GENETIC AMELIORATION FOR EARLINESS AND HIGH TEST WEIGHT THROUGH INDUCED CHEMICAL MUTAGENESIS IN RESTORER LINES OF SUNFLOWER

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Abstract

Two restorer lines of sunflower, viz., RHA 265 (nonbranching) and 6D-1 (branching) were treated with ethyl methane sulphonate (EMS) at 0.5% and 1.0% concentrations to induce variability for days to flowering and test weight. In general a wide range of variability in the M3 generation was observed for flowering and test weight in both the genotypes. Favorable mutant lines for the traits were recovered at 0.5% concentration in comparison with 1.0% concentration. Pedigree selection enabled isolation of early flowering and high test weight mutant genetic stock in both the restorer lines. In the RHA 265 mutant population, high estimates of heritability were accompanied by low genetic advance for flowering in contrast to test weight which was accompanied by high genetic advance. In 6D-1, a low to medium heritability estimate was observed for the traits studied.

Introduction

Mutation breeding in supplement to conventional breeding methods is helpful to widen genetic variability in the population for effective selection of desired traits (Brock, 1971). Earlier studies on induced mutagenesis in sunflower have been found to be effective in generating variability for quantitative traits (Giriraj et al., 1990; Encheva et al., 1993; Deshpande and Giriraj, 1997). In the present study ethyl methane sulphonate (EMS) was used to induce variability for days to flowering and test weight in two restorer lines of sunflower.

Materials and Methods

RHA 265, a nonbranching, downy mildew resistant and late-flowering restorer line is widely used in heterosis breeding. 6D-1 with branching habit, low test weight and late flowering is a pollen parent of the popularly cultivated KBSH-1 hybrid. A total of 100 presoaked seeds of these two R-lines were treated with 0.5% and 1.0% of EMS for 8 hours at

room temperature with intermittent shaking. The M1 generation consisted of all the treated and untreated seeds, which served as a control. The seeds collected from each selfed M1 plant were planted in unreplicated progeny rows to produce the M2 generation. None of the 6D-1 plants survived at 1.0% EMS concentration until flowering. The M3 generation was raised during the summer season of 2002 from selfed seeds of M2 progenies (single plant basis) along with corresponding control. A total of 400 and 350 individual progeny lines of RHA 265 and 6D-1 respectively were advanced to the M3 generation. Data was recorded on a population basis in each treatment for days to flowering and test weight. Genetic parameters were computed following the procedures outlined by Falconer (1986), Hanson et al. (1956) and Burton and de Vane (1953).

Results and Discussion

The range, mean and variance in the M3 generation for days to flowering and test weight are presented in Table 1.

Table 1. Mean, range and variance for days to flowering and test weight in the M3 generation of two restorer lines of sunflower.

Genotype/ Treatment	Days to flowering			Test weight (g)		
	Mean	range	Variance	Mean	range	Variance
RHA 265						
Control	66.7	62-69	4.49	7.6	6.0-9.0	0.59
0.5 % EMS	60.9	50-78	32.26	6.4	4.0-10.0	2.16
1.0 % EMS	59.7	54-68	10.11	6.9	4.0-11.0	2.56
6D-1						
Control	71.7	65-81	16.65	3.3	2.0-5.0	0.77
0.5 % EMS	63.5	54-75	28.62	4.9	2.0-7.0	1.02

A wide range of variability was evident in both the genotypes for flowering and test weight. Early and late-flowering genotypes were observed at 0.5% and 1.0% EMS concentration in RHA 265. In 6D-1 mutagenesis was helpful in isolating early flowering mutant lines as flowering ranged from 54 to 75 days in the mutant population against 65 to 81 days in the untreated population. For test weight mutagenesis had a negative effect in RHA 265 at both the concentrations (low mean values over control). The negative shift in mean values could be attributed to the occurrence of deletions or harmful mutations (Ram et al., 1987). However, the wide range of variance values offered a range for selecting genotypes with high test weight. The restorer line 6D-1 is characterized by low test weight. Mutagenesis treatment was found effective in isolating high test weight mutant lines as was evident from the higher mean and wide range values. Similar observations were made earlier by Giririj et al., 1990, and Deshpande and Giriraj, 1997.

The genetic variability parameters and heritability values are presented in Table 2. The magnitude of induced genetic variability in RHA 265 was high for days to flowering at 0.5% EMS. In contrast it was high at 1.0% EMS for test weight. Further the high estimates of heritability were accompanied by low genetic advance for days to flowering while for test weight it was accompanied by high genetic advance. It appeared both additive and nonadditive types of gene interaction were involved for days to flowering in the mutant population. However for test weight, the additive genetic portion was predominant. In the

Table 2. Genotypic variance (GV), genotypic coefficient of variation (GCV), heritability (H) and genetic advance (GA) in the M3 population.

Genotype/ Treatment	Days to flowering				Test weight (g)			
	GV	GCV	H %	GA	GV	GCV	H %	GA
RHA 265								
0.5 % EMS	32.26	9.30	86.00	16.50	1.57	19.60	72.60	34.40
1.0 % EMS	10.11	5.20	55.50	6.10	1.97	20.00	76.90	36.40
6D-1								
0.5 % EMS	28.62	8.4	41.82	7.19	0.25	10.20	24.50	10.42

case of 6D-1, the magnitude of genetic variability was low to medium for both the traits. The heritability estimates were low to medium coupled with low genetic advance for both the traits indicating the major role of nonadditive gene action along with epistatic interaction. The studies of Mahla et al., (1990) in *Brassica,* and Deshpande and Giriraj (1997) in sunflower have also demonstrated that variation induced in the mutant populations is dependent on genotype, mutagen dose and character under study.

Conclusions

The present study revealed the effectiveness of EMS in inducing the variability and isolation of desirable genotypes. The shift in mean values was in a positive direction for days to flowering in RHA 265 and 6D-1, while it was negative for test weight in RHA 265. Promising mutant lines isolated by pedigree method are being utilized in a heterosis breeding program for developing hybrids with different maturity groups.

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