-6924) and 23 (BD-6925).
III	11	4 (BARI Mung-5), 5 (BARI Mung-6), 6 (BD-6904), 8 (BD-6908), 9 (BD-6909), 11 (), 17 (BD-6918), 19 (BD-6921), 24 (BD-6926), 25 (BD-6927) and 26(BD-6928).

Table 6. Cluster means for 8 characters of 26 Mungbean genotypes

Characters	Clusters		
	I	II	III
Days to 50% flowering (days)	35.56	40.5	39.55
Days to 80% maturity (days)	62.67	65.08	65
Plant height (cm)	36.87	37.75	37.86
Number of pods per plant	12.22	23.53	20.55
Pod length (cm)	5.42	7.34	6.75
Number of seeds per pod	10.05	10.69	11.67
1000-grain weight (g)	28.65	27.13	26.25
Grain yield per plant (g)	8.23	8.65	8.55

Table 7. Relative contribution of the 8 characters to the total divergence of Mungbean genotypes

Characters	Vector-I	Vector-II
Days to 50% flowering (days)	0.31141	-0.32269
Days to 80% maturity (days)	0.04155	0.15203
Plant height (cm)	0.23083	-0.60723
Number of pods per plant	0.77602	0.50623
Pod length (cm)	0.07032	0.01332
Number of seeds per pod	0.17633	-0.03709
1000-grain weight (g)	-0.39379	0.4745
Grain yield per plant (g)	0.23387	0.14511

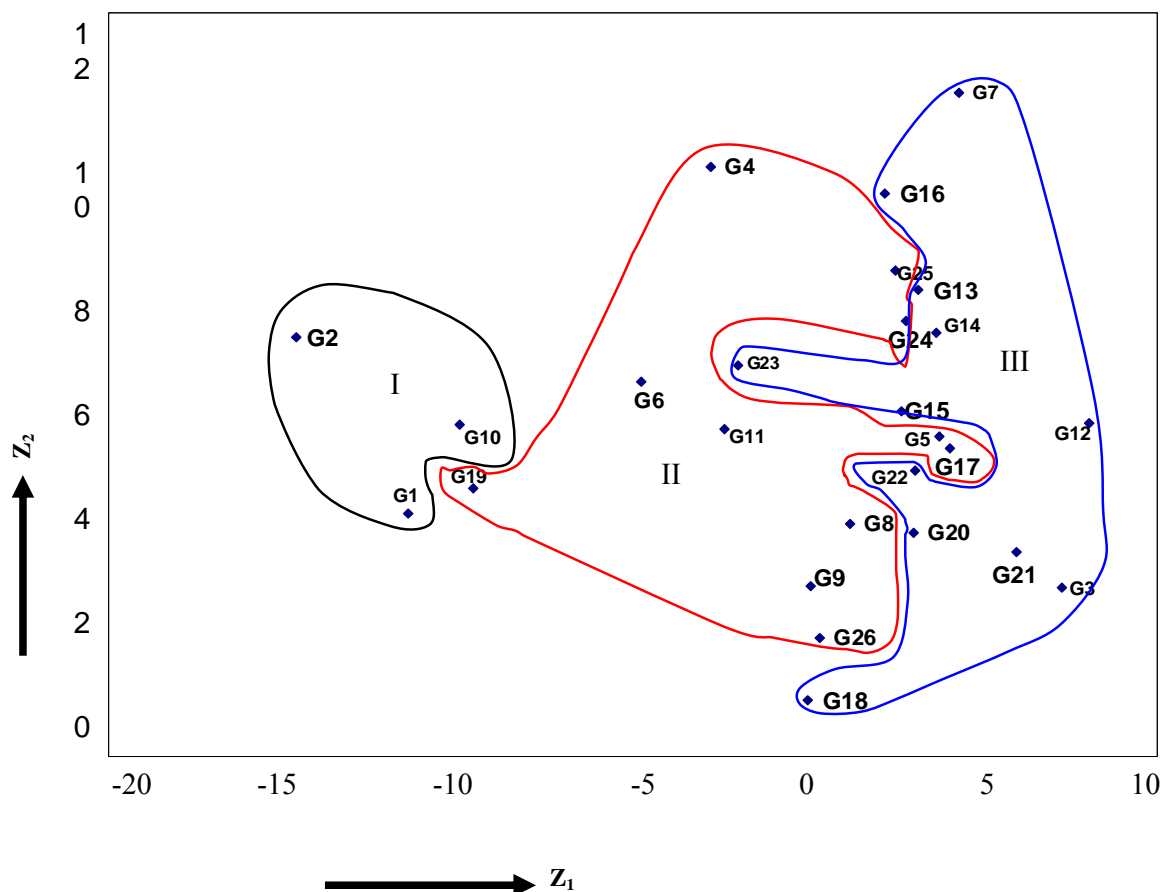


Fig 1. Scatter diagram of 26 Mungbean genotypes based on their principal component scores superimposed with clustering

indicated that the contribution of component character was 67.2 percent. The rest 32.8 percent was the contribution of other factors. The correlation and path coefficient study showed that number of pods per plant and number of seeds per pod are the important characters. Therefore, phenotypic selection can be effective for these characters in these rice genotypes.

Genetic divergence analysis

The analysis of variance showed significant differences among the genotypes for all the characters revealed the presence of notable genetic variability among 26 Mungbean genotypes. Twenty six Mungbean genotypes were grouped into three clusters through non-hierarchical clustering (Table 5). Kumar et al. (2009) grouped 60 genotypes into 13 clusters based on the divergence among Mungbean genotypes. Maximum number of genotypes (12) were grouped into cluster II, followed by 11 in clusters III and the lowest (3) in cluster I. Sandhu and Brar (2002) grouped 39 mutants of Mungbean into eight clusters. Table 6 showed that the mean value of cluster I ranked first for 1000-grain weight. Cluster II had the second highest cluster mean for days to 50% flowering, days to 80% maturity, number of pods per plant, pod length, grain yield per plant. Early maturing genotypes also found in this

cluster. This cluster also includes higher yielding genotypes. Cluster III constitutes genotypes with the highest mean values for number of seeds per pod and plant height indicating tallest genotypes were included in this cluster. The maximum range of variability was observed for number of pods per plant (12.22 -20.55) among all the characters in 3 clusters. A two-dimensional scatter diagram was constructed using component I as X-axis and component II as Y-axis, reflecting in the relative position (Figure 1). As per scatter diagram the genotypes were apparently distributed into five clusters. It was also revealed that the genotypes of cluster I was more diverse from the genotypes of cluster III. The canonical variate analysis revealed that the vectors (Vector-I and II) for days to 80% maturity, number of pods per plant, pod length and grain yield per plant were positive (Table 7). This result suggested that these four characters contributed maximum towards divergence. Roshan et al. (1998) reported that pods per plant contributed most to cluster differentiation. It is assumed that maximum amount of heterosis is manifested in cross combination involving the genotypes belonging to most divergent clusters. However, for a practical plant breeder, the objective is not only high heterosis but also to achieve high-level of production. In the present study, the maximum distance was between cluster I and III. Considering the yield

and growth duration, crosses involving cluster I and III may exhibit high heterosis for yield as well as earliness. Also the crosses between genotypes from cluster II with those of cluster I and III might produce high level of segregating population.

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