The Andhra Agric. J 62(2):293-296, 2015

Studies on Genetic Divergence 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 had 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 was observed for cluster XII (133.29) followed by cluster II (85.50) and cluster I (78.48). The inter cluster D2 values ranged from 43.11 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 III and XII clusters (1239.96), which indicated that the genotypes included in these clusters will give high heterotic responses and thus produce better segregants. Among the 12 clusters studied, seed yield contributed the most (95%) towards the divergence of genotypes.

Key words : Genetic divergence, Safflower.

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 earlier by 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 D^2 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 (Table 1). 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 yield (kg/ha). 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 revealed significant differences among the genotypes for all the traits studied. Through multivariate analysis, the

Table 1. Table showing 75 safflower germplasm accessions along with 5 checks included in the study.

GMU 3635	GMU 3650	GMU 3668	GMU 3684	GMU 3701
GMU 3636	GMU 3651	GMU 3670	GMU 3685	GMU 3702
GMU 3637	GMU 3652	GMU 3671	GMU 3686	GMU 3703
GMU 3638	GMU 3653	GMU 3672	GMU 3687	GMU 3704
GMU 3639	GMU 3654	GMU 3673	GMU 3689	GMU 3705
GMU 3640	GMU 3656	GMU 3674	GMU 3690	GMU 3706
GMU 3641	GMU 3658	GMU 3675	GMU 3691	GMU 3708
GMU 3642	GMU 3659	GMU 3676	GMU 3692	GMU 3709
GMU 3643	GMU 3660	GMU 3677	GMU 3693	GMU 3711
GMU 3644	GMU 3661	GMU 3678	GMU 3694	GMU 3713
GMU 3645	GMU 3662	GMU 3679	EC 523367	GMU 3715
GMU 3646	GMU 3663	GMU 3680	GMU 3696	GMU 3716
GMU 3647	GMU 3664	GMU 3681	GMU 3698	GMU 3718
GMU 3648	GMU 3666	GMU 3682	GMU 3699	GMU 3719
GMU 3649	GMU 3667	GMU 3683	GMU 3700	GMU 3720
Checks:				
Bhima	Manjira	A 1	JSF-1	HUS 305

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 I 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 2) 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 XII, 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 be helpful in generation of novel recombinants 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 3. 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

Table 2. 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 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	11.90	16.20	4.07	567.17
Cluster II	79.33	111.56	71.64	14.00	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	16.00	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	13.00	22.00	3.61	1199.00
Cluster VII	83.00	115.00	76.30	28.00	20.60	4.69	1243.00
Cluster VIII	75.00	107.00	69.80	16.00	18.20	4.27	1287.00
Cluster IX	84.00	117.00	63.60	8.00	26.00	5.90	1332.00
Cluster X	78.00	110.00	79.80	10.00	16.60	4.13	1376.00
Cluster XI	83.00	113.00	84.20	13.00	24.40	5.01	1465.00
Cluster XII	82.00	113.50	81.60	14.00	20.80	5.13	1931.50

Table 4. Percent contribution of different characters towards genetic divergence.

Character	Percent contribution 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

maximum (95.89%) towards total genetic divergence (Table 4) 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 will be used to select genetically diverse and agronomically superior genotypes and desirable recombinants. On the 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 3711and GMU 3716 selected for crossing may be to get promising segregants for seed yield and hence may be used in future breeding programmes for improvement of yield in safflower.

LITERATURE CITED

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, Muppidathi 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.

(Received on 06.07.2013 and revised on 04.06.2014)