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Short Comminication

Estimation of genetic variability for seed yield and yield related traits in mungbean [*Vigna radiata* (L.) Wilczek]

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ABSTRACT

Genetic variability is the most important factor for the success of any crop improvement program. Hence, the evaluation of genotypes has to be conducted as a preliminary step to study the extent of variability available in the genotypes and to identify suitable high-yielding genotypes that can be utilized in the crop improvement program. The present investigation was carried out to estimate genetic variability, heritability, and genetic advance for yield and yield contributing characters among 38 genotypes of mungbean for eleven quantitative traits. Significant differences were observed among genotypes for all eleven characters studied. The high degree of genetic variability along with high heritability and high genetic advance as percent of mean were recorded for seed yield per plant, harvest index, number of pods per plant, plant height, and the number of branches per plant which indicates that these characteristics were under the control of additive gene action and therefore, form the basis of selection for the mungbean improvement program.

Key words: Genetic advance, Genotypic coefficient of variation, Heritability, Mungbean, Phenotypic coefficient of variation, Seed yield

Mungbean is one of the most important pulse crops for protein supplements in subtropical zones of the world. Mungbean [*Vigna radiata* (L.)], which belongs to the angiospermic dicot family Leguminaceae. India is the principal producer of mungbean in the world with an annual production of 3.17 mt from an area of 5.50 mha with a productivity of 570 kg per ha and contributing 10.3 % to the total pulses production (Anonymous 2022-23). It is widely grown in the Indian subcontinent as an annual, semi-erect, and erect catch crop between two principal crops (Roy Chowdhury *et al*. 2012). Mungbean is an essential dietary component in India. It is the cheapest source of protein and provides nutritional security to vegetarians. It is also consumed in the preparation of other food products like *Papad, Namkeen, Mangori, Dal vada, etc*. *Mung Ki Dal Ki Khichadi* made with mungbean *Dal* and rice is easily digestible and therefore always recommended by doctors for sick people (Kumar *et al*. 2024). Mungbean is rich in necessary amino acids particularly lysine, which is lacking in most of the cereal crops (Suresh *et al*. 2010). Short duration, low input requirements, and high global demand make mungbean an ideal rotation crop for small and marginal farmers. It generates a triple benefit: additional income, additional supplements-rich food, and increased soil fertility by N_{2-} fixation (Nair *et al*. 2020).

The natural variability for yield and yield-related traits is very limited in those extremely self-pollinated crops for example mungbean and further preference for improvement becomes impractical due to its tough and fine floral parts and very accurate micro condition which is required for pollen cleave and fertilization. However, proper assessment of the extent of genetic variation available for yield traits, their heritability values, and genetic advancement help the breeders to choose excellent varieties for improvement. Estimates of inherited parameters provide a manifestation of the relative importance of the several types of gene effects that act on the total variation of a plant's character. GCV, PCV, and heritability along with genetic advance are very important parameters in the genetic enhancement of characters (Denton and Nwangburuka 2011). Therefore, present investigation aimed to estimate genetic variability for seed yield and yield-related traits in mungbean.

The present study was carried out during *Kharif*, 2019 at the experimental farm of ARS, Mandor, Agriculture University, Jodhpur (Rajasthan). The experimental material comprises 38 genotypes (Table 1) and was sown on July 23, 2019, in RBD with three replications. The row-to-row spacing was 30cm and plant-to-plant spacing was 10 cm for each genotype. The observations were recorded on 11 characters including days to 50% flowering, days to maturity, 100 seed weight (g) and protein content (%) on a whole plot basis while plant height (cm), pods/ plant, pod length (cm), number of branches/ plants, number of seeds/pod, seed yield/plant (g) and harvest index (%) were measured on five randomly selected plants and data were averaged (SPAR 3.0).

The ANOVA showed significant differences among genotypes for eleven characters (Table 2) and recommended that the material has appropriate genetic variability to sustentation the breeding programme for increasing the seed yield of mungbean (data presented).

A broad range of variability in the mungbean genotypes was depicted (Table 3) by different characteristics namely; days to 50% flowering (38 - 57 days), days to maturity (70 - 83 days), plant height (20.3 - 69.7 cm), pods/ plant (7.9 - 25.5), pod length (5.3 - 8.6 cm), branches/ plant (1.1 - 2.3), seeds/ pod (8.6 - 12.6), 100 seed weight (3.3 - 6.2 g), seed yield/ plant (4.2 - 11.6 g) harvest index (12.6 - 41.8%) and protein content (21.9 - 27.6%).

Table 2: Analysis of variance (ANOVA) for seed yield and other traits in 38 mungbean genotypes/ varieties

S. No.	Characters	Replications	Genotypes	Error
	Degree of freedom	2	37	74
1.	Days to 50% flowering	0.08	41.10**	1.23
2.	Days to maturity	1.32	24.30**	2.19
3.	Plant height (cm)	1.34	278.49**	1.37
4.	No. of pods per plant	0.57	46.79**	0.81
5.	Pod length (cm)	0.30	0.90**	0.37
6.	No. of branches per plant	0.01	0.35**	0.01
7.	Number of seeds per pod	0.27	1.97**	0.48
8.	100 seed weight (g)	0.09	1.15**	0.02
9.	Seed yield per plant (g)	0.33	8.48**	0.64
10.	Harvest Index (%)	1.72	132.74**	5.61
11.	Protein content (%)	1.38	6.55**	1.62

** = Significant at 1%., * = Significant at 5%.

In the present study, PCV values were moderately higher than that of GCV, indicating the influence of the environment on the traits. However,

Table 1. List of mungbean genotypes used for the present investigation.

S. No.	Name of genotypes	Source	S. No.	Name of genotypes	Source
1.	IPM 02-3M 02-	IIPR, Kanpur, U.P.	20.	Pusa M 1871	IARI, New Delhi
2.	IPM 604-1	IIPR, Kanpur, U.P.	21.	Pusa M 1872	IARI, New Delhi
3.	Virat	IIPR, Kanpur, U.P.	22.	OBGG 1011GG	OUAT, Bhubaneswar, Odisha
4.	Shikha	IIPR, Kanpur, U.P.	23.	OBGG 102	OUAT, Bhubaneswar, Odisha
5.	SKNM 1514	SDAU, S.K. Nagar, Gujarat	24.	IGKM 05-6-27KKM-	IGKVV, Raipur, Chhattisgarh
6.	SKNM 1516	SDAU, S.K. Nagar, Gujarat	25.	IGKM 06-18-3	IGKVV, Raipur, Chhattisgarh
7.	GM 4	SDAU, S.K. Nagar, Gujarat	26.	PM 1511	GBPUA&T, Pantnagar, Uttarakhand
8.	GM 6	SDAU, S.K. Nagar, Gujarat	27.	PM 1522	GBPUA&T, Pantnagar, Uttarakhand
9.	ML 818818	PAU, Ludhiana, Punjab	28.	CO-6GCG-6	Coimbatore, T.N.
10.	ML 2483	PAU, Ludhiana, Punjab	29.	COGG-912	Coimbatore ,T.N.
11.	SML 1901	PAU, Ludhiana, Punjab	30.	GAM 5	Anand, Gujarat
12.	SML 668	PAU, Ludhiana, Punjab	31.	LGG 630	ARS, Lam, A.P.
13.	MH 2-15	Hisar, Hariyana	32.	DGGV- 59	ARS,Dharwad, Karnataka
14.	MH 421	Hisar, Hariyana	33.	MGG 399	ARS,Madhira, Telangana
15.	MH 1344	CCS HAU, Hisar, Hariyana	34.	TRCM 171-B-12-6	Agartala, Tripura, Bangladesh
16.	SVM 6262	SVHS, Hisar, Hariyana	35.	OUM 11-5	Berhampur, Odisha
17.	VGG 17-002	NPRC, Vamban, T.N.	36.	JLM 707-5	MPKV, Jalgaon, MH
18.	VGG 17-009	NPRC, Vamban, T.N.	37.	AKM- 1604	PDKV, Akola, MH
19.	VGG 16-055	NPRC, Vamban, T.N.	38.	SKAU-M-365	Srinagar, J & K

smaller differences between phenotypic and genotypic coefficient variation values were noticed for eleven characters, as they are less affected by the environment indicating the reliability of selection based on these traits. Genetic variability parameters approximate for different characters of mungbean are given in Table 3, Fig 1. The highest GCV and PCV in mungbean genotypes were observed for seed yield/ plant followed by pods/plant, harvest Index, plant height, and branches/plant, indicating a good scope for producing variability through hybridization followed by selection. Similar findings were reported by Makeen *et al.* (2007), Garje *et al.* (2014), Hemavathy *et al.* (2015), Bhutia *et al.* (2016), Pulagampalli and Lavanya (2017), Muthuswamy *et al.* (2019), Talukdar *et al.* (2020), Wesly *et al.* (2020), Gaur *et al*. (2021) and Kumar (2022). The occurrence of moderate GCV and PCV was recorded for 100 seed weight which suggests that genetic enhancement in these traits might be obtained to a reasonable extent.

The response of selection depends upon the magnitude of heritable variation there in the population. A character with high GCV and high heritability will be additionally valuable in a selection program. In the present study, high heritability estimates were observed for plant height (98.5), pods/ plant (94.9), 100 seed weight (93.0), seed yield/ plant (89.8), harvest index (88.3) and branches/ plant (85.4). As per Panse and Sukhatme (1985), such traits are mainly governed by additive gene action and could be magnified through individual plant selection outstanding to their high heritability used and similar discovery were also reported by Bisht *et al.* (2014), Singh and Kumar (2014), Shiv *et al.* (2017), Sharma *et al.* (2018), Muthuswamy *et al.* (2019), Wesly *et al.* (2020) and Kumar (2022).

The genetic advance as % of the mean provides an intention of the amount of advance that can be achieved by selection for the perturbed characters. High genetic advance as % of the mean (5% level of significance) was estimated for pods/plant (56.0), seed yield/plant (54.4), plant height (45.9), harvest index (43.4), branches/plant (40.7) and 100 seed weight (27.2); although, moderate values were noticed for days to 50% flowering (16.2) and seeds/ pod (9.2).

The high heritability values coupled with genetic advances would be better founded and useful in forecasting the gain under selection than the heritability approximate uniquely. The high estimate of heritability coupled with high genetic advance as % of mean was recorded for plant height, pods/plant, 100 seed weight, seed yield/plant, branches/plant, and harvest index. Therefore; these traits are to be governed by additive gene effects and can be enhanced through straight selection. Similar findings were observed by Tiwari *et al.* (2014), Choudhary *et al.* (2017), Shiv *et al.* (2017), Pulagampalli and Lavanya (2017), Sharma *et al.* (2018), Muthuswamy *et al.* (2019) and Gaur *et al*. (2021).

The highest value of GCV and PCV observed for pods per plant indicated a greater phenotypic and genotypic variability among the genotypes which suggested that response to selection would be very high for these constituents ultimately leading to yield improvement in the mungbean crop.

The characters such as plant height, pods/ plant, branches/plant, harvest index, and seed yield per plant recorded high genetic variability, and high heritability in coincidence with high genetic advance as percent mean specify the prevalence of

Table 3. Estimates of genetic variability parameters for different characters of mungbean

S. No.	Characters	Mean ± SEm	Range	Coefficient of variance		Heritability (in broad sense)	GA as per cent of mean
				GCV (%)	PCV (%)		
1.	Days to 50% flowering	44±0.6	38.0-57.0	8.23	8.60	91.5	16.2
2.	Days to maturity	75±0.8	70.0-83.0	3.61	4.11	77.1	6.5
3.	Plant height (cm)	42.8±0.7	20.3-69.7	22.42	22.59	98.5	45.9
4.	No. of pods per plant	14.0±0.5	7.9-25.5	27.92	28.66	94.9	56.0
5.	Pod length (cm)	7.14±0.3	5.3-8.6	5.94	10.33	33.1	7.0
6.	No. of branches per plant	1.56±0.1	1.1-2.3	21.38	23.14	85.4	40.7
7.	Number of seeds per pod	9.86±0.4	8.6-12.6	6.65	9.84	45.8	9.3
8.	100 seed weight (g)	4.48±0.1	3.3-6.2	13.70	14.20	93.0	27.2
9.	Seed yield per plant (g)	7.72±0.4	4.2-11.6	27.90	29.44	89.8	54.4
10.	Harvest Index (%)	29.0±1.3	12.6-41.9	22.42	23.86	88.3	43.4
11.	Protein content (%)	24.3±0.7	21.9-27.7	5.28	7.45	50.3	7.7

Note: GCV and PCV = genotypic and phenotypic coefficient of variation, respectively.

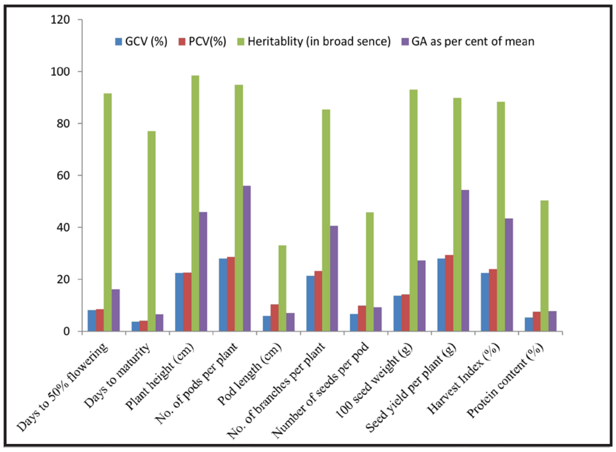

Fig. 1. Estimates of genetic variability parameters for different characters of mungbean

additive gene action and selection may be effectual in next generations for these traits.

Out of 38 genotypes, MH 421, IPM 604-1, Virat, SKNM 1514, SKNM 1516, Shikha, GM 4, MH 421, MH 1344, Pusa M 1871 and COGG-912 were found promising to days to 50% flowering; Shikha, SKNM-1514, IPM 604-1, and SKNM-1514 for days to maturity; Pusa M 1871, ML 818, SML 668, VGG 17-002, VGG17-009 and IGKM 06-18-3 for plant height; PM-1522, IGKM 06-18-3, IGKM 05-6-27, LGG-630, COGG-6 and OBGG 102 for the number of pods per plant; SKAU-M-365, GM-6, COGG-912 and VGG 16-055 for pod length; PM 1522, IGKM-05-6-27, OBGG-101, GAM-5, LGG 630 and DGGV 59 for the number of primary branches per plant. GM-6, MH2-15, PM 1522 for the number of seeds per pod, SKAU-M-365 JLM 707-5, SVM-6262 and Pusa M 1872 for the 100-seed weight; Virat, MH 1344, SVM 626, MH 421, Pusa M1871, Sikha and PM 1522 for harvest index; VGG 16-055, PM 1511, LGG 630 and AKM 1604 for protein content.

Out of 38 genotypes PM 1522, GM-6, IGKM 06-18-3, GM-4, SKAU-M 365, JLM707-5, SML 668 and Pusa M 1872 were found higher in seed yield and other traits based on mean performance. Hence, these genotypes would be used as parental origin for subsequent breeding programs.

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