



Research Paper

MULTIVARIATE STUDIES IN SAFFLOWER, *Carthamus tinctorius* L.

D. Shivani and Ch. Sreelakshmi

Agricultural Research Station, Tandur.

Abstract

A field experiment was conducted with eighty safflower germplasm lines to study the diversity among the germplasm lines, which were grouped into twelve clusters revealing the presence of considerable amount of genetic diversity in the material. Cluster II and the maximum number of 23 genotypes followed by cluster I with 22 genotypes and cluster V with 10 genotypes. The intra cluster distance ranged from 0.00 to 133.29. The highest intra cluster distance observed for cluster XII (133.29) followed by cluster II (85.50) and cluster I (78.48). The inter cluster D2 values ranged from 46.85 to 1506.01, the maximum inter cluster distance was observed between the clusters IV and XII (1506.01) followed by I and XII (1372) and the clusters (1239.96), which indicated that the genotypes included in these clusters will give high heterotic responses and thus better segregants. Among the 12 clusters studied, seed yield contributed the most (95%) towards the divergence of genotypes.

Key words: Safflower, Genetic divergence.

INTRODUCTION

Safflower, *Carthamus tinctorius* L. is an important oilseed crop of India and its oil is good for all cardiac problems. Safflower petals are an important source in the manufacture of carthamine dye, a natural colouring agent. There exists abundant variability among the safflower germplasm collections for various traits which need to be harnessed for breeding high yielding varieties. However, the proper and precise utilization of these lines in breeding programmes depends on their characterization for qualitative and quantitative traits. Information on nature and degree of genetic divergence would help the plant breeders in choosing the right type of parents for purposeful hybridization. The importance of selection of parents on the basis of genetic distance to get heterotic effect in F1 generation and higher frequency of better segregants in subsequent generations has been reported by earlier researchers in oilseed crop like linseed (Pyasi, 2000). Multivariate analysis is an important biometrical technique for quantifying the degree of divergence among different genotypes. Mahalanobis D² statistics (1936) as described by Rao, 1952 has been successfully used by plant breeders in different crops for isolating genetically diverse genotypes. In the present study an attempt has been made to utilize this useful technique for selection of parents for hybridization in safflower breeding programme.

MATERIAL AND METHODS

The material for the present study comprised of 75 safflower germplasm accessions and five released varieties viz., Bhima, Manjira, A-1, JSF-1 and HUS 305. The experiment was conducted at Agricultural Research Station, Tandur of Acharya N G Ranga Agricultural

University during rabi, 2011-12. Each genotype was sown in one row of 5m length spaced at 45 cm with inter plant distance of 20 cm. The experiment was laid out in augmented block design. In each entry five plants were randomly tagged and utilized to collect data on seed yield and associated attributes viz., days to 50% flowering, days to maturity, plant height (cm), number of capitula per plant, number of seeds per capitulum, 100-seed weight (g) and seed (kg/ha) (Table 1). The data were subjected to statistical analysis using Mahalanobis D^2 statistics and Tocher's method as described by Rao, 1952 for determining the group constellation.

RESULTS AND DISCUSSION

The analysis of variance significant differences among the genotypes for all the traits studied. Through multivariate analysis, the 80 genotypes based on D^2 values were grouped into 12 clusters. Cluster II had the maximum number of genotypes (23), followed by cluster by cluster with 22 genotypes and cluster V with 10 genotypes reflecting a narrow genetic diversity among them. Further, cluster III, cluster IV and cluster XII had 9, 8 and 3 genotypes, respectively while the rest of the clusters VI, VII, VIII, IX, X and XI were solitary clusters demonstrating the impact of selection pressure in increasing the genetic diversity. The average intra cluster distance (Table 1) revealed that the genetic diversity among the genotypes in cluster V was minimum (43.11) followed by cluster IV (49.67) indicating that the genotypes within these clusters were similar. The maximum intra cluster distance (133.29) was observed in cluster II, hence selection within these clusters might be carried out on the basis of highest mean for the desirable traits. Such intra cluster genetic diversity among the genotypes could be due to heterogeneity, genetic architecture of the populations, past history of selection in developmental traits and degree of general combining ability. These results are in agreement with the earlier reports of Murkute and Deshmukh, 2011.

The relative divergence of each cluster from other clusters (inter cluster distance) indicated high order of divergence between cluster XII and IV (1506.01) followed by that between cluster I and XII (1372.11). Hence, selection of parents from these clusters for hybridization programme would help create novel recombinant with maximum hybrid vigour. Hybridization between genetically distant genotypes to generate promising breeding material has been suggested by Sankarapandian *et al.*, (1996) and Shailaja *et al.*, (2011). The minimum inter cluster distance was observed between cluster VI and VII (46.85) indicating the close relationship among the genotypes in these clusters.

The cluster mean of each trait towards divergence are presented in Table 2. There was wide range of variation in the cluster mean values for most of the characters under study. Cluster IX had highest mean values for number of seeds per capitula and test weight whereas cluster VIII recorded least number of days for flowering and maturity. Cluster XI recorded highest mean values for plant height, cluster VII for number of capitula per plant and cluster XII for seed yield. Sreenivasa *et al.*, (2010) and Diwakar, *et al.*, (2006) reported similar results in safflower.

The characters contributing to most of the divergence should be given more importance for the purpose of effective selection and the choice of parents for hybridization. Seed yield contributed maximum (95.89%) towards total genetic divergence (Table 3) followed by plant height and number of seeds per capitula whereas all the other characters contributed the least divergence indicating narrow diversity for those characters among the genotypes under study. The data on cluster distances and per se performance of genotypes were used to select genetically diverse and agronomically superior genotypes and desirable recombinants. On this basis of the maximum inter cluster values and per se performance for seed yield and plant height, the genotypes GMU 3661, GMU 3672, GMU 3674, GMU 3684, GMU 3705, GMU 3708, GMU 3711 and GMU 3716 selected for crossing are expected to give rise to promising segregants for seed yield and hence may be used in future breeding programmes for improvement of yield in safflower.

Table. 1 Average intra and inter cluster distances (D^2 values) for twelve clusters of safflower germplasm

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII
I	78.48	521.64	147.20	149.18	353.33	639.22	683.27	726.94	771.88	815.74	904.65	1372.11
II		85.50	389.75	653.75	179.55	134.17	175.47	216.96	260.90	303.78	391.64	858.28
III			52.81	271.08	220.97	506.41	550.51	594.21	639.19	683.15	772.10	1239.96
IV				49.67	484.67	772.37	816.42	860.31	905.37	949.27	1038.28	1506.01
V					43.11	290.49	334.65	378.21	423.12	467.04	555.93	1024.14
VI						0.00	46.85	89.17	133.39	177.56	266.36	735.61
VII							0.00	47.50	92.29	134.50	222.69	691.88
VIII								0.00	48.70	89.88	179.00	648.12
IX									0.00	48.77	134.75	603.53
X										0.00	89.69	559.54
XI											0.00	471.56
XII												133.29

Table. 2 Eigene values, proportion of the total variance represented by first three principal components, cumulative percent variance and component loading of different characters in safflower germplasm

	PC1	PC2	PC3
Eigene value (root)	8085533.000	4143.403	2187.218
Percent Var. Exp	99.87786	0.05118	0.02702
Cumulative variance explained	99.87786	99.92904	99.95606
Days to 50% flowering	0.00017	0.09904	0.17319
Days to maturity	0.00027	0.10096	0.17959
Plant height (cm)	-0.00693	0.84836	0.44425
Number of capitula per plant	-0.00106	0.00623	0.28291
Number of seeds per capitula	-0.00592	-0.50983	0.81245
Test weight (g)	-0.00066	-0.01784	-0.01450
Seed yield (kg/ha)	-0.99996	-0.00281	-0.00810

Table 3: Cluster means of eighty germplasm accessions for six quantitative traits in safflower

Cluster No.	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of capitula per plant	Number of seeds per capitula	Test weight (g)	Seed yield (kg/ha)
Cluster I	80.48	112.58	68.97	11.9	16.2	4.07	567.17
Cluster II	79.33	111.56	71.64	14.0	19.76	4.49	1077.78
Cluster III	79.87	111.53	67.91	13.93	20.41	4.20	693.93
Cluster IV	81.50	113.75	70.95	16.0	14.83	4.10	427.38
Cluster V	79.89	112.67	70.40	13.22	22.78	4.24	910.00
Cluster VI	84.00	117.00	71.20	13.0	22.0	3.61	1199.00
Cluster VII	83.00	115.00	76.30	28.0	20.6	4.69	1243.00
Cluster VIII	75.00	107.00	69.80	16.0	18.2	4.27	1287.00
Cluster IX	84.00	117.00	63.60	8.0	26.0	5.90	1332.00
Cluster X	78.00	110.00	79.80	10.0	16.6	4.13	1376.00
Cluster XI	83.00	113.00	84.20	13.0	24.4	5.01	1465.00
Cluster XII	82.00	113.50	81.60	14.0	20.8	5.13	1931.50

Table 4: Percent contribution of different characters towards genetic divergence

Days to 50% flowering	0.32
Days to maturity	0.38
Plant height (cm)	1.84
Number of capitula per plant	0.66
Number of seeds per capitula	0.92
Test weight (g)	0.00
Seed yield (kg/ha)	95.89

REFERENCES

- Diwakar R, Sreedhar N and Mukta N 2006.** Studies on genetic diversity in safflower, *Carthamus tinctorius* L. Journal of Oilseeds Research, 23: 301-303.
- Mahalanobis, P .C. 1936.** On the generalized distance in statistics. *Proc. National Academy of Sci.*, 12: 49-55.
- Murkute, R.K and Deshmukh,, S.N. 2011.** Genetic divergence in selected germplasm of safflower, *Carthamus tinctorius* L. Journal of Oilseeds Research, 28 (2): 169-171.
- Pyasi, S.K. 2000.** Genetic divergence in linseed. Crop Research, 19(1): 158-161.
- Rao, C R 1952.** Advanced statistical methods in Biometrical research, John Wiley and Sons, New York: 390.
- Sankarapandian, R., Muppudathi, N.,Rajarathinam, S., and Chidambaram, S. 1996.** Genetic divergence in sunflower. Madras Agricultural Journal, 83: 637-639.
- Shailaja, M., Bharathi, M., Mukta, N., and Sreedhar, N. 2011.** Analysis of genetic divergence in safflower, *Carthamus tinctorius* L. Journal of Oilseeds Research, 28 (1):84-86.
- Sreenivasa V, Sreedhar N and Mukta N 2010.** Genetic divergence in selected germplasm of safflower, *Carthamus tinctorius* L. Journal of Oilseeds Research 27 (1): 85-87.