

Original Research Article

Genetic Variability, Heritability and Genetic Advance for Yield and its Related Traits in mungbean [*Vigna radiata* (L.) Wilczek] Genotypes

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ABSTRACT

The present study consists of 48 mungbean genotypes that were evaluated two years (2016 and 2017) to study genetic variability, heritability and genetic advance for yield and 13 yield associated traits. The analysis of variance revealed statistically significant differences ($p < 0.05$) indicating the existence of genetic variability among the 48 genotypes for all the traits studied. The genotypic coefficient of variations was the highest for characters viz., harvest index, number of effective branches/plant. The heritability was observed highest for seed yield per plant, days to maturity and days to 50% flowering. The higher estimates of heritability indicated that these characters were less affected by the environment and under the control of additive gene effect. High heritability and high genetic advance as percent of may be attributed due to additive gene action. Therefore, direct selection for characters viz., number of effective branches/plant, number of pods/cluster number of seeds/pod would be effective and therefore, considered to be of prime importance in formulating the selection programme. In both environments high estimates of variation were observed for number of effective branches/plant, seed index, seed yield/plant, biological yield/plant and harvest index, it indicates the existence of enormous inherent variability that remains unaltered by environmental conditions among the genotypes, which is more useful for exploitation in selection and hybridization programme. Consequently, based on the genetic parameter analysis days to 50% flowering, number of effective branches/plant, seed index, seed yield/plant, biological yield/plant and harvest index should be given significant precedence while formulating a selection strategy for effective improvement of mungbean varieties.

Keywords

Mungbean,
heritability,
genetic variability

Introduction

Greengram [*Vigna radiata* (L.) Wilczek] is one of the important grain legumes belongs to family Leguminosae and considered as a major pulse crop in Asia since ancient times. Genetically mungbean is self-pollinated diploid crop ($2n=2x=22$) and posses a relatively small genome (Ca. 560 Mb). Mungbean is a tropical grain legumes widely grown in the subtropical countries of

South and Southeast Asia. Mungbean cultivation spreads widely because of its superior digestibility in Africa, South America, Australia and in many Asian countries, and has been identified as high yielding pulse crop (Arshad *et al.*, 2009).

It is a rich source of proteins, vitamins and minerals. Plant parts and seeds being used as

animal feed. After harvesting of pods it also used as green manure. In addition, like other legumes it also improves the soil health by fixing the atmospheric nitrogen into the soil and increase the yield of subsequent crop (Biradar *et al.*, 2007 and Mehandi *et al.*, 2013). Despite its importance, the area, production and productivity of green gram is still low, which may due to lack of determinate and high yielding varieties. It warrants an urgent development of some high yielding varieties with determinate growth habit. Development of varieties with high yield, short duration with synchronous maturity may fit in rice-wheat cropping system and enhance the area of mungbean without reducing the area of other crop(s). To develop such desirable genotypes, recombination breeding and trait manipulation offer the potential alternatives which however require suitable parents for crossing programme. Assessment of existing genetic diversity especially in the primary gene pool remains the most crucial factor in success any crop improvement programme. Mungbean breeder needs to identify the cause of variability in seed yield and acquire information on the nature and magnitude of variation in the available materials in any given environment, since fluctuations in environment generally affects yield through its components. Knowledge of heritability and genetic advance of the characters is a pre-requisite for the improvement through selection (Titumeer *et al.*, 2014, Tiwari *et al.*, 2014). Lack of adequate variability has been implicated as one of the major bottleneck in improving the productivity of mungbean. The entire success of plant breeding programme of any crop basically depends on the wide range of genetic variability in respect of important economic characters present in the population. The genetic advance is the deviation in the characters of selected population over the base population. Gain under selection or

genetic advance is a measure to predict the expected progress under selection. The genetic advance helps to evaluate the selection procedures. If the value of genetic advance is more than in the succeeding generation there will be good progress over population mean. The estimation of heritability along with genetic advance is more applicable than the heritability value alone. Johnson *et al.*, (1955) reported that in study of estimated heritability in conjunction with genetic advance would provide more reliable information than the study of heritability alone. Keeping the above points under consideration the present experiment was undertaken to assess the genetic variability and isolate the suitable traits for genetic improvement programme through manipulation of genotypes.

Materials and Methods

The experimental material comprised of forty eight diverse genotypes of mungbean were sown in Randomized Block Design with three replications, during Kharif, 2016 and 2017 at Rajaula farm, M.G.C.G.V. Satna, Chitrakoot, Madhya Pradesh, India (Table 1).

Spacing between genotypes and between the plants of same genotype was maintained 10 cm and 30 cm respectively. The observations were recorded on 5 randomly selected plants from the plot of each replication on days to 50% flowering (DF), days to maturity (DM), plant height (PH), effective primary branches (EPB), cluster/plant (CP), -Number of pods/cluster (PC), Pod length (PL), Number of seeds/pod (SP), Seed index (SI), Seed yield/plant (SY), Biological yield/plant (BY) and Harvest index (HI). The plots were weeded manually to keep weed pressure low. Other recommended agronomic management practices were adopted for optimum crop

growth and development. The data were subjected to the analysis of variance (Panse and Sukhatme 1967) and further, biometrical procedures were followed to estimate genotypic and phenotypic coefficient of variation (Burton 1952), heritability in broad sense (Burton and Devane 1953), genetic advance (Johnson *et al.*, 1955) and correlation and path coefficient analysis (Singh and Chaudhry 1979).

Results and Discussion

Analysis of Variance (ANOVA)

The analysis of variance was revealed significant differences among mungbean genotypes for all traits studied ($P < 0.05$) (Table 2). The results showed that there is a presence of acceptable amount of variability among the genotypes. This gives an opportunity for mungbean breeders to improve those traits through selection and hybridization to improve the desired traits. Mehandi *et al.*, 2015 also reported similar result in 30 mungbean genotypes for all the traits they studied. Bisht *et al.*, 2014 and Ved *et al.*, 2007 reported significance differences among rice genotypes evaluated in different locations. Genotype \times location interactions were highly significant difference ($p < 0.01$). These significant difference of genotype \times location interactions implies that differential response of genotypes under the two locations for these traits. This indicates that the phenotypic expression of characters was different at the two locations.

Genotypic coefficient of variation and Phenotypic coefficient of variation

Estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) are indicated in Table 3. The genotypic coefficient of variation

(GCV) ranged from 5.14% for pod length to 30.87% for seed yield per plant and pod length 7.51% to harvest index 31.24% in both environments respectively. The genotypic coefficient of variations was the highest for characters *viz.*, Harvest index, Number of effective branches/plant. However, phenotypic coefficient of variation (PCV) ranged from 8.89% for days to maturity to 35.43 % for harvest index and 10.12% for days to maturity to 37.58 % for harvest index in both years respectively (Kant *et al.*, 2015).

Heritability and genetic advance

Heritability is an index of the transmission of characters from parents to their offspring. It is generally expressed in percentage. The estimation of heritability helps the plant breeder in selection of elite genotypes (Eswari *et al.*, 2006). Heritability in broad sense and genetic advances as percent mean are showed in Table 3. Heritability in broad sense estimates of the 12 quantitative traits ranged from 16.55% for pod length to 78.04% for seed yield per plant and 18.02% for pod per cluster to 80.61% for plant height in both years respectively. The heritability was observed highest for seed yield per plant followed by days to maturity, days to 50% flowering.

The higher estimates of heritability indicated that these characters were less affected by the environment and under the control of additive gene effect. High heritability and high genetic advance as percent of may be attributed due to additive gene action (Panse 1957). Therefore, direct selection for characters *viz.*, number of effective branches/plant, number of pods/cluster number of seeds/pod would be effective and therefore, considered to be of prime importance in formulating the selection programme (Lal and Singh 2014).

Table.1 List of 48 genotypes selected for the study

S. No.	Genotypes	Origin/Source	S. No.	Genotypes	Origin/Source
1	Samrat	IIPR, Kanpur	25	ML 818	PAU, Ludhiana
2	PDM 04-123	IIPR, Kanpur	26	ML 5	PAU, Ludhiana
3	PDM 281	IIPR, Kanpur	27	ML 512	PAU, Ludhiana
4	PDM 54	IIPR, Kanpur	28	ML 515	PAU, Ludhiana
5	PDM 262	IIPR, Kanpur	29	ML 682	PAU, Ludhiana
6	PDM 288	IIPR, Kanpur	30	ML 729	PAU, Ludhiana
7	PDM 178	IIPR, Kanpur	31	ML 935	PAU, Ludhiana
8	PDM 191	IIPR, Kanpur	32	ML 1059	PAU, Ludhiana
9	IPM 02-14	IIPR, Kanpur	33	ML 1256	PAU, Ludhiana
10	IPM 06-5	IIPR, Kanpur	34	ML 1257	PAU, Ludhiana
11	IPM 409-4	IIPR, Kanpur	35	AKM 99-4	PDKV, Akola
12	IPM 312-43K	IIPR, Kanpur	36	AKM 96-1	PDKV, Akola
13	Meha	IIPR, Kanpur	37	AKM 96-2	PDKV, Akola
14	IPM 2K-14-9	IIPR, Kanpur	38	EC 393410	Exotic collection
15	IPM 205-7	IIPR, Kanpur	39	PRATEEKSHA NEPAL	AVRDC, Taiwan
16	IPM 2-23	IIPR, Kanpur	40	EC 398894	Exotic collection
17	IPM 03-1	IIPR, Kanpur	41	Pusa Vishal	IARI, New Delhi
18	IPM 03-3	IIPR, Kanpur	42	IPM 312-394	IIPR, Kanpur
19	IPM 02-17	IIPR, Kanpur	43	Taram 1	BARC, Trombey
20	IPM 02-3-1	IIPR, Kanpur	44	Taram 18	BARC, Trombey
21	IPM 02-16	IIPR, Kanpur	45	TMB 37	BARC, Trombey
22	IPM 02-3	IIPR, Kanpur	46	TMB 96-2	BARC, Trombey
23	IPM 03-2	IIPR, Kanpur	47	RMG 991	RAU, Pusa
24	IPM 02-19	IIPR, Kanpur	48	MG 331	Gurdaspur, Panjab

Table.2 Analysis of variance for various traits in mungbean

Characters	Mean sum of squares (2016)			Mean sum of squares (2017)		
	Replications (df=2)	Treatments (df=47)	Error (df=94)	Replications (df=2)	Treatments (df=47)	Error (df=94)
DFP	51.67	96.06**	10.34	130.42	74.21**	10.18
DM	5.08	96.51**	12.72	47.51	129.1**	10.29
PH	115.29	169.38**	14.87	61.89	116.90**	8.67
EPB	0.37	1.32**	0.76	0.42	1.18**	0.45
CP	0.36	7.27**	1.48	1.48	6.22**	1.19
PC	0.13	1.03**	0.47	0.09	0.83**	0.50
PL	0.26	1.22**	0.76	0.08	0.10**	0.93
SP	5.76	3.83**	2.16	0.16	3.43**	1.52
SI	0.21	0.42**	0.20	0.02	0.70**	0.19
SY	6.51	20.45**	1.75	5.65	7.95**	1.98
BY	17.04	49.14**	18.65	11.92	21.41**	25.34
HI	80.13	262.87**	35.28	34.95	134.05**	58.28

**Significant at 1%. DFP-Days to 50% flowering, DM-Days to maturity, PH-Plant height (cm), EPB-Number of effective branches/plant, CP- cluster/plant, PC-Number of pods/cluster, PL-Pod length (cm), SP-Number of seeds/pod, SI-Seed index (g), SY-Seed yield/plant (g), BY-Biological yield/plant (g) and HI-Harvest index (%).

Table.3 Genetic parameters for 12 characters in mungbean

Characters	Mean		GCV		PCV		h ² (%) (b.s.)		GA % as mean	
	2016	2017	2016	2017	2016	2017	2016	2017	2016	2017
DFF	35.51	37.43	14.25	12.34	16.63	15.00	73.43	67.72	25.16	20.92
DM	71.71	69.79	7.37	9.02	8.89	10.12	68.70	79.38	12.58	16.55
PH	41.82	40.87	17.16	14.69	19.48	16.36	77.60	80.61	31.14	27.17
EPB	2.56	2.24	16.92	22.08	37.98	37.21	19.86	35.21	15.54	26.99
CP	6.66	6.18	20.86	19.64	27.74	26.11	56.52	56.56	32.30	30.43
PC	4.16	3.99	10.36	8.32	19.49	19.60	28.25	18.02	11.34	7.27
PL	7.57	7.38	5.14	7.51	12.64	13.10	16.55	19.33	4.31	0.36
SP	10.40	9.25	7.19	8.64	15.84	15.83	20.58	29.79	6.72	9.71
SI	3.77	3.79	7.20	10.06	13.99	15.39	26.48	42.68	7.63	13.53
SY	8.09	7.64	30.87	18.45	34.49	26.08	78.04	50.04	56.18	26.88
BY	27.87	26.95	11.44	17.22	19.26	31.32	35.27	30.24	14.00	19.51
HI	29.76	29.18	29.27	31.24	35.43	37.58	68.26	76.47	49.82	47.54

Table.4 Range, Mean, Standard error and Coefficient of variance for 12 characters in mungbean

Characters	Range		SEm ±		CV (%)	
	2016	2017	2016	2017	2016	2017
DFF	27.33-47.67	29.33-45.67	1.857	1.84	8.57	8.52
DM	55.33-79.67	54.33-77.33	2.059	1.85	4.97	4.60
PH	23.35-60.66	29.98-60.66	2.226	1.70	9.22	7.21
EPB	1.24-5.03	1.41-4.73	0.405	0.39	28.48	29.95
CP	3.65-11.48	4.73-11.60	0.751	0.63	19.43	17.64
PC	2.87-5.20	3.27-5.33	0.405	0.41	17.05	17.74
PL	6.35-9.88	5.62-8.55	0.51	0.56	11.67	13.08
SP	6.88-12.53	6.95-11.20	0.831	0.71	13.57	13.31
SI	2.03-4.67	2.17-4.57	0.272	0.26	12.53	11.68
SY	4.45-16.08	5.26-11.62	0.764	0.81	16.33	18.43
BY	18.05-35.98	18.75-32.73	2.562	2.91	15.96	18.67
HI	14.45-59.74	19.83-48.35	4.351	4.41	25.07	26.16

Moreover, genetic advance as percent of mean varied from 4.31% for pod length and 56.18% for seed yield per plant whereas in the second year genetic advance as percent of means ranged from 0.36% for pod length and 47.54% for harvest index. The presence of sufficient variability indicated that the materials of mungbean under study were good enough for further study.

Means and range

The range and mean of genotypes for all studied traits also indicated wide ranges of variation which also revealed possible amount of variability among the genotypes (Table 3). A wide range of variation was observed in the mungbean genotypes for all the quantitative characters and yield (Table

3). However, widest range of variability was recorded for harvest index (14.45-59.74) followed by biological yield (18.05-35.98), seed yield (4.45-16.08) etc. and similar result sown in next year (Mathivathana *et al.*, 2015, Rahim *et al.*, 2010). The range of variation obtained for number of effective primary branches (1.24 to 5.03) and seed index (2.03- 4.67 g) was least when compared to all the other characters. Therefore, the presence of such range of variations of the traits indicated that the existence of enough variability among the genotypes which is the source of variable genetic materials.

Coefficient of variation

The estimates of coefficient of variations were in general higher in second year environments than in first year environment.

In both environments high estimates of variation were observed for number of effective branches/plant. Seed index, seed yield/plant, Biological yield/plant and Harvest index, it indicates the existence of enormous inherent variability that remains unaltered by environmental conditions among the genotypes, which is more useful for exploitation in selection and hybridization programs (Rao *et al.*, 2006, Rohman *et al.*, 2003).

In conclusion, the present study identified the presence of adequate genetic variability among 348 tested genotypes. Hence, the information generated from this study, mungbean breeder can be exploited for future mungbean breeding program. The study was also carried out for two crop season. Therefore, it is advisable to repeat the study at least more than one season considering major mungbean growing areas to make sound recommendations. Moreover, it is recommended that future mungbean

research explore molecular means to further confirm the outcome of this study findings.

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