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## Path and variability in parents and F<sub>2</sub> population of different crosses

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### Abstract

Pulses in India have long been considered as only source of poor man's protein. India is the largest importer, producer and consumer of pulses (Jitendra *et al.*, 2011). India accounts for 33% of the world area and 22% of the world production of pulses (Amarender, 2009). Pulses production in India 18.34 million tonne (ICAR 2013-14). Combining ability analysis is frequently employed to identify the desirable parents for inclusion in hybridization programme. Highest yield in F<sub>2</sub> population was envisaged in the crosses HUM-12 × PS-16 and HUM-12 × Bireswar. HUM-12 × PS-16 F<sub>2</sub> population was also found superior for plant height and as well as earliness. HUM-12 × Bireswar were found superior for a number of yield contributing characters like number of seeds pod<sup>-1</sup>, pod width and pods plant<sup>-1</sup>. Derivatives from these two hybrids may help to develop high yielding early maturing genotypes with significant improvement of many yield components through selection in progressive generation. HUM-12 × PS-16 and HUM-12 × Bireswar with high protein content could be involved for tailoring genotypes with high yield, protein content and early maturity. Likewise per se performance of WBM-314 × Hum-12 followed by Hum-12 × Bireswar were found to be superior with respect to protein and Hum-12 × PS-16 and Hum-12 × Basanti for earliness.

**Keywords:** path, variability, F<sub>2</sub> population

### Introduction

Mung bean (*Vigna radiata* L. Wilczek) is a pulse species of the pan-tropical region (kumar *et al.*, 2004) [3]. But (Tomooka *et al.*, 1992) [4], considered it as native to Asia and widely cultivated in Africa, Asia and Latin America. They also examined the variations of seed proteins in mung bean landraces from Asia, and proposed it as diverse region for mung bean. According to their study, the region of protein type diversity is found in West Asia (Afghanistan-Iran-Iraq area) rather than in India. Judging from the geographical distribution of protein types, mung bean might have spread mainly to the east by two routes, one route is from India to Southeast Asia strains consisting of a few protein types with prominent protein type were disseminated by this route and another dissemination pathway may have been the route known as the Silk Road. By this route, protein type 7 and 8 strains spread from West Asia or India to China and Taiwan via the Silk Road, not by the route from Southeast Asia. A large proportion of alleles of higher productivity have been lost in the present populations of mung bean due to overriding role of natural selection even long after the crop domestication (Jain, 2004) [5]. The interrelationship of quantitative traits with yield determines the efficiency of selection in breeding programmes. It indicates the intensity and degree of association between different character pairs. To improve mung bean for both yield and yield components, an understanding of their association among themselves is necessary. Variability and correlation studies help in selection of reliable yield components for efficient yield improvement (Vijayalaxmi *et al.*, 2000) [6]. The use of diverse germplasm as a significant factor contributing to high yield and quality characteristics had been also stressed by (Gopalakrishnan and Dwivedi, 2008). Heritability in conjunction with genetic advance is more useful than heritability alone in the prediction of resultant effect of selecting the best individual (Singh *et al.*, 2010) [7]. Correlation analysis provides information on inter-relationship of important plant characters and hence, leads to a directional model of selection providing scope for direct and or indirect improvement in grain yield (khan *et al.*, 2004) [8]. The correlation values decide only the nature and degree of association existing between pairs of characters.

### Materials and Methods

The field experiment was conducted at Jaguli instructional farm Bidhan Chandra Krishi Viswavidyalaya, Nadia district, West Bengal during 27 genotypes were sown in the 1<sup>st</sup> of

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March 2014. The farm is located at 22.93° (N), latitude, 88.53° (E) longitude and at 9.75m. Above main sea level. Five plants were selected at random from each entry in each replication for recording data. For estimation of protein by Lowry's Method, 27 genotypes and 21 genotypes of mung bean from each genotype was pipette in different test tube separately. In this method, the blue colour developed by the reduction of the phosphomolybdic-phosphotungstic components in the Folin-Ciocalteu's reagent by the amino acids tyrosine and tryptophan present in the protein plus the colour developed by the biuret reaction of the protein with alkaline cupric tartrate are measured in the Lowry's Method at 660nm with the help of spectrophotometer. Reagents used in this method are phosphate buffer (pH 8.0) for extraction protein and bovine serum albumin (BSA) for working standard. Preparation of different buffer solutions with their composition are listed below. Reagent A: 2% sodium carbonate in 0.1(N) sodium hydroxide. 0.4g sodium hydroxide pellet was dissolved in 100ml distilled water to prepare 0.1(N) sodium hydroxide solution. 2g sodium carbonate was added and dissolved in 0.1(N) sodium hydroxide solution. Reagent B: 0.5% copper sulphate (CuSO<sub>4</sub> 5H<sub>2</sub>O) in 1% potassium sodium tartrate. 0.5% copper sulphate was dissolved in 100ml distilled water. Then 1g potassium sodium tartrate was added and dissolved completely. Reagent C: alkaline copper solution: Mixture of 50ml of reagent A and 1ml of Reagent B. Reagent D: Folin and Ciocalteu's Phenol Reagent 1(N).

### Results and discussion of path and variability in parents and F<sub>2</sub> population of different crosses

Plant height is an important growth index of plant. WBM-314 is the shortest genotype (38.7) and Hum-12 is the tallest genotype (72.5), Marginal difference between PCV and GCV was recorded and so the character may be less influenced by the environment and selection on the basis of phenotypic value may provide worthwhile step to improve the character. Presence of high heritability (99.991%) coupled with high genetic advance over percent of mean indicated the character was predominantly controlled by additive gene action. The mean data revealed that Basanti × PS-16 as the early flowering genotype and Basanti as late flowering genotype. The PCV value (3.733) was higher than the GCV value (3.729). Marginal difference between PCV and GCV was recorded and so the character may be less influenced by the environment and selection on the basis of phenotypic value may provide worthwhile step to improve the character. Presence of high heritability (99.807%) coupled with low genetic advance over percent of mean indicated the character was predominantly controlled by non-additive gene action. The maximum 100 seed weight was observed in WBM-314 × Bireswar (4.74) and minimum HUM-12 × Bireswar (2.25). The PCV value (15.214) was higher than GCV value (15.039) which indicated is influence of the environment on the character. Presence of high heritability (97.712%) coupled with high genetic advance over percent of mean suggested that the character was influenced predominantly by additive gene action. Basanti × TM-99-50 was found to be poor in protein content while the genotype HUM-12 × Basanti was found to be high in protein content and their respective protein content was 17.35% and 23.20%. Marginal difference between PCV and GCV was recorded and so the character may be less influenced by the environment. With the presence of high heritability (97.411) and low genetic advance indicated that the character was influenced predominantly by

additive gene action. Genotype with lowest yield was PS-16 × TM-99-50 (4.15) and highest yield was HUM-12 × PS-16 (11.7). The PCV value (11.19) differed least from GCV (10.438) which indicated influence of the environment on the character. With the presence of high heritability (87.018) and average genetic advance over percent of mean indicated the influence of both additive and non-additive gene action on the expression of the character. From the above results it could be suggested that the genotypes differed significantly for all the studied characters as was observed by Roychowdhury *et al.*, (2012). PCV was found to be marginally higher than GCV for most of the characters, the difference for characters like number of days to 50% flowering, number of branches plant<sup>-1</sup> and pod length showed wider differences between GCV and PCV which might be due to higher environmental influence on these characters. Alie *et al.*, (2008) <sup>[9]</sup>, carried out experiment to estimate the variability and character association analysis between seed yield and its component characters were carried out in four F<sub>2</sub> populations of mung bean. The estimates of coefficient of variability and heritability were high for all the characters except number of seeds pod<sup>-1</sup>. The correlation and path coefficient analysis revealed that biological yield, harvest index and number of pods per plant were the major yield contributing characters and an emphasis should be given to these characters while making selection for realizing improvement in seed yield in mung bean. Miah *et al.*, (1989) <sup>[10]</sup>, estimated on genetic variance and heritability from data on yield and 8 yield components in 7 varieties of *Vigna radiata* and their 21 F<sub>2</sub> hybrids and 21 reciprocals. High values for expected genetic advance were found for number of days to flowering, plant height and number of pods and seeds plant<sup>-1</sup>, and it was suggested that selection for these traits would be effective. The genotypic and phenotypic correlation coefficients among eleven characters are presented in table 3. Correlation studies among the eleven characters indicated different degree of association between characters at genotypic and phenotypic levels. Both positive and negative correlations was found between different pairs of characters. The correlation coefficient at genotypic level was in general higher than their phenotypic correlations. Plant height showed significant positive correlation with number of seeds pod<sup>-1</sup> and pod length at both the phenotypic and genotypic levels. Number of branches plant<sup>-1</sup> showed significant positive correlation with number of seeds pod<sup>-1</sup> at both the phenotypic and genotypic levels. Protein content showed significant positive correlation with seed yield plant<sup>-1</sup> only at phenotypic level. Plant height showed significant negative correlation with pod width and seed weight (100 seeds) at both the phenotypic and genotypic levels. Number of seeds pod<sup>-1</sup> showed significant negative correlation with pod width and number of pod plant<sup>-1</sup> at both the phenotypic and genotypic levels. Pod length showed significant negative correlation with protein content at both the phenotypic and genotypic levels. Seed weight (100 seeds) showed significant negative correlation with seed yield plant<sup>-1</sup> at the phenotypic level. The correlation is a measure of the degree of which variables vary together or a measure of intensity of association (Steel and Torrie, 1980) <sup>[12]</sup>. Hakim (2008) <sup>[13]</sup>, mentioned that yield had positive correlation with number of pods plant<sup>-1</sup>. Rahim *et al.*, (2010) <sup>[14]</sup>, observed number of pods plant<sup>-1</sup> and number of seeds plant<sup>-1</sup> were positively correlated with grain yield plant<sup>-1</sup>. Pods plant<sup>-1</sup> and plant height were reported by Hakim (2008) <sup>[13]</sup> to be positively correlated with seed yield. In addition, selection for pods plant had frequently been regarded as important for seed

yield production of mung bean by various authors like Makeen *et al.*, (2007) [16], Gul *et al.*, (2008) [17], Hakim (2008) [13], Tabasum *et al.*, (2010) [18].

The direct and indirect effects of different characters on the yield plant<sup>-1</sup> are presented in table 4. The direct and indirect contribution of yield attributing characters on yield following path analysis was worked out in *phenotypic* as well as genotypic levels. Residual effect was low (0.14765) indicating the number of characters chosen for the study were sufficient for yield determination in mung bean. Path coefficient analysis revealed that among the studied characters four characters out of eleven viz... Plant height, days to maturity, number of seeds pod<sup>-1</sup> and pod length (100 seeds) had positive direct effect on yield. Protein content showed negative direct effect on yield. Number of pods plant<sup>-1</sup> imparted the highest direct effect on yield per plant followed by, number of seeds pod<sup>-1</sup>, pod length, plant height (100 seeds). Number of pods plant<sup>-1</sup> had significantly positive relation with yield plant<sup>-1</sup>. Therefore direct selection through this trait would be effective to improve yield potential of a

genotype. Though plant height, days to maturity, number of seeds pod<sup>-1</sup> and pod length had positive direct effect on yield but showed non-significant correlation with yield. Five characters out of eleven viz. Days to 50% flowering, number of branches plant<sup>-1</sup>, Pod width, seed weight and protein content showed negative direct effect on yield. On the basis of path analysis studied number of pods plant<sup>-1</sup> found to be the most important attributable components for yield improvement. Alie *et al.*, (2008) [9], the variability and character association analysis between seed yield and its component characters were carried out in four F<sub>2</sub> populations of mung bean. The estimates of coefficient of variability and heritability were high for all the characters except number of seeds per pod. The correlation and path coefficient analysis revealed that biological yield, harvest index and number of pods plant<sup>-1</sup> were the major yield contributing characters and an emphasis should be given to these characters while making selection for realizing improvement in seed yield in mung bean.

**Table 1:** Mean performance of parents and F<sub>2</sub> population for different characters of mung bean

Sl. No	Parents and crosses	Plant height	Days to 50% flowering	Days to maturity	No. of branches plant <sup>-1</sup>	No. of seeds pod <sup>-1</sup>	Pod length	Pod width	No. of pods plant <sup>-1</sup>	Seed weight (100 seeds)	Protein content	Seed yield
1	BASANTI	58.4	54.5	77.5	2.43	12.65	7.95	0.42	21.00	2.66	23.16	4.16
2	BIRESWAR	48.9	48.8	74.5	4.22	8.25	6.75	0.37	21.35	2.97	19.15	7.60
3	HUM-12	72.5	52.5	73.5	4.54	12.45	8.35	0.40	15.90	4.66	19.02	9.22
4	PS-16	46.5	49.5	83.5	3.45	10.35	8.55	0.42	16.05	3.58	20.05	7.12
5	TM-99-50	52.6	48.0	75.5	3.66	13.5	7.95	0.41	15.00	2.28	22.01	5.27
6	WBM-314	38.7	47.0	78.5	2.87	8.25	6.75	0.38	27.25	3.87	22.32	9.96
7	BASANTI×BIRESWAR	39.2	44.0	81.6	2.65	11.7	6.76	0.35	25.70	3.73	22.05	6.91
8	BASANTI×PS-16	41.2	43.0	76.0	3.25	11.1	7.43	0.36	23.85	3.82	20.95	7.91
9	BASANTI×TM-99-50	40.6	44.5	76.5	3.70	11.3	8.65	0.42	23.35	2.53	17.30	6.55
10	HUM-12×BASANTI	39.8	45.5	73.0	3.85	10.2	7.74	0.38	25.80	3.01	23.20	8.49
11	HUM12×BIRESWAR	39.8	44.5	80.0	2.45	12.7	7.19	0.45	26.85	2.25	19.80	10.2
12	HUM-12×PS-16	48.2	47.0	75.0	2.55	10.7	6.68	0.40	26.60	3.11	18.95	11.7
13	HUM-12×TM-99-50	42.0	45.0	76.0	3.15	8.1	6.48	0.42	26.30	3.20	21.35	6.90
14	PS-16×BIRESWAR	41.1	44.5	72.5	3.50	9.4	6.84	0.39	25.95	3.23	18.95	6.55
15	PS-16×TM-99-50	42.5	51.5	74.5	2.65	9.6	7.22	0.36	26.45	2.53	17.35	4.15
16	TM-99-50×BIRESWAR	40.6	44.0	76.5	3.85	10.5	6.40	0.41	25.70	2.85	19.55	8.92
17	WBM-314×BASANTI	39.2	46.5	76.5	3.70	9.4	7.04	0.40	23.45	3.24	22.60	8.98
18	WBM-314×BIRESWAR	49.6	49.0	80.5	2.65	9.3	7.43	0.42	20.50	4.74	21.35	7.25
19	WBM-314 × HUM-12	44.5	45.0	76.0	3.50	9.5	6.68	0.38	26.42	3.46	19.46	7.21
20	WBM-314×PS-16	49.5	48.0	74.5	4.68	10.5	8.81	0.39	14.95	3.47	22.45	7.22
21	WBM-314 ×TM-99-50	48.2	45.5	76.0	3.72	9.1	7.19	0.43	26.82	3.09	19.45	9.16
22	C.D. AT 5%	9.008	3.114	3.732	3.868	1.174	0.938	0.177	3.750	0.675	0.526	1.274
23	SE(m)	4.504	1.057	1.866	1.934	0.862	0.469	0.059	1.250	0.226	0.263	0.079

**Table 2:** Mean, Range And Other Genetic Characters Of Parents And F<sub>2</sub> Population:

Sl. no	Character	Range		Mean	SED	Variances					H2	GA	% mean		
		Min	Max			PV	GV	EV	CV	GCV				PCV	ECV
1	Plant height	38.7	72.5	39.3	4.5	667.9	667.8	0.0	1.1	32.3	32.3	4.6	100.0	17.5	66.6
2	Days to 50% flowering	43.0	54.5	48.9	1.1	8.4	8.4	0.0	0.4	3.7	3.7	3.1	99.8	3.8	7.7
3	Days to maturity	73.0	81.6	71.3	1.9	7.0	6.9	0.0	0.4	3.2	3.2	4.5	99.4	5.2	6.6
4	No. of branches plant <sup>-1</sup>	2.4	4.7	3.9	1.9	177.0	171.8	5.2	0.4	16.3	16.6	48.6	97.1	1.0	33.1
5	No. of seeds pod <sup>-1</sup>	8.1	12.7	9.6	0.9	51.5	51.2	0.4	0.6	9.5	9.6	15.1	99.3	2.2	19.6
6	Pod length	6.4	8.7	7.8	0.5	839.8	684.6	155.1	0.5	32.2	35.7	279.7	81.5	0.3	59.9
7	Pod width	0.4	0.5	0.5	0.1	176.9	176.1	0.9	0.4	16.6	16.7	20.4	99.5	2.8	34.2
8	No. of pods plant <sup>-1</sup>	14.9	27.2	20.4	1.3	103.2	102.5	0.7	0.3	12.9	12.9	19.0	99.3	2.1	26.5
9	Seed weight (100 seeds)	2.3	4.7	3.7	0.2	152.6	149.1	3.5	1.5	15.0	15.2	40.1	97.7	1.1	30.6
10	Protein content	17.4	23.2	18.8	0.3	229.0	228.9	0.1	0.5	20.4	20.4	7.9	99.9	7.4	42.0
11	Seed yield plant <sup>-1</sup>	4.2	11.7	6.8	0.1	82.9	72.1	10.8	0.6	10.4	11.2	77.7	87.0	1.7	20.1

**Table 3:** Genotypic and Phenotypic Correlation among the Elven Characters of parents and F<sub>2</sub> (*Vigna radiata* L. Wilczek)

Sl. no	Characters		Plant height	Days to 50% flowering	Days to maturity	No. of branches plant <sup>-1</sup>	No. of seeds pod <sup>-1</sup>	Pod length	Pod width	No. of pods plant <sup>-1</sup>	Seed weight (100 seeds)	Protein content	Seed yield plant <sup>-1</sup>
1	Plant height	G		-0.012	-0.104	-0.086	0.388*	0.445**	-0.420**	-0.189	-0.589**	-0.043	0.264
		P		-0.012	-0.104	-0.085	0.386*	0.402*	-0.419**	-0.189	-0.582**	-0.043	0.247
2	Days to 50% flowering	G			-0.252	0.116	0.14	0.236	-0.013	0.311	0.088	-0.011	-0.096
		P			-0.252	0.114	0.14	0.213	-0.013	0.309	0.087	-0.011	-0.085
3	Days to maturity	G				-0.131	0.043	-0.22	0.264	0.084	-0.037	0.099	0.082
		P				-0.134	0.043	-0.204	0.264	0.086	-0.041	0.098	0.074
4	No. of branches plant <sup>-1</sup>	G					0.383*	0.031	-0.011	0.139	0.04	-0.138	-0.185
		P					0.376*	0.038	-0.01	0.136	0.037	-0.134	-0.176
5	No. of seeds pod <sup>-1</sup>	G						0.045	-0.448**	-0.332*	-0.241	-0.03	0.206
		P						0.028	-0.445**	-0.331*	-0.24	-0.03	0.191
6	Pod length	G							-0.088	-0.132	-0.165	-0.399*	0.286
		P							-0.089	-0.107	-0.121	-0.361*	0.296
7	Pod width	G								0.202	0.614**	0.018	-0.221
		P								0.202	0.603**	0.018	-0.208
8	No. of pods plant <sup>-1</sup>	G									-0.235	0.051	0.320*
		P									-0.235	0.051	0.320*
9	Seed weight (100 seeds)	G										-0.173	-0.390*
		P										0.051	0.051
10	Protein content	G											-0.232
		P											0.320*

\*significant at 5% level, \*\*significant at 1% level

**Table 4:** Path Coefficient Analysis at Genotypic Level of 11 Elven Characters parents and F<sub>2</sub> (*Vigna radiata* L. Wilczek)

Sl. No	Characters	Plant height	Days to 50% flowering	Days to maturity	No. of branches plant <sup>-1</sup>	No. of seeds pod <sup>-1</sup>	Pod length	Pod width	No. of pods plant <sup>-1</sup>	Seed weight (100 seeds)	Protein content	Seed yield
1	Plant height	-0.16426	0.00951	0.01482	0.06266	0.39687	0.30227	0.09916	-0.22936	-0.22896	0.00094	0.264
2	Days to 50% flowering	0.00204	-0.76711	0.03594	-0.08508	0.14362	0.16007	0.00303	0.37709	0.03408	0.00024	-0.096
3	Days to maturity	0.01709	0.19349	-0.14248	0.096	0.04441	-0.14925	-0.06229	0.10136	-0.01443	-0.00216	0.082
4	No. of branches plant <sup>-1</sup>	0.01408	-0.08928	0.01871	-0.73103	0.39147	0.0214	0.00271	0.16863	0.01544	0.003	-0.185
5	No. of seeds pod <sup>-1</sup>	-0.06373	-0.1077	-0.00619	-0.27975	1.02298	0.03057	0.10581	-0.40273	-0.09374	0.00066	0.206
6	Pod length	-0.07306	-0.18067	0.03129	-0.02302	0.04602	0.67963	0.02076	-0.15966	-0.06421	0.00867	0.286
7	Pod width	0.06894	0.00983	-0.03757	0.00839	-0.45815	-0.05973	-0.23625	0.24519	0.23901	-0.00039	-0.221
8	No. of pods plant <sup>-1</sup>	0.0311	-0.23881	-0.01192	-0.10177	-0.34011	-0.08958	-0.04782	1.2113	-0.09125	-0.0011	0.320*
9	Seed weight (100 seeds)	0.09669	-0.06722	0.00529	-0.02902	-0.24655	-0.11219	-0.14517	-0.28416	0.38896	0.00376	-0.390*
10	Protein content	0.00707	0.00836	-0.01416	0.10078	-0.03105	-0.27098	-0.00426	0.06127	-0.06727	-0.02175	-0.232

Residual are 0.14765.

**References**

- Jitendra Kumar, Arbind K. Choudhary, Ramesh K. Solanki and Aditya Pratap Plant Breed. 2011; 130:297-313.
- Amarender Reddy. Economic & Political Weekly. 2009; XLIV(52):73-80.
- Kumar R, Thakral SK, Kumar S. Response of green gram (*Vigna radiata* L.) to weed control and fertilizer application under different planting systems. Indian J Weed Sci. 2004; 36:131-2.
- Tomooka N, Lairungreang C, Nakeeraks P, Egawa Y, Thavarasook C. Center of genetic diversity and dissemination pathways in mung bean deduced from seed protein electrophoresis. Theoretical and Applied Genetics. 1992; 83:289-293.
- Jain HK. Pulses-The wonder plants of world agriculture. In: Twenty Five years of Pulses Research in India (Ali, M., Asthana, A.N., Mehta, S.L. Ed). Indian Institute of Pulses Research, Kanpur, India, 2004, 1-4.
- Vijayalaxmi NVS, Kumar J, Rao N. Variability and correlation studies in desi, kabuli and intermediate chickpea. Legume Res. 2000; 23:232-236.
- Singh M, Singh TP, Sharma SK, Thakur HL. Influence of cropping system on combining ability and gene action for grain yield and its components in black gram (*Vigna mungo*). Indian J Agri. Sci. 2010; 73:356-357.
- Khan MD, Khalil IH, Khan MA, Ikramullah. Genetic divergence and association for yield and related traits in mash bean. Sarhad J Agric. 2004; 20:555-56.
- Alie FA, Tejbir-Singh. Variability and character association analysis in F<sub>2</sub> populations of mung bean (*Vigna radiata* (L.) Wilczek). Advances-in-Plant-Sci. 2008; 21(2):637-640.
- Miah NN, Bhadra SK. Genetic variability in the F<sub>2</sub> generation of mung bean Bangladesh J of Agri. Res., 1989; 14(1):72-75.
- Roychowdhury R, Datta S, Gupta P, Tah J. Analysis of genetic parameters on mutant populations of mung bean (*Vigna radiata* L.) after ethyl methane sulphonate treatment. Nat. Sci. Biol. 2012; 4(1):137-143.
- Steel RGD, Torrie JH. Principles and Procedures of Statistics. McGraw-Hill Book Co. Inc., New York, USA, 1980.
- Hakim. Variability and correlation of agronomic characters of mung bean germplasm and their utilization for variety improvement program. Indonesian-Jrnl. of Agri. Sci. 2008; 9(1):24-28.

14. Rahim MA. Genetic variability, character association and genetic divergence in mung bean (*Vigna radiata* L. Wilczek). Plant omics Journal. 2010; 3(1):1-6.
15. Rahim MA, Mia AA, Mahmud F, Afrin KS. Multivariate analysis in some mung bean accessions on the basis of agronomic traits. American-Eurasian J Sci. Res. 2008; 3(2):217-221.
16. Makeen K, Abraham G, Jan A, Singh AK. Genetic variability and correlations studies on yield and its components in mung bean (*Vigna radiata* L. Wilczek.). J Agron. 2007; 6(1):216-218.
17. Gul R, Khan H, Mairaj G, Ali S, Farhatullah, Ikramullah. Correlation study on morphological and yield parameters of mung bean (*Vigna radiata*). Sarhad J Agric. 2008; 24(1):37-42.
18. Tabasum A, Saleem M, Aziz I. Genetic variability, trait association and path analysis of yield and yield components in mung bean (*Vigna radiata* L. Wilczek). Pak. J Bot. 2010; 42:3915-3924.