

Genetic Variability for some Quantitative Traits Related to Yield in Mungbean (*Vigna radiata* L. Wilezek)

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Abstract—Genotypic variability, heritability, genetic advance and genetic advance expressed as percentage of mean for yield and some of its attributing traits were studied in 30 genotypes of mungbean (*Vigna radiata* L. Wilezek) The observations taken from five randomly selected plants from each genotype with three replications were recorded for ten characters which indicated wide spectrum of variation among the genotypes studied. Analysis of variance further revealed considerable differences among the genotypes for all the characters studied. The genotypic and phenotypic variances were high for plant height (78.175 and 79.461), number of pods plant⁻¹ (14.990 and 16.217) and seed yield plant⁻¹ (4.288 and 4.427). Moderate to high heritability was observed for all the characters studied. High heritability combined with high genetic advance expressed as percentage of mean were observed for plant height, number of branches plant⁻¹, number of pods plant⁻¹ and 100 seed weight, indicating the influence of additive gene effects on these traits. The result of the study suggested sufficient genetic variability for most of the economic traits in the genetic material and there is ample scope for genetic improvement through selection.

1. INTRODUCTION.

Pulses are an important commodity group of crops that provide high quality protein complementing cereal proteins for pre-dominantly substantial vegetarian population of the country. Mungbean or greengram (*Vigna radiata* L. Wilezek) is one of the leading pulse or legume crop in India and an important legume crop of many Asian continent [1]. It is rich in protein can be cultivated as an inter-crop and also as mixed crop. They are mostly cultivated under rainfed conditions and do not require intensive irrigation facility. Apart from this, pulses like mungbean possess several other qualities such as they are rich in protein, improve soil fertility and physical structure, fit in mixed/inter-cropping system, crop rotations and dry farming and provide green pods for vegetable and nutritious fodder for cattle as well. In addition they are highly water efficient, can grow in drought prone areas and help improve soil fertility by fixing soil nitrogen [9, 21].

Mungbean is a highly self-pollinated crop with very narrow variability for yield and its component traits resulting

in limited scope for selection opportunity. However, efficiency of selection depends upon the existence and magnitude of genetic variability for yield and its contributing traits in the breeding material. Reports on significant variation among yield and its contributing traits in mungbean were observed earlier by various authors [3 - 4, 6, 8 - 9, 16, 18, 21]. For any yield improvement programme, selection of superior parents possessing better heritability and genetic advance for any quantitative trait is an essential pre-requisite. Heritability indicates the relative success of selection. Heritability in conjunction with genetic advance is more useful than heritability alone in prediction of resultant effect of selecting the best genotype [7]. Proper evaluation of the genetic variation available for yield components, their heritability values and genetic advance could be of great help to the breeders to provide the basis for effective selection [18]. Therefore, an attempt was made in the present study to estimate the extent of variability, heritability and genetic advance by utilizing 30 mungbean genotypes.

2. MATERIALS AND METHODS.

The experimental material for the present study comprised of 30 mungbean genotypes viz., TM-99-50, TM-99-21, WBM-220, SUBLOBATA-2, BASANTI, TARM-1, TARM-2, PDM-84-139 (Samrat), KOPERGAON, TM-99-37, TM-98-50, SUBLOBATA-14, HUM-12, B-1 (Sonali), PUSA VISHAL, PANT MUNG-2, WBM-611-2, WBM-659, K-851, WBM-4131, WBM-314, MALDA-95-13, MIDNAPUR LOCAL, WBM-04-05, PDM-54, WBM-6-34-1-1 (Bireswar), PDM-11, PDM-54 (Moti), PUSA BAISAKHI and PS-16 were grown during the *Kharif* season of 2012 at experimental fields of the Instructional Farm, Department of Plant Breeding, Bidhan Chandra Viswavidyalaya, Jaguli, Nadia, West Bengal. The material was planted in a randomized block design with three replications. Each genotype was grown in three rows of 2 meter length with row to row and plant to plant spacing of 30cm and 10cm respectively. All the recommended cultural

practices were followed up to harvest. Days to 50% flowering, days to maturity (90%), plant height (cm) and number of branches plant⁻¹ were recorded in the field. At maturity, data were collected for pod length (cm), pod width (cm), number of seeds pod⁻¹, 100 seed weight (g), number of pods plant⁻¹ and seed yield plant⁻¹ on five competitive plants randomly selected from each of the three replications. The mean value of data were subjected to statistical analysis to obtain analysis of variance [12], genotypic and phenotypic coefficients of variation [2], heritability in broad sense [5] and expected genetic advance [8].

3. 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 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 plant height (32.800 to 67.167) followed by number of pods plant⁻¹ (11.273 to 27.333), seed yield plant⁻¹ (2.560 to 12.617), days to maturity (75.333 to 81.000), days to 50% flowering (46.000 to 51.000), 100 seed weight (2.487 to 6.830), number of branches plant⁻¹ (2.397 to 6.577), number of seeds pod⁻¹ (9.367 to 12.693) and pod length (6.207 to 8.547). Similar findings for most of the traits have also been reported by [6, 17].

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 (>25%) were recorded for seed yield plant⁻¹ (29.722 and 29.254) and number of branches plant⁻¹ (28.132 and 25.871), moderate (10-25%) for number of pods plant⁻¹, 100 seed weight and plant height. Further, the estimates of PCV were higher than GCV for all the other traits studied indicating that the environment influencing those traits. High and moderate values of PCV and GCV for these traits have also been reported by others working on mungbean [19, 17, 15, 4, 8, 14]. Low (<10%) values of PCV and GCV were observed for number of seeds pod⁻¹, pod length, pod width, days to 50% flowering and days to maturity. Similar findings were earlier reported by other authors [14, 15]. Further the present findings showed that estimates of PCV were generally higher than their corresponding GCV for all the traits studied [13, 14].

Genetic coefficient of variation together with heritability estimates would give the best indication of the amount of gain due to selection [17]. Therefore, there could be better chance for improvement of the above traits with the relatively highest value of genotypic coefficient of variation.

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

Traits	M.S.S.		Mean ±S.E.	Range of variatio n	Variances			Coefficient of variatio n		Heritability (%)	Genetic adv ance (% of mean)	Genetic adv ance (% of mean)
	Genotype	Error			G V	P V	E V	G C V (%)	P C V (%)			
Days to 50% flowering	5.056**	0.658	48.422±0.662	46.000 - 51.000	1.466	2.124	0.658	2.500	3.010	69.01	3.020	4.279
Days to maturity	9.854**	0.658	77.922±0.660	75.333 - 81.000	3.067	3.720	0.653	2.248	2.475	82.45	6.319	4.204
Plant height (cm)	235.810**	1.287	48.420±0.926	32.800 - 67.167	78.175	79.461	1.287	18.260	18.410	98.38	61.038	37.311
Number of branches plant ⁻¹	2.830**	0.162	3.645±0.329	2.397 - 6.577	0.889	1.052	0.162	25.871	28.132	84.57	1.833	49.010
Pod length (cm)	0.790**	0.207	6.848±0.371	6.207 - 8.547	0.194	0.401	0.207	6.433	9.246	48.42	0.400	9.221

Pod width (cm)	0.003**	0.001	0.430±0.018	0.343-0.467	0.001	0.001	0.000	7.367	8.956	67.67	0.001	12.485
Number of seeds pod ⁻¹	3.190**	0.488	10.546±0.569	9.367-12.693	0.902	1.387	0.486	9.003	11.169	64.98	1.857	14.951
100 seed weight	2.195**	0.052	3.762±0.187	2.487-6.830	0.714	0.767	0.052	22.464	23.274	93.16	1.472	44.665
Number of pods plant ⁻¹	46.197*	1.227	17.584±0.904	11.273-27.333	14.990	16.217	1.227	22.018	22.901	92.44	30.881	43.608
Seed yield plant ⁻¹	13.0037**	0.138	7.079±0.304	2.560-12.617	4.288	4.427	0.138	29.254	29.722	96.88	8.835	59.315

** = Highly significant, M.S.S. = Mean Sum of Square, S.E. = Standard Error, GV= Genetic Variance, PV= Phenotypic Variance, EV= Environmental Variance, GCV= Genotypic Coefficient of Variation, PCV= Phenotypic Coefficient of Variation

(Table 1) were high (>50%) for all the traits studied except for pod length (48.42) [16, 18]. The genetic advance as per cent of mean was highest for seed yield plant⁻¹ followed by number of branches plant⁻¹, 100 seed weight, number of pods plant⁻¹, plant height, number of seeds pod⁻¹, pod width, pod length, days to 50% flowering and days to maturity. 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 [16].

The high heritability coupled with high genetic advance for particular character indicates suitability of being selected for further improvement. High heritability and high expected genetic advance were recorded for plant height (98.38 and 37.31), number of branches plant⁻¹ (84.57 and 49.01), number of pods plant⁻¹ (92.44 and 43.608), 100 seed weight (93.16 and 44.665) and seed yield plant⁻¹ (96.88 and 59.315) indicating that these traits were governed by additive gene effects and selection would be effective for these traits and can be easily transferred to succeeding generations [3, 9, 10, 16, 20]. While characters like days to 50% flowering (69.01 and 4.279), days to maturity (82.45 and 4.204), pod length (48.42 and 9.221),

pod width (67.67 and 12.485) and number of seeds pod⁻¹ (64.98 and 14.951) showed that high heritability is coupled with low genetic advance, so non-additive (dominant and epistasis) effects are more for these characters [10].

In order to explore the full potentiality of the varieties, varietal selection is an important task. Due to the presence of enough and wide genetic variation among the genotypes, there is a good scope of selection for improvement in quantitative characters.

The result of the present study suggests sufficient genetic variability for most of the economic traits in the studied mungbean genotypes and there is ample scope for genetic improvement through selection. Characters like plant height, number of branches plant⁻¹, number of pods plant⁻¹, 100 seed weight and seed yield plant⁻¹ will be effective for selection in mungbean improvement programme involving these genotypes.

4. REFERENCES

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