

Evaluation of Recurrent Selection Derived Lines in Safflower (*Carthamus tinctorius* L.)

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Abstract The present study was undertaken to evaluate the expected genetic gain for seed yield and its components from half-sib selection method. The 105 half-sib families developed were grown in *rabi* of 2011 along with check viz. Bhima, A-1, AKS-207 and AKS-68 for evaluation in augmented block design with five blocks. Expected genetic advance was 42.48% and 48.23 at 10% selection intensity over population mean and Bhima respectively for the seed yield plant⁻¹. This indicate that the half-sib recurrent selection is effective for increasing population mean and extraction of superior recombinant lines better than check varieties.

Keywords Safflower, Half sib-families, Random mating population, Genetic advance.

Introduction

Safflower (*Carthamus tinctorius* L.) is a member of the composite, family Asteraceae. There are twenty five species in this genus. Out of which only *Carthamus tinctorius* L. (2n = 24) is cultivated. In India safflower is grown on 1.95 lakh hectares with total production of 1.00 lakh tonnes. Maharashtra occupies pride place in safflower production and it is grown 1.23 lakh hectares with a total production 0.67 lakh tonnes and productivity 545 kg ha⁻¹. In Vidharbha safflower is grown on 1900 ha with total production 1000 tonnes and productivity 368 kg ha⁻¹ [1].

Safflower is cultivated mainly for its seeds, which yield edible oil traditionally. Besides, it contains 30% oil in Indian varieties. The oil constitutes 76% of linoleic acid (PUFA) which helps in reducing cholesterol level in human blood. Earlier varieties of safflower have the genetic potential to give yield of 15-20 q/ha with oil content of about 30-40% under optimum condition. However attempts to further improve the yield and oil content were not successful for the last three decades. This may be due to, use of pedigree selection technique in population derived from two line crosses and negative correlation between seed yield and oil content. Conventional breeding methods have not been very efficient for improving quantitatively inherited characters like seed yield and oil content. Moreover regular methods of breeding have several limitations to use available genetic resource. These limitations

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may be overcome by application of recurrent selection method in self-pollinated crop.

Materials and Methods

The experimental material consisted of safflower population developed by crossing HUS-MS-305 and 62 male parents out of which 25 crosses were developed at AICRP, Akola, 25 crosses at AICRP, Solapur and 12 crosses were developed at Botany section, College of Agriculture, Nagpur during 2008. The F_{15} were raised in 2009 in respective research stations and equal amount of F_{15} seeds were mixed and base population was constructed. The base population was raised in 2010 and composited to form random mating population. Half sib seed were harvested from individual male sterile plants. One hundred five families were developed from random mating population. These 105 half-sib families developed were grown in *rabi* of 2011 along with check viz. Bhima, A-1, AKS-207 and AKS-68 for evaluation in augmented block design with five blocks. Each block consisted of 21 half-sibs and 4 checks. Row to row and plant to plant spacing was maintained as 45×45 cm. The recommended packages of practices were followed to raise good crop. The data were recorded on five competitive fertile plants from each family on seven characters viz. plant height (cm), number of primary branches plant⁻¹, number of ca-

pitula plant⁻¹, number of seeds capitulum⁻¹, 100 seed weight (g), oil content (%) and seed yield plant⁻¹ (g) except days to 50% flowering and days to maturity for which data were recorded on plot basis. The mean data of five observational plants from each family were used for statistical analysis.

Results and Discussion

Analysis of variance

The analysis of variance for the half-sib families were estimated for nine characters viz. days to 50% flowering, plant height, days to maturity, number of primary branches plant⁻¹, number of capitula plant⁻¹, number of seed capitulum⁻¹, 100 seed weight oil content and seed yield plant⁻¹ and presented in Table 1. The mean squares due to half -sib families were significant for all the characters except days to maturity, number of primary branches plant and 100 seed weight indicating existence of substantial genetic variability among half-sib families for six characters i.e. days to 50% flowering, plant height, number of capitula plant⁻¹, number of seed capitulum⁻¹, oil content and seed yield plant⁻¹ after one cycle of recurrent selection. The basic objective of all recurrent selection method is to increase the frequency of favorable genes in a population so that the

Table 1. Analysis of variance for half-sib families. * Significance level at 5%, ** Significance level at 1%.

Source of variances	DF	Days to 50% flowering	Plant height (cm)	Days to maturity	Mean squares			100 seed weight (g)	Seed yield plant (g)	Oil content (%)
					No. of primary branches plant ⁻¹	No. of capitula plant ⁻¹	No. of seed capitulum ⁻¹			
Block (ignoring treatments)	4	30.10**	426.29**	64.50*	7.90*	107.44*	62.30	0.38	102.75	9.28**
Treatments (eliminating block)	108	15.04**	82.45**	40.72	4.54*	138.46**	66.29*	0.90	313.80*	1.84**
Checks	3	16.33*	42.68*	20.40	1.40	28.97	83.53*	1.84*	46.49	0.22**
Checks + Var vs Var	105	15.01**	83.59**	41.30	4.63*	141.59**	65.79*	0.87	321.44*	1.89**
Error	12	3.37	10.32	18.73	1.64	26.15	21.55	0.38	101.66	0.01
Block (eliminating check + Var)	4	8.57	12.37	14.28	1.71	73.92	10.73	0.32	156.32	0.004
Entries (ignoring blocks)	108	15.84**	97.78**	42.58	4.77*	139.70**	68.20*	0.90	311.82*	2.18**
Checks	3	16.33*	42.68*	20.40	1.40	28.97	83.53*	1.84*	46.49	0.22**
Half-sib	104	14.97**	92.69**	41.58	4.67	140.52**	62.82*	0.88	321.61*	2.23**
Checks vs Varieties	1	105.00**	792.52**	213.14**	25.03**	386.76**	580.85**	0.26	89.72	3.12**
Error	12	3.37	10.32	18.73	1.64	26.15	21.55	0.38	101.66	0.01

opportunities to extract superior genotypes are enhanced.

Mean performance of half-sib families

Maximum, minimum, range and mean values of agronomic characters were measured on 105 half-sib families and presented in Table 2. In the present study, the days to 50% flowering ranged from 91 to 109 days with mean value of 96.60 days. Plant height ranged from 88.8 to 144 cm with mean height of 113.37 cm. Number of capitula plant⁻¹ ranged from 17.8 to 80.2 with mean of 39.22. Number of seeds capitulum⁻¹ ranged from 20.0 to 57.8 with 38.86 mean. Seed yield plant⁻¹ ranged from 15.62 to 78.90 g with mean seed yield of 50.80 g. Oil content ranged from 24.7 to 31.63% with 28.33% mean oil content. The maximum range was recorded by seed yield plant⁻¹ (63.28 g) followed by number of capitula plant⁻¹ (62.4), plant height (55.2 cm), days to maturity (41), number of capitulum⁻¹ (37.8), days to 50% flowering (18), number of primary branches plant⁻¹ (10.4), oil content (6.93%) and 100 seed weight (3.72 g) indicating considerable amount of genetic variance in random mating population which will facilitate selection of superior families. These results revealed that characters like seed yield plant⁻¹, number of capitula plant⁻¹ and plant height showing maximum range in the 105 half-sib families studied can

be considered as traits for selecting superior families. Similar to these results earlier [2—4] also found the importance of seed yield plant⁻¹ and number of capitula plant for selecting superior families based on means and range. Mean values of half-sib families when compared with check varieties, upper limit values of half-sib families for all the nine characters studies were found to be higher than the best check variety for the respective characters. This indicates the availability of promising half-sib families superior than check. Hence the half-sib families can be subjected to selection of superior families for the above mentioned characters i.e. seed yield plant⁻¹, number of capitula plant⁻¹ and plant height if these traits also record a good extent of heritability and genetic advance.

Expected genetic advance with half-sib selection

The expected genetic advance per cycle from single trait selection using half-sib family selection and expected genetic advance expressed as percent of population mean are presented in Table 3. Genetic advance is a measure of expected progress under selection and it depends on the magnitude of genetic variance, heritability and selection intensity. The information about magnitude of genetic variance and heritability can be used in ascertaining the possibility of extracting superior progenies for use in the

Table 2. Mean values of agronomic characters measured on selected half-sib families. * Mean performance of 105 half-sib families. ** Mean performance of 4 lines of check from five blocks.

Characters	Days to 50% flowering	Plant height (cm)	Days to maturity	No. of primary branches plant ⁻¹	No. of capitula plant ⁻¹	No. of seed capitulum ⁻¹	100 seed weight (g)	Seed yield plant ⁻¹ (g)	Oil content (%)
Maximum	109	144	167	15.8	80.2	57.8	6.9	78.90	31.63
Minimum	91	88.8	126	5.4	17.8	20.0	3.18	15.62	24.7
Range	18	55.2	41	10.4	62.4	37.4	3.72	63.28	6.93
Mean (HS)*	96.60	113.37	136.76	8.91	39.22	38.86	5.31	50.80	28.33
Check varieties**									
Bhima	95.20	108.72	136.20	9.54	43.00	35.72	4.56	44.74	29.06
A-1	94.80	106.96	132.40	10.52	41.28	37.20	5.62	50.32	28.64
AKS-207	91.40	102.26	131.80	10.64	44.96	30.04	5.94	51.52	28.79
AKS-68	95.00	108.08	132.40	9.84	46.84	28.96	5.64	47.37	28.57

Table 3. Expected genetic advance per cycle from single trait selection using half-sib family selection system. # Response to selection of top 5% (K = 2.06), 10% (K=1.76) of large number of families where K is standardized selection differential.

Unit of evaluation and selection	Gener- ation cycle	Selection intensity (#)	Days to 50% flowering	Plant height (cm)	Days to maturity	No. of primary branches plant ⁻¹	No. of capitula plant ⁻¹	No. of seed capitulum ⁻¹	100 seed weight (g)	Seed yield plant ⁻¹ (g)	Oil (%)
Half-sib	2	5	6.17	17.62	7.29	2.88	19.87	10.72	1.09	25.26	3.07
		10	5.27	15.05	6.23	2.46	16.98	9.16	0.93	21.58	2.62
Expected genetic advance as percent mean of population											
Half-sib	2	5	6.38	15.54	5.33	32.32	50.66	27.58	20.52	49.72	10.83
		10	5.45	13.27	4.55	27.60	43.29	23.57	17.51	42.48	9.24
Expected genetic advance as percent mean over Bhima											
Half-sib	2	5	6.48	16.20	5.35	30.18	46.20	30.01	23.90	56.45	10.56
		10	5.53	13.84	4.57	25.78	39.48	25.64	20.39	48.23	9.01

development of superior safflower varieties. The expected genetic advance from single trait selection at 5 and 10% of half-sib families was high for seed yield plant⁻¹ (25.26 and 21.58 respectively), followed by number of capitula plant⁻¹ (19.87 and 16.98), plant height (17.62 and 15.05), number of seeds capitulum⁻¹ (10.72 and 9.16), days to maturity (7.29 and 6.23), days to 50% flowering (6.17 and 5.27), oil content (3.07 and 2.62), number of primary branches plant⁻¹ (2.88 and 2.46) and 100 seed weight (1.09 and 0.93). The expected genetic advance expressed as percent of population mean at 5 and 10% was highest for number of capitula plant⁻¹ (50.66 and 43.29) followed by seed yield plant⁻¹ (49.72 and 42.48), number of primary branches plant⁻¹ (32.32 and 27.60), number of seeds capitulum⁻¹ (27.58 and 23.57), seed weight (20.52 and 17.51), plant height (15.54 and 13.27), oil content (10.83 and 9.24), days to 50% flowering (6.38 and 5.45) and days to maturity (5.33 and 4.55).

The expected genetic advance expressed as percent over Bhima at 5 and 10% selection intensity was highest for seed yield plant⁻¹ (56.45 and 48.23) followed by number of capitula plant⁻¹ (46.20 and

39.48), number of primary branches plant⁻¹ (30.18 and 25.78), number of seed capitulum⁻¹ (30.01 and 25.64), 100 seed weight (23.90 and 20.39), plant height (16.20 and 13.84), oil content (10.56 and 9.01), days to 50% flowering (6.48 and 5.53) and days to maturity (5.35 and 4.57) respectively. The expected genetic advance from single trait selection, expressed as percent of population mean and over check Bhima revealed the importance of seed yield plant⁻¹ and number of capitula plant⁻¹ as they exhibited maximum genetic advance. Hence, selection of 5% or 10 % superior half-sibs based on seed yield plant⁻¹ and number of capitula plant⁻¹ will definitely result in improved performance in the next cycle.

In accordance to this study in safflower, Kumar [5] observed that the expected genetic advance percent over Bhima at 5, 10 and 20% selection intensity was high for seed yield plant⁻¹ in third cycle (27.12, 35.98 and 28.62), followed by second cycle (27.93, 23.87 and 18.98) and first cycle (12.01, 10.26 and 8.11) respectively. The expected genetic advance obtained from second cycle of recurrent selection was 28.8, 23.99 and 19.08% in seed yield plant⁻¹ and 29.19, 24.94 and 19.83 in number of ca-

pitula plant⁻¹ at 5, 10 and 20% selection intensity as reported by Naole [6]. In third cycle Goyal [7] reported 49.49, 42.29 and 33.64% genetic advance in seed yield plant⁻¹ and 30.67, 26.20 and 20.84 in number of seed capitulum⁻¹ from 5, 10 and 20% selection intensity. Deshmukh [2] reported expected genetic advance as 39.68% and 45.68% at 10% selection intensity over population mean and Bhima respectively for seed yield plant⁻¹ and 27.52% and 28.02% for capitula plant⁻¹ after one cycle of recurrent selection. Gawande [3] reported that expected genetic advance was 28.88% and 22.78% 10% selection intensity over population mean and Bhima respectively for seed yield plant⁻¹ and 8.86% and 8.37% for number of capitula plant⁻¹ after third cycle of recurrent selection. This clearly indicates the accumulation of favorable genes for yield and important yield component number of capitula plant⁻¹.

The present study on recurrent selection in safflower revealed that an expected genetic advance was 42.48 and 48.23% at 10% selection intensity over population mean and Bhima respectively for the seed yield plant⁻¹ which indicates accumulation of desirable genes for seed yield. The half-sib recurrent selection was effective for increasing population mean

and extraction of superior recombinant lines better than check varieties. This study also indicated that the selection of half-sib families superior over check goes on increasing with the number of cycle and break in linkage group were observed between earliness and yield plant⁻¹ due to recurrent selection in random mating.

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