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Estimation of Genetic Variability for Seed Yield and Yield Related Traits in Mungbean [*Vigna radiata* (L.) Wilczek]

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ABSTRACT: A field experiment was conducted to study the genetic variability involve 38 genotypes for seed yield and its component traits in mungbean at ARS (Agriculture University, Jodhpur), Mandor, Jodhpur during *Kharif* 2019. Good amount of genetic variability has been reported in green gram for various characters such as days to flowering, days to maturity, plant height, harvest index, pods per plant, protein content etc. and their utilization in breeding programme resulted in identification and release of good number of improved varieties. However, these released types cannot be continued longer due to genetic erosion and susceptibility to diseases and pests. Thus, pulse improvement programmes emphasized the urgency of generating variability for high yield potential and identify the genotypes for new niches. It is very essential to understand the genetic nature of varieties, gene action governing yield and its component traits increase yield per unit area. Under this study, eleven characters were analysed and significant differences were observed among genotypes for all the characters. The magnitudes of phenotypic coefficients of variation were slightly higher over genotypic values showing smaller effect of environment in the expression of all studied characters including seed yield. The highest magnitudes of PCV and GCV were observed for seed yield per plant followed by pods/ plant, harvest index, plant height, branches/ plant. High heritability coupled with high genetic advance as 5 per cent of mean were altogether at a glance and observed for the traits like plant height (98.5, 45.9), pods/ plant (94.9, 56.0), 100-seed weight (93.0, 27.2), seed yield/ plant (89.8, 54.4), number of branches/ plant (85.4, 40.7) and harvest index (88.3, 43.4) suggesting additive gene action in the expression of these characters, hence these characters may be proved as effective criteria for selection to improve the seed yield in mungbean. Genotypes exhibited higher seed yield along with other desirable traits were PM 1522, GM-6, IGKM 06-18-3 and GM-4. Besides quantitative traits, all these variety were also found early in flowering and maturity, which are considered as the most desirable characters for crop cultivation.

Keywords: Genotypic variability, mungbean, phenotypic variability, seed yield.

INTRODUCTION

Mungbean is one of the most important pulses crops for protein supplement in subtropical zones of the world. Mungbean [*Vigna radiata* (L.)], which belongs to the angiospermic dicot family: Leguminaceae is one of the most important pulse crops. India is the principle producer of mungbean in the world with an annual production of 2.5 mt from an area of 4.5 mha with the productivity of 556 kg per ha and contributing 10.3 percent to the total pulses production (Anonymous 2020-21). It is widely grown in Indian subcontinent an annual, semi erect and erect catch crop between two principle crops (Roy Chowdhury *et al*. 2012). Protein content of mungbean varies from 21to 26%. Mungbean contains 51% carbohydrate, 4% minerals and 3% vitamins and it also helps in increase nitrogen by fixing the atmospheric nitrogen through root nodulation (Idress *et al*., 2006). Mungbean is wealthy 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 benefits: 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 elements, their heritability values and genetic advance could be of great help for the breeders in order to choose excellent variety for improvement. Estimates of inherited parameters provide a manifestation of the relative importance of the several types of gene effects act on the total variation of a plant character. GCV, PCV and heritability go with genetic advance are very major parameters in enhancing characters (Denton and Nwangburuka, 2011).

MATERIAL AND METHODS

The current study was carried out during *Kharif*, 2019 at experimental farm of ARS, Mandor, Agriculture University, Jodhpur (Rajasthan). The experimental material comprises of 38 genotypes (Table 1) and was sown on July 23, 2019 in RBD with 03 replications. The trial was sown R x R spacing was 30cm and P x P spacing was 10cm. The observations were set down for 11 characters in which days to 50% flowering, days to maturity, 100 seed weight (g) and protein content (%) were recorded on whole plot basis while plant height (cm), pods/ plant, pod length (cm), number of branches/ plant, number of seeds/ pod, seed yield/ plant (g) and harvest index (%) were measure on 05 competitive plants in every one genotype/ replication, and data were averaged.

RESULT AND DISCUSSION

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

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

Sr. No.	Name of genotypes	Source	S. No.	Name of genotypes	Source
1.	IPM 02-3M 02-	IIPR, Kanpur, U.P.	20.	Pusa M 1871871	IARI, New Delhi
2.	IPM 604-1	IIPR, Kanpur, U.P.	21.	Pusa M 1872	IARI, New Delhi
3.	Viratt	IIPR, Kanpur, U.P.	22.	OBGG 1011GG	OUAT, Bhubaneswa, Odisha
4.	Shikha	IIPR, Kanpur, U.P.	23.	OBGG 102	OUAT,Bhubaneswa, 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, M. H.
18.	VGG 17-009	NPRC,Vamban, T.N.	37.	AKM- 1604	PDKV , Akola, M.H.
19.	VGG 16-055	NPRC,Vamban, T.N.	38.	SKAU-M-365	Srinagar, J & K

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

Sr. 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%.

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

Sr. 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.

A broad range of variability in mungbean genotype was depicted (Table 2) by different characters 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%).

In this research, PCV values were moderately higher than that of GCV, indicates the influence of environment on the traits. But, smaller differences between phenotypic and genotypic coefficient variation values were notice for total the characters, as they are less effect by the environment indicating reliability of selection based on these traits. Genetic variability parameters approximate for different characters of mungbean are given in Table 2. The highest GCV and PCV in mungbean genotypes were observed for seed yield/ plant followed by pods/ plant, harvest Index, plant height, branches/ plant so that, recommend a good scope of enhancement, produce variability through hybridization followed by selection. Similar findings were reported by Makeen *et al.* (2007); Hemavathy *et al.* (2015); Pinchhyo *et al.* (2016); Pulagampalli and Lavanya (2017); Muthuswamy *et al.* (2019); Talukdar *et al.* (2020); Wesly *et al.* (2020); Gaur *et al*. (2021); Kumar (2022). The occurrence of moderate GCV and PCV was recorded for 100 seed weight which suggests that enhancement in these characters 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 additional valuable in a selection programme. 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 magnify 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); Kumar (2022).

The genetic advance as % of mean provides an intention of the amount of advance that can be achieve by selection for the perturbed characters. High genetic advance as % of 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 notice for days to 50% flowering (16.2) and seeds/ pod (9.2).

The high heritability values coupled with genetic advance would be better founded and useful in forecast 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 enhanceed through straight selection. Similar discovery 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); Gaur *et al.*(2021).

CONCLUSION

The highest value of GCV and PCV observed for pods/ plant indicated a greater phenotypic and genotypic variability among the genotypes which suggested that response to selection would be very high for these constituent which 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, high heritability in coincidence with high genetic advance as per cent mean specify the prevalence of additive gene action and selection may be effectual in next generations for these traits.

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 for other characters based on mean performance. Hence, these genotypes would be used as parental origin for subsequent breeding programmes.

FUTURE SCOPE

The assessment of genetic variability parameters like genotypic and phenotypic coefficient of variation, heritability and genetic advance are important for the effective selection as well as improvement of the breeding population. The genotypes namely; PM 1522, GM-6, IGKM 06-18-3, GM-4, SKAU-M 365, JLM707-5, SML 668 and Pusa M 1872 will helpful for developing high yielding varieties as well as future breeding programmes.

Conflict of Interest. None.

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