Induced Mutations for Yield Contributing Traits in Green Gram

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ABSTRACT

In the present investigation, variability induced by ethylmethane sulphonate (EMS) for four quantitative traits viz., fertile branches/plant, pods/plant, 100-seed weight (g) and yield/plant (g) was studied in M_2 and M_3 generations of green gram (*Vigna radiata* L. Wilczek) var. Asha. A significant shift in mean values in the positive direction was observed for all the quantitative traits studied. High values of heritability and genetic advance over the control indicate the possibility of inducing desirable mutations for polygenic traits accompanied with effective selection in M_2 and later generations. Yield/plant was positively correlated with various yield contributing traits, but did not show any association with seed protein content.

Key Words: Green gram; EMS; Quantitative traits; Correlations; Protein content

INTRODUCTION

Variability in base population becomes essential when breeding objectives are more complex. Main interests of a plant breeder are quantitative traits, which are controlled by polygenic interactions. A series of experiments carried out with various crops have established that chemical mutagens induce polygenic variability (Kharkwal, 1999; Rajput *et al*., 2001; Singh & Singh, 2001; Khan *et al.*, 2004). Since green gram is a self-pollinating crop, limited variability is available for its improvement programmes. Induced mutagenesis thus seems to be an ideal methodology for the induction of desirable genetic variability.

The present study was undertaken to evaluate the extent of genetic variability in M_2 and M_3 generations for the four quantitative traits of green gram var. Asha following mutagenesis with ethylmethane sulphonate (EMS). An attempt was also made to find out the association between yield and yield components.

MATERIALS AND METHODS

A field experiment was conducted during kharif season of 2000/01, 2001/02 and 2002/03 at the Agricultural Farm, Aligarh Muslim University, Aligarh, India. Uniform and healthy seeds of green gram (*Vigna radiata* L. Wilczek) var. Asha were presoaked in distilled water for 9 h followed by the treatment with EMS (0.1 – 0.3%), prepared in phosphate buffer of pH 7 for 6 h. Seeds soaked in distilled water were used as control. After completion of treatment period for 6 h, the treated seeds were washed thoroughly in running tap water to reduce the residual effect of the mutagen sticking to the seed coat. The treated and control seeds were sown in the field in complete randomized block design (CRBD). Seeds harvested from individual M_1 plants were sown as M_2 families in three replications in the field. For raising M_3 generation, such 10 M_2 progenies were selected, which showed significant deviations in mean values in the positive direction from the mean values of control, particularly for the yield and yield components in M_2 generation. Seeds from each selected M_2 progeny were bulked by taking an equal amount of seeds from all M_2 plants from a single M_2 progeny and thoroughly mixed. A random sample of this bulk was sown to obtain M_3 progeny.

ANOVA was performed to test the significance of variance. Heritability (h^2) in broad-sense and phenotypic correlation among various character pairs were calculated by the formulae suggested by Singh and Chaudhary (1985) and Khan and Khanum (1994), respectively and the genetic advance by the method outlined by Johnson *et al.* (1955). The protein content of seeds was determined by the method of Lowry *et al.* (1951).

RESULTS AND DISCUSSION

The data recorded for various quantitative traits in green gram are presented in Tables I and II. It is clear from the tables that the mean values increased significantly for all the yield contributing traits under study. Higher values of mean for number of fertile branches, number of pods/plant and total plant yield were recorded with 0.2% EMS treatment in both M_2 and M_3 generations. It has been observed that during mutagenesis, if mutations occur at random for the quantitative traits, no significant change is expected in the mean values. However, the shift in mean values in the positive direction indicates that more positive mutations have occurred for these traits. Plant yield was found to be associated with the increase in the number of fertile branches, pods, and 100-seed weight. A high degree of correlation between number of pods/plant and number of fertile branches was reported earlier by Khan and Siddiqui (1997) in mungbean and Kharkwal (2003) in chickpea. The values for genotypic variability, heritability and genetic advance also showed an increase over control in most of the

Table I. Estimates of mean values and genetic parameters for different yield contributing traits in M_2 generation of green gram var. Asha

Treatment	Mean±S.E.	Shift in $\overline{X}$	GCV (%)	h^2(%)	GA(% of $\overline{X}$)
		Fertile branches / plant			
Control	6.77±0.18	-	7.30	20.35	6.95
0.1% EMS	7.34±0.21	+0.57*	10.81	25.90	13.89
0.2 % EMS	7.83±0.27	+1.06*	18.67	54.08	36.25
0.3% EMS	7.10±0.25	+0.33*	11.80	25.00	11.43
		Pods / plant			
Control	47.97±1.60	-	1.38	15.06	1.53
0. 1% EMS	49.61±0.25	+1.64*	11.10	60.55	16.15
0. 2% EMS	51.70±0.26	+3.73*	3.40	69.10	22.50
0.3% EMS	48.33±0.25	+0.36*	7.50	66.85	7.62
		100 seed-weight (g)			
Control	4.10±0.06	-	3.40	14.30	2.40
0.1% EMS	4.55±0.03	+0.45*	7.10	33.36	10.55
0.2% EMS	4.20±0.05	+0.10	6.15	42.75	10.38
0.3% EMS	4.29±0.06	+0.19	5.21	21.75	5.85
		Yield / plant (g)			
Control	8.60±0.19	-	4.36	44.80	4.80
0.1% EMS	9.02±0.21	+0.42*	7.35	60.00	14.75
0.2% EMS	9.50±0.23	+0.90*	17.41	48.70	32.07
0.3% EMS	8.87±0.19	+0.27*	9.10	45.98	16.20

* = Significant at p = 0.05; GCV = Genotypic coefficient of variation; h^2 = Heritability, GA = Genetic advance.

Table II. Estimates of mean values and genetic parameters for different yield contributing traits of the mutants isolated in M_3 generation of green gram var. Asha

Treatment	Mean±S.E.	Shift in $\overline{X}$	GCV (%)	h^2(%)	GA(% of $\overline{X}$)
		Fertile branches / plant			
Control	6.80±0.17	-	6.06	17.53	6.66
0.1% EMS	7.56±0.21	+0.76*	20.49	72.07	45.76
0.2 % EMS	7.96±0.22	+1.16*	21.86	76.71	50.36
0.3% EMS	7.44±0.19	+0.64*	17.01	66.11	36.30
		Pods / plant			
Control	47.94±0.15	-	2.56	14.24	2.50
0. 1% EMS	52.13±0.73	+4.19*	12.46	84.55	30.25
0. 2% EMS	53.23±0.72	+5.29*	11.86	83.14	28.48
0.3% EMS	47.73±0.57	-0.21	8.15	68.14	17.71
		100 seed-weight (g)			
Control	4.03±0.10	-	5.54	14.28	5.41
0.1% EMS	4.84±0.17	+0.81*	7.73	14.89	7.83
0.2% EMS	4.73±0.15	+0.70*	8.72	19.10	9.93
0.3% EMS	3.90±0.13	-0.13	9.59	22.58	11.88
		Yield / plant (g)			
Control	8.53±0.02	-	6.93	44.87	12.20
0.1% EMS	9.13±0.15	+0.60*	12.59	73.74	28.47
0.2% EMS	9.86±0.33	+1.33*	21.49	63.59	45.03
0.3% EMS	8.63±0.24	+0.10	17.30	60.92	35.58

* = Significant at p = 0.05; GCV = Genotypic coefficient of variation; h^2 = Heritability, GA = Genetic advance.

treatments. The high heritability estimates in the quantitative characters have been found to be useful for selecting suitable types based on their phenotypic performance. The data, in general, indicate a relatively higher estimated heritability (broad-sense) for various quantitative traits in M_3 generation. The increased heritability values in M_3, in comparison to M_2 generation, may be due an increased homozygosity of the genes involved. Johnson *et al.* (1955) advocated that heritability estimates along with genetic advance is usually more helpful than the heritability value alone in predicting the resultant effects of selection. Genetic advance is indicative of the expected genetic progress for a particular trait under suitable selection procedure (Kaul & Garg, 1982) and consequently carries much significance in self-pollinated crops. The results are in conformity with other reports (Khan *et al.*, 2001; Singh *et al.*, 2001; Raut *et al.*, 2004). In the present study, the higher values of heritability and genetic advance suggest that the variability so evolved can be effectively exploited for further genetic improvement of green gram.

Table III. Phenotypic correlation between various character pairs of the mutants isolated in M$_3$ generation of green gram

Treatment	Fertile branches/plant vs. pods/plant	Fertile branches/plant vs. yield/plant	Pods/plant vs. yield/plant	100-seed weight vs. yield/plant
Control	+ 0.022	+ 0.161	+ 0.330	- 0.301
0.1% EMS	+ 0.482**	+ 0.326	+ 0.449*	- 0.205
0.2% EMS	+ 0.522**	+0.487**	+ 0.292	- 0.550
0.3% EMS	+ 0.045	+ 0.186	+ 0.392*	- 0.102

*,**Significant at 5% and 1% levels of probability, respectively.

Table IV. Total seed protein content (%) of the mutants isolated in M$_3$ generation of green gram

Treatment	Seed protein content (%)				Yield/plant vs. Seed protein content (r)
	Mean ±S.E.	Shift in $\overline{X}$	Range	CV (%)	
Control	21.38±0.33	-	20.10-22.10	3.50	- 0.183
0.1% EMS	22.92±0.85	+ 1.54	19.80-24.85	8.28	- 0.723
0.2% EMS	23.18±0.97	+ 1.80	19.55-24.95	9.40	- 0.059
0.3% EMS	23.02±0.74	+ 1.64	20.08-23.40	7.17	- 0.674

CV = Coefficient of variation; r = Correlation coefficient

Correlation coefficients among four characters under study were estimated at phenotypic level (Table III). In all the mutagenic concentrations, the correlations were found to be higher than the control. Yield/plant was found to have significant positive correlation with number of pods/plant and fertile branches/plant. These findings are in conformity with those reported by Vijayalakshmi *et al.* (2000) in chickpea. 100-seed weight was not correlated with yield per plant in the present study. However, Amaranath *et al.* (1990) and Singh and Singh (1999) reported positive correlation of 100-seed weight with total plant yield in soybean.

Seed protein content of the mutants did not alter significantly in any of the EMS treatments studied (Table IV). However, the coefficient of variation was higher in mutagenic treatments as compared to control, indicating that improvement in seed protein content is possible. Seed protein did not show any association with yield/plant, indicating the independent genetic control of protein content and total plant yield. Sandhu *et al.* (1979) suggested that the lack of association between grain yield and grain protein can be easily combined in a single genotype.

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