

**GENETIC VARIABILITY, CHARACTER ASSOCIATION AND
GENETIC DIVERGENCE IN MUNGBEAN (*VIGNA RADIATE*
L. WILCZEK)**

GENETSKA VARIJABILNOST, ZNAČAJKE I GENETSKA
RAZLIČITOST AZIJSKOG GRAHA (*VIGNA RADIATE* L. WILCZEK)

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ABSTRACT

Genetic variability, correlation coefficient, path coefficient and genetic diversity were determined among fifty mungbean genotypes. There was a great deal of significant variation for all the characters among the genotypes. Considering genetic parameters high genotypic co-efficient of variation (GCV) was observed for no. of primary branches, seed yield per plant but no. of seed per pod and days to 80% maturity showed low GCV. In all the cases, phenotypic variances were higher than the genotypic variance. High heritability with low genetic advance in percent of mean was observed for days to 50% flowering suggesting non-additive gene effects for the expression of the character and selection for such trait might not be rewarding. High heritability with high genetic advance in percent of mean was observed for no. of primary branches per plant and a thousand seed weight indicating that this trait was under additive gene control and selection for genetic improvement for this trait would be effective. Seed yield per plant showed highest significant positive correlation with a thousand seed weight. It also has a significant positive correlation with seed per pod at genotypic level and a non-significant positive correlation with seed per pod at phenotypic level. Therefore, these traits could be important for the direct selection to improve yield. Total six clusters were formed for fifty genotypes. Considering group distance, cluster mean values, and other agronomic performances, inter genotypic crosses between G16 and G47; G16 and G13; G47 and G13; G21 and G19; G8 and G21, G21 and G35, G3 and G8, G3 and G35, G3 and G19, G8 and G19 might be suggested for future hybridization program.

Keywords: genetic variability, genetic divergence, mungbean, *Vigna Radiate* L. Wilczek

SAŽETAK

Među pedeset genotipova azijskog graha određeni su genetska varijabilnost, koeficijent korelacije, koeficijent putanje i genetska različitost. Među genotipovima bilo je mnogo značajnog variranja u svim značajkama. U genetskim parametrima primijećen je značajno visoki koeficijent raznolikosti (GLV) u broju primarnih grančica i prinosu sjemena po biljci, ali je broj sjemenki po mahuni dana do 80% zrelosti pokazao niski GLV. U svim slučajevima fenotipska variranja bila su viša nego genotipska variranja. Visoka nasljednost s niskim genetskim napretkom u postotku prosjeka primijećeni su za dane do 50% do cvatnje, što pretpostavlja djelovanje neaditivnog gena za izražavanje značajki pa selekcija za takve osobine možda nije korisna. Visoka nasljednost s visokim genetskim napretkom u postotku prosjeka primijećena je za broj primarnih grančica po biljci i težinu 1000 sjemenki, što upućuje da je ova osobina pod kontrolom aditivnog gena, te da bi selekcija za genetsko poboljšanje ove osobine bila djelotvorna. Prinos sjemena po biljci pokazao je najvišu značajnu pozitivnu korelaciju s težinom 1000 sjemenki. Isto tako ima pozitivnu korelaciju sa sjemenom po mahuni na razini fenotipa. Stoga bi ove značajke mogle biti važne za izravnu selekciju radi poboljšanja prinosa. Formirano je ukupno šest klastera za pedeset genotipova. S obzirom na grupnu udaljenost, srednju vrijednost klastera i druge agronomske rezultate/performance može se preporučiti međugenetsko križanje za buduće programe hibridizacije između G16 i G47; G16 i G13; G47 i G13; G21 i G19, G8 i G21, G21 i G35, G3 i G8, G3 i G35, G3 i G19, G8 i G19.

Ključne riječi: genetska varijabilnost, genetska različitost, azijski grah, *Vigna Radiate* L.Wilczek

INTRODUCTION

Mungbean (*Vigna radiate* L.Wilczek) is one of the important pulse crops in Bangladesh. It belongs to Leguminosae family. The climatic conditions of Bangladesh favour mungbean cultivation throughout the year. Pulses constitute the main source of protein for the people of Bangladesh. In addition, it is also considered as the best source of protein for domestic animals. It holds the 3rd in protein content and 4th in both acreage and production in Bangladesh (Sarkar et al., 1982). Besides, this crop has the capability to enrich soils through biological nitrogen fixation (Robertson, 2004). Mungbean contains 51% carbohydrates, 26% proteins, 4% minerals and 3% vitamins. From the nutritional point of view, it is one of the best among pulses (Khan, 1985). It is widely used as “Dal” in the

country like other pulses. Genetic variability is crucial for a successful breeding program for any crops and a critical survey of genetic variability is essential before initiating any crop improvement program. The correlation coefficients between yield and its components usually show a complex chain of interacting relationship while 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 most important criteria for the genetically diverse parent selection for a meaningful plant breeding program. It can be estimated through biometrical procedures using Mahalanobis's D2-statistic (Rahim et al., 2010). In this study, our objective is to select genetically diverse mungbean genotypes with respect to yield for future hybridization program.

MATERIALS AND METHODS

The experiment was carried out at the experimental farm of Sher-e-Bangla Agricultural University, Dhaka, Bangladesh during March to June, 2010. Fifty mungbean genotypes including varieties and advanced lines (Table 1) were used in the study. The seeds were collected from Bangladesh Agricultural Research Institute (BARI), Gazipur. Seed was sown in the experimental field using a Randomized Complete Block Design (RCBD) with three replications and spacing was 30 cm x 15 cm. The unit plot was of 3 m long with three rows. N, P and K fertilizers @ 20-40-20kg/ha were applied as a basal dose during final land preparation. The standard agronomic practices were applied to raise a healthy growth. Data were recorded from 10 randomly selected plants for each plot on 8 characters such as days to 50% flowering (days), days to 80% maturity (days), plant height (cm), number of primary branches per plant, 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 described by Miller et al. (1958) and path coefficient analysis was done according to the method suggested by Dewey and Lu (1959). Genetic diversity was found through cluster analysis, principal component analysis and D2-statistic.

Table 1. List of Mungbean genotypes with their sources

Tablica 1 Popis genotipova azijskog graha s njihovim izvorima

Serial no.	Genotypes	Serial no.	Genotypes
1	BM x K1-01019-2	26	BD-6904
2	BM X K2-0300011-1	27	BD-6905
3	BM x K1-0300011-6	28	BD-6906
4	BM x K1-0300013-1	29	BD-6907
5	BM x K2-0300	30	BD-6908
6	BM x K2-030005-4	31	BD-6909
7	BM x K2-0300011-4	32	BD-6910
8	BM x K2-04005-3	33	BD-6911
9	BM x K1-0300013-10	34	BD-6912
10	BD-6888	35	BD-6913
11	BD-6889	36	BD-6916
12	BD-6890	37	BD-6918
13	BD-6891	38	BD-6920
14	BD-6892	39	BARI Mung-2
15	BD-6893	40	BARI Mung-3
16	BD-6894	41	BARI Mung-4
17	BD-6895	42	BARI Mung-5
18	BD-6896	43	BARI Mung-6
19	BD-6897	44	BINA Mung-2
20	BD-6898	45	BINA Mung-5
21	BD-6899	46	BINA Mung-6
22	BD-6900	47	BINA Mung-7
23	BD-6901	48	BAU Mung-1
24	BD-6902	49	BAU Mung-3
25	BD-6903	50	BAU Mung-4

RESULTS AND DISCUSSION

Genetic variability

All the genotypes showed significant variations for all the traits studied except for number of seeds per pod. The estimate of genotypic variance, phenotypic variance, heritability, genetic advance and coefficient of variation for different traits are presented in Table 2.

Table 2. Genetic variability, genetic parameter, heritability (h²b), GA and GA in percent of mean for nine yield contributing characters of 50 Mungbean genotypes

Tablica 2 Genetska varijabilnost, genetski parametar, nasljednost (h²b), GA i GA u postotku prosjeka za devet značajki prinosa 50 genotipova azijskog graha

	DFE	50%F	80%M	PH	NPB	Npod	PL	NSP	TSW	SYP
GM	36.673	42.900	75.907	61.549	1.993	22.727	7.126	11.39	31.47	8.12
MSS	13.789**	14.398**	9.715**	125.349**	1.895**	48.88**	2.163**	0.84 ^{NS}	113.05**	10.55**
Error	1.713	1.207	1.647	47.388	0.031	11.769	0.452	0.71	1.48	1.60
σ^2_g	4.03	4.40	2.69	25.99	0.62	12.37	0.57	0.04	37.19	2.98
σ^2_p	5.74	5.60	4.34	73.38	0.65	24.14	1.02	0.75	38.67	4.58
σ^2_e	1.71	1.21	1.65	47.39	0.03	11.77	0.45	0.71	1.48	1.60
GCV	5.47	4.89	2.16	8.28	39.55	15.48	10.60	1.84	19.38	21.28
PCV	6.53	5.52	2.74	13.92	40.53	21.62	14.19	7.61	19.76	26.38
ECV	3.57	2.56	1.69	11.18	8.83	15.09	9.43	7.38	3.87	15.58
h ² b	70.15	78.46	62.02	35.42	95.25	51.25	55.79	5.86	96.17	65.11
GA	3.46	3.83	2.66	6.25	1.58	5.19	1.16	0.10	12.32	2.87
GA in % of mean	9.44	8.92	3.50	10.15	79.52	22.82	16.31	0.92	39.14	35.38
CV%	3.57	2.56	1.69	11.18	8.85	15.10	9.44	7.38	3.87	15.58

** Significant at 1% level of probability, * Significant at 5% level of probability; DFE= Days to 1st flowering, 50%F= Days to 50% flowering, 80% M= days to 80% maturity, PH= Plant height (cm), NPB= number of Primary branches, NPod= Number of Pod per Plant, PL= Pod length (cm), NSP= No. seed per pod, TSW= Thousand seed wt. (g) and SYP=Seed yield per plant.

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

Tablica 3 Genotipska i fenotipska korelacija koeficijena između prinosa i komponente značajki u azijskom grahu

Parameters		Days to 50% Flowering	Days to 80% Maturity	Plant height	No. of primary branch	No. of pod per plant	Pod length	No. seed per pod	Thousand weight	Seed yield per plant
Days to first flowering	r _g	0.999**	0.805**	0.711**	-0.143	-0.418**	0.072	0.144	-0.016	-0.308*
	r _p	0.818**	0.491**	0.317*	-0.100	-0.197	0.056	0.001	-0.023	-0.241
Days to 50% Flowering	r _g		0.804**	0.680**	-0.204	-0.364**	-0.031	-0.054	-0.074	-0.379**
	r _p		0.603**	0.316*	-0.166	-0.233	0.010	-0.039	-0.078	-0.259
Days to 80% Maturity	r _g			0.281*	-0.201	-0.249	-0.262	-0.277	-0.028	-0.406**
	r _p			0.104	-0.175	-0.131	-0.071	-0.093	-0.050	-0.194
Plant height	r _g				0.496**	0.094	-0.495**	0.342*	-0.480**	-0.446**
	r _p				0.308*	0.078	-0.204	0.213	-0.278	-0.162
No. primary branch	r _g					0.479**	-0.476**	0.762**	-0.282*	0.071
	r _p					0.329*	-0.342*	0.203	-0.269	0.044
No. of pod per plant	r _g						-0.535**	-0.004	-0.289*	0.327*
	r _p						-0.282*	0.027	-0.225	0.372**
Pod length	r _g							0.494**	0.710**	0.508**
	r _p							0.224	0.495**	0.315*
No. seed per pod	r _g								-0.051	0.538**
	r _p								-0.020	0.109
Thousand weight	r _g									0.740**
	r _p									0.581**

** Significant at 1% level of probability, * Significant at 5% level of probability; g=Genotypic, p=Phenotypic.

The results showed that phenotypic coefficient of variations was higher than the phenotypic coefficient of variation for all the traits. Similar results were found by Kumar and Dubey (2001), Ali et al. (2005) and Rai et al., (2014). The genotypic and phenotypic variances were higher for plant height, no. of pods per plant and a 1000-seed weight. Rahim et al. (2010) found similar results for these traits. The highest genotypic variance was recorded for no. of primary branches per plant while the lowest was for no. of seeds per pod suggesting higher magnitude of variability for those traits. Moderate to high heritability

(broad sense) was found in all the traits except in no. of seeds per pod. The highest heritability and genetic advance in percent of mean were observed for a 1000-seed weight followed by no. of primary branches per plant and seed yield per plant. Thus reveals that additive genetic effect plays an important role and the expression of these characters and phenotypic selection would be rewarding. Similar results were reported by Noor et al., (2003), Atta et al., (2008), Rahim et al., (2010), Naveed et al., (2012).

CORRELATION COEFFICIENT ANALYSIS

Genotypic and phenotypic correlation co-efficients are presented in Table 3. Days to first flowering were found to display highly significant positive relationships with days to 50% flowering, days to 80% maturity, plant height, pod length and number of seeds per pod at genotypic level and significant relationships with days to 50% flowering, days to 80% maturity, plant height, pod length and number of seeds per pod at phenotypic level. The character reflected highly significant positive association with days to 50% flowering, days to 80% maturity, plant height, pod length and number of seeds per pod at genotypic and phenotypic level and a highly significant positive association with days to 50% flowering at genotypic and phenotypic level. It appeared from the results that increasing days to first flowering caused the plant to produce lesser length and pod length. Days to 50% flowering showed a highly significant positive association with days to 80% maturity ($G = 0.804$), plant height ($G = 0.680$), genotypic level and days to 50% flowering showed a highly significant positive association with days to 80% maturity ($GP = 0.6034$), and plant height ($P = 0.3.16$), at phenotypic level. The result revealed that if days to 50% flowering increased, then days to 80% maturity and plant height also increased. Days to 50% flowering showed a highly significant negative association with number of pods ($G = -0.364$) and seed yield per plant ($G = -0.379$) at genotypic level. Rao et al. (2006), Yaqoob et al. (1997) reported that days to 50% flowering were positive and significantly associated with seed yield. Rahman (1982) obtained a positive correlation of days to 50% flowering with days to maturity. Days to 80% maturity showed a highly significant positive association with plant height ($G = 0.281$), at genotypic level. Plant height showed a significant positive correlation with number of primary branch ($G = 0.496$.) number of seeds per pod ($G=0.342$) at genotypic level and number of primary branches ($P=0.308$) at the phenotypic level. On the other hand plant height showed a significant negative correlation with pod length ($G=-0.495$), a thousand seed weight was $G=-0.48$ and seed yield per plant was $G = - 0.446$ at

genotypic level. Makeen et al. (2007), Islam et al. (1999), Niazi et al. (1999) indicated that plant height had a significant positive correlation with seed yield. Number of primary branches per plant showed a highly significant positive correlation with (G = 0.479) and number of seeds per pod at genotypic level and a significant positive correlation with number of pods per plant (p = 0.329) at the phenotypic level. A significant negative correlation was found with pod length (G = -0.476) and a thousand seed weight at genotypic level. Islam et al. (1999) found yield per plant was significantly and positively correlated with number of primary branches per plant. Pods per plant showed a significant negative correlation with pod length (G = -0.535, P = -0.282) at genotypic and phenotypic level. Pods per plant showed a significant positive correlation with seed yield per plant (G = 0.327, P = 0.372) at genotypic and phenotypic level as reported by Makeen et al. (2007), Rao et al. (2006), Islam et al. (1999). Pod length showed a significant highly positive correlation with seed per pod (G = 0.494), a thousand seed weight and seed yield per plant at genotypic level. Pod length showed a significant highly positive correlation with a thousand seed weight and seed yield per plant at phenotypic level. Similar result was reported by Islam et al. (1999), Singh et al. (1993). Rahman (1982) found a positive correlation for pod length with a 1000-seed weight. Seeds per pod showed significant positive correlation only with seed yield per plant (G = 0.538) and a non-significant positive correlation with seed yield per plant (P = 106) at phenotypic level. Similar results were obtained by Islam et al. (1999). A thousand seed weight showed most highly significant positive correlation with yield per plant (G = 0.740, P = 0.581) at genotypic and phenotypic level. Similar results were obtained by Islam et al. (1999), Sharma et al. (1999), Yaqoob et al. (1997). Shamsuzzaman and Shaikh (1982) reported a 1000-seed weight exhibited a negative correlation with seed yield.

Path co-efficient analysis

The direct and indirect effects of different characters on yield are presented in Table 4 and Figure 1. Days to first flowering had a negative direct effect (-0.290) on yield per plant. Days to first flowering had a positive indirect effect on days to 50% flowering (0.412), days to maturity (0.029) and pod length (0.066). A negative indirect effect was found for plant height (-0.113), number of primary branches (-0.075), pod per plant (- 0.307), number of seeds per pod (-0.024) and a thousand seed weight (- 0.006). Days to 50% flowering had a positive direct effect (0.412) on yield per plant. Days to 50% flowering had a positive indirect effect on 80% maturity (0.029), and seed per pod (0.009).

A negative indirect effect was found for plant height (-0.108), number of primary branches (-0.107), pod per plant (- 0.267), pod length (-0.029) and a thousand seed weight (- 0.028). Yaqoob et al. (1997), Rahman (1982) observed a positive direct effect of days to 50% flowering on seed yield. Days to 80% maturity had a positive direct effect (0.036) on yield per plant. Days to 80% maturity had a positive indirect effect on seed per pod (0.046). A negative indirect effect was found for plant height (-0.045), number of primary branches (-0.105), pod per plant (- 0.182), pod length (-0.243) and a thousand seed weight (- 0.011). Plant height had a negative direct effect (-0.159) on yield per plant and a positive indirect effect through days to 50% flowering (0.28), 80% maturity (0.010), number of primary branches per plant (0.26), number of pods (0.069). On the other hand, plant height showed a negative indirect effect on yield per plant via pod length (-0.458), number of seeds per plant (-0.057) and thousand seed weight (-0.185). The previous studies reported maximum direct effect on seed yield by plant height (Makeen et al., 2007; Sharma et al., 1999). Rao et al. (2006), Yaqoob et al. (1997) showed that plant height had a direct negative effect on seed yield. Pod per plant showed a positive direct (0.734) effect on yield per plant and a positive indirect effects through days to first flowering (0.121) and seed per pod (0.001). Pod per plant had a negative indirect effect on all other characters. Makeen et al. (2007), Rao et al. (2006), Sharma et al. (1999) found maximum positive direct effect on seed yield in pods per plant. Pod length had a direct positive effect (0.925) on yield per plant. This trait also had an indirect positive effect on thousand seed weight (0.273). Pod length had a negative indirect effect on all other characters. Similar results were found by Bhaumik and Jha (1980). Seeds per pod had a negative direct effect (-0.168) on yield per plant and a positive indirect effect on primary branch (0.400) and pod length (0.457). On the other hand, this trait showed a negative indirect effect on all other parameters. Rahman (1982) found number of seeds/pod (-0.800) had a negative direct contribution to yield. Thousand seed weight had a high positive direct effect on yield per plant (0.385) and a positive indirect effect on days to first flowering (0.005), plant height (0.076), pod length (0.657) and number of seeds per pod (0.009). A thousand seed weight had a negative indirect effect on days to 50% flowering (-0.030), days to 80% flowering (-0.001), primary branches (-0.148) and pods per plant (-0.212). Singh and Malhotra (1976) observed a 1000-seed weight had a negative indirect effect on yield by affecting the number of seeds/pod.

Table 4. Direct (Diagonal) and indirect effect of some yield contributing characters on *Vigna radiata* L.Wilczek

Tablica 4 Direktno (dijagonalno) i indirektno djelovanje nekih značajki prinosa na *Vigna radiata* L.Wilczek

	DFF	50%F	80%M	PH	NPB	Npod	PL	NSP	TSW	Genotypic correlation with yield
DFF	-0.290	0.412	0.029	-0.113	-0.075	-0.307	0.066	-0.024	-0.006	-0.3077*
50%F	-0.290	0.412	0.029	-0.108	-0.107	-0.267	-0.029	0.009	-0.028	-0.3794**
80%M	-0.234	0.331	0.036	-0.045	-0.105	-0.182	-0.243	0.046	-0.011	-0.4056**
PH	-0.206	0.280	0.010	-0.159	0.260	0.069	-0.458	-0.057	-0.185	-0.4456**
NPB	0.042	-0.084	-0.007	-0.079	0.524	0.351	-0.440	-0.128	-0.109	0.0706
Npod	0.121	-0.150	-0.009	-0.015	0.251	0.734	-0.495	0.001	-0.111	0.3266*
PL	-0.021	-0.013	-0.010	0.079	-0.249	-0.393	0.925	-0.083	0.273	0.5084**
NSP	-0.042	-0.022	-0.010	-0.054	0.400	-0.003	0.457	-0.168	-0.020	0.5383**
TSW	0.005	-0.030	-0.001	0.076	-0.148	-0.212	0.657	0.009	0.385	0.7395**

Residual effect (R): 0.2639; ** Significant at 1% level of probability, * Significant at 5% level of probability; DFF= Days to 1st flowering, 50%F = Days to 50% flowering, 80% M= days to 80% maturity, PH = Plant height (cm), NPB=number of Primary branches, , NPod= Number of Pod per Plant, PL=Pod length (cm), NSP= No. seed per pod, TSW= Thousand seed wt. (g) and SYP=Seed yield per plant.

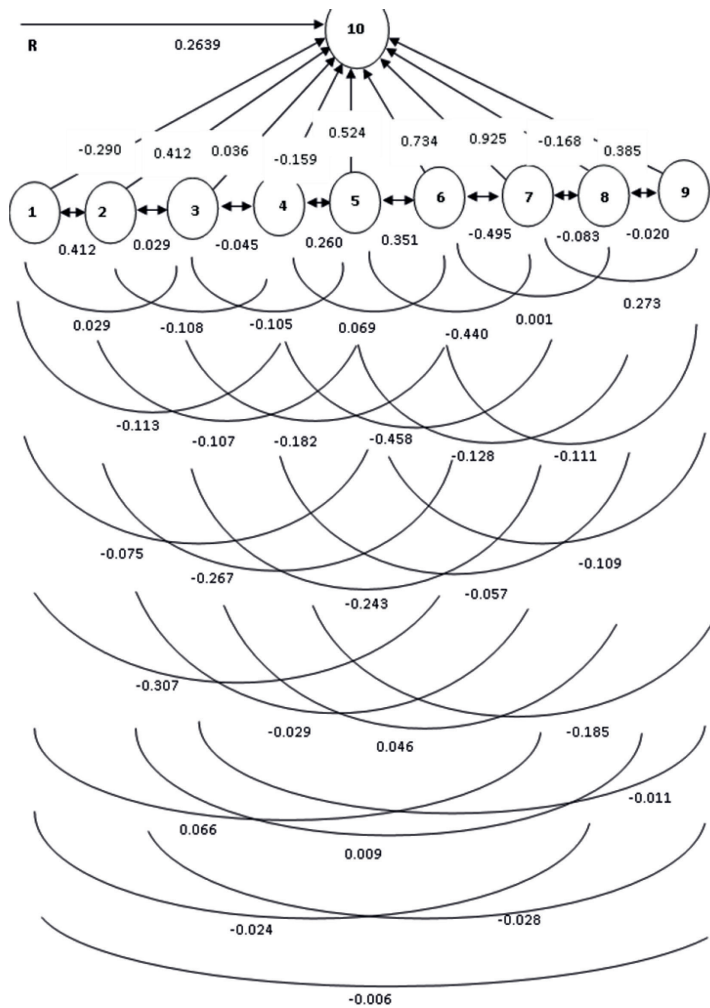


Fig. 1. Path diagram of 10 yield contributing traits in 50 Mungbean genotypes
 [1 = days to first flowering, 2 = days to 50% flowering, 3=Days to 80% maturity 4= plant height, 5 = , Primary branch,, 6 = No. of pod, 7 = pod length, 8 = No. seed /pod, 9 = 1000 seed weight 10 = yield/plant; R= residual effect].

Graf 1 Dijagram putanje 10 osobina prinosa u 50 genotipova azijskog graha

Table 5. Eigen value and percent contribution of 10 yield contributing characters of fifty Mungbean genotypes

Tablica 5 Vrijednost eigena i postotak doprinosa deset značajki pedeset genotipova azijskog graha

Parameters	Eigen values	Percentage of total variation accounted for individual characters	Percentage of cumulative variation
DFP	4.3236	44.01	44.01
50%F	3.1366	31.92	75.93
80%M	1.2348	12.57	88.50
PH	0.4884	4.97	93.47
NPB	0.3197	3.25	96.72
Npod	0.148	1.51	98.23
PL	0.1044	1.06	99.29
NSP	0.0526	0.54	99.83
TSW	0.0095	0.10	99.93
SYP	0.0073	0.07	100.00

Genetic Divergence

The principal component analysis (PCA) was performed using fifty mungbean genotypes where first three eigen values for three principal coordination axes of genotypes accounted for 88.50% variation (Table 5). A two dimensional scattered diagram was drawn on the basis of the principal component score, Z1 and Z2 score (Fig. 2). Fifty mungbean genotypes were clustered into six groups using non-hierarchical clustering. Abbas et al. (2010) grouped 40 mungbean genotypes into 8 different clusters using Metroglyph analysis. Rahim et al., (2010) reported 3 clusters for 26 mugbean genotypes using non-hierarchical clustering. Among six clusters, cluster I (five) contained the highest number (15) of genotypes (Table 7). Cluster II, cluster III, cluster IV, cluster V and cluster VI consisted of two, five, six, fifteen and thirteen genotypes, respectively. Cluster means for different clusters are

presented in Table 8. Cluster I showed maximum cluster mean for days to maturity, plant height, days to first flowering and days to 50% flowering. Similarly, cluster II ranked first for number of primary branches and number of seeds per pod. Cluster V ranked first for no. of seeds per pod. Cluster VI represented highest mean for pod length, a thousand seed weight and seed yield per plant. The principal coordinate analysis revealed the highest inter genotypic distance between genotypes G20 and G5 followed by G5 and G1 and the lowest distance was observed between genotypes G18 and G13 followed by the distance between genotypes G41 and G32 (Table 6).

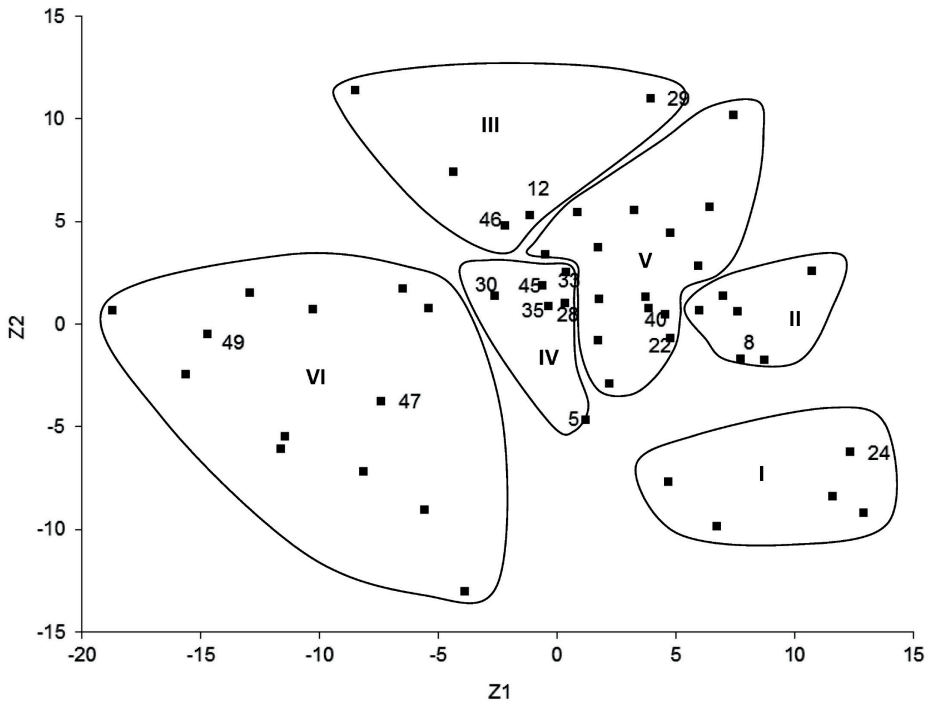


Fig. 2. Scattered diagram of 50 mungbean genotypes superimpose cluster

Graf 2 Razbacani dijagram 50 genotipova klastera azijskog graha

Table 6. Ten highest and ten lowest inter genotypic distance among the fifty Mungbean genotypes

Tablica 6 Deset najvećih i deset najmanjih udaljenosti unutar genotipa među pedeset genotipova azijskog graha

Sl. No.	Genotypic combination	Distances
A. 10 highest inter genotypic distance		
1	G20-G05	1.3060
2	G05-G01	1.3045
3	G33-G20	1.2870
4	G33-G01	1.2827
5	G49-G14	1.2552
6	G49-G20	1.2156
7	G49-G21	1.2000
8	G43-G14	1.1844
9	G49-G11	1.1826
10	G45-G20	1.1620
B. 10 lowest inter genotypic distance		
1	G18-G13	0.1302
2	G41-G32	0.1313
3	G17-G06	0.1320
4	G41-G23	0.1421
5	G41-G39	0.1433
6	G21-G14	0.1533
7	G44-G22	0.1627
8	G23-G22	0.1636
9	G03-G02	0.1637
10	G28-G23	0.1751

Table 7. Distribution of fifty Mungbean genotypes in six clusters

Tablica 7 Raspodjela pedeset genotipova azijskog graha u šest klastera

Cluster	Genotype number	Designation
1	4, 24, 25, 26, 31 (5)	BM x K1-0300013-1, BD-6902, BD-6903, BD-6904, BD-6909
2	8, 11, 13, 18, 19, 21 (6)	BM x K2-04005-3, BD-6889, BD-6891, BD-6896, BD-6897, BD-6899,
3	12, 16, 29, 46, 50 (5)	BD-6890, BD-6894, BD-6907, BINA Mung-6, BAU Mung-4
4	5, 28, 30, 33, 35, 45 (6)	BM x K2-0300, BD-6906, BD-6908, BD-6911, BD-6913, BINA Mung-5,
5	14, 15, 22, 23, 27, 32, 34, 36, 37, 38, 39, 40, 41, 44, 48 (15)	BD-6892, BD-6893, BD-6900, BD-6901, BD-6905, BD-6910, BD-6912, BD-6916, BD-6918, BD-6920, BARI Mung-2, BARI Mung-3, BARI Mung-4, BINA Mung-2, BAU Mung-1,
6	1, 2, 3, 6, 7, 9, 10, 17, 20, 42, 43, 47, 49 (13)	BM x K1-01019-2, BM X K2-0300011-1, BM x K1-0300011-6, BM x K2-030005-4, BM x K2-0300011-4, BM x K1-0300013-10, BD-6888, BD-6895, BD-6898, BARI Mung-5, BARI Mung-6, BINA Mung-7, BAU Mung-3,

Table 8. Cluster mean distance of 50 Mungbean genotypes

Tablica 8 Prosječna udaljenost klastera 50 genotipova azijskog graha

Parameters	Cluster					
	I	II	III	IV	V	VI
DFE	39.74	36.33	34.20	37.39	36.67	36.28
50%F	46.00	42.50	40.40	44.11	42.96	42.23
80%M	77.40	74.50	73.93	77.06	76.36	75.69
PH	72.83	68.38	55.00	59.24	62.72	56.29
NPB	2.26	2.61	1.93	1.45	2.13	1.72
Npod	18.93	25.33	22.07	17.78	26.09	21.64
PL	7.29	7.03	7.04	7.02	6.44	7.98
NSP	11.53	11.83	11.20	11.33	11.27	11.38
TSW	30.11	27.09	26.79	29.08	28.39	40.47
SYP	6.47	8.45	7.27	5.84	7.95	10.16

The difference between the highest and the lowest inter genotypic distance indicated the moderate variability among the fifty mungbean genotypes. The maximum intra cluster distance was found in cluster VI containing thirteen genotypes while the lowest intra cluster distance was observed in cluster IV having six genotypes (Table 9 and Fig. 3). The highest inter cluster distance was observed between clusters I and VI followed by clusters II and VI (Table 9 and Fig. 3). The intra clusters distance was the highest in cluster I and the lowest inter cluster distance was observed between clusters IV and V followed by cluster III and IV. The higher inter-cluster distances between these clusters indicate possibilities of having a diverse segregating population if parents are chosen from these clusters for hybridization program. However, the highest inter cluster distance was observed between cluster I and VI indicating the genotypes in these clusters were more diverged than other clusters. Similarly, the lowest inter cluster distance was observed between cluster IV and V and moderate distance was found between cluster I and III, cluster III and VI. The inter cluster distances were higher than the intra cluster distances suggesting wider genetic diversity among the genotypes of different groups. Results obtained through different multivariate analysis were superimposed in Figure 2 and confirmed that different multivariate techniques supplemented one another. It is expected that maximum amount of heterosis will be manifested in cross combination involving the genotypes belonging to the distant clusters. However, for a practical plant breeding, the objective is not only high heterosis but also to achieve high level production. In the present study the maximum distance exists between cluster I and VI. But considering the yield and duration crosses involving clusters cluster I and VI may exhibit high heterosis for yield. Main and Bahl (1989) reported that the parents separated by D2 values of moderate generally showed higher heterosis. The values of Vector I and Vector II are presented in Table 10. Vector I obtained from PCA expressed that days to 50% flowering, plant height, no. of seeds per pod and yield per plant were major characters that contribute to the genetic divergence. It was the reflection of first axis of differentiation. In vector II days to 50% flowering, days to 80% flowering, plant height, no. of primary branches, no of pods, pod length and a thousand seed weight, showed their important role toward genetic divergence. Negative values in both vectors for days to first flowering had a lower contribution towards the divergence. Considering the magnitude of cluster mean and agronomic performance genotype G16 (BD-6894) for minimum days of first flowering from cluster I; G47 (BINA Mung-7) for maximum pod length and thousand seed weight form cluster VI; G13 (BD-6891) for maximum number of pod per plant from cluster II were found promising.

Table 9. Average Inter and intra cluster distance of 50 Mungbean genotypes

Tablica 9 Prosječna udaljenost unutar i među 50 genotipova azijskog graha

cluster	Cluster					
	1	2	3	4	5	6
1	0.416					
2	2.532	0.429				
3	6.190	4.102	0.514			
4	4.450	2.821	1.917	0.405		
5	4.087	2.147	2.103	0.782	0.458	
6	6.338	6.233	5.188	4.105	4.816	0.534

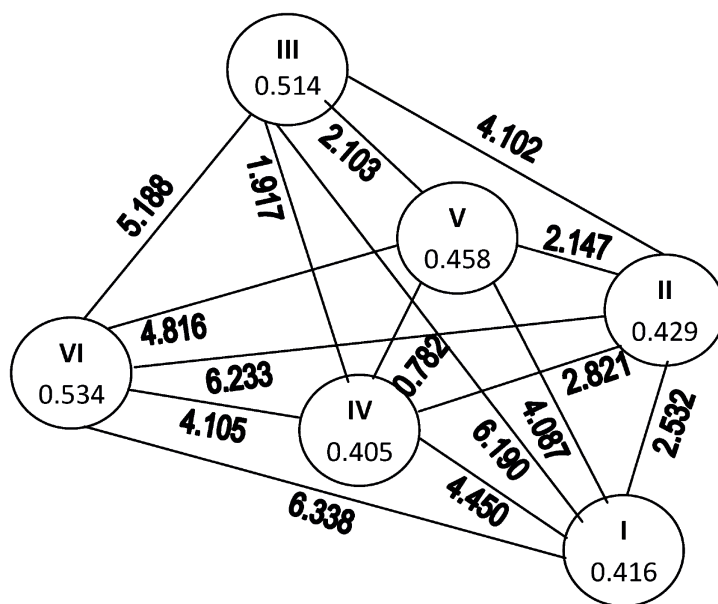


Fig. 3. Cluster diagram with Inter and intra cluster distance

Graf 3 Dijagram klastera s udaljenosti unutar i među klasterima

Table 10. Latent vectors for 10 principal component characters of 50 genotypes of Mungbean

Tablica 10 Latentni vektori za 10 glavnih značajki komponenata 50 genotipova azijskog graha

Parameters	Vectors 1	Vectors 2
DFE	-0.1485	-0.1750
50%F	0.1078	0.0501
80%M	-0.1157	0.3140
PH	0.1987	0.2556
NPB	-0.3461	0.4696
Npod	-0.0199	0.0051
PL	-0.1056	1.1704
NSP	0.0825	-0.2127
TSW	-0.3025	0.1545
SYP	0.0763	-0.1191

CONCLUSION

Considering group distance and other agronomic performance, inter genotypic crosses between G16 and G47; G16 and G13; G47 and G13; G21 and G19; G8 and G21, G21 and G35, G3 and G8, G3 and G35, G3 and G19, G8 and G19 might be suggested for future hybridization program.

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