Breeding strategy for improvement of flower and seed yields in safflower

Vrijendra Singh, N. M. Kolekar and N. Nimbkar
Nimbkar Agricultural Research Institute, Lonand Road, Phaltan 415523,
Maharashtra, India   nariphaltan@gmail.com

Abstract
Variability in flower yield and its components and seed yield was assessed in spiny and non-spiny genotypes to know the extent of diversity for these traits in safflower. High estimates of genotypic and phenotypic coefficients of variation and heritability estimates coupled with high genetic advance as percent of mean were obtained for flower yield/plant, seed yield/plant, number of primary branches/plant, number of capitula/plant, capitulum diameter, number of seeds/capitulum and number of flowers/capitulum. This suggested the presence of a wide variability for these traits. Both flower and seed yields were significantly and positively associated with the number of primary branches/plant, number of capitula/plant, capitulum diameter, number of seeds/capitulum, 100-seed weight, number of flowers/capitulum, corolla tube length, stigma length and petal area/flower. The association between flower yield and seed yield/plant was found to be significant and positive.

The nature of gene action for expression of flower and seed yields/plant and their component traits was observed to be both additive and non-additive. To exploit both of these gene actions for different traits it is suggested that hybrid vigour should be harnessed by using existing genetic male sterility systems in the crop as well as by resorting to biparental mating followed by individual plant selections in the crosses showing dominant X recessive gene action. The existence of very high standard heterosis for flower yield (188%), number of capitula/plant (173%), seed yield/plant (171%) and number of seeds/capitulum (63%) further emphasizes the need to exploit hybrid vigour in order to enhance productivity of safflower.

Key words: Breeding strategy - safflower - flower yield – heterosis - gene action.

Introduction
Safflower (*Carthamus tinctorius* L.) is an important oilseed crop producing quality-oil rich in polyunsaturated fatty acids, which helps in reducing cholesterol level in blood. In addition, safflower also produces brightly coloured flowers which are known as a source of natural colour for food and have many pharmacological properties to cure several chronic diseases. Recently, an increasing demand for safflower flowers due to their popularization as herbal health tea and potential for their export to Japan and European countries has been witnessed.

Although recently developed non-spiny cultivars NARI-6, JSF-97, PBNS-40 and hybrid NARI-NH-1 are available for the production of both flowers and seed, their development has been carried out with an emphasis on seed yield superiority rather than flower yield. Therefore, whatever flower production is available from these cultivars is a byproduct. In view of increasing international demand for safflower flowers it has become imperative not only to increase seed yield but also to maximize flower production so as to make this crop more remunerative than the competing crops. Therefore, in order to devise a breeding strategy to optimize both seed and flower production, experiments were carried out to study genetic variability, correlation, combining ability and heterosis.

Material and Methods
I.   A trial consisting of 39 safflower genotypes-six of spiny and 33 of non-spiny nature was laid out in a randomized block design with three replications during winter 2002-03 to study the variability for flower yield and its components in safflower.

II. Another trial consisting of 55 entries comprising of 45 diallel-based F_1s and their 10 parents (MSN-3-8-5, GMU-3195, MSV-6, MSN-8, GMU-4808, GMU-2937, NARI-6, CO-1, C 2708-2-2, 126-8-2) was conducted in a randomized block design with three replications during winter 2002-03 to study the correlation and the inheritance of flower yield and its components and the extent of heterosis for these traits. Each entry in both the trials was sown in two rows of 5 m length with inter and intra row spacings of 45 and 20 cm respectively. Observations on floral and other physiological traits were recorded from five random plants of each entry. However the whole plot was used to record flower and seed yields of test entries.

Ten flowers from main capitulum of each of the five plants of each entry were selected to record observations on corolla tube length, petal length, anther length, stigma length and petal area/flower. Except petal area all other floral traits were measured by using precision vernier calipers with a least count of 0.001 cm. For recording petal area, a digital planimeter was used. Average values for five plants in each entry were used for statistical analysis. Heritability (broad sense) was estimated according to Hanson et al. (1956). Phenotypic and genotypic coefficients of variation (PCV, GCV) were estimated as per Burton (1952). Genetic advance (G.A.) as percent of mean was estimated according to Johnson et al. (1955) and genotypic correlations were determined by the method of Al-Jibouri et al. (1958). The combining ability analysis was carried out according to Method 2, Model I of Griffing (1956).

Results and Discussion

Genetic variability: The 39 genotypes showed highly significant differences for all the physiological and floral traits, thereby indicating the presence of a wide variability among them for different traits. Number of flowers/capitulum exhibited the maximum range of estimates. This trait also showed the maximum genotypic coefficient of variation (GCV), as well as genotypic and phenotypic variances. Similarly number of seeds/capitulum, number of capitula/plant and flower yield/plant also showed high estimates of GCV and PCV. The characters number of flowers/capitulum, number of seeds/capitulum, number of capitula/plant, flower yield/plant and seed yield/plant gave high estimates of both heritability and genetic advance (G.A.) as percent of mean indicating the usefulness of selection in these traits for improvement of the crop. These results are in conformity with the findings of Patil et al. (2002).

Correlation studies: Flower yield was significantly and positively associated with number of primary branches/plant, number of capitula/plant, capitulum diameter, number of flowers/capitulum, stigma length, petal area/flower and seed yield/plant in non-spiny safflower hybrids (Table 1). All the traits which showed positive and significant association with flower yield except number of primary branches/plant and stigma length also exhibited highly significant and positive association with seed yield. In addition, seed yield was significantly and positively associated with number of seeds/capitulum, 100-seed weight and corolla tube length. Of these three, number of seeds/capitulum and corolla tube length also showed positive association with flower yield, but it was of low magnitude. However, the remaining trait i.e. 100-seed weight recorded negative association of very low magnitude with flower yield. Therefore the study suggested that the selection for the component traits which exhibited positive association with both flower and seed yield would result in simultaneous improvement in both.

Inheritance of flower yield and its components in safflower : The 10-parent diallel analysis indicated that the variances due to general combining ability (gca) and specific combining ability (sca) were highly significant for all the characters studied (Table 2). Thus the importance of both additive as well as non-additive gene actions in the expression of different traits in safflower was seen. The variances due to gca were found to be considerably higher than those due to sca for all the characters except flower yield/plant, thus suggesting the predominant role of additive and additive X additive epistatic components of genetic variance which are fixable. In case of flower yield, non-additive gene action was found to be important.

Table 1. Genotypic correlation coefficients for flower yield and its components in non-spiny safflower hybrids

Sr. no.	Characters	Flower yield/plant	Seed yield/plant
1.	Days to 50% flowering	- 0.478**	- 0.527**
2.	Plant height (cm)	- 0.198	0.011
3.	No. of primary branches/plant	0.432**	0.035
4.	No. of capitula/plant	0.710**	0.384**
5.	Capitulum diameter (cm)	0.312*	0.485**
6.	No. of seeds/capitulum	0.258	0.513**
7.	100-seed weight (g)	- 0.075	0.298**
8.	Days to maturity	- 0.542**	- 0.534**
9.	No. of flowers/capitulum	0.392**	0.275*
10.	Corolla tube length (cm)	0.176	0.290*
11.	Petal length (mm)	0.201	0.254
12.	Anther length (mm)	0.161	0.015
13.	Stigma length (mm)	0.377**	0.233
14.	Petal area/flower (cm^2)	0.374**	0.459**
15.	Flower yield/plant (g)	-	0.578**

**, * Significant at P = 0.01 and P = 0.05 respectively.

Table 2. ANOVA for combining ability for flower yield and its components in safflower

Sr. No.	Mean sum of squares	Source of variation		
		gca	sca	Error
		d.f.		
		9	45	108
1.	Days to 50% flowering	39.59**	6.75**	0.66
2.	Plant height (cm)	351.59**	25.75**	2.50
3.	No. of primary branches/plant	10.35**	1.62**	0.36
4.	No. of capitula/plant	73.05**	29.08**	1.11
5.	Capitulum diameter (cm)	0.08**	0.02**	0.004
6.	No. of seeds/capitulum	62.11**	25.50**	1.90
7.	100-seed weight (g)	0.36**	0.24**	0.06
8.	Days to maturity	28.94**	6.01**	0.50
9.	No. of flowers/capitulum	670.20**	89.52**	13.61
10.	Corolla tube length (cm)	0.05**	0.03**	0.009
11.	Petal length (mm)	0.27**	0.05**	0.014
12.	Anther length (mm)	0.61**	0.10**	0.02
13.	Stigma length (mm)	0.27**	0.10**	0.023
14.	Petal area/flower (cm^2)	0.004**	0.002**	0.0004
15.	Flower yield/plant (g)	0.36**	0.54**	0.0005
16.	Seed yield/plant (g)	30.032**	27.986**	0.911

** Significant at P = 0.01

The importance of additive gene effect for seed yield in safflower has also been reported by Ragab and Friedt (1992). However the present findings are in contrast with those of Ranga Rao (1983).

The magnitude and direction of combining ability effects provide guidelines for selecting parents and their utilization in crop breeding. In the present study the estimates of gca effects of the parents showed that the parents MSN-3-8-5 and GMU-3195 were good general combiners for all the characters studied except number of primary branches/plant, 100-seed weight and corolla tube length in case of MSN-3-8-5 and number of primary branches/plant,

capitulum diameter, number of seeds/capitulum, 100-seed weight and number of flowers/capitulum in case of GMU-3195 (Table 3). The parent MSV-6 was also estimated to give high gca effects for days to 50% flowering, plant height, number of capitula/plant, days to maturity, flower yield/plant and seed yield/plant.

Table 3. Per-se performance of superior general combiners in safflower with desired significant gca effects for different characters

Sr. No.	Character	Parents					
		MSV-6		MSN-3-8-5		GMU-3195	
		Per-se performance	gca effects	Per-se performance	gca effects	Per-se performance	gca effects
1.	Days to 50% flowering	79.67	- 1.66	78.67	- 2.29	78.67	- 2.54
2.	Plant height (cm)	97.47	- 1.64	93	-3.93	85	- 5.02
3.	No. of capitula/plant	25	3.14	26.87	1.82	18.07	1.48
4.	Capitulum diameter (cm)	-	-	2.23	0.04	-	-
5.	No. of seeds/capitulum	-	-	30.6	2.42	-	-
6.	Days to maturity	120.33	- 1.33	120	- 2.53	121.33	- 1.61
7.	No. of flowers/capitulum	-	-	113.87	12.59	-	-
8.	Corolla tube length (cm)	-	-	-	-	2.49	0.07
9.	Petal length (mm)	-	-	8.81	0.06	8.41	0.10
10.	Anther length (mm)	-	-	6.29	0.11	5.96	0.15
11.	Stigma length (mm)	-	-	6.50	0.12	5.92	0.12
12.	Petal area/flower (cm²)	-	-	0.57	0.01	0.54	0.02
13.	Flower yield/plant (g)	1.86	0.08	2.95	0.4	0.95	0.03
14.	Seed yield/plant (g)	13.04	1.34	20.69	2.17	11.46	0.97

The sca analysis of the crosses for different traits indicated that the parents in them had either high x high, high x low or low x low gca effects. The high sca effects in the cross MSN-8 X GMU-3195 for seed yield/plant involving parents with high x high gca effects can be attributed to additive type of interaction between the parents and thus can be utilized in a variety of ways for improving the crop. In view of considerable importance of additive effects and possibility of their fixation, single plant selections may be carried out in segregating generations for evolving superior inbreds. The high sca effects in the crosses MSV-6 X C 2708-2-2 and MSN-8 X CO-1 for seed yield/plant and MSN-3-8-5 X 126-8-2 for flower yield/plant involving one parent with high gca and the other with low gca are probably due to dominant x recessive interaction. Epistatic interactions seem to be responsible for high sca effects in the crosses involving both parents with low gca effects.

Heterosis for flower yield and its components in safflower : The development of genetic male sterile lines of varied nature from different sources has made it possible to harness non-additive gene interaction (observed to be predominant in certain crosses for flower and seed yield) through exploitation of hybrid vigour on commercial scale. The 10-parent diallel analysis showed that the safflower hybrids exhibit highly significant standard heterosis for flower yield and its components. The highest significant standard heterosis in favourable direction was recorded for flower yield/plant (188%), which was followed by number of capitula/ plant (173%), seed yield per plant (171%), number of primary branches/plant (81%), number of seeds/capitulum (63%), number of flowers/capitulum (52%), 100-seed weight (34%), petal area/flower (33%), capitulum diameter (20%), days to 50% flowering (-16%), and plant height (13%). Singh et al. (2000) recorded a high heterosis of 81% over the highest flower yielding parent for flower yield in safflower. High heterosis for seed yield and its components in safflower has been reported by several workers such as Ramachandram and Goud (1982). Thus the results suggest that high heterosis for economic traits existing in safflower can be harnessed successfully with the use of genetic male sterility system in the crop.

Proposed breeding strategy: Thus, based upon the present findings, a breeding plan to improve flower and seed yield in safflower has been envisaged. It includes the evaluation of available genotypes for different physiological and floral traits to generate information on genetic variability existing in them. The genotypes giving high per-se performance for the traits giving high estimates of PCV and GCV, heritability and G.A. as percent of mean (for example number of flowers/capitulum, number of seeds/capitulum, number of capitula/plant, flower yield and seed yield in the present study) can be selected for crossing. The resultant crosses may be studied for the nature of inheritance of different floral and physiological traits and for the existence of heterosis apart from associations between flower yield and its components. The crosses exhibiting high heterosis for both seed and flower yield can be exploited commercially if economic means of hybrid seed production is available. In addition, depending upon the nature of gene action responsible for the inheritance of seed and flower yields in different crosses, the segregating populations of such crosses may be subjected to single plant selections to develop superior lines if additive effects are predominant. In case of the crosses exhibiting dominant x recessive interactions, adoption of biparental mating may be useful to break the undesirable linkages and through recombination may produce transgressive segregants in the subsequent generations. For selecting single plants of desirable type in the segregating generations, the characters like number of primary branches/plant, number of capitula/plant, capitulum diameter, number of seeds/capitulum, number of flowers/capitulum, stigma length and petal area/flower which have shown significant and positive association with both flower and seed yield may be considered to achieve simultaneous improvements in both flower and seed yields in safflower.

Acknowledgements

References

Al-Jibouri, H. A., Miller, P. A. and Robinson, H. F. 1958. Genotypic and environmental variances and covariances in an upland cotton cross of interspecific origin. Agron. J. 50: 633-636.

Burton, G. W. 1952. Quantitative inheritance in grasses. Proc. Sixth Int. Grassland Cong. 1: 277-283. National Publishing Co., Washington D.C.

Griffing, B. 1956. A generalized treatment of the use of diallel crosses in quantitative inheritance. Heredity 10: 31-50.

Hanson, C. H., Robinson, H. F. and Comstock, R. E. 1956. Biometrical studies of yield in segregating populations of Korean Lespedeza. Agron. J. 48: 268-272.

Johnson, H. W., Robinson, H. F. and Comstock, R. E. 1955. Estimates of genetic and environmental variability in soybeans. Agron. J., 47: 314-318.

Patil, A. J., Murumkar, D. R. and Tambe, S. I. 2002. Genetic variability studies in safflower germplasm screened for early rabi situations. Sesame and Safflower Newsletter 17: 85-88.

Ragab, A. I. And Friedt, W. 1992. Combining ability and reciprocal effects for some agronomic and oil quality traits in safflower (*Carthamus tinctorius* L.). Sesame and Safflower Newsletter 7: 62-69.

Ramachandram, M. and Goud, J. V. 1982. Heterosis for seed yield and oil content in safflower. Indian J. Agric. Sci. 52 (9): 561-563.

Ranga Rao, V. 1983. Combining ability for yield, percent oil and related components in safflower. Indian J. Genet. 43(1): 68-75.

Singh, Vrijendra, Deshpande, M. B. and Nimbkar, N. 2000. Potential for commercial exploitation of hybrid vigour for flower yield in safflower and popularization of safflower flowers as herbal health tea. In : Proc. National Seminar on the Frontiers of Research and Development in Medicinal Plants. Journal of Medicinal and Aromatic Plant Sciences. 22/4A and 23/1A. pp. 303-307.