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## Genetic variability analysis for yield and yield components in mungbean [*Vigna radiata* (L.) Wilczek]

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#### Abstract

Mungbean is the most important pulse crop after chickpea and pigeon pea. The present experiment was conducted at College Farm, College of Agriculture, Navsari Agricultural University, Bharuch Campus during kharif 2021. The Experimental materials consist of 19 genotypes of mungbean representing different geographical origins. The experiment was laid out in Randomized Block Design (RBD) with three replications for various traits to assess the genetic variability, heritability and genetic advance in mungbean. The analysis of variance revealed a highly significant difference for all the eleven characters. Higher heritability coupled with high genetic advance as per cent mean is observed for seed yield per plant, branches per plant and pods per cluster. This confirms higher additive gene action and thus improvement could be brought about by direct phenotypic selection over the genotypes.

**Keywords:** mungbean, variability, heritability, genetic advance

#### Introduction

One of the most valuable pulse crops is the mungbean [*Vigna radiata* (L.) Wilczek], also known as green gram or Moong in India. *Vigna* is a pantropical genus with 150 species, the majority of which are found in Asia and Africa. Only two species of *Vigna*, which are of African origin, and five species, which are of Asian origin, are grown as pulse crops. Mungbean is an ancient and well-known crop in Asia, particularly in the Indian subcontinent and now becoming popular in other continents (Rehman *et al.*, 2009) [21]. *Vigna radiata* is divided into three subgroups: one domesticated (*Vigna radiata* subsp. *radiata*) and two wild (*Vigna radiata* subsp. *sublobata* and *Vigna radiata* subsp. *glabra*). It is a wonderful source of easily digested and high-quality protein for India's mostly vegetarian population. It has a dry weight of 59 to 65% carbohydrates, 22 to 28 % total protein, 21 to 25 % amino acids, 1.5 to 2.63 % lipids, 1.0 to 1.5 % fat, 3.5 to 4.5 % fiber and 4-5 % ash and it has 334 to 344 kcal of energy per serving (Srivastava and Ali, 2004). It fulfills the country's vegetarian population's protein needs. It contains a lot of important amino acids, including phenylalanine, isoleucine, leucine and lysine (Lambrides and Godwin, 2007) [13].

India is the world's greatest mungbean producer, accounting for 65% area and 54% of production. In India, mungbean occupies an area of 4.34 million hectares with a production of 2.12 million tones and 489 kg per hectares productivity (Anon., 2020) [2]. The area under mungbean cultivation in Gujarat is about 154690 hectares with the production of 110140 tones and 711 kg per hectare productivity (Anon., 2021) [3].

The entire success of the plant breeding program of any crop largely depends on the wide range of variability present in that crop. The effectiveness of selection is based on the genetic variability which occurs about key economic traits that are present in the population. The economically significant traits, which are quantitatively inherited, are strongly influenced by the environment. It is also difficult to determine whether the observed variability is caused by heritable factors or by the environment, and it is required to separate it into heritable and non-heritable components.

#### Materials and Methods

The present research work was conducted at College Farm, College of Agriculture, Navsari Agricultural University, Bharuch Campus during kharif 2021. The Experimental materials consist of 19 (18 + 1 check) genotypes of mungbean representing different geographical origins. The pure seeds of these genotypes were provided by Pulse Research Station, Navsari Agricultural University, Navsari. The details of the genotypes are GP – 6, GP – 7, GP – 16, GP – 17, GP – 19, GP – 20, GP – 24, GP – 25, GP – 26, GP – 27, GP – 28, GP – 30, GP – 38, GP

– 39, GP – 45, GP – 48, GP – 63, GP – 70 and GM – 7 (check). The experiment is laid out in Randomized Block Design (RBD) with three replications. Each entry was accommodated in a single row of 2 m with a spacing of 45 x 15 cm. A line of 12 plants was grown as a gross plot and from both sides, 1 plant each was excluded to consider 10 plants as a net plot. Observations were taken on 5 random plants in the plot. All cultural practices were followed and timely plant protection measures were taken to avoid damage through pests and diseases.

The following characters like days to 50% flowering, days to maturity, plant height (cm), branches per plant, pods per cluster, pods per plant, pod length (cm), seeds per pod, seed yield per plant (g), 100 seed weight (g), protein content (%), mungbean yellow mosaic virus (MYMV) incidence %. The observations were recorded on five randomly selected plants from each line in each replication except for days to 50% flowering and days to maturity where all 10 plants of the net plot are considered. All the weights were recorded in grams with the help of Precisa Analytical Weight balance. In this experiment, MYMV incidence was not observed, so it was not calculated. Representative sample of seeds was taken at maturity from each entry per replication and dried in an oven at 60°C for 24 hrs. and then was grinded in a grinder-cum-

mixer. The nitrogen content in seeds was determined with micro-kjeldhal procedure (Jackson, 1967) and the percentage of protein was calculated using the factor 6.25. The analysis of the variance of RBD and their significance for all the characters were worked out as suggested by Panse and Sukhatme (1967) [17]. Environmental, genotypic and phenotypic variances were estimated as follows as suggested by Johnson *et al.* (1955) [11]. The heritability in a broad sense and genetic advance were estimated according to the method given by Allard (1960) [1].

**Results and Discussion**

The significant mean sum of square values for all the traits for all the genotypes studied evidenced the presence of sufficient variability in the material under study. Analysis of variance revealed highly significant differences among the mean sum of squares concerning genotypes for yield attributing traits under study. This result evidenced that a sufficient amount of variability is present within the material used. The mean sum of square values is described in Table 1.

Mean values and components of variance of all the nineteen genotypes of mungbean for eleven characters are given in Tables 2 and 3.

**Table 1:** Result of analysis of variance for different characters of mungbean

Character	d.f.	Mean sum of square										
		DFFF	DTM	PH	BPP	PPC	PPP	PL	SPP	SYP	HSW	PC
Replication	2	0.86	3.84	48.75	0.44	0.13	8.55	0.11	3.09	2.62	0.00	0.87
Genotypes	18	10.61**	19.18**	91.76**	3.42**	3.98**	41.43**	0.98**	3.74**	9.95**	0.39**	7.39**
Error	36	1.27	5.58	16.61	0.14	0.48	7.67	0.17	0.98	0.88	0.05	0.82
S. Em. ±		0.65	1.36	2.35	0.22	0.40	1.60	0.23	0.57	0.54	0.13	0.52
CD at 5%		1.86	3.91	6.75	0.63	1.15	4.59	0.67	1.64	1.56	0.37	1.50
CD at 1%		2.50	5.25	9.05	0.84	1.54	6.15	0.90	2.20	2.09	0.50	2.01
CV %		3.14	3.17	8.11	6.42	11.50	13.04	5.53	8.93	13.96	6.76	4.11

\*\* - Significant at 1% level, \* - Significant at 5.0% level, d.f. – degrees of freedom

**Where,**

- DFFF – Days to 50% flowering
- DTM – Days to maturity
- PH – Plant height (cm)
- BPP – Branches per plant
- PPC – Pods per cluster
- PPP – Pods per plant
- PL – Pod length
- SPP – Seeds per pod
- SYP – Seed yield per plant (g)
- HSW – 100 Seed weight (g)
- PC – Protein content (%)

**Table 2:** Mean values of all the nineteen genotypes of mungbean for eleven characters

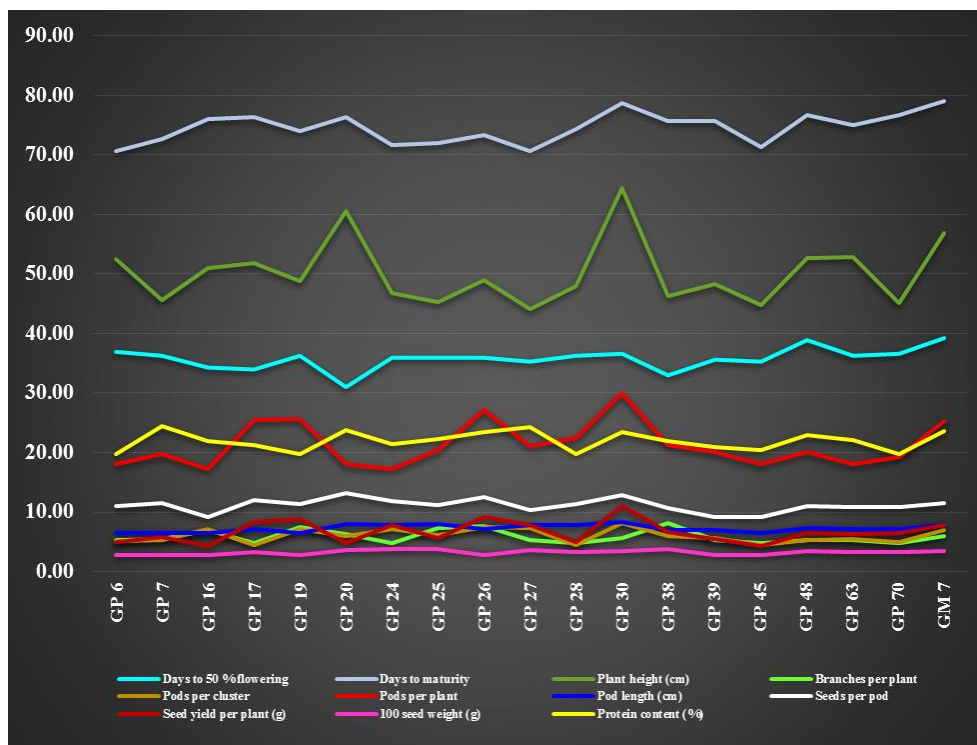
Sr. no.	Genotypes	DFFF	DTM	PH	BPP	PPC	PPP	PL	SPP	SYP	HSW	PC
1	GP – 6	37.00	70.67	52.53	5.20	5.13	18.07	6.75	10.87	5.01	2.80	20.02
2	GP – 7	36.33	72.67	45.58	5.47	5.27	19.67	6.80	11.40	5.90	2.93	24.52
3	GP – 16	34.33	76.00	50.97	7.00	7.13	17.27	6.41	9.20	4.22	2.73	21.97
4	GP – 17	34.00	76.33	51.83	4.87	4.40	25.47	7.18	12.00	8.38	3.39	21.26
5	GP – 19	36.33	74.00	48.77	7.53	7.20	25.60	6.44	11.27	8.86	3.08	20.06
6	GP – 20	31.00	76.33	60.51	6.27	5.93	17.93	8.01	13.13	4.79	3.73	23.79
7	GP – 24	36.00	71.67	46.85	5.07	7.07	17.33	7.95	11.73	7.93	3.82	21.46
8	GP – 25	36.00	72.00	45.28	7.33	6.07	20.33	8.02	11.20	5.74	3.85	22.36
9	GP – 26	36.00	73.33	48.99	7.60	7.53	27.07	7.26	12.53	9.20	3.25	23.56
10	GP – 27	35.33	71.00	44.16	5.20	7.27	21.07	7.82	10.33	7.85	3.67	24.39
11	GP – 28	36.33	74.33	47.95	5.00	4.47	22.40	7.96	11.33	4.99	3.27	20.10
12	GP – 30	36.67	78.67	64.43	5.67	8.13	29.93	8.39	12.73	11.06	3.52	23.51
13	GP – 38	33.00	75.67	46.36	8.13	5.93	21.27	7.04	10.53	6.62	3.84	21.98
14	GP – 39	35.67	75.67	48.34	5.20	5.67	20.00	7.03	9.27	5.47	3.06	21.06
15	GP – 45	35.33	71.33	44.79	5.07	4.47	17.93	6.96	9.13	4.69	2.88	20.53
16	GP – 48	39.00	76.67	52.66	5.27	5.27	20.07	7.41	11.00	6.49	3.49	23.07
17	GP – 63	36.33	75.00	52.84	5.20	5.47	17.93	7.28	10.80	6.42	3.31	22.10
18	GP – 70	36.67	76.67	45.06	5.07	5.00	19.13	7.24	10.80	6.45	3.41	19.75
19	GM – 7	39.33	79.00	56.86	6.00	7.00	25.27	7.81	11.53	7.84	3.56	23.73

**Table 3:** Range, mean and components of variance for different characters of mungbean

Sr. no.	Characters	Range		Mean	Component of variance		
		Minimum	Maximum		Genotypic	Phenotypic	Environmental
1	Days to 50% flowering	31.00	39.33	35.82	3.11	4.38	1.27
2	Days to maturity	70.67	79.00	74.58	4.53	10.12	5.58
3	Plant height (cm)	44.16	64.43	50.25	25.05	41.66	16.61
4	Branches per plant	4.87	8.13	5.90	1.09	1.24	0.14
5	Pods per cluster	4.40	8.13	6.02	1.17	1.64	0.48
6	Pods per plant	17.27	29.93	21.25	11.25	18.93	7.67
7	Pod length (cm)	6.41	8.39	7.36	0.27	0.44	0.17
8	Seeds per pod	9.13	13.13	11.09	0.92	1.90	0.98
9	Seed yield per plant (g)	4.22	11.06	6.73	3.02	3.90	0.88
10	100 seed weight (g)	2.73	3.85	3.35	0.11	0.16	0.05
11	Protein content (%)	19.75	24.52	22.06	2.19	3.01	0.82

The variation of days to 50% flowering ranged from 31.00 days (GP – 20) to 39.33 days (GM – 7) and Genotype GP – 20 (31.00 days) was the earliest to flower. Mean values of days to maturity range from 70.67 days (GP – 6) to 79.00 days (GM – 7) and genotype GP – 27 (71.00 days) had the least maturity period. The range of variation for plant height lies between 44.16 (GP – 27) to 64.43 cm (GP – 30) with the overall mean of 50.25 cm and genotype GP – 30 (64.43 cm) exhibiting maximum plant height followed by the GP – 20 (60.51 cm), GM – 7 (56.86 cm). The mean values for the branches per plant ranged from 4.87 (GP – 17) to 8.13 (GP – 38) and genotype GP – 38 (8.13) had maximum branches per plant. Mean data revealed that among 19 genotypes, GP – 30 (8.13) possessed maximum pods per cluster. The tune of variation for pods per plant lies between 17.27 (GP – 16) to 29.93 (GP – 30) pods per plant. Mean data revealed that

among 19 genotypes, GP – 30 (29.93) possessed maximum pods per plant. Variations for pod length ranged between 6.4 (GP – 16) to 8.39(GP–30). Mean data revealed that among 19 genotypes, GP – 20 (13.13) maximum seeds per pod. The spectrum of variation seed yield per plant ranged from 4.22 (GP – 16) to 11.06 g (GP – 30) while the general mean was 6.73 g. Among all the genotypes, GP – 30 (11.06 g) recorded the highest seed yield per plant. The quantum of variation for 100 seed weights ranged between 2.73 (GP – 16) to 3.85 g (GP – 25). Genotype GP – 7 (24.52%) had highest protein content, whileGP – 70 (19.75%) had lowest protein content value. A graphical representation of the mean performance of nineteen genotypes for different characters in mungbean is given in Fig.



**Fig 1:** Mean performance of nineteen genotypes for different characters in mungbean

Phenotypic and genotypic coefficients of variation, heritability, genetic advance for all the characters are given in Table 4. The highest phenotypic coefficient of variation was

observed for seed yield per plant (29.35%), pods per cluster (21.30%), pods per plant (20.47%). Branches per plant (18.83%), plant height (12.84%), seeds per pod (12.42%) and

**Table 4:** Genotypic and phenotypic coefficient of variation, heritability, expected genetic advance and genetic advance as per cent of mean for different characters of mungbean

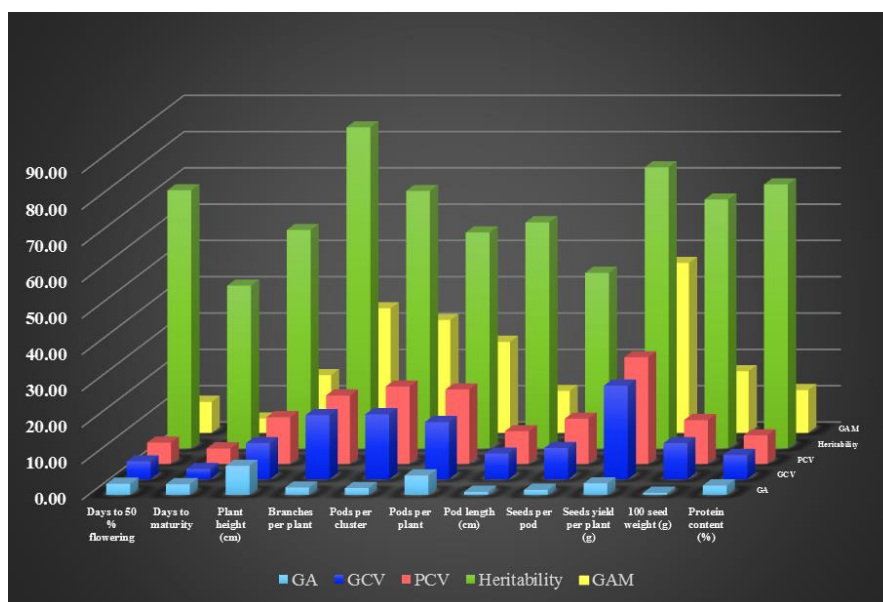
Sr. no.	Characters	GCV%	PCV%	Heritability Broad sense (%)	Genetic Advance	Genetic Advance (% of mean)
1	Days to 50% flowering	4.92	5.84	71.07	3.06	8.55
2	Days to maturity	2.85	4.27	44.81	2.94	3.94
3	Plant height	9.96	12.84	60.13	7.99	15.91
4	Branches per plant	17.70	18.83	88.38	2.02	34.29
5	Pods per cluster	17.93	21.30	70.87	1.87	31.10
6	Pods per plant	15.78	20.47	59.44	5.33	25.07
7	Pod length	7.10	9.00	62.22	0.85	11.54
8	Seeds per pod	8.64	12.42	48.35	1.37	12.38
9	Seed yield per plant	25.82	29.35	77.38	3.15	46.79
10	100 seed weight	9.97	12.04	68.52	0.57	17.00
11	Protein content	6.70	7.87	72.68	2.60	11.78

100 seed weight (12.04%) had moderate values. Pod length (9.00%), protein content (7.87%), days to 50% flowering (5.84%) and days to maturity (4.27%) had low values for the phenotypic coefficient of variation.

The highest genotypic coefficient of variation was observed for seed yield per plant (25.82%). Pods per cluster (17.93%), branches per plant (17.70%) and pods per plant (15.78%) had moderate values for the genotypic coefficient of variation. 100 seed weight (9.97%), plant height (9.96%), seeds per pod (8.64%), pod length (7.10%), protein content (6.70%), days to 50% flowering (4.92%) and days to maturity (2.85%) exhibited a very low genotypic coefficient of variation. High heritability estimates were observed for branches per plant (88.38%) followed by seed yield per plant (77.38%) protein content (72.68%), days to 50% flowering (71.07%), pods per cluster (70.87%), 100 seed weight (68.52%), pod length (62.22%), plant height (60.13%). The highest genetic advance was

observed for plant height (7.99%).

Higher heritability coupled with high genetic advance as per cent mean is observed for seed yield per plant, branches per plant, pods per cluster. This confirms higher additive gene action and thus improvement could be brought about by direct phenotypic selection over the genotypes. These findings are similar to results by Reddy *et al.* (2011) [20], Gadakh *et al.* (2013) [8], Bhanu *et al.* (2016) [6], Jagdhane *et al.* (2017) [10], Asari *et al.* (2019) [4], Dutt *et al.* (2020) [7], Kumar *et al.* (2020) [12]. Plant height, protein content, pod length and 100 seed weight showed high heritability with a moderate genetic advance which indicates that the genotypes under study have the moderate potential for genetic improvement under selection. Similar results were recorded by Narasimhulu *et al.* (2013) [15], Nagrale *et al.* (2018) [14]. A graphical representation of GCV, PCV, heritability, genetic advance and genetic advance percent of mean of nineteen genotypes in fig. 2.



**Fig 2:** GCV, PCV, heritability, genetic advance (GA) and genetic advance as % of mean (GAM) for eleven quantitative characters in mungbean

Higher heritability with low genetic advance as per cent mean is observed in day to 50% flowering indicating the effect of non-additive gene action. The higher heritability might be due to the favorable environment rather than the genotype. Reddy *et al.* (2011) [20], Prasanna *et al.* (2013) [19] and Payasi (2015) [18] reported similar findings. Moderate heritability with moderate genetic advance as per cent of mean was observed for seeds per pod. The result of the present study was in

agreement with the finding of Pandey *et al.* (2007) [16], Azam *et al.* (2018) [5] and Sirohi *et al.* (2018) [22].

The heritability estimate provides information on the magnitude of inheritance of quantitative character but does not indicate the magnitude of the genetic gain obtained by the selection of the best individual from the best population. Heritability associated with genetic advance is much more beneficial than heritability alone.

**References**

1. Allard RW. Principles of Plant Breeding. John Wiley and Sons. Inc., New York. 1960, 85-95.
2. Anonymous. Directorate of Agriculture, Government of India. 2020.
3. Anonymous. Directorate of Agriculture, Government of India. 2021.
4. Asari T, Patel BN, Patel R, Patil GB, Solanki C. Genetic variability, correlation and path coefficient analysis of yield and yield contributing characters in mungbean (*Vigna radiata* (L.) Wilczek). Int. J Chem. Stud. 2019;7(4):383-387.
5. Azam MG, Hossain MA, Alam MS, Rahman KS, Hossain M. Genetic variability, heritability and correlation path analysis in mungbean (*Vignaradiata* (L.) Wilczek). Bang. J Agric.Res. 2018;43(3):407-416.
6. Bhanu AN, Singh MN, Singh M. Genetic variability, correlation and path coefficient analysis for quantitative traits in mungbean genotypes. J Food Legumes. 2016;29(3 and 4):199-205.
7. Dutt A, Singh PK, Dutt A, Singh M, Singh A. Study of genetic variability heritability and genetic advance for seed yield in mungbean (*Vigna radiata* (L.) Wilczek). J. Pharmacogn. and Phytochem. 2020;9(6):2245-2246.
8. Gadakh SS, Detha AM, Kathale MN. Genetic variability, correlations and path analysis studies on yield and its components in mungbean (*Vigna radiata* (L.) Wilczek). J Life Sci. 2013;10(2a):441-447.
9. Jackson MT. Soil chemical analysis, Prentice Hall Int., New Delhi. 1967.
10. Jagdhane NM, Suresh BG, Ram BJ, Yadav P. Genetic variability and character association for seed yield in mungbean (*Vigna radiata* (L.) Wilczek). J. Pharmacogn. and Phytochem. 2017;6(4):1388-1390.
11. Johnson HW, Robinson HF, Comstock RE. Genotypic and phenotypic correlation in soybean and their implications in selection. Agron. J. 1955;47:477-483.
12. Kumar A, Sharma NK, Kumar R, Sanadya SK, Sahoo S, Yadav MK. Study of genetic variability parameters for seed yield and its component traits in mungbean germplasm under arid environment. Int. J Chem. Stud. 2020;8(4):2308-2311.
13. Lambrides CJ, Godwin ID. Mungbean. In *Pulses, sugar and tuber crops*. Springer, Berlin, Heidelberg. 2007, 69-90.
14. Nagrale SC, Jadhav PV, Tayade N, Patil AN. Assessment of genetic variability and correlation in mungbean (*Vigna radiata* (L.) Wilczek). J. Pharmacogn. and Phytochem. 2018;7(5):708-710.
15. Narasimhulu R, Naidu NV, Shanthi PM, Rajarajeswari V, Reddy KHP. Indian J Plant Sci. 2013;2(3):82-66.
16. Pandey MK, Srivastava N, Kole CR. Selection strategy for augmentation of seed yield in mungbean (*Vigna radiata* (L.) Wilczek). Legume Res. 2007;30(4):243-249.
17. Panse VG, Sukhatme PV. Statistical Methods for Agricultural workers. Indian Council of Agricultural Research, New Delhi. 1967.
18. Payasi DK. Genetic variability analysis for seed yield and its components in mungbean (*Vigna radiata* (L.) Wilczek). Int. J. Plant Breed and Genet. 2015;9(3):177-188.
19. Prasanna BL, Rao PJM, Murthy K GK, Prakash KK. Genetic variability, correlation and path coefficient analysis in mungbean. Environ. Ecol. 2013;31:1782-1788.
20. Reddy KDR, Venkateswarlu O, Obaiiah MC, Jyothi GLS. Studies on genetic variability, character association and path coefficient analysis in green gram (*Vigna radiata* (L.) Wilczek). Legume Res. 2011;34(3):202-206.
21. Rehman A, Khalil SK, Nigar S, Rehman S, Haq I. Phenology, plant height and yield of mungbean varieties in response to planting date. Sarhad J Agric. 2009;25:147-151.
22. Sirohi SPS, Tyagi M, Mohit SS. Assessment of genetic variability and character association in promising genotypes of mungbean (*Vigna radiata* (L.) Wilczek). J. Pharmacogn and Phytochem. 2018;7(5):2513-2516.
23. Srivastava RP, Ali M. Nutritional quality of common pulses, Kanpur. Indian Institute of Pulses Research, Kanpur, 2004, 1-65.