

Study of genetic variability and correlation in mungbean

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SUMMARY

In order to access the genetic variability, seventy seven diverse genotypes of mungbean [*Vigna radiata* (L.) Wilczek] were evaluated for ten characters viz., days to 1st flowering, days to 50% flowering, days to maturity, plant height (cm), primary branches per plant, secondary branches per plant, seed per pod, pod per plant, seed yield per plant (g) and 100 seed weight (g). High heritability coupled with high expected genetic advance observed for 100 seed weight, pod per plant, secondary branches per plant, plant height and primary branches per plant revealed the preponderance of additive gene effects in the expression of these traits. Seed yield per plant exhibited positive and significant association with days to 50% flowering followed by days to maturity, secondary branches per plant and days to 1st flowering at genotypic and phenotypic levels. Based on these findings it is suggested that selection may be an effective tool for the genetic improvement in mungbean.

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Mungbean is the major pulse crop of India, yet limited success has been achieved so far in augmenting its yield. The information on the nature and magnitude of variation in the available gene pool and knowledge of association among different economic traits is important for any crop improvement programme. Heritability and genetic advance of yield and its components is prerequisite for the improvement through selection. Similarly studies on association of different traits help to identify the real components of yield and provide an effective basis for selection. Therefore, an attempt was made to gather information on extent of variability, heritability, genetic advance and interrelationship between seed yield and component traits in genotypes of mungbean.

MATERIALS AND METHODS

The experimental material for the present study was consisted of seventy seven diverse genotypes of mungbean procured from the germplasm stock maintained at the IIPR, Kanpur, were grown during the *Kharif* season of 2009 at Regional Research Station, Saini, Kaushambi of Chandra Shekhar Azad University of Agriculture and Technology, Kanpur. The material was planted in a Randomized Block Design with three replications. Each genotype was grown in three rows of 3 meter length with

row to row and plant to plant spacing of 30 and 10 cm, respectively. The observations on the ten characters were recorded on five randomly selected plants in each of the three replications/blocks for days to 1st flowering, days to 50% flowering, days to maturity, plant height (cm), primary branches per plant, secondary branches per plant, seed per pod, pod per plant, seed yield per plant (g) and 100 seed weight (g). The mean value of data were subjected to statistical analysis to obtain analysis of variance using Panse and Sukhatme (1985), genotypic and phenotypic coefficients of variation as suggested by Burton and Devance (1953), heritability in broad sense by Hanson *et al.* (1956) and expected genetic advance and correlation coefficient by Johnson *et al.* (1955).

RESULTS AND DISCUSSION

The existence of genetic variability present in the breeding programme is responsible for the effective selection. Larger is the variability, greater the scope of selection and improvement. The main objective of any breeding programme is to study the genetic variability in the material under study and utilization of suitable breeding procedure with the help of selection in the desired direction. The results revealed the presence of wide range of variability among the genotypes of mungbean. The estimates of mean, range, genotypic and phenotypic coefficients of variation, heritability and expected genetic advance to all the characters are presented in Table 1.

The treatment mean squares were significant for all

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Table1: Analysis of variance and estimates of genetic parameters for ten characters in mungbean

Traits	M.S.S.		Mean \pm S.E.	Range of variation	Coefficient of variation		Heritability (%)	Genetic advance (% of mean)
	Genotype	Error			GCV	PCV		
Days to 1 st flowering	46.48**	3.73	40.09 \pm 1.93	32 – 52	11.53	12.50	85.1	29.73
Days to 50% flowering	37.54**	6.36	46.31 \pm 2.52	37 – 58	8.53	10.12	71.0	19.26
Days to maturity	74.62**	11.56	66.36 \pm 3.40	54 – 75	8.46	9.89	73.2	19.54
Plant height (cm)	72.71**	6.23	33.01 \pm 2.49	23 – 49	17.46	19.03	84.2	44.66
Primary branches/plant	1.49**	0.47	4.01 \pm 0.68	2 – 6	17.86	24.74	52.1	32.11
Secondary branches/plant	11.20**	1.26	5.94 \pm 1.12	2 – 13	37.49	41.97	79.8	91.32
Seed per pod	2.68**	1.16	8.00 \pm 1.08	6 – 10	10.89	17.35	39.4	16.23
Pod per plant	98.55**	4.31	15.48 \pm 2.07	4 – 37	44.34	46.33	91.6	120.6
Seed yield per plant (g)	0.37**	0.07	3.12 \pm 0.26	2.31 – 4.40	12.49	15.18	67.8	26.85
100-seed weight (g)	5.51**	0.03	3.16 \pm 0.16	0.60 – 8.30	52.30	52.56	99.0	148.40

Table 2 : Genotypic (G) and Phenotypic (P) correlation coefficients among yield and component traits in mungbean

Characters		Days to 1 st flowering	Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches /plant	Secondary branches /plant	Seed per pod	Pod per plant	Seed yield per plant(g)	1000-seed weight(g)
Days to 1 st flowering	G	1.00	0.965**	0.819**	-0.187	0.015	-0.037	-0.156	-0.175	0.274*	-0.225*
	P		0.885**	0.766**	-0.091	0.095	0.021	-0.004	-0.144	0.273*	-0.191
Days to 50% flowering	G		1.000	0.928**	-0.197	-0.032	-0.044	-0.139	-0.237*	0.390**	-0.290**
	P			0.803**	-0.091	0.119	0.047	0.041	-0.153	0.398**	-0.226*
Days to maturity	G			1.000	-0.183	-0.034	0.020	-0.031	-0.219*	0.303**	-0.257*
	P				-0.045	0.052	0.072	0.089	-0.171	0.394**	-0.204
Plant height (cm)	G				1.000	-0.153	-0.158	0.048	-0.170	-0.003	-0.625**
	P					-0.137	-0.149	0.138	-0.162	-0.060	-0.581**
Primary branches/plant	G					1.000	0.665**	-0.299**	0.609**	0.070	0.512**
	P						0.442**	-0.094	0.420**	0.040	0.389**
Secondary branches/plant	G						1.000	-0.022	0.605**	0.320**	0.521**
	P							0.020	0.529**	0.249*	0.472**
Seed per pod	G							1.000	-0.060	0.106	-0.102
	P								-0.030	0.048	-0.047
Pod per plant	G								1.000	0.096	0.924**
	P									0.066	0.887**
Seed yield per plant(g)	G									1.000	0.068
	P										0.077
100-seed weight(g)	G										1.000
	P										

the characters studied, suggesting the presence of substantial variability for various characters studied in genotypes evaluated. Analysis of variance revealed that high variability was observed for the 100 seed weight (0.60 to 8.30 g) followed by pods per plant (4 to 37), days to 1st flowering (32 to 52), plant height (23 to 49 cm), secondary branches per plant (2 to 13), days to maturity (54 to 75), days to 50% flowering (37 to 58), seed yield per plant (2.31 to 4.40 g), primary branches per plant (2 to 6) and seeds per pod (6 to 10). Similar findings for

most of the traits have also been reported by Singh *et al.* (2009).

The relative contribution of genotype and environment could be judged by computing phenotypic and genotypic coefficient of variation. The high magnitude of PCV and GCV were recorded for 100 seed weight, pod per plant and secondary branches per plant. Further the estimates of PCV were higher than GCV for all the traits indicating that the environment influences the traits. High values of PCV and GCV for these traits have also

been reported by Yadav *et al.* (2001) and Singh *et al.* (2009).

Heritability is the measurement of transmission of an attribute from one generation to the other. An estimate of heritable fraction of variability is of paramount importance in any crop improvement programmes. The present study revealed that estimates of broad sense heritability (Table 1) were high (>50%) for all the traits studied except seed per pod. The results of present study on heritability aspect are strongly supported by the findings of Yadav *et al.* (2001) and Singh *et al.* (2009). The genetic advance as per cent of mean was highest for 100 seed weight followed by pod per plant, secondary branches per plant, plant height, primary branches per plant, days to 1st flowering, seed yield per plant, days to maturity, days to 50% flowering and seed per pod. A character having high heritability and high genetic advance generally indicates that heritability is more due to the additive gene effects and advocated the use of high estimate of heritability along with high magnitude of genetic advance for genetic improvement in any trait through selection as reported earlier by Yadav *et al.* (2001) and Singh *et al.* (2009).

The high heritability coupled with high genetic advance for particular character indicates its suitability of being selected for further improvement. High heritability and high expected genetic advance were recorded for 100 seed weight, pod per plant, secondary branches per plant, plant height and primary branches per plant indicating that these traits were governed by additive gene effects and selection would be effective for these traits as reported by Yadav *et al.* (2001).

Genotypic correlation coefficient was in general, observed to be higher than that of phenotypic correlation coefficient indicating the existence of strong inherent association for the various traits studied and phenotypic selection may be rewarded. Seed yield per plant exhibited positive and significant association with days to 50% flowering followed by days to maturity, secondary branches per plant and days to 1st flowering at genotypic and phenotypic levels (Table 2). Thus, it can be inferred that selection based on any one of these traits either alone or in combination, will result in identifying high yielding strains. Similar findings for most of the traits have also been reported by Ahuja and Chaudhary (1991), Joshi and Kabaria (1973), Natrajan and Palanisamy (1988), Singh *et al.* (1990) and Yadav *et al.* (2001).

When inter relationship of different characters was monitored it was observed that days to maturity exhibited positive and significant association with days to 1st flowering, days to maturity and seed yield per plant, which closely agreed with the observations of Natrajan and Palanisamy (1988), Singh *et al.* (1990) and Yadav *et al.* (2001). Further 100 seed weight was observed positive and significant association with primary branches per plant, secondary branches per plant, pod per plant and seed yield per plant. Negative and significant association of plant height with 100 seed weight was also supplements the findings of Singh *et al.* (1990), Yadav *et al.* (2001) and Singh *et al.* (2009).

The results of the present study suggest that sufficient genetic variability for most of the economics traits in the above genetic material and there is ample scope for genetic improvement through selection.

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