Studies on Genetic Divergence in Safflower (*Carthamus tinctorius* L.)

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Euclidean cluster analysis was used for the characterization of 36 exotic germplasm accessions of different geographical origin and four check varieties of safflower (*Carthamus tinctorius* L.). A quantitative assessment of genetic divergence for eleven characters using Mahalanobis D^2 statistics revealed the presence of considerable genetic diversity.The forty genotypes were grouped into seven well defined clusters with variable number of genotypes. The inter-cluster distances (D value) ranged from 8.27 to 25.68. Among the plant attributes, hull content, number of seeds in main capitulum, seed yield/plant and number of effective capitula were found to be important in the present study. Accessions GMU 848, 4097, 4095, 5110 from Cluster V and GMU 1727, 1747, 5111 from Cluster VII were identified as potential parents in future hybridization programmes for genetic improvement in safflower.

Key Words: Safflower, Genetic divergence, Cluster, Cluster means

Introduction

Safflower (*Carthamus tinctorius* L.) is one of humanity's oldest crops, cultivated mainly for the orange red dye extracted from its coloured florets and the highly valued edible oil obtained from the seeds. Oil has been produced commercially and for export for about 50 years, first as an oil source for the paint industry, now as an edible oil for cooking. Over 60 countries grow safflower, but more than half is produced in India. Production in the USA, Mexico, Ethiopia, Argentina and Australia comprises most of the remainder (Li Dajue and Mündel, 1996). India occupies a premier position in the world in safflower area and production, however, its productivity is only about 80% of the world's productivity. Though there has been an increasing trend in area, production and productivity of safflower in the country during the past 30 years (Hegde and Sudhakara Babu, 2002), concerted efforts are still required towards breeding highly productive cultivars to bridge the gap between the domestic and international levels of productivity.

The role of plant genetic resources in the improvement of cultivated plants has been well recognized. Characterization and evaluation of both exotic and indigenous collections for information on useful traits forms the basic step for crop improvement programmes. Study of genetic divergence among a set of genotypes will therefore enable a plant breeder to choose suitable parents and plan an appropriate hybridization programme. D^2 statistics has proved to be a powerful tool in discerning genetic divergence among groups based upon multiple growth characters, assessing relative characters and assessing relative contribution of different components to total divergence (Bhatt, 1973). The present study was conducted to determine the magnitude of variability in yield and various agronomic traits and the degree of inter-relationship among traits in the exotic accessions of safflower and their performance against released high yielding varieties for identification of promising germplasm.

Materials and Methods

Forty diverse genotypes of safflower of different geographical origin were selected for the present study. Of these, thirty six exotic accessions were acquired from fifteen countries (Turkey, USA, Pakistan, Egypt, Iran, Jordan, Portugal, Germany, Israel, Spain, USSR, China, Argentina, Ethiopia and Canada), while four cultivated varieties (A-1, CO-1, Bhima, JSI-7) were included as checks. The experimental material was sown in Randomized Block Design with three replications at College Farm, Acharya NG Ranga Agricultural University, Rajendranagar, Hyderabad. Each entry was represented by three rows of 2.5 m length. The inter-row and inter-plant spacings were 60 cm and 20 cm, respectively. Five randomly selected plants of each genotype in each replication were used for recording observations on ten characters, *viz.*, days to 50% flowering, plant height (cm), diameter of main capitulum (mm), number of effective capitula, number of seeds in main capitulum, 100-seed weight, hull content (%), oil content (%), seed yield per plant (g) and oil yield per plant (g). Divergence was studied by multivariate analysis using Mahalanobis D^2 statistics and the genotypes were

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grouped into different clusters by employing Euclidean method as described by Rao (1952).

Results and Discussion

Multivariate analysis based on D^2 statistics indicated the presence of considerable amount of genetic diversity among the genotypes studied. This statistical tool has been widely employed to resolve genetic divergence at inter-varietal and sub-species level in classifying the crop plants (FAO, 1997). The forty genotypes were grouped into seven clusters by using Euclidean cluster method (Table 1). Cluster II was the largest consisting of 10 genotypes followed by cluster III, I and VI having 7, 6 and 5 genotypes, respectively. Clusters IV, V and VII consisted of four genotypes each. The pattern of distribution of genotypes into various clusters was at random suggesting that geographical distribution and genetic diversity were not related. This was in accordance with the results reported by Patil *et al.* (1984) and Patel *et al.* (1989). The magnitude of D^2 values suggested presence of considerable amount of diversity in the experimental material. Similar results were obtained by Ranga Rao *et al.* (1980), Agarwal *et al.* (1982), Mandal and Banerjee (1991), Patil *et al*. (1991), Dingming *et al.* (1993), and Ghongade and Navale (1995).

The analysis of dispersion for the test of significance of differences in the mean values based on Wilk's criterion revealed highly significant differences between the genotypes for the aggregation of ten characters.

The maximum intra-cluster distance was observed in cluster VII (9.96) and this might have been due to limited gene exchange or selection practiced among the genotypes for diverse characters. This was followed by cluster VI (7.74), cluster V (7.44), cluster I (7.31), cluster IV (7.28) and cluster II (6.62). Cluster III (6.17) displayed the least intra-cluster divergence revealing the similarity of genotypes within the cluster. Based on the inter-cluster distance, it was found that cluster IV was highly divergent from cluster V (25.68) followed by cluster II and cluster V (21.27) (Table 2). In the present study, inter-cluster distances were found to be greater than intra-cluster distances revealing considerable amount of genetic diversity among the genotypes evaluated.

Table 1. Clustering pattern of 40 genotypes of safflower

No. of Cluster	No. of genotypes	Genotypes/Check varieties
I	6	GMU 683, 807, 1186, 1232, 1238, 1872
II	10	GMU 740, 871, 874, 1037, 1209, 1233, 1240, 1778, 5121, 5127
III	7	GMU 1163, 1193, 1237, 1749, 1868, 5117, JSI-7
IV	4	GMU 1160, 1241, 1246, CO-1
V	4	GMU 848, 4097, 4095, 5110
VI	5	GMU 1230, 1402, 1429, 1741, A-1
VII	4	GMU 1727, 1747, 5111, Bhima

Table 2. Intra and inter-Euclidean cluster distances

Cluster No.	I	II	III	IV	V	VI	VII
I	**7.31**	8.50	8.58	12.11	20.57	15.22	14.88
II		**6.62**	8.27	9.65	21.27	14.86	15.88
III			**6.17**	11.84	16.95	10.84	12.84
IV				**7.28**	25.68	18.58	20.77
V					**7.44**	11.38	12.44
VI						**7.74**	11.75
VII							**9.96**

Values in bold are intra-cluster distances

The presence of variability in the 40 germplasm accessions was also reflected in the cluster means for the ten traits evaluated (Table 3). Genotypes in cluster III were early to flower (79.52) while maximum days to 50 per cent flowering was observed for cluster VI (81.40). Cluster IV recorded the maximum plant height (86.70 cm) but minimum values for 6 other traits, viz., diameter of main capitulum, number of effective capitula, number of seeds per capitulum, oil content, seed and oil yield were observed. Maximum diameter of main capitulum (25.26 mm), highest oil content (26.60%) and oil yield per plant (16.10 g) were recorded in Cluster V. Highest cluster mean for number of effective capitula was observed in Cluster I (33.63) which also recorded the least hull content (35.53%). Maximum number of seeds per capitulum (25.45) and seed yield per plant (60.67 g) were recorded in Cluster VII whereas maximum 100-seed weight was recorded in Cluster VI (5.51 g).

The number of times that each of the ten quantitative characters appeared in combination and their respective per cent contribution towards diversity is presented in Table 4. Greater emphasis should be laid on those characters contributing maximum to the D^2 values for the purpose of further selection and choice of parents for hybridization. Highest contribution in this regard was of hull content (46.79%) followed by number of seeds in main capitulum (17.05%), seed yield per plant (15.38%), number of effective capitula per plant (11.15%), plant height (6.03 %), oil content (1.67 %), oil yield per plant (0.77), diameter of main capitulum (0.64 %) and 100-seed weight (0.51 %). Days to 50 per cent flowering did not contribute towards genetic divergence.

The present findings can be used for the selection of suitable parents based on the traits identified for

Table 3. Cluster means for ten characters in 40 safflower genotypes

Cluster No.	Days to 50% flowering	Plant height (cm)	Diameter of main capitulum (mm)	No. of effective capitula	No. of seeds in main capitulum	100 seed weight (g)	Hull content (%)	Oil content (%) (g)	Seed yield plant (g)	Oil yield plant
I	80.72	80.88	23.19	33.63	23.42	4.56	35.53	25.13	29.30	7.41
II	79.93	74.47	22.49	29.24	19.45	4.82	35.69	26.28	29.34	7.76
III	79.52	80.52	22.69	27.75	22.19	4.64	38.02	26.08	28.28	7.34
IV	81.25	86.70	20.20	20.65	17.48	5.07	35.74	23.93	20.36	4.88
V	79.58	84.05	25.46	33.01	25.26	5.25	43.52	26.80	60.15	16.10
VI	81.40	79.26	22.68	29.74	20.86	5.51	41.84	24.33	38.77	9.41
VII	81.08	78.83	24.06	30.11	25.45	4.84	39.34	24.32	60.67	14.71

Table 4. Contribution of different characters towards genetic divergence (D^2) in 40 genotypes of safflower

Source	No of times ranked first	Per cent contribution towards divergence
Days to 50% flowering	0	0
Plant height (cm)	47	6.03
Diameter of main capitulum (mm)	5	0.64
No. of effective capitula	87	11.15
No. of seeds in main capitulum	133	17.05
100-seed weight (g)	4	0.51
Hull content (%)	365	46.79
Oil content (%)	13	1.67
Seed yield/plant (g)	120	15.38
Oil yield/plant (g)	6	0.77

improvement. Accessions GMU 848, 4097, 4095, 5110 from Cluster V and GMU 1727, 1747, 5111 from Cluster VII were identified as potential parents in future hybridization programmes for genetic improvement in safflower.

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