



Research Note

Genetic Divergence Studies in Safflower, *Carthamus tinctorius* L.

D. Shivani, Ch.Sreelakshmi and C.V.Sameer Kumar

(Received: 13 Aug 2010; Accepted: 24 Aug 2010)

Abstract:

The present study was carried out to study the genetic divergence among 75 germplasm lines of safflower. Analysis of variance revealed significant variation among the genotypes for all the characters studied. Among the genotypes, GMU 3327, GMU 3279, GMU 3325 and GMU 3313 were found to be promising on the basis of *per se* performance for seed yield. Seed yield exhibited maximum contribution towards genetic divergence followed by number of capitula per plant, number of seeds per capitulum, oil content, days to 50% flowering and days to maturity. The genotypes were grouped into 8 clusters out of which cluster II is having maximum of 23 genotypes followed by cluster I with 20 genotypes. Maximum inter cluster distance was observed between clusters VII and VIII followed by clusters VI and VIII, clusters IV and VIII and clusters I and VIII.

Key words:

Safflower, divergence

Safflower is an important oil seed crop and its oil constitutes an important source of PUFA in the oil based diets of many people in India. For improvement programme of existing safflower varieties, the selection of suitable diverse parents for hybridization is an important step for getting desired recombinations in the segregating generations. The D^2 classifies the genotypes into homogenous groups / clusters with little diversity within cluster while diversity between two clusters is usually high. Thus representative genotypes from diverse clusters can be earmarked for utilization in hybridization programme depending upon breeding objective. Since, the literature in respect of genetic divergence studies in safflower is meager, therefore present investigation was undertaken to assess the presence of genetic diversity among safflower germplasm lines.

The experimental material for the present investigation consists of 75 genotypes which were obtained from Directorate of Oilseeds Research

Hyderabad. The experiment was conducted at Agricultural Research Station, Tandur during *rabi* 2009-10 in augmented block design. The entries were grown in 5m long single row plots with a spacing of 20 cm between the plants and 45 cm between the rows. Recommended cultural practices were followed to raise a good crop. Five competitive plants from each line were randomly selected for recording observations for seven metric characters viz., days to 50% flowering, days to maturity, number of capitula per plant, number of seeds per capitulum, test weight (g), seed yield (kg/ha) and oil content(%). Genetic divergence among 75 genotypes was analyzed by using Mahalanobis' D^2 statistic (Rao, 1952).

Analysis of variance was performed to test the significance of difference among the genotypes for the characters studied. Partitioning the variance and co-variance into genotypic, phenotypic and environmental components was done as suggested by Fisher and Yates (1958) and Mahalanobis generalized distance (Mahalanobis, 1936 and Rao, 1952) for computing genetic divergence for the characters studied. Selection of parents for hybridization from different clusters was performed

on the basis of mean statistical distance as suggested by Bhatt (1970).

Analysis of variance revealed that the variation among the genotypes was significant for all the characters studied and indicated the presence of significant genetic variability for the characters. Among 75 genotypes, GMU 3327, GMU 3279, GMU 3325 and GMU 3313 were found to be promising on the basis of *per se* performance for seed yield. In this investigation seed yield and number of capitula per plant were found to be significant and important source of variation. Gajbhiye, 2000 also noticed that 100-seed weight, plant height, numbers of pods per plant were important source of variation in lathyrus. The percent contribution of individual characters towards genetic divergence is taken as a measure for relative importance of the characters towards genetic divergence (Table 2). Seed yield exhibited maximum contribution towards genetic divergence (96.79%) followed by number of capitula per plant (1.33%), number of seeds per capitulum (0.65%), oil content (0.54%), days to 50% flowering (0.43%) and days to maturity (0.25%). These results are in agreement with the earlier findings of Diwakar *et al.*, (2006).

For selection of parents for hybridization programme, information on clusters, intra and inter cluster distance and cluster mean should be of paramount importance. In the present study, 75 genotypes were grouped into 8 clusters (Table 1) out of which three clusters comprised only one genotype each. Cluster II is having maximum of 23 genotypes followed by cluster I with 20 genotypes, cluster III with 13 genotypes, IV with 10 genotypes and V with 6 genotypes. The average inter, intra cluster distance and cluster mean have been presented in Table 3.

In the present study, all possible combinations beyond the mean statistical distance D formed from different clusters have been arranged in descending order of magnitude of genetic distance and promising four cluster combinations. For practical consideration, characters like earliness, seed yield and high oil content while choosing the genotypes as parents from different clusters should be given due importance. The clusters containing only one genotype appeared to be genetically diverse from each other and also from other genotypes under study. In Tocher's method, (Rao, 1952) maximum inter cluster distance was observed between clusters VII and VIII (D=2044) followed by clusters VI and VIII (D=1867.05), clusters IV and VIII (D=1628.27)

and clusters I and VIII (D=1372.01). Thus, crossing among parents from these clusters would give the desirable transgressive segregates. The clusters VI and VII showed the lowest degree of divergence indicating a close relationship between them. Therefore, crossing to genotypes belonging to these clusters may not result into improvement in the desired direction as there might be closeness in respect of their origin. These findings are in close agreement with those reported by Patil *et al.*, (1991) and Ghongade and Navale (1995). However, Gajbhiye (2000) suggested that mean statistical distance may be considered arbitrarily as a guide line and crosses between parents belonging to different clusters having same higher inter cluster distance than mean statistical distance may be attempted.

The parents for crossing should be chosen from widely distant clusters but, it was observed in the present investigation that several genotypes were included in widely separated clusters. Then the question arises which of the genotypes from these more diverse clusters may be used for crossing. The problem can be solved safely considering the cluster means (Table 4) and the mean performance of each genotype for the trait selected for improvement. The potential parents selected for hybridization in combination are GMU 3279, GMU 3325, GMU 3313, GMU 3324, GMU 3314, GMU 3319 GMU 3327

References :

- Bhatt, G.M. 1970. Multivariate analysis approach for selection of parents for hybridization aiming at yield improvement in self pollinated crops. *Australian J. Agric. Res.*, **21**:1-17.
- Diwakar, R., Sreedhar, N. and Mukta, N. 2006. Studies on genetic diversity in safflower, *Carthamus tinctorius* L. *J.Oilseeds Res.*, **23**: 301-303.
- Fisher, R.A. and Yates, F. 1958. *Statistical tables for biological, agricultural and medicinal research*. 5th Edn. Halner Publishing Company, New York.
- Gajbhiye, V.R. 2000. D² analysis in land races and some promising germplasm lines in lathyrus. *M.Sc (Agri) Thesis*, Dept of Botany, College of Agri., Nagpur, Dr. Punjab Rao Deshmukh Agri. Univ., Akola.
- Ghongade, R.A. and Navale, P.A. 1995. Genetic divergence in safflower. *J.Maharashtra agric. Univ.*, **20**:249-251.
- Mahalanobis, P.C. 1936. On the generalized distance in statistics. In : *Proceed. on Natural Institute of Sciences, India*, **2**; 49-55.
- Patil, B.R., Dubhe, R.S., Ghorpade, P.B., Dhumale, D.B. and Deshmukh, M.P. 1991. Studies on genetic

- divergence in safflower. *Indian J. Genet.*, **40**:73-85.
- Rao, C.R. 1952. *Advanced statistical methods in biometrical research*. John Wiley and Sons, Znc. New York.

Table 1: Grouping of 75 genotypes of safflower in different clusters

Cluster No.	Number of genotypes	Name of the genotype
I	20	GMU 3275, GMU 3340, GMU 3272, GMU 3306, GMU 3294, GMU 3258, GMU 3299, GMU 3292, GMU 3276, GMU 3341, GMU 3284, GMU 3316, GMU 3332, GMU 3278, GMU 3260, GMU 3264, GMU 3330, GMU 3259, GMU 3297, GMU 3262.
II	23	GMU 3290, GMU 3304, GMU 3295, GMU 3273, GMU 3331, GMU 3282, GMU 3311, GMU 3323, GMU 3215, GMU 3256, GMU 3329, GMU 3339, GMU 3286, GMU 3322, GMU 3281, GMU 3333, GMU 3287, GMU 3303, GMU 3300, GMU 3301, GMU 3328, GMU 3307, GMU 3285.
III	13	GMU 3302, GMU 3305, GMU 3289, GMU 3309, GMU 3280, GMU 3326, GMU 3342, GMU 3320, GMU 3277, GMU 3253, GMU 3265, GMU 3310, GMU 3336.
IV	10	GMU 3257, GMU 3296, GMU 3283, GMU 3261, GMU 3317, GMU 3270, GMU 3341, GMU 3268, GMU 3334, GMU 3263.
V	6	GMU 3279, GMU 3325, GMU 3313, GMU 3324, GMU 3314, GMU 3319.
VI	1	GMU 3269
VII	1	GMU 3266
VIII	1	GMU 3327

Table 2: Percent contribution of 7 traits towards genetic divergence in 75 germplasm lines of safflower

Character	% contribution
Days to 50% flowering	0.43
Days to maturity	0.25
Number of capitula per plant	1.33
Number of seeds per capitulum	0.65
Test weight (g)	0.00
Seed yield (kg/ha)	96.79
Oil content (%)	0.54



Table 3: Average intra (diagonal) and inter cluster distances in 75 germplasm lines of safflower

	I	II	III	IV	V	VI	VII	VIII
I	81.19	281.95	526.88	271.82	797.93	499.35	675.54	1372.01
II		110.16	273.29	531.97	537.24	765.62	941.93	1107.87
III			96.37	781.71	289.21	1018.06	1194.80	853.66
IV				108.79	1053.53	251.27	423.96	1628.27
V					106.06	1291.00	1467.81	581.94
VI						0.00	177.70	1867.05
VII							0.00	2044.00
VIII								0.00

Table 4: Mean of cluster from 75 germplasm lines of safflower for 7 traits

	Days to 50% flowering	Days to maturity	Number of capitula per plant	Number of seeds per capitulum	Test weight (g)	Seed yield (kg/ha)	Oil content (%)
I	81.25	110.90	23.35	17.40	5.43	895.15	22.44
II	80.13	110.57	24.39	17.09	5.34	1160.78	22.73
III	80.77	110.85	27.62	17.38	5.68	1414.92	22.60
IV	80.20	110.00	26.10	21.10	5.33	639.40	22.93
V	80.33	110.50	25.33	18.33	5.34	1688.17	22.25
VI	78.00	111.00	26.00	23.00	3.55	399.00	25.00
VII	81.00	112.00	15.00	15.00	5.28	222.00	17.90
VIII	82.00	112.00	18.00	16.00	4.74	2266.00	18.40