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MMS and SA induced genetic variability for quantitative traits in mungbean

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ABSTRACT

An experiment was conducted to evaluate the extent of genetic variability in three quantitative traits *viz.*, plant height and days to flowering and maturity in M_2 and M_3 generations following mutagenesis with methylmethane sulphonate (MMS) and sodium azide (SA) in mungbean (*Vigna radiata* (L.) Wilczek) var. T 44. Higher genetic variability for various quantitative traits was recorded in M_2 in comparison to M_3 generation, indicating that potential gain could be achieved through selection in early generation.

Key words: Chemical mutagens, Mungbean, Quantitative traits, *Vigna radiata*

Mutation breeding offers scope for achieving in many instances what cannot be accomplished through backcrossing and selection. The advantage of mutation breeding is that it can be applied for changing specific characters in otherwise good varieties by incorporating some useful variations in comparatively shorter period of time than the conventional breeding methods. So the induced mutations supplement plant breeding and confer specific improvements on a variety without significantly altering its otherwise acceptable phenotype. Since the induction of mutations has been accepted as a useful tool in plant breeding programme, a systematic study of induced mutagenesis creating variability for quantitative traits appears to be very essential in a crop like mungbean.

MATERIALS AND METHODS

A field experiment was conducted during the summer season of 2002, 2003 and 2004 at the Agriculture Farm, Aligarh Muslim University, Aligarh. Uniform and healthy seeds of mungbean (*Vigna radiata* (L.) Wilczek) var. T 44 were presoaked in distilled water for 9 hours prior to treatment with mutagenic solution. Two concentrations (0.01% and 0.02%) of MMS and SA were prepared in phosphate buffer of pH 7 for MMS and pH 3 for SA. Control was maintained by soaking seeds in distilled water only. After completion of treatment period for 6 hours, seeds were thoroughly washed in running tap water to reduce the residual effect of the mutagens sticking to the seed coat. Three replications of 100 seeds each were sown for every treatment in the field in a complete randomized block design (CRBD) to raise M_1 generation. Twenty healthy seeds from each normal looking M_1 plant of all different treatments and control were sown in plant progeny rows in M_2 generation. Different treatments and control comprised 30 progenies. The distances between plants in a row and between rows were kept at 30 and 60 cm, respectively. The 10 M_2 progenies were used to raise M_3 generation. Seeds from each selected M_2 progeny were sown in plant progeny rows. Data collected for three quantitative characters *viz.*, plant height, days to flowering and days to maturity were subjected to statistical analysis according to the method suggested by Singh and Chaudhary (9).

RESULTS AND DISCUSSION

The mutagenic treatments cause reduction in various parameters like seed germination, seedling height and pollen fertility, which, in turn, can be used as indices to test the mutagenic sensitivity of an organism. In this study, it was noticed that both the mutagens (MMS and SA) brought about dose dependent reduction in all the three biological parameters under study (Table 1). Inhibition in seed germination and seedling height was recorded maximum with SA treatments whereas the maximum reduction in pollen fertility was noticed in MMS treatments. The reduction in seed germination, seedling height and pollen fertility might be due to gross injury caused at cellular level either due to genes controlling biochemical processes or acute chromosomal aberrations or both (2, 3, 6, 8).

Table 1. Effect of chemical mutagens on seed germination, pollen fertility and seedling height of mungbean var. T 44 in M_1 generation

Treatment	Germination		Seedling height		Pollen fertility	
	%	Inhibition (%)	Mean (cm)	Injury (%)	%	Reduction %
Control	96.50	-	10.27±0.10	-	97.00	-
0.01% MMS	88.89	7.88	9.21±0.08	10.32	84.86	12.51
0.02% MMS	82.50	14.50	8.97±0.08	12.66	82.25	15.20
0.01% SA	75.80	21.45	7.91±0.09	22.98	90.15	7.06
0.02% SA	70.21	27.24	6.55±0.08	36.22	90.10	7.11

The data recorded on plant height, days to flowering and days to maturity in M_2 and M_3 generations are presented in Table 2. The treatments of SA gave the maximum reduction in plant height in both the generations. The extent of reduction in growth is related to the mechanisms of action of a given mutagen. As a respiratory inhibitor, azide may inhibit an energy system resulting in the inhibition of mitosis which can be associated with seedling growth depression. Ismail *et al.* (4) in *Vicia faba*, Singh *et al.* (10) in *Vigna mungo* and Khan *et al.* (7) in *Lens culinaris* reported an increase in plant height after mutagen treatment. The MMS treatments seem to be more effective in reducing the flowering as well as maturity period

Table 2. Estimates of mean values ($\bar{X}$) and genetic parameters for various quantitative traits in M_2 and M_3 generations in mungbean

Treatment	M_2					M_3				
	Mean±SE	Shift in $\bar{X}$	$\delta^2 g$	h^2	Gs	Mean±SE	Shift in $\bar{X}$	$\delta^2 g$	h^2	Gs
Plant height (cm)										
Control	47.05±0.62	-	3.70	0.33	2.90	46.40±1.28	-	1.26	0.17	2.73
0.01% MMS	47.00±1.23	-0.05	11.32	0.73	7.55	45.67±0.46	-0.73	6.29	0.23	3.12
0.02% MMS	44.90±0.57	-2.15	4.16	0.31	2.95	45.20±0.39	-1.20	2.78	0.18	1.82
0.01% SA	43.27±0.33	-3.78	8.08	0.74	6.44	44.47±0.57	-1.93	3.69	0.25	2.50
0.02% SA	42.43±0.41	-4.62	3.58	0.22	8.76	43.93±0.43	-2.47	3.01	0.12	3.25
CD (p=0.05)		2.38					4.24			
Days to flowering										
Control	47.57±0.32	-	2.09	0.32	2.15	46.43±0.37	-	0.60	0.15	0.78
0.01% MMS	48.73±1.07	+1.16	13.01	0.34	3.73	48.20±1.02	+1.77	2.31	0.74	3.44
0.02% MMS	44.30±0.39	-3.27	14.10	0.37	10.21	43.54±0.70	-2.89	1.76	0.20	1.55
0.01% SA	47.00±0.44	-0.57	2.46	0.32	3.11	48.60±0.30	+2.17	0.85	0.13	0.87
0.02% SA	44.85±0.38	-2.72	1.72	0.35	2.04	44.43±0.34	-2.00	0.71	0.15	0.83
CD (p=0.05)		2.09					3.09			
Days to maturity										
Control	64.40±0.36	-	7.31	0.52	5.11	65.03±0.52	-	2.02	0.27	1.93
0.01% MMS	65.27±0.49	+0.87	10.22	0.56	9.34	63.77±0.45	-1.26	10.00	0.30	4.72
0.02% MMS	59.87±0.31	-4.53	12.16	0.81	8.28	62.07±0.42	-2.96	7.06	0.29	3.74
0.01% SA	64.20±0.39	-0.20	6.38	0.58	5.05	63.47±0.44	-1.56	7.00	0.27	3.88
0.02% SA	61.40±0.44	-3.00	7.99	0.54	5.48	62.97±0.53	-2.06	7.83	0.26	4.29
CD (p=0.05)		1.39					1.41			

$\delta^2 g$ = Genotypic variation; h^2 = Heritability; Gs = Genetic advance

in both the generations. Flowering was early by three days with 0.02% of MMS treatment in M_2 generation. The data obtained on days to maturity resulted in a significant gain in reducing the maturity period by approximately four days with 0.02% MMS treatment in M_2 generation. The mean of days to maturity was 59.87 in 0.02% MMS treatment, whereas it was 64.40 in control. Kaul (5) reported that the mutation of two dominant genes to their recessive forms led to early flowering in peas.

Improvement of cultivated plants largely depends on the extent of genetic variability available within the species. Since most of the economically important characters are influenced by environment, estimates of genetic parameters like genotypic variation, heritability and genetic advance help to formulate suitable breeding procedures and to foresee the possibilities upto which a particular trait could be improved. The study of genetic parameters, such as genotypic variation ($\delta^2 g$), heritability (h^2) and genetic advance (Gs), revealed that various mutagenic treatments used in the present study had induced a higher genetic variability for various polygenic traits and the degree of increase differed with the mutagenic treatment and the character under study. In general, MMS treatments induced the maximum genetic variability in comparison to SA treatments. The genetic variability was higher in M_2 than M_3 generation. Differences in the expression of variability in different generations have been reported by Borojevic and Borojevic (1) in *Triticum aestivum*. Efficient use of induced variability in breeding through selection would be possible when the generation in which maximum variability is likely to be released. All the three characters in the present study showed higher genetic variability in M_2 than M_3 generation, indicating that effective selection can be made in M_2 itself.

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