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GENETIC DIVERGENCE IN SAFFLOWER (*CARTHAMUS TINCTORIUS* L.)

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ABSTRACT

Genetic diversity in a population of 60 representative genotypes of safflower (*Carthamus tinctorius* L.), assessed using Mahalanobis's D^2 value, indicated considerable diversity in the material studied. Plant height, seed yield, branching height and 1000-seed weight contributed considerably, accounting for 80% of total divergence. The results obtained by D^2 analysis were confirmed by canonical analysis. Using multivariate analysis, the 60 genotypes were divided in 14 clusters. The pattern of distribution of genotypes from different geographical regions into various clusters was random, demonstrating that geographical isolation may not be the only factor causing genetic diversity.

Key words: Genetic divergence, safflower.

Safflower has been under cultivation in India for a long time [1] as an important source of edible oil and is also used in the manufacture of 'carthamine' and safflower-yellow dye. A logical way to start any breeding programme is to survey the variation present in the germplasm. Precise information on the nature and degree of genetic divergence would help the plant breeder in choosing the right type of parents for purposeful hybridization or heterosis breeding programmes.

MATERIALS AND METHODS

Sixty representative genotypes were chosen for this study from the safflower germplasm collection of about 2000 lines maintained at the Agricultural Research Institute, Rajendranagar, Hyderabad. These included 26 lines from India and 30 introductions from most of the safflower growing countries of the world.

The experiment was laid out in randomised block design with three replications with single row-plots of 3 m length and 45 × 30 cm spacing. Data were recorded on five plants chosen at random for 11 economic traits (Table 1), and means of the 15 plants over three replications used for analysis. From the estimates of variances

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and covariances, V statistic, which utilizes Wilk's Λ criterion, a simultaneous test of differences between mean values of a number of correlated variables was done. Further, the analysis of genetic divergence using Mahalanobis's D^2 statistic was carried out as described by Rao [2]. On the basis of the magnitude of the D^2 values the varieties were grouped into a number of clusters as suggested by Tocher [2]. The mutual relationship among populations was also determined by using the principal component analysis.

Table 1. ANOVA and coefficients of variability for 60 safflower genotypes in respect of 11 characters

Source	d.f.	Plant height	Days to flower	No. of primaries	No. of secondaries	Branching height	Capsules per plant	Seeds per capitulum	1000-seed weight	Seed yield per plant	Oil content	Oil yield per plant
Replications	2	6.1	1.4	2.0	13.9	1.0	16.4	0.5	1.2	3.3	1.5	0.2
Genotypes	59	489.1**	35.1**	24.3**	114.6**	415.1**	241.8**	151.7**	198.6**	343.5**	14.1**	36.1**
CV %		25.8	8.0	45.3	47.8	70.3	45.2	64.8	34.6	93.2	11.6	93.5

**Significant at 1% level.

Table 2. Distribution of 60 genotypes of safflower in 14 clusters

Cluster	Total No. of genotypes	Genotypes with origin
I	15	SS-16-4-2, 53-3, 1547-2, 1617, 1618, 1635, 1899 (India), 682-3, 687-2(Australia), 620-1 (Iraq), 643 (Israel), 641 (Italy), 991 (Portugal), 1015-1 (Egypt)
II	14	60, 65, 437, 445, 458, 1244-1, 1399, 1579-3, 1627 (India), 631 (USA), 660 (Spain), 694-1 (Australia), 771 (USSR), 1194 (Pakistan)
III	5	628 (Hungary), 1174 (Pakistan), 1368-1, 1371-3, 1575 (India)
IV	6	431-1, 438 (India), 1223-1, 1230 (Pakistan), 791-1 (Sudan), 932 (Portugal)
V	8	597-1 (Algeria), 611-1 (Rumania), 627-1 (Hungary), 647 (Morocco), 961 (Portugal), 1028-1 (Egypt), 1601-11 (India), 1916 (USSR)
VI	3	597-1 (Algeria), 836 (Turkey), 1625 (India)
VII	2	740-1 (Spain), 1878-1 (India)
VIII	1	598 (Algeria)
IX	1	618-1 (Iraq)
X	1	781-2 (Sudan)
XI	1	877 (Turkey)
XII	1	1008 (Egypt)
XIII	1	1114 (Iran)
XIV	1	1349 (India)

RESULTS AND DISCUSSION

Analysis of variance (Table 1) reveals highly significant differences among the genotypes for all the characters studied, indicating the existence of genetic diversity among the varieties. The highest variability was observed for seed as well as oil yield per plant (CV 93%), and the least variability for days to flower (CV 8%) and oil content (CV 11%). The significance of Λ statistic indicates that the differences between the means in respect of the pooled effect of all the characters between different populations were significant. Hence, further analysis to estimate D^2 values was done and on the basis of relative magnitude of D^2 values. All the 60 genotypes were grouped into 14 clusters (Table 2).

Table 3. Mean intra- and intercluster distance (D^2 values) in safflower

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV
I	13.5	18.6	22.6	16.6	17.0	22.4	19.2	18.3	23.5	18.6	19.8	18.3	30.5	33.4
II		13.4	16.8	18.7	20.6	18.1	19.0	24.2	30.6	19.3	26.1	26.5	38.1	26.1
III			11.6	21.3	20.4	24.6	16.9	31.2	37.8	22.7	30.3	32.3	40.2	18.4
IV				13.5	19.0	26.3	22.6	17.8	27.0	18.6	21.0	23.2	35.9	31.4
V					12.7	26.1	16.7	24.2	32.3	17.1	20.5	18.6	25.1	31.9
VI						12.4	20.0	28.3	33.0	22.6	30.9	28.5	39.2	32.2
VII							11.5	29.6	36.0	20.0	27.7	26.4	32.0	26.7
VIII								0.0	19.7	20.3	16.9	19.3	35.6	43.6
IX									0.0	30.8	28.6	25.3	40.8	47.5
X										0.0	24.7	21.1	31.8	35.5
XI											0.0	17.1	26.2	41.3
XII												0.0	18.3	44.0
XIII													0.0	50.1
XIV														0.0

The pattern of distribution of genotypes from different geographical regions into different clusters was at random. This tendency of genotypes (exotic and indigenous) occurring in clusters cutting across geographical boundaries demonstrates that geographical isolation is not the only factor causing genetic diversity [3, 4]. Plant populations restricted to small geographical areas or subjected to identical environmental pressures help evolve adaptive gene complexes. These gene complexes are conserved by genetic linkages or stringent natural or human selections. Changes in the breeding systems have also accelerated genetic divergence in natural populations [5]. On the other hand, Murty and Arunachalam [6] have suggested that genetic drift and natural selection forces under diverse environmental conditions within a country could cause considerable diversity than geographical isolation.

Maximum intercluster divergence (Table 3) was observed between varieties of clusters XIII and XIV (D^2 50.68), while the closest proximity was noticed between clusters I and IV (D^2 16.58). The intracluster divergence varied from 0.0 to 13.5, maximum being for cluster IV which comprised six varieties of diverse origin.

The cluster constellations obtained by D^2 analysis were also confirmed by canonical analysis (Table 4). The first two vectors accounted for only 57.6% variability and the first three canonical vectors accounted for 72.6% of total genetic divergence. For getting a clear two-dimensional representation, the contribution by three canonical roots should be more than 95%. Therefore, a slight deviation is expected in such analysis. More or less similar observations were reported by Murty et al. [7] and Dhagat and Singh [8] in brown sarson and kodo millet, respectively.

Table 4. Canonical vectors for different characters in safflower

Character	Canonical vectors		
	Z_1	Z_2	Z_3
Plant height	0.6803	0.0428	0.1533
Days to flower	0.1815	−0.1567	0.1461
No. of primary branches	−0.2039	0.1288	0.0080
No. of secondary branches	−0.1866	0.1428	−0.0464
Branching height	0.3655	−0.6093	0.2948
Capitula/plant	0.0398	0.2117	0.1927
Seeds/capitulum	0.3094	0.0694	−0.4458
1000-seed weight	0.0492	0.4950	−0.3336
Oil content	−0.1014	−0.1006	−0.0592
Oil yield/plant	−0.0074	−0.0233	−0.0771
Variation % accounted for	36.74	20.88	14.94

The analysis for estimating the contribution of various characters towards the expression of genetic divergence (Table 5) indicated that plant height (22.0%), seed yield/plant (20.6%), branching height (19.7%), and 1000-seed weight (18.0%) contributed maximum to the total genetic divergence in this collection. They accounted for more than 80% of total divergence in the material. It is clear that these are the basic attributes of plant architecture which need greater attention. Ranga Rao et al. [4] reported branching height, 1000-seed weight, plant height and capitula/plant to contribute more towards diversity in the safflower collections studied under two environments.

Table 5. Contribution of different quantitative characters to diversity (D^2) in safflower

Character	Contribution, %
Plant height	22.0
Days to flower	2.3
No. of primary branches	0.3
No. of secondary branches	2.4
Branching height	19.7
No. of capitula/plant	4.7
Seeds/plant	9.8
1000-seed weight	18.0
Seed yield/plant	20.6
Oil content	0.1
Oil yield/plant	—

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