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

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Genetic divergence analysis revealed that twenty eight genotypes were grouped in 12 clusters. Cluster II comprised five genotypes one each from Australia, GDR, Pakistan, Japan and USSR whereas clusters VIII to XII were represented by single genotype from Iran, Greece, Syria and India respectively. The common evolutionary trends were obvious, since the genotypes spaced apart were grouped together. It was also revealed from grouping pattern that the nature of selection forces operating under domestic conditions seems to be unidirectional for accumulating similar gene pool across the geographical barriers since genotypes from countries far apart got grouped together. The present study helped in isolating genotypes with high cluster means which are useful for breeding programme. However, geographical diversity was observed to be not strictly related to genetic diversity. This analysis also helped in identifying genotypes which are genetically divergent.

Variability in the population, especially for characters where improvement is sought for, is an indispensable pre-requisite for successful crop improvement programme. A broad spectrum of variability in segregating generation can be generated by crossing genetically diverse parents. The D^2 technique (Mahalanobis, 1936) has been found to be a powerful tool to estimate genetic divergence among populations of different yield components to total diversity. To identify the genotypes of distinct characteristics to be utilized as donor parents, the present investigation was planned to evaluate 28 promising safflower germplasm lines originating from twenty six countries.

MATERIALS AND METHODS

Twenty eight promising safflower lines were chosen from large number of collections maintained at the NBPGR, Regional Station, Akola and Oilseed Research Station (Mahatma Phule Krishi Vidyapeeth), Jalgaon. One culture from each country source along with 3 lines from India namely 'Tara'; IC 1394 and CTS 7218 were selected on the basis of its yield performance. The trial of 28 varieties was conducted in randomized block design replicated thrice. The plot size being 2 rows of 3 metres long and 75

cm apart, number of plants/row being 20. The sowing was done on 12th Nov., 1980. The crop was raised under irrigated conditions with standard cultural practices.

The observations on fifteen quantitative characters viz. days to 50 per cent flowering, plant height, height up to Ist primary branch, number of primary branches, angle of Ist primary branch, days to 50 per cent maturity, number of capitula per plant, capitulum length, capitulum diameter, size of outer involucral bracts (OIB), number of seeds per capitulum, 100 seed weight, seed yield per plant, oil content and oil yield per plant were recorded on five random plants. For estimation of genetic divergence, D^2 statistics (Mahalanobis, 1936) was used. The cluster formation was done by Tocher's method (Rao, 1952).

RESULTS AND DISCUSSION

Based on D^2 values, the twenty eight genotypes of safflower could be grouped in 12 clusters. The cluster means for each group for 15 characters are given in Table-1. The grouping pattern of 28 varieties of safflower in different clusters is presented in Table 2. Cluster-I consisting of four genotypes representing Afghanistan, Egypt, Kenya and Spain. Cluster-II was the largest having five varieties from Australia, GDR, Pakistan, Japan and USSR. Cluster-III was formed by varieties from Algeria, Sudan and USA and Cluster-IV with four genotypes from Mexico, Morocco, Philippines and India. The Cluster-V and VI both comprised two cultures each from Ethiopia and Jordan (Cluster-V) and France and Israel (Cluster-VI). In Cluster-VII, three genotypes were from Portugal, Turkey and Rumania. Cluster-VIII to XII were represented by single genotype originating from Iran, Greece, Syria and India respectively. The clusters with single genotype were characterized distinctly. Genotype JL-1329 from Iran (Cluster-VIII) is very late in flowering, tall growing, low seed and oil yielding and JL-1462, ex-Greece, falling in Cluster-IX was the dwarfest, early with appressed branching habit and very small seeds. JL-1439 in Cluster-X, JL-1394 in Cluster-XI and CTS-7218 in Cluster-XII were also characterized by maximum oil content and seed yield; bold seeds, widest angle and bold capitulum, with maximum seeds per capitulum repsectively.

Marked differences between different clusters in respect of all the characters under study were observed (Table 1). The variability range observed for days to 50 per cent flowering (92–113 days), plant height (80–147 cm), height up to Ist primary branch (21—77 cm), number of primary branches (5.3 – 9.9), angle of 1st primary branch (27–44°), days to 50 per cent maturity (124–138 days), number of capitula per plant (20–33),

Table 1. Cluster means for 28 varieties of safflower for genetic divergence

Cluster group	Varieties/ cluster	Source country	Days to 50 % flowering	Plant height (cm)	Height up to 1st branch (cm)	No. of primary branches	Days to 50 % maturity
I	1,6,11,20	Afghanistan, Egypt, Kenya and Spain	106.25	123.62	50.37	7.63	135.47
II	2,4,19,22,24	Australia, GDR, Pakistan, Japan and USSR.	98.20	98.25	27.69	8.31	127.19
III	9,17,25	Algeria, Sudan and U.S.A.	100.60	95.80	32.22	9.13	133.09
IV	12,13,21,26	Mexico, Morocco, Philippines, India	97.91	95.60	21.03	9.89	127.83
V	3,10	Ethiopia and Jordan	106.80	127.03	42.73	7.57	133.00
VI	7.23	France and Israel	101.36	121.23	51.23	7.12	127.87
VII	14,16,18	Portugal, Turkey and Rumania	99.44	108.89	42.87	7.40	130.70
VIII	5	Iran	112.13	146.40	76.87	8.07	137.57
IX	8	Greece	99.50	79.87	34.13	5.33	126.73
X	15	Syria	108.20	128.53	51.00	7.80	138.27
XI	27	India	92.07	89.13	33.27	9.13	124.07
XII	28	India	98.93	100.73	36.00	8.13	132.00

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Table 1. Cont'd...

Cluster group	Varieties/ cluster	Source Country	Angle of Ist primary branch	No. of capitula per plant	Capitulum length (mm)	Capitulum diameter (mm)	Size of involucral bract (sq. mm)
I	1,6,11,20	Afghanistan, Egypt, Kenya and Spain	31.43	24.92	22.05	18.89	16.33
II	2,4,19,22,24	Australia, GDR, Pakistan Japan and USSR	35.95	24.87	21.69	18.10	18.21
III	9,17,25	Algeria, Sudan and U.S.A.	36.49	23.36	20.20	16.93	16.29
IV	12,13,21,26	Mexico, Morocco, Philippines, India	43.08	32.68	20.35	16.48	15.10
V	3,10	Ethiopia and Jordan	32.20	21.48	19.03	15.33	15.58
VI	7,23	France and Israel	36.13	22.98	19.53	15.97	15.10
VII	14,16,18	Portugal, Turkey and Romania	35.56	23.78	21.64	18.49	11.79
VIII	5	Iran	38.67	22.00	18.93	16.13	15.17
IX	8	Greece	26.40	22.13	19.80	17.00	13.33
X	15	Syria	38.55	30.80	21.60	18.00	13.13
XI	27	India	43.67	27.40	21.60	18.07	19.03
XII	28	India	38.33	20.00	24.73	20.53	19.0

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Table 1 Contd...

Cluster group	Varieties/ Cluster	Source country	No. of seeds per capitulum	100-seed weight (g)	seed yield per plant (g)	Oil content (%)	Oil yield per plant (g)
I	1,6,11,20	Afghanistan, Egypt, Kenya and Spain	48.52	3.37	35.08	37.10	12.88
II	2,4,19,22,24	Australia, GDR, Pakistan, Japan and USSR.	37.73	3.50	30.99	37.19	11.49
III	9,17,25	Algeria, Sudan and U.S.A.	37.33	2.88	24.21	38.79	9.19
IV	12,13,21,26	Mexico, Morocco, Philippines and India	32.93	3.74	34.77	37.74	13.23
V	3,10	Ethiopia and Jordan	39.17	2.70	22.08	41.08	9.05
VI	7,23	France and Israel	39.10	4.93	36.79	42.40	15.73
VII	14,16,18	Portugal, Turkey and Romania	36.39	3.87	31.19	37.14	11.61
VIII	5	Iran	26.60	2.23	12.61	39.40	5.19
IX	8	Greece	34.13	1.73	19.81	38.43	4.97
X	15	Syria	48.33	4.29	61.60	36.70	22.56
XI	27	India	31.20	5.93	45.80	35.73	16.83
XII	28	India	72.40	3.39	48.74	42.43	20.63

capitulum length (19–25 mm), size of OIB (12–20 sq mm), seeds per capitulum (27–72), 100 seed weight (1.73–5.92 g), oil content (35.7–42.4%), seed yield per plant (12.6–61.6 g), oil yield per plant (4.97–22.56 g). Maximum genetic diversity was present between Cluster-IX and X (27.77) represented by Iran and Syria respectively, followed by Cluster-IX and XII (23.43). The minimum divergence was exhibited between Cluster-III & VII (8.96) represented by genotypes from Algeria, Sudan and USA and Portugal, Turkey and Rumania respectively. The combinations of clusters which exhibited higher magnitude of genetic divergence were cluster-VIII and XI (22.37), IX and XI (22.21), VIII and XII (22.09), III and X (21.20) and XI and XII (21.03).

Table 2. Clustering pattern of 28 safflower lines

Cluster No.	No. of varieties	Name of the varieties with origin	
I	4	JL–1446	Afghanistan
		JL–1284	Egypt
		JL–1006	Kenya
		JL–1375	Spain
II	5	JL—1518	Australia
		EC–36340	GDR
		JL–1325	Pakistan
		JL–1570	Japan
		JL–1544	USSR
III	3	JL–985	Algeria
		JL–1035	Sudan
		JL–127	USA
IV	4	EC-42477	Mexico
		JL–1038	Morocco
		JL–1136	Philippines
		Tara	India
V	2	JL–896	Ethiopia
		JL-1342	Jordan
VI	2	JL–915	France
		JL–1337	Israel
VII	3	JL–1391	Portugual
		JL–1356	Turkey
		JL–991	Romania
VIII	1	JL–1329	Iran
IX	1	JL–1462	Greece
X	1	JL–1439	Syria
XI	1	IC–1394	India
XII	1	CTS–7218	India

The Intra-cluster distance ranged from 0 : 00 to 12.24. The intra-cluster distance was highest in Cluster-I (12.24) followed by Cluster-VI (11.02). The minimum intra-cluster distance other than those where single genotype formed clusters was 6.80 for cluster VII represented by JL 1391, JL 1356 and JL 991 from Portugal, Turkey and Romania, respectively.

It would be interesting and perhaps also more useful for the breeders to assess whether the genotypes differ when all the characters are considered simultaneously. It was also helpful in the choice of the parent material for specific breeding objectives, since it is known that exploitation of heterosis for yield and success of obtaining desirable recombinnats is dependent on degree of divergence between the parents chosen. The utility of multivariate analysis and D^2 analysis in quantifying the degree of divergence between populations to understand the trend of evolutionary pattern, to assess the relative combination of different components of yield to the total divergence and to determine the nature of forces operating at intra and inter cluster levels has been emphasised by various workers in different crops. viz. brown *sarson* (Murthy and Quadri, 1966), groundnut (Sangha, 1973), *rai* (Trehan *et al*, 1975), and in safflower (Patil *et al.*, 1982; Agrawal *et al.*, 1982; Alba *et al.*, 1984 and Patil *et al.*, 1984). Such study would also help in picking up genetically divergent parents to obtain desirable recombinants in segregating generation (Ram and Pawar, 1970).

The represenation of various clusters showed that in many clusters, the genotypes falling in them originated wide apart in space suggesting thereby that distance in space is not related to genetic divergence in safflower crop. However, the representation of genotypes in few clusters have showed the geographical relationship in safflower (Agrawal *et al.*, 1982, Alba *et al.*, 1984 and Patil *et al.*, 1984). Twenty three varieties were grouped into seven clusters and remaining five in single variety clusters confirming different genetic base even in the strains of same origin, eg., three varieties of indigenous origin grouped in 3 clusters i.e. Cluster-IV, XI and XII. The maximum genetic diversity was observed between Cluster IX and Cluster X represented by genotypes from Iran and Syria respectively, while minimum divergence was exhibited between Cluster-III and VII. This offers ample scope for selecting desired genotypes from cross combinations involving genotypes from these diverse groups, rather than utilizing genotypes falling within the same group, since this will be based on narrow genetic differences and is bound to limit the scope for useful genetic advance.

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