**RESEARCH ARTICLE**

# Evaluation of recurrent selection derived lines in safflower (*Carthamus tinctorius* L.)

■ N.G. GAWANDE, A.E. PATIL, P.C. AWACHAR AND P.B. GHORPADE

## SUMMARY

The present study was undertaken; to evaluate the response of recurrent selection derived lines by the testing of $(C_3)$ derived lines for genetic variability, genetic advance and heritability and to assess the effect of selection on other quantitative traits. The 16 half-sib families were selected from 3rd cycle of recurrent selection were grown for evaluation in Randomized Block Design in *Rabi* 2009 -10 along with check varieties Bhima and $A_1$. The expected genetic advance expressed as per cent of population mean at 10 per cent was high for seed yield per plot (48.84) followed by seed yield per plant (28.88). The expected genetic advance per cent over Bhima at 10 per cent selection intensity was high for seed yield per plot (28.27) followed by seed yield per plant (22.78). In safflower seed yield per plant was positively and significantly correlated with days to maturity, number of capitula per plant, number of seeds per capitulum and 100 seed weight. Days to maturity and seed yield per plant had exhibited significant and positive correlation. Two half-sib families were identified for testing in preliminary yield evaluation trial.

**Key Words :** Safflower, Random mating population, Evaluation

Safflower (*Carthamus tinctorius* L.) is a member of the family Asteraceae. There are twenty five species in this genus. Out of which only *Carthamus tinctorius* L. (2n = 24) is cultivated. Safflower is cultivated mainly for its seeds, which yield edible oil traditionally. This crop was grown for its flowers, used for colouring and flavoring foods and making dyes. The medicinal uses of flower in China have become known to the rest of the world in last few years rekindling the interest in this crop, because of its superior adoptability under drought conditions. Besides, it contains 30 per cent oil in Indian varieties. The oil constitutes 76 per cent of Linoleic acid (PUFA) which helps in reducing cholesterol level in human blood (Anonymous, 2007).

Earlier varieties have the genetic potential to give yield of 15-20 q/ha with oil content of about 30 per cent under optimal condition. However, attempts to further improve the yield and oil content were not successful for the last four decades. Due to pedigree selection techniques in population derived from two line crosses, negative correlation between seed yield and oil content was observed so conventional breeding methods have been useful only recombining simple inherited characters. Therefore, these conventional breeding

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methods have not been very efficient for improving quantitatively inherited characters like seed yield, oil content, tolerance to stresses and horizontal resistance to diseases and insects. Conventional method have several limitations such as limited use of available genetic variability resulting in the development of varieties with a narrow genetic base, successive loss of genes in the segregating generation with no chance of recombination for genes linked for yield and oil content (Jensen, 1970). Therefore, the present investigation was conducted to evaluate the response of recurrent selection derived lines for seed yield and its components after $3^{rd}$ cycle ($C_3$) of recurrent selection.

## MATERIAL AND METHODS

The experimental material consisted of six half-sib families selected from $3^{rd}$ cycle of recurrent selection *i.e.* HS-68, HS-109, HS-92, HS-117, HS-127, RS-9; (Goyal, 2006 and Metkar, 2008) and ten half-sib families selected for $2^{nd}$ cycle of recurrent selection HS-10, HS-21, HS-23, HS-47, HS-54, HS-55, HS-57, HS-60, HS-129, HS-171 (Deshmukh,2009) were planted in *Rabi* 2009 along with check varieties *viz.,* Bhima, $A_1$ for a evaluation in RBD with three replications. The plant spacing within a row was 30 cm and row to row spacing was 45 cm. The plot size was 5 x 1.80 m (four row plot).

Two seeds per hill were initially sown in each dibble and latter thinning was practiced to retain only one plant per hill. Recommended package of practices was followed to raise the good crop. The data were recorded on five competitive fertile plants for days to 50 per cent flowering, days to maturity, plant height (cm), number of branches per plant, number of

capitula per plant, number of seeds per capitulum, 100 seed weight (g), seed yield per plant (g), seed yield per plot (kg). Statistical analysis was carried out for analysis of variance, estimation of family components as suggested by Hallaur and Miranda (1989).

## RESULTS AND DISCUSSION

The development of half-sib families in safflower segregating for male sterility expects the half-sib families testing and selection utilizes one fourth of additive genetic variance ($1/4\sigma_A^2$) Therefore, it is important to study the response of lines derived from recurrent selection for genetic variability, genetic advance and heritability and to assess its effect of selection on other quantitative characters.

### Analysis of variance and mean performance of half-sib families :

The analysis of variance for the half-sib families has been presented in Table 1. The mean square due to half-sib families were significant for all the characters except plant height indicating substantial genetic variability existed among half-sib families after third cycle of recurrent selection. The basic objective of all recurrent selection method is to increase the frequency of favourable genes in a population so that the opportunities to extract superior genotypes are enhanced. Maximum, minimum, range and mean values of agronomic characters measured on selected 16 half-sib families have been presented in Table 2. In the present study, the days to 50 per cent flowering ranged from 85 to 94 days. Days to maturity ranged from 127 to 144.66 days. Number of primary branches

### Table 1 : Analysis of variance for half- sib families

| Source of variation | d.f. | Days to 50 % flowering | Days to maturity | Plant height (cm) | No. of primary branches / plant | No. of capitula/ plant | No. of seeds/ capitulum | 100 seed weight (g) | seed yield/ plant (g) | Seed yield/ plot (kg) |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | Mean squares | | | | | |
| Replication | 2 | 11.72 | 161.69 | 0.58 | 0.80 | 56.08 | 1.08 | 0.25 | 266.43 | 0.056 |
| Half –sib families | 17 | 21.25* | 108.54* | $25.86^{NS}$ | 3.22* | 61.56* | 45.09* | 1.30* | 197.47** | 0.21** |
| Error | 34 | 10.08 | 49.80 | 32.20 | 1.44 | 25.60 | 19.23 | 0.61 | 60.39 | 0.047 |

\* and ** indicate significance of values at P=0.05 and 0.01, respectively                     NS = Non-significant

### Table 2 : Mean value of agronomic characters measured on randomly chosen half-sib families

| Statistic | Days to 50 % flowering | Days to maturity | No. of primary branches / plant | No. of capitula/ plant | No.of seeds / capitulum | 100 seed weight (g) | Seed yield/ plant (g) | Seed yield /plot (kg) |
|---|---|---|---|---|---|---|---|---|
| Maximum | 94.0 | 144.66 | 14.33 | 47.26 | 32.21 | 4.91 | 42.69 | 1.14 |
| Mimimum | 85.0 | 127.0 | 10.08 | 28.66 | 19.81 | 3.0 | 16.25 | 0.20 |
| Range | 9.0 | 17.66 | 3.53 | 18.60 | 12.29 | 1.91 | 26.44 | 0.94 |
| Mean (H.S.)* | 88.54 | 132.29 | 13.02 | 38.83 | 24.28 | 3.94 | 27.04 | 0.61 |
| Check varieties | | | | | | | | |
| $A_1$ ** | 88.66 | 137.0 | 10.93 | 34.53 | 25.52 | 4.07 | 22.13 | 0.92 |
| Bhima** | 92.66 | 144.66 | 12.66 | 41.13 | 32.31 | 4.85 | 34.27 | 1.05 |

\* Mean performance of 16 half- sib families,  ** Mean performance of check varieties

per plant ranged from 10.80 to 14.33. Number of capitula per plant ranged from 28.66 to 47.26. Number of seeds per capitulum ranged from 19.81 to 32.21, 100 seed weight ranged from 3 to 4.91 (g). Seed yield per plant ranged from 16.25 to 42.69. Seed yield per plot ranged from 0.20 to 1.14. The maximum range was recorded by seed yield per plant (26.44 g) followed by number of capitula per plant (18.60), days to maturity (17.66), number of seeds per capitulum (12.29), days to 50 per cent flowering (9.0), number of primary branches per plant (3.53) and 100 seed weight (1.91 g) and seed yield per plot (0.94 kg). The comparison of range indicated that marginal reduction of range for most of the traits under study. However, there was no reduction in variation for range seed yield per plant indicating significant genetic variation available for selection. In the present study, two half- sib families recorded at par increased seed yield over check Bhima and $A_1$. Reddii (2002), Naole (2004), Goyal (2006) and Metker (2008) also reported superior performance of families developed in safflower random mating population.

**Half-sib family components of variance and heritability :**

The significant and large genetic variation among half-sib families is prerequisite for recurrent selection programme. The estimates of half- sib family components of variance and heritability for each agronomic trait have been presented in Table 3. The genetic variance among half- sib families ($\sigma^2_{H.S}$) and additive variance ($\sigma^2_A$) was high and significant for seed yield per plant (45.69 and 182.77) followed by days to maturity (19.58 and 78.32), number of capitula per plant (11.99 and 47.95), number of seeds per capitulum (8.62 and 34.47), days to 50 per cent flowering (3.72 and 14.89), number of primary

branches per plant (0.59 and 2.37), 100 seed weight (0.23 and 0.92) and seed yield per plot (0.054 and 0.214 ), respectively. The significant and high genetic variance among half-sib families was reported by Reddii (2002), Mummaneni (2003), Naole (2004), Panchbhai (2004), Goyal (2006) and Metker (2008) in random mating population of safflower. Estimates of heritability in a safflower populations segregating for genetic male sterility are useful in determining the best method of selection to improve these population for specific traits. The most important function of heritability in determining the best method of selection to improve population for specific traits and the genetic study of quantitative traits in its predictive role, expressing the reliability of the phenotypic value as a guide to the breeding value. The narrow sense heritability estimates on family means basis were high for seed yield per plot (0.53) followed by seed yield per plant (0.43), number of capitula per plant (0.32), number of seeds per capitulum (0.31), number of primary branches per plant (0.29), days to maturity(0.28),100 seed weight (0..27) and days to 50 per cent flowering (0.27). High estimates of heritability has been reported in random mating population of safflower for several agronomic traits by Reddii (2002), Mummaneni (2003), Naole (2004), Goyal (2006), Pavithran (2007) and Metker (2008). Similarly high estimates of heritability has been reported in sorghum for several agronomic and quality traits by Eckebil *et al.* (1977).

**Genetic advance :**

Genetic advance is a measure of expected progress under selection and it depends on the magnitude to genetic variance, heritability and selection intensity. The information about

**Table 3 : Estimates of half-sib family components of variance and heritability for different agronomic traits**

| Half sib family components | Days to 50 % flowering | Days to maturity | No. of primary branches / plant | No. of capitula/ plant | No. of seeds/ capitulum | 100 seed weight (g) | Seed yield/ plant (g) | Seed yield /plot (kg) |
|---|---|---|---|---|---|---|---|---|
| $\sigma^2_{H.S}$ | 3.72 | 19.58 | 0.59 | 11.99 | 8.62 | 0.23 | 45.69 | 0.054 |
| $\sigma^2_A = 4 \sigma^2_{H.S.}$ | 14.89 | 78.32 | 2.37 | 47.95 | 34.47 | 0.92 | 182.77 | 0.214 |
| $\sigma^2_P = \frac{1}{4}\sigma^2_A + \sigma^2_e$ | 13.80 | 69.38 | 2.04 | 37.59 | 27.84 | 0.84 | 106.08 | 0.10 |
| $H^2 \text{ (n.s.)} = \dfrac{\frac{1}{4}\sigma^2_A}{\frac{1}{4}\sigma^2_A < \sigma^2_e}$ | 0.27 | 0.28 | 0.29 | 0.32 | 0.31 | 0.27 | 0.43 | 0.53 |

**Table 4 : Expected genetic advance per cycle from single trait selection using half- sib family selection system**

| Unit of evaluation and selection | Generation /cycle | Selection intensity # | Days to 50 % flowering | Days to maturity | No. of primary branches / plant | No. of capitula / plant | No. of seeds/ capitulum | 100 seed weight (g) | Seed yield/ plant (g) | Seed yield /plot (kg) |
|---|---|---|---|---|---|---|---|---|---|---|
| Half-sib | 2 | 10 | 1.76 | 4.13 | 0.68 | 4.03 | 2.87 | 0.44 | 7.81 | 0.30 |
| Expected genetic advance per cent mean of population | | | | | | | | | | |
| Half-sib | - | 10 | 1.99 | 3.12 | 5.21 | 8.86 | 11.83 | 11.21 | 28.88 | 48.84 |
| Expected genetic advance per cent over Bhima | | | | | | | | | | |
| Half-sib | - | 10 | 1.90 | 2.86 | 5.35 | 8.37 | 8.90 | 9.11 | 22.78 | 28.27 |

\# Response to recurrent selection of top 10 per cent (k = 1.76) of large number of families where 'k' is standardized selection differential

magnitude of genetic variance and heritability can be used in ascertaining the possibility of extracting superior progenies for use in the development of superior safflower varieties. 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 4. In the present study, the expected genetic advance from single trait- selection at 10 per cent of half-sib families was high for seed yield per plant (7.81) followed by days to maturity (4.13), number of capitula per plant (4.03), number of seeds per capitulum (2.87), days to 50 per cent flowering (1.76), number of primary branches per plant (0.68), 100 seed weight (0.44) and seed yield per plot (0.30). The expected genetic advance expressed as per cent of population mean at 10 per cent was high for seed yield per plot (48.84) followed by seed yield per plant (28.88), number of seeds per capitulum (11.83), 100 seed weight (11.21), number of capitula per plant (8.86), number of primary branches per plant (5.21), days to maturity (3.12) and days to 50 per cent flowering (1.99). The expected genetic advance per cent over Bhima at 10 per cent selection intensity was high for seed yield per plot (28.27) followed by seed yield per plant (22.78), 100 seed weight (9.11), number of seeds per capitulum (8.90), number of capitula per plant (8.37), number of primary branches per plant (5.35), days to maturity (2.86) and days to 50 per cent flowering (1.90). This indicating scope for further improvement of yield and it's contributing traits. In safflower, Reddii (2002) reported 9.483 per cent genetic advance in seed yield per plant from at 10 per cent selection intensity in random mating population of safflower after one cycle of recurrent selection. The expected genetic advance obtained from second cycle of recurrent selection was 23.99 per cent at 10 per cent selection intensity (Naole, 2004). In third cycle Goyal (2006) reported 42.29 per cent genetic advance from 10 per cent selection intensity.

The significant genetic advance for yield has been reported in sorghum which ranged from 13.8 to 40.4 per cent per cycle (Lothrop et al., 1985) and 6.2 to 16.3 91 q/ha (Bittinger et al., 1981). Brim (1978) and Burton and Brim (1981) reported increase in protein per cent in soybean from 42.8 to 46.3 per cent after five cycles of selection. Brim (1978) reported 16 per cent increase in soybean yield and $C_3$ composite yielded 20 per cent more than check variety. Onim (1981) reported average increase in grain yield was 2.3 to 4.3 per cent per cycle. Kadappa (1995) reported 106 per cent increase in yield in improved population than original population. The comprehensive studies on recurrent selection in different self- pollinated crops indicated that there is a significant increase in seed yield, protein content and oil content. The present study on recurrent selection in a safflower population segregating for genetic male sterility also indicated that the improvement in seed yield and its components by adopting half- sib family testing and selection.

**Phenotypic correlations :**

The recurrent selection experiments are mainly designed and conducted for improving seed yield per plant. However, this does not mean that other traits are unimportant. Selection for high yield does to some extend is indirect selection for disease and insect resistance and for traits correlated with yield (Gardner, 1978). However, if selection is for high seed yield alone undesirable correlated response may occur in other traits as pointed out by Doggett (1972). The phenotypic correlations among different traits were estimated and have been presented in Table 5. The days to maturity exhibited significant and positive correlation with days to 50 per cent flowering (0.674**), number of seed per capitulum (0.542*), seed yield per plant (0.549*). Number of capitula per plant exhibited significant and positive correlation with number of primary branches per plant (0.529*). Seed yield per plant had significant and positive correlation with number of capitula per plant (0.493*), number of seeds per capitulum (0.590**) and 100 seed weight (0.504*). Days to maturity and seed yield per plant had exhibited significant and positive correlation. These results indicate that half-sib families behave as like pureline due to continuous selection of fertile plants. This result of estimates are in agreement with those reported in safflower true breeding lines (Pure lines) by various worker Argikar et al. (1957); Reddii (2002); Mummaneni (2003); Naole (2004) and Goyal (2006) reported that the correlation between days to 50 per cent flowering and days to maturity was negative indicating breaking of linkage. Goyal (2006) reported negative and significant correlation between seed yield and days to 50 per cent flowering and also Metker (2008) indicating that unfavorable gene combination can be broken by recurrent

**Table 5 : Phenotypic correlation among seven quantitative characters for half- sib family selection**

| Characters | Days to maturity | No. of primary branches / plant | No. of capitula/ plant | No. of seeds/ capitulum | 100 seed weight (g) | seed yield/ plant (g) |
|---|---|---|---|---|---|---|
| Days to 50 % flowering | 0.674** | 0.060 | 0.353 | 0.291 | 0.181 | 0.457 |
| Days to maturity | | -0.108 | 0.204 | 0.542* | 0.356 | 0.549* |
| No. of primary branches / plant | | | 0.529* | -0.162 | -0.165 | 0.035 |
| No. of capitula / plant | | | | 0.318 | -0.116 | 0.493* |
| No. of seeds / capitulum | | | | | 0.231 | 0.590** |
| 100 seed weight (g) | | | | | | 0.504* |

* and ** indicate significance of values at P=0.05 and 0.01 is (0.4685), (0.5901), respectively

selection. This will facilitate selection recombinant lines with high yield and earliness.

**Identification of promising half-sib families :**

The objective of any recurrent selection method is to increase the frequency of desirable genes thereby increase frequency of lines than check varieties. Hallaur (1985) suggested to test 200-300 progenies which provide 20-30 progenies for recombination with a selection intensity 10 per cent. In the present study out of 16 half-sib families two half-sib families recorded at par to Bhima for seed yield and have been RS-68 and HS-57. Two half-sib families were identified for testing in preliminary yield evaluation trial. The result obtained in the present study, clearly indicate that yield plateau can be raised by adopting recurrent selection method in safflower.

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