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Induced genetic variability and divergence in M_3 generation in mungbean

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ABSTRACT

Genetic variability and divergence for nine economically important metric traits in 140 variant lines in M_3 generation and base genotype (PDM 84-139) of mungbean were studied in the present study. Leaf area, plant height, number of pods/plant and grain yield/plant showed high heritability coupled with high genetic advance. Other characters showed medium heritability and low to medium genetic advance. On the basis of D^2 values, variants (mutants) could be grouped into eight clusters, indicating that induced mutations are effective in creating genetic divergence. Maximum number of variants was recorded in cluster I (26) and minimum in cluster IV (2). Cluster VIII having maximum intra- and inter-cluster divergence had high mean values for leaf area, number of primary branches/plant, plant height, number of pod clusters/plant, number of pods/plant, pod length, number of seeds/pod, test weight and grain yield/plant. On the contrary, cluster I had minimum mean values for all the characters under study. The parental genotype (PDM 84-139) was accommodated in cluster VIII. The other clusters had low to medium mean values of the characters. This fact indicates the distinctness of the eight clusters, as the cluster showing high mean values of the characters had high performing variants (*i.e.* cluster VIII-V70, V78, V129) and *vice-versa*.

Key words: D^2 analysis, Divergence, Genetic variability, Induced mutations, *Mungbean, Vigna radiata*

Genetic variability is essential for any crop improvement programme and its creation and management are central to plant breeding. Induced mutations play important role in crop improvement (4) and several popular mutant varieties have been developed in diverse crop plants including grain legumes. Although, heritability is a useful parameter for comparing and improving efficiency of selection methods, genetic advance has an added advantage over heritability. Mungbean (*Vigna radiata* (L.) Wilczek) is an important pulse crop of semi-arid tropics and sub-tropics. Factors like limited genetic variability, genome plasticity and self-pollination have yielded little success in augmenting yields through conventional breeding approaches. It necessitates generation of wide genetic variability through mutation breeding.

Sarma and Talukdar (12) have reported genetic divergence in irradiated populations in mungbean for different yield components. In the present study, an attempt was made to assess the quantum of genetic variation and to quantify the extent of genetic diversity in the derived M_3 mungbean mutants.

MATERIALS AND METHODS

The present study was carried out with mungbean variety PDM 84-139 obtained from I.I.P.R., Kanpur. Hundred seeds/dose were irradiated with 0, 5, 10, 20, 40 and 80 kR doses of γ-rays using the gamma chamber facility (Co^{60} as source) of N.B.R.I., Lucknow at the dose rate of 55 Sec/kR. The moisture content of seeds used for irradiation was 12.5+0.5% (w/W). The 100 irradiated seeds/dose of uniform size were sown within 24 hours of irradiation in the experimental plot at Department of Life sciences, CSJMU, Kanpur for raising M_1 generation in march 1999 and data were recorded on each plant.

Each plant of M_1 generation was studied for various traits along with 10 randomly chosen plants from the check in order to mark variants (mutants) plants. From each plant of M_1 generation, seeds were collected separately and seeds of marked 141 variants were sown in a randomized block design with four replications for raising M_2 progeny in March 2000. Seeds of each variant (mutants) collected in M_2 progeny were used to raise M_3 generations in March 2001 following the same layout and method and package of practices as were adopted during the M_2 generation. The data were recorded on nine metric traits (leaf area, number of primary branches/plant, plant height, number of pod clusters/plant, number of pods/plant, pod length, number of seeds/pod, test weight and grain yield/plant). Comparison of data for various metric traits in variants in M_1, M_2 and M_3 generations furnished maximum stability in M_3. Therefore, this data was used for estimation of the extent of variability and other genetic parameters. Heritability was estimated using the formula of Burton and De Vane (2) and genetic advance by the formula proposed by Robinson *et al.* (10). For working out the genetic divergence among 141 lines, the procedure suggested by Rao (9) was followed. The related statistics, such as intra- and inter-cluster divergences, formation of clusters on the basis of closeness in terms of divergence and performance of individual character across the clusters formed were also estimated.

RESULTS AND DISCUSSION

The analysis of variance revealed that variation among variants was significant for all the characters (Table 1). The estimates of various genetic parameters (Table 2) showed that very high magnitude of genotypic coefficient of variability was observed for grain yield/plant followed by number of

Table 1. Analysis of variance (MSS) for nine characters in mungbean in M_3 generation

Source of variation	d.f.	m.s.s.								
		Leaf area (cm^2)	Primary branches per plant	Plant height (cm)	Pod clusters per plant	Pods per plant	Pod length (cm)	Seeds per pod	Test weight (g)	Yield per plant (g)
Replication	3	0.57	1.85	0.073	0.77	50.86**	0.24	1.03	0.29	3.34**
Treatment	140	121.83**	4.96**	116.55**	2.51**	47.33**	1.09**	5.72**	0.76**	5.37**
Error	420	0.22	1.23	0.23	0.64	9.58	0.27	1.39	0.17	0.99

Table 2. Estimation of variability parameters for different characters in mungbean in M_3 generation

Parameter	Leaf area (cm^2)	No. of primary branches/ plant	Plant height (cm)	No. of pod clusters/ plant	No. of pods/ plant	Pod length (cm)	No. of seeds/ pod	Test weight (g)	Grain yield/ plant (g)
Genotypic coefficient of variation	34.65	24.85	20.43	21.63	38.03	8.33	15.24	10.49	49.25
Phenotypic coefficient of variation	34.78	37.88	20.51	33.24	53.98	12.46	23.04	15.33	68.19
Heritability	99.20	43.20	99.50	42.30	49.60	44.00	43.70	47.20	52.30
Genetic advance (as % of mean)	71.15	33.76	41.95	29.02	55.20	11.27	20.82	14.91	73.58

pods/plant and leaf area. Pod length and test weight had low genetic variability thus suggesting limited scope for altering the mean values of these characters through selection from the variant (mutant) populations. These two traits have been found to show high and positive association with the grain yield. The leaf area and plant height showed similar magnitude of genotypic and phenotypic coefficients of variability. High heritability was observed for leaf area, plant height and grain yield/plant whereas rest of the characters showed medium heritability. Previous studies (6, 7, 8, 11) also reported high heritability for leaf area, plant height and grain yield/plant in mungbean mutants and the same was found true in the present study.

High heritability coupled with high genotypic coefficient of variation was recorded for leaf area (99.2 and 34.65), plant height (99.50 and 20.43), number of pods/plant (49.6 and 38.03) and grain yield/plant (52.3 and 49.5). However, heritability estimates together with the estimates of genetic advance are more reliable in suggesting the selection method to improve a particular trait. In the present study, leaf area, plant height number of pods/plant and grain yield/plant showed high heritability coupled with high genetic advance indicating additive gene action governing these traits and the possible improvement even through simple selection. High heritability coupled with high genetic advance for number of pods/plant and grain yield/plant has been reported by Rosaiah *et al.* (11), Ignacimuthu and Babu (3) and Sahu and Patra (13). On the other hand, rest of the characters showed medium heritability and low to medium genetic advance. High heritability values for most of the characters in the present investigation indicate that heritable variations have been created through mutation breeding. The magnitude of heritable variability is the most important aspect of the genetic constitution to predict the breeding value of a trait and has a close relationship on its response to selection.

Genetic divergence is the measure of genetic distance among the variants (mutants) present in the population under study. A set of 141 variants lines (including check) of the present study was grouped into eight clusters based on divergence analysis. Cluster I had maximum lines (26) and cluster IV had minimum (2) lines. The divergence in mutants may be due to different genes being subjected to changes in different plants at the same time due to induced mutagenesis. Sarma and Talukdar (12) have reported similar genetic divergence in irradiated populations in mungbean using eight yield component traits. The wide variation in number of clusters may be due to the base population and effect of γ radiation on the traits used for divergence estimation. The clustering behaviour of the mutants indicated that mutations followed by advancement of generations are useful in obtaining genetically diverse mutants. The divergence within the cluster (intra-cluster) indicates the divergence among the lines falling in that particular cluster. On the other hand, the inter-cluster divergence suggests the distance (divergence) between the lines of different clusters. The intra- and inter-cluster distances are given in Table 3. The minimum and maximum values for intra-cluster distance were found with cluster V and VIII. In general, cluster VIII had maximum inter-cluster divergence from the other 7 clusters, most distant being

Table 3. Intra- and inter-cluster distance among 8 clusters of 141 variant lines of mungbean in M_3 generation

Cluster	I	II	III	IV	V	VI	VII	VIII
I	2.105	2.269	2.731	4.560	2.522	4.885	4.788	7.208
II		1.784	1.977	3.230	2.236	2.889	3.647	5.568
III			1.913	2.982	1.958	2.784	2.542	4.923
IV				1.908	3.821	2.669	3.478	3.691
V					1.586	3.492	3.150	5.864
VI						1.943	2.383	3.112
VII							1.831	3.278
VIII								2.486

Table 4. Number of 141 lines of mungbean belonging to different irradiation treatments among 8 clusters in M_3 progeny

Cluster	No. of lines	No. of lines belonging to treatments					
		0 (Control)	5 kR	10 kR	20 kR	40 kR	80 kR
I	26	-	6	2	5	7	6
II	25	-	5	4	1	14	1
III	24	-	2	3	8	8	3
IV	2	-	1	1	-	-	-
V	21	-	12	-	7	-	2
VI	17	-	2	8	7	-	-
VII	16	-	1	3	8	1	3
VIII	10	1	-	2	5	-	2

cluster I and closest being cluster VII. Different clusters were also analyzed for the number of lines contained therein, their origin and their behavior (Table 4). Cluster I, II and III had maximum lines from 40 kR, cluster IV had equal lines from 5 kR and 10 KR, respectively, cluster V from 5 kR, VI from 10 kR, VII from 20 kR and VIII from 20 kR. The comparison of various clusters for the origin of the lines comprised therein indicates that the variation arose randomly in all directions for each trait by different radiation treatments.

The mean values for different characters were compared across clusters (Table 5). It was observed that the cluster VIII having maximum intra- and inter-cluster divergence had high mean values for leaf area, number of primary branches/plant, plant height, number of pod clusters/plant, number of pods/plant, pod length, number of seeds/pod, test weight and grain yield/plant. On the contrary, cluster I furnished minimum mean values for all the characters under study. The other clusters had low to medium mean values for the characters. This fact indicates the distinctness of the eight clusters, as the clusters showing high mean values of the characters had high performing variants and *vice-versa*. Estimation of genetic divergence among the mutants has immense bearing on identifying potential crosses, which produce broad spectrum of variability with transgressive segregants.

Table 5. Cluster-wise mean values of 9 characters of 141 lines of mungbean in M_3 generation

Character	I	II	III	IV	V	VI	VII	VIII
Leaf area (cm^2)	11.82	19.27	11.83	17.39	15.80	22.80	12.32	18.27
No. of primary branches/plant	2.90	3.72	4.17	3.65	2.86	4.88	4.64	5.81
Plant height (cm)	20.85	27.16	25.49	26.83	23.25	31.55	30.80	34.62
No. of pod clusters/plant	2.48	2.95	3.01	3.95	2.55	3.75	3.53	4.94
No. of pods/plant	4.72	6.58	7.70	12.73	5.88	9.75	9.55	15.22
Pod length (cm)	4.96	5.23	5.50	5.23	5.72	5.69	6.09	6.04
No. of seeds/pod	5.86	5.91	6.61	6.00	7.60	7.23	8.44	8.03
Test weight (g)	3.30	3.49	3.91	4.13	3.72	3.96	3.72	3.86
Grain yield/plant (g)	0.92	1.39	1.98	3.14	1.66	2.78	2.99	4.84

The present results confirmed not only to the random, polydirectional, quantitative nature of induced mutations but also put a note of caution to recommendation of Khan (6) who suggested possibility of selection of superior mutants in M_1 and M_2 generations. The present findings suggest that selection in mutant populations should be carried from M_3 or late generations when the population subjected to study has attained stability. Differences in expression of variability in different generations for the same trait in mutants have also been reported by Borojevic and Borojevic (1) in wheat and Khan (5) in mungbean. The above study suggests that efficient use of induced genetic variability in genetic improvement through selection would be possible when the generation in which maximum variability and optimum stability is likely to be released, is known.

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