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GENETIC POTENTIAL OF INDUCED MUTANT RESTORER LINES FOR PRODUCING HIGH YIELDING EARLY MATURING SUNFLOWER HYBRIDS

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ABSTRACT

Twenty five M_2 mutant lines, derived from 0.3 and 0.4% ethyl methane sulphonate (EMS) treatment of RHA-298 were crossed with two standard cytoplasmic male sterile lines, viz., CMS-234A and CMS-851A. The resultant 50 hybrids along with two check hybrids, analysed in line x tester design, exhibited significant gca and sca variance. Some mutant lines (P_1, P_8 and P_{15}) with very high gca effects for majority of characters were identified for use in breeding programme. Crosses with high sca effects involved parents with low x low gca effects. The CMS-234A x P_{15} hybrid showed higher heterosis for seed yield than the control F_1 hybrids and was also early.

Key words: Induced mutants, combining ability, sunflower.

Because of wide adaptability, sunflower is grown in varied agroclimatic conditions and there is scope to extend its cultivation to nontraditional areas [1]. However, late maturing commercial varieties/hybrids restricts the cultivation of sunflower in rainfed conditions. Successful cultivation of sunflower in such areas demands the development of early maturing hybrids/varieties. The restorer line RHA-298 is widely used in sunflower hybrid breeding programmes. It is resistant to rust, downey mildew and *Verticillium* wilt [2], but late in maturity and hence the derived hybrids using it as a parent are also generally late. The use of induced mutation to overcome such defects is well known. In many instances early mutations have been induced [3].

In the present study an attempt has been made to assess the nature and magnitude of induced variability for combining ability and explore the possibility of exploiting the same for developing early maturing hybrids.

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MATERIALS AND METHODS

Presoaked seeds of a potential restorer, RHA-298, were treated with 0.3 and 0.4% ethyl methane sulphonate (EMS). Twenty five randomly selected M_2 plants (P_1 to P_{15} from 0.3% dose, and P_{16} to P_{25} from 0.4% dose) were crossed with two male sterile lines, viz., CMS-234-A and CMS-851A, for early generation testing of the combining ability of the mutant lines for subsequent use of the selected early flowering lines. The 50 F_1 hybrids thus derived were evaluated in randomised block design with three replications along with two check F_1 hybrids obtained by crossing untreated RHA-298 (P_{26}) as male with the same two male sterile lines. Twenty eight parental entries (25 mutant lines, one untreated restorer line, and two maintainer lines in lieu of the two male sterile lines) were also grown in contigous blocks in the same manner. Each entry was grown in a single row of 4 m length with a spacing of 60 x 20 cm. Observations were recorded for five quantitative traits on five random plants in each line. Combining ability was analyzed following Kempthrone [4]. The comparative performance of F_1 hybrids was judged from their heterosis over the check hybrids.

RESULTS AND DISCUSSION

The analysis of variance (Table 1) indicated significant variation for seed yield, stem girth and leaf area. Although both the male sterile lines (CMS-234A and CMS-851A) were derived from *Petiolaris* source, wide genetic variability was evident in the cms lines. The higher magnitude of sca variance as compared to gca variance (except stem girth) implied that seed yield, days to flowering, plant height and leaf area were predominantly under the control of nonadditive gene action. However, Putt [5] reported that additive gene action was important in the inheritance of days to flowering. The nonadditive gene action observed in the present study is in agreement with the reports of Patil et al. [3] in sorghum. These results suggest that the breeding programme should be formulated to exploit nonadditive genetic variance in the present material.

Table 1. Analysis of variance (M.S.S.) for combining ability in sunflower

Source	d.f.	Seed yield	Days to flowering	Plant height	Stem girth	Leaf area
Crosses	51	40.1**	2.3	0.01	0.05*	87.3**
Lines	25	50.3**	1.6	0.01	0.04	84.3**
Testers	1	31.8**	52.0**	0.07**	0.10	1072.5**
Lines x testers	25	30.2**	0.9	0.01	0.03	50.8
Error	102	2.0	2.4	0.01	0.04	46.6
Estimate of variance components:						
Gca		0.26	0.03	0.00	0.00	0.6
Sca		31.39	0.14	0.01	0.00	62.4
Gca : sca		1:121.2	1:4.0	—	—	1:109.5

*,**Significant at 0.05 and 0.01 levels, respectively.

The gca effects of inbreds (Table 2) revealed that none of the parents was superior for all the characters studied. Nevertheless, P_1, P_8 and P_{15} recorded high gca effects for most of the characters. P_1 showed high gca for seed yield, stem girth and leaf area, while P_8 and P_{15} showed significant positive gca for seed yield and desirable significant gca for days to flowering. Similar observations were reported by Giriraj et al. [6]. It is noteworthy that for all the characters gca effects of mutant lines were higher than that of the untreated restorer line, RHA-298, suggesting the possibility of obtaining desirable variation for combining ability by induced mutagenesis. Similar conclusions were made by Patil et al. [3].

Table 2. Mean performance and gca effects of the top five mutant lines in respect of seed yield and other yield components in sunflowe

Character	Line	Mean	Gca effects
Seed yield (g/plant)	P_{10}	12.01	7.96**
	P_1	11.24	7.55**
	P_6	11.17	6.18*
	P_8	14.64	5.95**
	P_{15}	15.37	5.38**
Days to flowering	P_5	76.00	- 1.34*
	P_{15}	75.00	- 1.33
	P_8	76.00	0.97
	P_{18}	79.00	- 0.81
	P_{20}	77.00	- 0.81
Plant height (cm)	P_6	1.44	0.08**
	P_9	1.30	0.06*
	P_5	1.37	0.06*
	P_{25}	1.21	0.06*
	P_{26}	1.41	0.06*
Stem girth (cm)	P_1	2.32	0.29*
	P_9	2.26	0.29*
	P_{14}	2.44	0.20*
	P_{12}	2.24	0.12
	P_{26}	2.19	2.12
Leaf area (dm^2)	P_8	54.88	15.79**
	P_4	52.51	10.08**
	P_{10}	54.22	7.73**
	P_9	46.15	7.17**
	P_1	47.70	5.53*

*,**Significant at 0.05 and 0.01 levels, respectively.

In respect of specific combining ability also, many crosses involving mutant derivatives appeared to be promising (Table 3). They also exhibited high heterosis in the desirable direction over respective control F_1. In majority of crosses, high sca effect was observed either in low x low or high x high gca parent crosses, however, low x low gca combinations were more frequent. The results are in agreement with the findings of Vranceaneu and Stoenenscu [7].

As mentioned earlier, one of the limitations in cultivation of RHA-298 is its late maturity, due to which the hybrids derived from it are also late. The induced mutant lines proved effective in obtaining hybrid combination with earliness. The performance of the best four early hybrids as compared to the control F_1s is presented in Table 4. Among these 4 hybrids, CMS-234A x P_{15} was early and also a high yielding (Table 3). Gregory [8] and Carlson et al. [9] also reported early flowering hybrids involving mutant lines.

Table 3. Mean performance, heterosis and parental gca status of five crosses exhibiting maximum sca effects in respect of seed yield and components in sunflower

Character	Cross	Mean	Heterosis over control F_1	Sca effect	Gca status of parent	
					female	male
Seed yield (g/plant)	CMS-234A x P_{14}	36.36	0.56	11.33**	Low	Low
	CMS-234A x P_{15}	60.37	66.95**	10.43**	Low	High
	CMS-234A x P_{18}	52.33	24.33**	6.27**	Low	High
	CMS-851A x P_{21}	41.33	16.88**	4.92**	Low	High
	CMS-234A x P_6	55.40	53.21**	4.66**	Low	High
Days to flowering	CMS-234A x P_{24}	66.00	- 4.35*	- 2.17*	High	Low
	CMS-234A x P_{21}	66.00	- 4.35*	1.17	High	Low
	CMS-234A x P_{16}	66.00	- 2.89*	- 1.17	High	Low
	CMS-234A x P_{23}	68.00	- 1.45	- 1.01	High	Low
	CMS-851A x P_4	68.00	- 1.43	- 0.99	High	Low
Plant height (cm)	CMS-851A x P_6	1.97	8.83**	0.09*	Low	High
	CMS-234A x P_{19}	1.82	2.25	0.09*	Low	High
	CMS-234A x P_{11}	1.82	2.24	0.08	Low	Low
	CMS-234A x P_{16}	1.82	- 1.12	0.05	Low	Low
	CMS-234A x P_{25}	1.76	3.93	0.05	Low	Low
Stem girth (cm)	CMS-851A x P_{19}	3.08	12.00	0.24	Low	Low
	CMS-234A x P_{17}	2.95	10.90	0.23	Low	Low
	CMS-851A x P_{18}	3.12	13.45	0.21	Low	Low
	CMS-234A x P_7	3.10	7.52	0.21	Low	Low
	CMS-851A x P_{26}	2.75	—	0.17	Low	Low
Leaf area (dm^2)	CMS-851A x P_{14}	79.30	24.68*	12.12**	High	Low
	CMS-851A x P_3	78.72	0.77	12.08**	High	High
	CMS-234A x P_{19}	71.41	10.87	11.13**	High	Low
	CMS-851A x P_{19}	69.59	9.42	9.50**	High	Low
	CMS-234A x P_{13}	79.12	22.84*	9.24*	High	Low

*,**Significant at 0.05 and 0.01 levels, respectively.

The present study has thus helped in isolating better combining mutant lines with respect to earliness as well as yield. Keeping in view the obvious advantages of early generation testing, which have been clearly demonstrated in different crop species, the superior mutant lines identified in the present study may be carried forward

Table 4. Heterotic hybrids involving induced mutant lines for days to flowering in sunflower

With CMS-234A		With CMS-851A	
cross	heterosis over control F_1 (%)	cross	heterosis over control F_1 (%)
CMS-234A x P_{15}	- 5.79**	CMS-851A x P_5	- 2.86*
CMS-234A x P_{16}	- 2.89*	CMS-851A x P_8	- 2.86*
CMS-234A x P_{21}	- 4.35**	CMS-851A x P_{15}	- 2.85**
CMS-234A x P_{24}	- 4.35**	CMS-851A x P_{15}	- 4.28**

*,**Significant at 0.05 and 0.01 levels, respectively.

which may (after reaching desired level of homozygosity) prove to be promising for developing early and high yielding sunflower hybrids.

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