

Evaluation of third cycle of half-sib recurrent selection using genetic male sterility in safflower (*Carthamus tinctorius* L.)

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Safflower is member of the composite, family Asteraceae. There are twenty five species in the genus. Out of which only *Carthamus tinctorius* L. $2n = 24$ is cultivated and used for oil production, the rest are the wild species. Safflower contains 30% oil in Indian varieties. The oil constitutes 76 per cent of Linoleic acid (PUFA) which helps in reducing cholesterol level in human blood.

The present-day breeders are interested in applying more efficient breeding method to self-pollinated species to improve productivity, potentials of these crops [1, 2, 3, 4]. One method utilizing to accumulate desirable genes and facilitate breaking of linkages i.e. recurrent selection [5]. This method is substantially more efficient in breeding for quantitatively inherited characters than conventional breeding programme. However, due to necessity for recombination in each cycle, this system has been principally used in out crossing species. In past 30 years some recurrent selection schemes designed for self pollinated crop utilizing both hand crossing and out crossing mechanisms like male sterility have been proposed [6, 7, 8].

The present study was conducted during *rabi*, 2004-05 at the Institutional Farm of Department of Agricultural Botany, College of Agriculture, Nagpur. The experimental material was developed from safflower population segregating for genetic male sterility. The remnant seeds from top 13 per cent half – sibs families (26) selected from 2nd cycle of recurrent selection was

planted in *rabi*, 2004 for random mating. At flowering, male sterile plants were identified (morphological markers and aborted male organ), tagged and harvested separately as half-sibs. Out of which 174 half – sibs were selected for evaluation sufficient seeds so as to keep remnant seeds for the next recombination cycle. In *rabi*, 2005, 174 half-sib families along with 5 checks viz., Bhima, A1, AKS-207, HUS-305 and Phule-kusum were grown for evaluation in augmented block design in six blocks. Each block consisted twenty nine half-sibs along with 5 randomized checks in each block. The plant spacing within a row between plant to plant was 30 cm and two row spacing was 45 cm, the recommended cultural practices were followed to raise the good crop. The data was recorded on five competitive fertile plants for each type of family for the following characters as days to 50% flowering, Plant height (cm), days to maturity, primary branches per plant, capitula per plant, seeds per capitulum, 100 seed weight (g) and seed yield per plant (g). The analysis of variance for augmented block design was carried as per the standard method [9]. The estimation of half-sib family components of variances and expected genetic advance per cycle (Gc) was worked out from the family mean squares [6].

Analysis of variance for the half-sib families are presented in Table 1. The mean squares due to the half-sib families were significant for all the characters except primary branches, capitula per plant and 100 seed weight (g). This showed that substantial genetic variability existed among half-sib families for five

characters in a random mating population under study.

The days to 50 per cent flowering ranged from 84.79 to 103.79 days with 95.36 mean days. The plant height recorded maximum range (45.32) with 116.74 mean plant height of all half-sib families. The days to maturity ranged from 130.84 to 157.16 with 144.86 mean. For primary branches per plant, capitula per plant and 100 seed weight, the genetic variation was non significant. The maximum seeds per capitulum were 42.58 and minimum seeds per capitulum were 17.74 with a range of 24.84 and with the mean of 30.99. Seed yield per plant ranged from 19.14 to 51.09 g. The mean performance of seed yield per plant for all half-sib families was 34.88 g. The highest seed yield per plant was recorded by half-sib family number 127 (51.09g.). The maximum range was recorded by plant height (45.32 cm) followed by seed yield per plant (31.95 g.), days to maturity (26.32), seeds per capitulum (24.84 and days to 50 per cent flowering (19.0).

The estimates of half sib family components of variance and heritability for each agronomic trait have been present in Table (2). The genetic variance among half-sib families ($\sigma^2_{H.S.}$) and additive variance (σ^2_A) was maximum respectively for seed yield per plant (79.44 and 317.76), followed by plant height (73.97 and 295.88), seeds per capitulum (29.95 and 119.80), days to 50% flowering (22.87 and 91.48) and days to maturity (14.49 and 57.96), respectively. The estimates of heritability on family mean basis was high for seed yield

per plant (0.88) followed by days to 50% flowering (0.82), days to maturity (0.76), seeds per capitulum (0.71) and plant height (0.67), respectively.

The expected genetic advance per cycle from single trait selection using half-sib family selection and expected genetic advance expressed as per cent of population mean have been presented in Table 3. The expected genetic advance per cycle from single trait selection at 5, 10 and 20 per cent selection intensity was high for seed yield per plant (17.26, 14.75 and 11.73) followed by plant height (14.46, 12.35, 9.83), seeds per capitulum (9.50, 8.12 and 6.46), days to 50 per cent flowering (8.94, 7.64 and 6.08) and days to maturity (6.82, 5.83 and 4.64), respectively indicating effectiveness of recurrent selection.

The expected genetic advance as per cent of population mean at 5, 10 and 20 per cent was high for seed yield per plant (49.49, 42.29 and 33.64) followed by seeds per capitulum (30.67, 26.20 and 20.84), plant height (12.39, 10.58 and 8.42), days to 50 per cent flowering (9.38, 8.01 and 6.37) and days to maturity (4.71, 4.02 and 3.20), respectively.

The expected genetic advance per cent over Bhima at 5, 10 and 20 per cent was high for seed yield per plant (42.12, 35.98 and 28.62), followed by seeds per capitulum (29.67, 25.34 and 20.16), plant height (13.95, 11.92 and 9.48), days to 50 per cent flowering (9.20, 7.86 and 6.25) and days to maturity (4.40, 3.76 and 2.99), respectively.

Table 1. Analysis of variance of half-sib families

Characters	DF	Mean sum of squares							
		Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches per plant	Capitula/ plant	Seeds/ capitulum	100 seed weight (g)	Seed yield plant (g)
Blocks (Ignoring treatments)	5	754.27**	33.01**	819.94**	29.44**	434.13**	228.00**	1.16**	2113.89**
Treatment (eliminating blocks)	178	8.8	23.84**	79.76*	1.43	26.44	29.83*	0.14	40.08**
checks	4	29.69**	18.80*	86.83	7.31*	150.46*	57.84**	0.52*	258.68**
Checks + Var. vs. Var.	174	8.32	23.96**	79.60*	1.29	23.59	29.23*	0.13	35.06**
Error	20	4.85	4.61	36.92	1.94	45.73	12.19	0.15	10.39
Block (eliminating checks + var.)	5	117.80**	3.44	88.36	4.03	59.07	44.37*	0.15	209.72**
Entries (Ignoring Blocks)	178	26.68**	24.67**	100.31**	2.14	36.98	35.03**	0.17	93.57**
Checks	4	29.69**	18.80*	86.83	7.31*	150.46*	57.84**	0.52*	258.68**
Varieties	173	25.47**	15.91**	79.32*	2.03	34.56	32.51**	0.15	89.42**
Checks vs. Varieties	1	223.04**	1563.95**	3785.90**	0.75	2.50	378.77**	0.85*	151.60**
Error	20	4.85	4.61	36.92	1.94	45.73	12.19	0.15	10.39

The expected genetic advance per cycle from single trait selection using half-sib family selection at 5, 10 and 20 per cent selection intensity for seed yield per plant was relatively high in third cycle (17.26, 14.75 and 11.73) followed by second cycle (10.92, 9.33 and 7.42) and in first cycle (4.76, 4.07 and 3.23), respectively. The expected genetic advance as per cent of population mean at 5, 10 and 20 per cent was high in third cycle (49.49, 42.29 and 33.64 respectively) followed by second cycle (28.08, 23.99 and 19.08) and in first cycle (11.51, 9.84 and 7.82), respectively. The expected genetic advance per cent over Bhima at 5, 10 and 20 per cent was also high in third cycle (42.12, 35.98 and 28.62), followed by second cycle (27.93, 23.87 and 18.98) and in first cycle (12.01, 10.26 and 8.11), respectively.

The number of half-sib families for next recombination was also high in third cycle as forty-one followed by twenty-six in second cycle and four in first cycle owing to random-mating, accumulation of favorable alleles and effective selection. Present study revealed that half-sib recurrent selection method of population improvement is also effective in self-pollinated crops by using genetic male sterility mechanism, avoiding the tedious task of hand emasculation and pollination, for further improvement of existing elite varieties by incorporation of exotic germplasm (as original base population was developed in 1998). Good amount of genetic variation, high heritability, high expected genetic advance and breaking of undesirable linkages after three cycles are the supporting evidences for the improvement due to the

Table 2. Estimates of half-sib family components of variance and heritability for different agronomic traits

Half-sib family components	Days to 50% flowering	Plant height (cm)	Days to maturity	Seeds/capitulum	Seed yield/plant (g)
$\sigma^2_{H.S.}$	22.87	73.97	14.49	29.95	79.44
$\sigma^2_A = 4\sigma^2_{H.S.}$	91.48	295.88	57.96	119.80	317.76
$\sigma^2_p = 1/4\sigma^2_A + \sigma^2_e$	27.72	110.89	19.10	42.14	89.83
$h^2_{(N.S.)} = \frac{1/4\sigma^2_A}{1/4\sigma^2_A + \sigma^2_e}$	0.82	0.67	0.76	0.71	0.88

Table 3. Expected genetic advance per cycle from single trait selection using half-sib family selection system

Unit of evaluation selection	Concentration cycle	Selection intensity#	Days to 50%	Plant height (cm)	Days to maturity	Seeds/ capitulum	Seed yield/ plant (g)
Half-sib	2	5	8.94	14.46	6.82	9.50	17.26
		10	7.64	12.35	5.83	8.12	14.75
		20	6.08	9.83	4.64	6.46	11.73
Expected genetic advance per cent mean of population							
Half-sib	2	5	9.38	12.39	4.71	30.67	49.49
		10	8.01	10.58	4.02	26.20	42.29
		20	6.37	8.42	3.20	20.84	33.64
Expected genetic advance per cent over Bhima							
Half-sib	2	5	9.20	13.95	4.40	29.67	42.12
		10	7.86	11.92	3.76	25.34	35.98
		20	6.25	9.48	2.99	20.16	28.62

#Response to selection of top 5 per cent ($K = 2.06$), 10 per cent ($K = 1.76$) and 20 per cent ($K = 1.40$) of large number of families where 'K' is standardized selection differential

increased concentration of favorable recombinant gene constellations, allowing them to further produce new recombinants and repeatedly selection of them.

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