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Assessment of Genetic Variability, Heritability and Genetic Advance for Yield and its Component Traits in Green Gram [*Vigna Radiata* (L.) Wilczek] Genotypes

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Abstract

An investigation with thirty four genotypes of green gram (*Vigna radiata* L.) including 10 parents and their 24 hybrids obtained by line x tester mating design was carried out to assess the variability, heritability and genetic advance at research farm of BNV College Rath, Hamirpur (Uttar Pradesh) during zaid season of 2019. Observations were recorded for yield and its 12 component traits. Results revealed that seed yield per plant ranged from 3.82 to 5.70g per plant in parents while it was 5.47 to 8.30g per plant in hybrids. The component characters also showed considerable range between the genotypes. Genotypic and phenotypic variations were recorded highest for pods per plant (55.29 and 58.41 respectively) followed by days to maturity, harvest index, days to 50% flowering, biological yield per plant and seed yield per plant. Heritability in narrow sense was observed highest for pods per plant (89.18) while it was lowers for harvest index (27.24). Heritability in broad sense was recorded highest for seed yield per plant (99.34) and it was lowest for seeds per pod (82.32). Genetic advance as % of mean at 5% selection intensity was recorded maximum for pods per plant (62.27%) followed by seed yield per plant (59.48), biological yield per plant (48.84) and pods per cluster (42.19). Improvement in seed yield per plant might be achieved by hybridization between desired parents followed by recurrent selection for traits exhibiting, high heritability and high genetic advance as percent of mean.

Key words *: Green gram, variability, heritability, genetic advance.*

Introduction

Greengram [*Vigna radiata* (L.) Wilczek] being one of the significant pulse crops has a place to family Leguminoceae and considered as a significant pulsecrop in Asia since old times. Mungbean is a self-pollinated diploid (2n=2x=22) legume cropand broadly cultivated in the subtropical nations of South and Southeast Asia. Mungbean development spreads generally in light of its predominant preference in Africa, South America, Australia and in numerous Asian nations, and has been recognized as one of the high yielding pulse crop (1).

India is the major producer of greengram in the world and grown in almost all the states. It is grown in 4.31 m ha with the production of 2.07 mt and 481 Kg ha^{-1} productivity.

Green gram seed is a rich source of nutrients like proteins, vitamins and minerals. Its plant parts and seeds both are being used as animal feed. Being fast growing and luxurious, it is also used as green manuring crop. Moreover, as other pulses, it additionally improves the soil wellbeing by fixing the atmospheric nitrogen into the soil and results increment in the yield of subsequent crop (2,3). In spite of its significance, the area, production and yield of green gram is still low, which may because of absence of determinate and high yielding cultivars. It warrants an earnest improvement of some high yielding varieties with determinate development propensity. Advancement of cultivars with high yield, brief term with coordinated development may fit in soybean-wheat cropping framework and improve the area of mungbean without lessening the acreage of other crop(s). Trait manipulation through recombination breeding is an appropriate measure for development of desirable genotypes. However, it requires diversity in parents, hence, sufficient variability is a pre-requisite for such breeding programme. Information on heritability and hereditary development of the characters is a pre-imperative for the improvement through choice (4). The hereditary development is the alteration in the characters of chosen populace over the base population. Genetic advance is a measure to foresee the normal advancement under choice. The genetic advance assists with determining the proper breeding system. In the event that the estimation of genetic advance is more than in the succeeding generation, there will be acceptable advancement over population mean. The assessment of heritability along withgenetic advance is more appropriate than the measure of heritability alone. (5) reported “in study of estimated heritability in conjunction with genetic advance provided more reliable information than the

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study of heritability alone”. Considering the above mentioned points, the present experiment was undertaken to assess the genetic variability and isolate the suitable traits for genetic improvement of genotypes through manipulation of traits ingenotypes.

Materials and Methods

The experimental material comprised of thirty four genotypes of mungbean, including 10 parents and 24 hybrids prepared by mating in line x tester mating design (6 x 4), were sown in Randomized Block Design with three replications, duringzaid 2019 at Research Farm, Brahmanand PG College, Rath (Hamirpur, UP) India (Table-1). Spacing between genotypes and between the plants of same genotype was maintained 30 cm and 10 cm respectively.

The observations were recorded on five randomly selected plants from the plot of each replication on days to 50% flowering, days to maturity, plant height, effective primary branches per plant, cluster/plant, pods/cluster, pods per plant, biological yield per plant, seeds/pod, seed weight per pod, harvest index and seed yield/plant. The plots were weeded manually to keep weed pressure low. Other recommended agronomic management practices were adopted for optimum cropgrowth and development. The data were subjected to the analysis of variance (6) and further, biometrical procedures were followed to estimate genotypic and phenotypic coefficient of variation (7), heritability in broad and narrow sense (8), genetic advance (5).

Results and Discussion

Analysis of Variance (ANOVA) : The analysis of variance revealed significant differences among mungbean genotypes for all traits studied (Table-2). The results revealed the 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. (2) also reported similar result in 30 mungbean genotypes for all the traits they studied.

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-2). A wide range of variation was observed in the mungbean genotypes for all the attributing characters and yield per plant. The widest range of variability in parents was recorded for days to 50% flowering and days to maturity (32.33–49.33 and 61.33 to 78.33 respectively) fallowed by pods per plant (13.66–30.00), harvest index (30.81–40.51), plant height (42.90–52.40), biological yield per plant (9.30–46.40) etc. and similar result sown in next year (Rahim et al., 2010,). However, in hybrids the highest range was observed for pods per plant (18.00-41.00) followed by harvest index (38.29–55.57), days to 50% flowering, days to maturity and biological yield per plant. The lowest range was observed for seed weight per pod in both the generations i.e., parents and hybrids (0.36–0.55 and 0.35–0.50 respectively). The range of variation obtained for remaining characters was also observed low. Therefore, the presence of such range of variations of the traits indicated the existence of enough variability among the genotypes which is the source of variable genetic materials.

Genotypic and phenotypic coefficient of variation : Estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) are indicated in Table-3. Phenotypic coefficient variation was little greater than the genotypic coefficient of variation. The genotypic coefficient of variation (GCV) ranged from 0.002 % for seed weight per pod to 55.29 % for pods per plant while the phenotypic coefficient of variations ranged from 0.002 % for seed weight per pod to 58.41% for pods per plant. Both GCV and PCV were highest for pods per plant and lowest for seed weight per pod. The magnitude of GCV and PCV values were higher for pods per plant, days to 50% flowering, days to maturity, harvest index, biological yield per plant, plant height and seed yield per plant while for remaining traits these value were low. The values of PCV and GCV revealed very close correspondence which indicated insignificant influence of environment on most of the traits. The results are in agreement with (9,10).

Heritability and genetic advance : Heritability is an index of the inheritance of characters from parents to their offspring generally expressed in percentage. The estimation of heritability helps the plant breeder in selection of elite genotypes (11). Heritability in broad sense and narrow sense and genetic advances as percent mean are showed in Table-3. The estimates of heritability in broad sense of the 13 quantitative traits were higher than the heritability in narrow sense. The heritability in broad sense and narrow sense ranged from 82.32% for seeds per pod to 99.34% for seed yield per plant and 27.24% for harvest index to 89.18% pods per plant respectively. The heritability in broad sense was observed highest for seed yield per plant followed by days to maturity, days to 50% flowering while in narrow sense it was highest for pods per plant followed by seed weight per pod, clusters per plant, pods per cluster and days to maturity.Moreover, genetic advance as percent of mean at 5% selection intensity varied from 11.27% for seeds per pod to 62.27% for pods per plant. The highest genetic advance as percent of mean was recorded for pods per

Table-1 : List of 34 genotypes (10 parents and 24 hybrids) taken for the study.

S.No.	Parental genotypes	Source	S.No.	Hybrid genotypes	S.No.	Hybrid genotypes
1.	JM 721	JNKVV	1.	JM 721 x AKM 8802	13.	TARM 2 x AKM 8802
2.	BM 4	MAU	2.	JM721 x TJM 3	14.	TARM 2 x TJM 3
3.	PKVAKM 4	PDKV	3.	JM721 x PDM 1	15.	TARM 2 x PDM 1
4.	TARM 2	BARC & PKV	4.	JM721 x HUM 1	16.	TARM 2 x HUM 1
5.	ML 131	PAU Ludhiana	5.	BM 4 x AKM 8802	17.	ML131 x AKM 8802
6.	JM 10	JNKVV	6.	BM 4 x TJM 3	18.	ML131 x TJM 3
7.	AKM 8802	PKV	7.	BM 4 x PDM 1	19.	ML131 x PDM 1
8.	TJM3	BARC & JNKVV	8.	BM 4 x HUM 1	20.	ML131 x HUM 1
9.	PDM 1	IIPR	9.	PKVAKM 4 x AKM 8802	21.	JM 10 x AKM 8802
10.	HUM 1	BHU	10.	PKVAKM 4 x TJM 3	22.	JM 10 x TJM 3
			11.	PKVAKM 4 x PDM 1	23.	JM 10 x PDM 1
			12.	PKVAKM 4 x HUM 1	24.	JM 10 x HUM 1

Table-2 : Pooled ANOVA with Mean and range of Parents and F_1s for 13 characters in 6x4 Line x Tester cross in green gram.

Characters	Mean sum of squares			Mean			Range			
	Replication (df=2)	Treatment (df=33)	Error (df=66)	Parents	F_1s	Grand	Parents		F_1s	
							Min.	Max.	Min.	Max.
Days to 50% flowering	3.95	51.97**	0.254	42.57	41.74	41.98	32.33	49.33	33.66	48.33
Days to maturity	6.24	58.41**	0.22	72.46	68.16	69.43	61.33	78.33	62.33	74.66
Primary branches/plant	0.30	0.71**	0.01	2.94	3.95	3.40	2.36	3.50	2.86	4.36
Plant height (cm)	7.71	37.01**	0.61	48.00	51.88	50.74	42.90	52.40	45.66	55.66
Pods per cluster	0.53	2.47**	0.04	3.87	4.43	4.27	2.50	5.40	3.13	6.16
Clusters per plant	0.77	3.18**	0.05	3.96	5.28	4.89	2.56	5.86	4.20	7.06
Pods per plant	26.50	169.00**	3.12	18.50	26.19	23.93	13.66	30.00	18.00	41.00
Biological yield (g)	5.44	38.27**	0.07	11.40	16.50	15.00	9.30	16.40	12.53	23.33
Seeds per pod	1.53	1.21*	0.08	9.72	10.36	10.17	8.43	10.60	9.66	11.20
Seed weight per pod (g)	0.002	0.006**	0.000	0.39	0.41	0.40	0.36	0.55	0.35	0.50
100-Seed weight (g)	0.106	0.991**	0.006	4.80	4.59	4.65	3.43	6.63	3.83	5.24
Harvest index (%)	0.18	59.58**	1.57	38.54	43.71	42.19	30.81	40.51	38.29	55.57
Seed yield per plant (g)	1.08	10.26**	0.02	4.34	7.11	6.37	3.82	5.70	5.47	8.30

Table-3 : Coefficient of variation, heritability and genetic advance in 34 genotypes (including 10 parents and 24 hybrids).

Character	GCV	PCV	Heritability		GA	GA as % of mean at 5% SI
			NS	BS		
Days to 50% flowering	17.24	17.49	76.29	98.54	8.49	20.22
Days to maturity	19.39	19.62	77.37	98.85	9.02	12.99
Primary branches/plant	0.23	0.24	58.09	95.09	0.97	28.65
Plant height (cm)	12.13	12.75	41.62	95.16	7.00	13.79
Pods per cluster	0.80	0.85	76.58	94.61	1.80	42.19
Clusters per plant	1.04	1.10	76.76	94.67	2.04	41.82
Pods per plant	55.29	58.41	89.18	94.65	14.90	62.27
Biological yield (g)	12.73	12.80	55.38	99.39	7.32	48.84
Seeds per pod	0.37	0.45	52.15	82.32	1.14	11.27
Seed weight per pod (g)	0.002	0.002	87.64	96.66	0.09	23.03
100-Seed weight (g)	0.32	0.33	43.06	98.18	1.16	25.13
Harvest index (%)	19.33	20.91	27.24	92.46	8.70	20.64
Seed yield per plant (g)	3.41	3.43	52.17	99.34	3.79	59.48

plant followed by seed yield per plant, biological yield per plant, pods per cluster and clusters per plant. The presence of sufficient variability indicated that the materials of mungbean under study were good enough for further study.

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 mean may be attributed due to additive gene action (12). Therefore, direct selection for characters *viz.,* pods per plant, seed yield per plant, biological yield per plant, number of pods/cluster clusters per plant and branches per plant would be effective and therefore, considered to be of prime importance in formulating the selection programme. Similar findings were reported by (2,13).

Conclusions

The present study identified the presence of adequate genetic variability among the tested genotypes. Hence, the information generated from this study of green gram, the variability can be exploited for future mungbean breeding program. However, the study was carried out for one crop season. Therefore, it is advisable to repeat the study at least for more than one season considering major mungbean growing areas to make sound recommendations. Moreover, it is recommended that the future mungbean research should explore molecular means to further confirm the outcome of these findings.

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