Utilization of genetic male sterility system toward recurrent selection in safflower and genetic gain realized

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Abstract

Two random-mating populations in safflower were synthesized, i.e. RMP-I and RMP-II using genetic male sterility factor. Selected 196 and 171 progenies in each were evaluated separately during rabi 2005-06 to constitute next cycle population and to predict genetic gains in 1st cycle recombination. Considerable genetic variability for all seven traits existed in both populations. Highest range was noticed for plant height (50 cm) in RMP-I followed by number of seeds per capitulum (47.6) and yield / plant (46.8 g). In RMP-II highest range was observed for yield/plant (49.5 g). Predicted genetic gain after 1st cycle of random-mating was as high as 51.9% in RMP-II for number of capitula/plant over check AKS 207 at 20% selection intensity. For yield/plant in both populations expected genetic gain was higher than the mean of populations (39.2% in RMP-I and 36.6% in RMP-II). Within these two populations predicted gain was high in RMP-I for yield /plant and for days to maturity (26.4%) and oil content (8.7%) it was also high in RMP-II indicating that for these traits either RMP-I or RMP-II may reward in future. On the basis of result obtained 39 and 34 superior progenies were selected from RMP-I and RMP-II respectively for construction of next cycle population. Thus, constructed improved populations of RMP-I and RMP-II and these were evaluated further against their respective base population during rabi 2006-07 and result revealed that improved populations realized genetic gain of 14.8% and 13.0% respectively.

Key words: Recurrent selection - Random-mating population - genetic gain expected/realized

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Introduction

Safflower (*Carthamus tinctorius* L.) is one of the oldest crops of the world. In India, it is grown since time immemorial. Today, it is a minor but important rabi oilseed crop usually cultivated in vertisols under residual moisture. India, USA and Mexico are the major producers of this crop. It is also grown in Ethiopia, Kazakhstan, China, Argentina and Australia and other countries. World wide, it is grown on 0.9 million ha. with a production of 0.7 million tonnes and productivity of 784 kg/ha (FAO, 2005). In India, it is grown in an area of 0.36 million hectares. with a production of 0.23 million tonnes and productivity of 625 kg/ha (2005-06). Indian productivity of safflower is till low, needs further attention through crop improvement.

It is proved in the case of safflower that conventional breeding methods are not very efficient for improving quantitatively inherited characters, like seed yield, oil content etc. and, therefore, there is no breakthrough in spite of several releases. Recurrent selection in broad based genetic populations is one method to accumulate desirable genes and facilitate breaking of undesirable linkages. Recurrent selection procedures for improvement of plant population have, in general, been restricted to cross-pollinated species. Therefore, to implement recurrent selection programme as alternative to traditional breeding procedure in autogamous species requires techniques that would increase natural crossing. Genetic male sterility virtually produce seed on sterile plants by natural crossing. The presence of genetic male sterility system in safflower affords an opportunity to adopt recurrent selection procedures in crop improvement. Genetic male sterility in safflower was first reported by Deshpande (1940) and subsequently by several workers like Joshi *et al.* (1983) and Ramachandran and Sujatha (1991).

Apparently phenotype of the male sterile plants has altered which facilitated for identification and tagging of sterile plants at flowering stage. Seed set on sterile plants were low when compared with fertile siblings (Brim and Stuber, 1973). The objectives of the present study was to predict genetic gains, constitute second cycle populations and to find out actual improvement realized in two random-mating populations developed by utilizing genetic male sterility in safflower.

Materials and Methods

Safflower hybrids segregating for genetic male sterility were used for synthesis of random-mating populations. It is actually another application of genetic male sterility to initiate recurrent selection programme. Random-mating population-I (RMP-I) was constructed from 54 crosses involving nine GMS lines (MMS, MS(O) 9, MS 1-1, NGMS, GMS 102, GMS 104, GMS 105, MS(O)6 and AKSMS-1) and six pollen parents (Bhima, N 7, AKS 207, AKS 68, AKS 215 and AKS 152). Equal amount of seed from these 54 crosses were composited and sown for recombination in open pollinated condition in isolation during rabi 2004-05 and 256 male sterile plants were tagged at the time of flowering. These plants were harvested individually. Out of which 196 individual plants were selected for evaluation during 2005-06. Random-mating population-II (RMP-II) was developed from male sterile plants located in the breeding field of safflower at Oilseeds Research station, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola during rabi season 2003-04. Seed set on sterile plants were composited in equal proportion and sown for recombination in open pollinated condition in isolation. Two hundred and fifty male sterile plants were tagged at the time of flowering during rabi season 2004-05 and harvested individual plant separately. Out of that, 171 progenies with sufficient seeds were selected for evaluation during rabi season 2005-06.

2005-06: Selected 196 progenies from RMP-I and 171 progenies from RMP-II along with check either Bhima or AKS 207 were grown for evaluation in separate experiment having single row plot of five meter length in modified randomized block design (Eckebil, 1977) with two replications and each replication consisted of ten and nine blocks respectively. Each block was having 20 prgenies along with one check i.e. Bhima in RMP-I and AKS 207 in RMP-II. Spacing between rows and within row was 45 cm and 20 cm. respectively. Ten quantitative traits were studied and observations were recorded on five randomly selected fertile plants. The predicted

responses or genetic gains from selections were calculated as suggested by Brim and Stuber (1973) and Eckebil (1977).

2006-07: To judge the actual improvement in yield in first cycle recombination an experiment was laid out with improved population which was constituted by compositing an equal amount of remnant seed of superior progenies selected from the earlier year testing. There were six treatments, viz., improved populations and base populations of both RMP-I and II along with two checks, viz., Bhima and AKS 207. Design of experiment was randomized block design with four replications. Plot size was 2.25 m x 5.0 m (Gross) and 1.35 m x 4.60 m (Net) and spacing was 45 cm x 20 cm. The sowing was done during last week of September (Both years). Uniform cultural practices were followed and need based plant protection measures were taken.

Results

The analysis of variance revealed that the differences among progenies for all characters in both populations viz., RMP-I and RMP-II were highly significant. It indicated the presence of considerable genetic variability for characters under study. Mean performance of the population for most of the traits were more or less similar, except yield/plant which is observed to be low in RMP-I and RMP-II when compared to their respective checks Bhima (37.5 g) and AKS 207 (41.7 g). However, the ranges were very high in all most all traits. Highest range was noticed for plant height (50 cm) in RMP-I, followed by number of seeds per capitulum (47.6) and yield/plant (46.8 g). In RMP-II, highest range was observed for yield/plant (49.5 g), followed by number of capitula/plant (43.8), days to maturity (32.0), number of seeds/capitulum (31.7) and plant height (30.5) (Table-1).

Predicted genetic gain after Ist cycle was estimated and it was as high as 51.9% in RMP-II for number of capitula/plant over check variety AKS 207 at 20% selection intensity. For yield/plant in both populations, expected gain was highest over mean of populations (39.2% in RMP-I and 36.6% in RMP-II), followed by number of primary branches/plant (28.9%) and number of seed/capitulum (28.0%) in RMP-I and number of capitula/plant (27.5%) in RMP-II. In respect of yield, predicted gain for RMP-I (39.2%) was higher than in RMP-II (36.6%) and similarly for days to maturity (26.4%) and oil content (8.7%) it was higher in RMP-II. It indicated that for seed yield RMP-I and for days to maturity and oil content RMP-II are having more expectation (Table-2).

Experimental results for realized genetic gain indicated that RMP-I was superior over RMP-II for yield/plant. Yield differences were statistically significant at 5 % . Improved populations realized genetic gains of 14.8% and 13.0% respectively over their respective base populations. However, it was observed that the performances of checks were superior after first recombination cycle   (Table-3).

Discussion

Considerable genetic variability was observed for the characters under study. Though the mean yield of progenies under study were observed to be low (29.2 g/plant in RMP-I and 35.2 g/plant in RMP-II), the ranges were high (46.8 in RMP-I and 49.5 in RMP-II) indicating scope for exerting selection pressure. Ghorpade (2001) reported similar type of results in safflower. Estimated genetic gain after Ist cycle was high for number of capitula/plant in RMP-I (51.9%) over check AKS 207, followed by yield/plant in both RMP-I (39.2%) and RMP-II (36.6 %) over population mean. The results of the present investigation were in conformity with the findings of Ghorpade (2001). The significant genetic advance for yield was reported in sorghum ranging from 13.8 % to 40.4 % per cycle (Obilana and Rouby, 1980) and 6.2 q/ha to 16.3 q/ha grain yield in sorghum (Eckebil *et al.* 1977). Burton and Brim (1981) reported increase in protein content in soybean from 42.8 to 46.3 per cent after five cycles of selection. Onim (1981) reported average increase in grain yield was 2.3 to 4.3 % per cycle in pigeonpea. Kadappa (1995) reported 106% increase cotton yield in improved population than original population.

In any recurrent selection programme, development of population, selection, evaluation of selected progenies, selection of superior progenies and construction of improved population

from remnant seed for next recombination cycle are the basic principles. Hallaur (1985) suggested testing 200-300 progenies which would provide 20-30 superior progenies for next recombination cycle. In the present study, out of 196 and 171 progenies evaluated in RMP-I and RMP-II respectively and 20% progenies had been selected on the basis of high yield, high oil, more number of primary branches/plant, more number of capitula/plant and higher number of seed/capitulum.

The remnant seed of selected progenies (39 in RMP-I and 34 in RMP-II) were composited in equal proportion and constructed improved RMP-I and improved RMP-II which were sown for recombination in isolation during 2006-07. Simultaneously, to realize actual genetic gain, trial was formulated and results given in table 4 revealed that there must be accumulation of desirable genes in each of both improved populations i.e. improved RMP-I (14.8% yield increase) and improved RMP-II (13.0% yield increase) over their respective base populations. Similarly yield improvement in improved population over base population was reported by Kadappa (1995) in cotton.

Conclusion:

It is confirmed from the estimated genetic gain and yield increase in improved population in present study that the recurrent selection, alternative to the other conventional breeding methods, accumulates desirable genes. Estimated genetic gain, after Ist cycle of recombination was high in both populations (39.2 % in RMP-I and 36.6 in RMP-II) over their respective mean of population for yield per plant.

Realized genetic gain for seed yield (kg/ha) was 14.8 % in RMP-I and 13.0 % in RMP-II over their respective base population. However, national check Bhima and local check AKS 207 yielded highest by producing 1389 and 1338 kg seed yield per hectare respectively.

Table-1 : **Mean performance of progenies derived from random-mating populations of safflower**

Sr. No.	Traits	RMP-I			RMP-II		
		Range	Mean	Bhima(C)	Range	Mean	AKS 207(C)
1.	Days to 1st flowering	74.0-103.0 (29.0)	85.8	86.4	75.5-95.5 (20.0)	83.7	88.5
2.	Days to 50% flowering	82.0-110.0 (28.0)	91.1	92.1	81.0-99.5 (18.5)	90.9	82.5
3.	Days to maturity	139.0-160.0 (21.0)	145.8	145.7	119.0-151.0 (32.0)	145.6	93.0
4.	Plant height (cm)	75.2-125.2 (50.0)	95.9	93.4	75.7-106.2 (30.5)	91.9	99.0
5.	Number of primary branches/ plant	3.8-17.4 (13.6)	9.9	10.1	5.2-17.0 (11.8)	11.4	12.5
6.	Number of capitula/plant	6.4-42.4 (36.0)	25.1	26.3	10.9-54.7 (43.8)	29.1	15.5
7.	Number of seeds/capitulum	10.4-58.0 (47.6)	27.5	27.3	9.4-41.1 (31.7)	26.9	18.0
8.	100 seed weight (g)	4.7-7.3 (2.6)	5.9	5.6	5.0-7.4 (2.4)	6.1	6.4
9.	Oil content (%)	27.0-33.5 (6.5)	29.4	31.3	23.4-31.8 (8.4)	27.3	28.2
10.	Yield/plant (g)	8.7-55.5 (46.8)	29.2	37.5	15.7-65.2 (49.5)	35.2	41.7

Figures in parentheses indicated range.

Table-2 : Predicted genetic gain from recombination of 20% progenies to form next generation random-mating populations of safflower

Sr. No.	Trait	Expected genetic advance per cycle (%)			
		RMP-I		RMP-II	
		Over mean of population	Over check Bhima (C)	Over mean of population	Over check AKS 207 (C)
1.	Days to 1st flowering	5.2	5.2	4.0	4.3
2.	Days to 50% flowering	4.5	4.4	6.0	6.8
3.	Days to maturity	2.5	2.5	15.7	26.4 $
4.	Plant height (cm)	7.6	7.8	8.0	8.2
5.	Number of primary branches/ plant	28.9	28.2 $	21.6	16.5
6.	Number of capitula/plant	26.0	24.9 $	27.5	51.9 $
7.	Number of seeds/ capitulum	28.0	28.1 $	17.2	19.6
8.	100 seed weight (g)	9.9	10.4	7.8	9.8
9.	Oil content (%)	4.3	4.0	8.7	8.1 @
10.	Yield/plant (g)	39.2 @	31.2	36.6	32.5 @

Response to selection of top 20% (K=1.40) of progenies, where 'K' is the standardized selection differential.
$ - Indicated agronomically beneficial gains
@ - Indicated economically beneficial gains
These gains (@ and $) are breeder relevant for variety improvement.

Table-3 : Genetic gain realized over base populations of safflower

Sr. No.	Population	Seed Yield (kg/ha)	% increase over base population
1.	Improved population (RMP-I)	1280	14.8
2.	Base population (RMP-I)	1115	-
3.	Improved population (RMP-II)	1248	13.0
4.	Base population (RMP-II)	1104	-
5.	Bhima (C)	1389	-
6.	AKS 207 (C)	1338	-
	S.Em +	60.7	
	C.D. (at 5%)	170.7	

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