Genetic Divergence in Sunflower (*Helianthus annuus* L.)

S Sridhar, M Reddi Sekhar and V Anil Kumar
Department of Genetics and Plant Breeding, SV Agricultural College, Tirupathi-517 502 (Andhra Pradesh)

Thirty-nine genotypes of sunflower were evaluated for their genetic divergence by D^2 analysis for a set of 14 divergent characters. The D_2 analysis revealed that genotypes exhibited considerable diversity and were grouped into nine clusters. Twenty-seven genotypes representing different eco-geographical regions were grouped into cluster I indicating that genetic divergence and geographical divergence were not related. The characters, oil content, total number of seeds/head and total dry matter/plant, contributed maximum towards genetic divergence in D_2 analysis. Based on Tocher's clustering pattern the genotypes with accession numbers 1144, 780, 1164, 1217 and 1220 were suggested for inclusion into hybridization for obtaining desirable recombinants.

Key Words: Clustering, D^2 analysis, Genetic Divergence, *Helianthus annuus* L., Sunflower

Sunflower is an important non-traditional oilseed crop. Extension of sunflower crop to different areas, seasons and situations has necessitated diversification of varietal/ hybrid base in the country. Genetic divergence among parents is essential since a crossing programme involving genetically diverse parents is likely to produce high heterotic effects and also more variability could be expected in segregating generations. Mahalonobis D^2 Statistic has been employed widely to resolve genetic divergence at inter-varietal and sub-species level in classifying the crop, therefore, an attempt was made in sunflower to study genetic divergence.

Materials and Methods

Thirty-nine genotypes of sunflower (Table 1) with different origins were raised in a randomized block design replicated thice, during *rabi* 1997-98 at college farm, SV Agricultural College, Triupathi. In each replication each genotype was sown in a row of 4 m length with a spacing of 60 x 30 cm. Recommended agronomic practices were followed during the entire growth period under protective irrigation. In each replication five competitive plants were tagged and observations were recorded for 14 characters, namely, days to flowering, days to maturity, plant height (cm), number of leaves, stem diameter (cm), head diameter (cm), leaf area index, total number of seeds/head, seed filling (%), 100-seed weight (g), oil content (%), total dry matter (g), Harvest index (%) and seed yield/plant (g). The data were subjected to analysis of variance followed by multivariate analysis (Mahalanobis, 1930). The genotypes were further grouped into different clusters based on Tocher's method (Rao, 1952)

Results and Discussion

The analysis of variance revealed significant differences among genotypes for all the 14 characters studied. The analysis of variance of dispersion of 39 genotypes was significant indicating the significant pooled effect among all the characters studied between different genotypes.

The 39 genotypes were grouped into 9 clusters using Tocher's method (Table 1). Cluster 1 consisted of maximum number of 27 genotypes representing different eco-geographical regions whereas as six in Table 1 were included in cluster II. The remaining six clusters *viz.*, III, IV, V, VI VII, VIII and IX had one genotype each.

The clustering pattern revealed that the genotypes originating from different geographical regions had been grouped in cluster I which indicated that there was no association between genetic diversity and geographical diversity. Similar results were reported by Anand and Chandra (1980), Yadav *et al.* (1988), Haile (1994) and Sankarapandian *et al.* (1996). The genotypes that originated in one region had been distributed into different clusters, indicating that genotypes with same geographic origin could have undergone change for different characters under selection. This could be due to genetic drift, selection pressure and environment, which creates greater diversity rather than genetic distance (Murthy and Arunachalam, 1966).

The intra- and inter-cluster distances among the genotypes studied was of varying magnitude (Table 2). Intra-cluster D^2 values were ranged from 0 to 21.623, cluster II has maximum intra-cluster distance (21.623) followed by cluster I (20.453) indicating that selection of parents for hybridization within the cluster is advisable. Low intra-cluster D^2 values were recorded for cluster III, IV, V, VI, VII, VIII and IX as they included only single genotype in each cluster. The maximum inter-cluster D^2 value (1656.24) was observed between cluster

Table 1. Distribution of 39 sunflower genotypes into different clusters along with their origin

Cluster number	Number of genotype	Genotype (accession number)	Origin
I	26	350, 38, 1227, 315, 342	USA
		1172, 1148, 1206, 1160	Turkey
		95	South Africa
		652	Russia
		16	Hungary
		146	Italy
		93, 2, 52, 183, 385, 216, 18, 174, 451, 390, 365, 150, 159	—
II	6	1156,1177	Turkey
		702, 1180, 666	USA
		61	Bulgaria
III	1	1144	Turkey
IV	1	30	—
V	1	780	Romania
VI	1	1164	Turkey
VII	1	433	Hungary
VIII	1	1217	Iran
IX	1	1220	Yugoslavia

Table 2. Intra- (diagonal) and inter-cluster average D^2 values of 39 genotypes of sunflower

Cluster	I	II	III	IV	V	VI	VII	VII	IX
I	418.32 (20.45)	957.59 (30.91)	597.65 (24.44)	649.74 (25.49)	1202.97 (34.68)	714.81 (26.73)	753.94 (27.45)	1344.33 (36.66)	1656.24 (40.69)
II		467.77 (21.62)	1232.71 (35.11)	751.25 (27.40)	595.99 (24.41)	671.48 (25.93)	628.85 (25.07)	831.74 (28.84)	783.10 (27.98)
III			0.00	769.89 (28.74)	1620.62 (40.25)	357.58 (18.91)	1063.21 (32.60)	1382.94 (37.18)	1524.66 (39.04)
IV				0.00	873.79 (29.56)	909.08 (30.15)	471.32 (21.77)	667.49 (30.05)	1193.63 (34.54)
V					0.00	1036.00 (32.18)	560.03 (23.66)	667.49 (25.83)	1402.27 (37.44)
VI						0.00	852.99 (29.20)	839.26 (28.97)	752.40 (27.43)
VII							0.00	944.76 (30.73)	934.76 (30.57)
VIII								0.00	990.42 (31.47)
IX									0.00

I and IX indicating wider genetic diversity between the genotypes in these groups. Since, these clusters have more inter-cluster distance among them, selection of parents from such clusters for hybridization programme would help to achieve novel hybrids. Inter-cluster distance is found to be minimum (357.58) between cluster III and VI indicating close relationship and similarly for most of the characters of the genotypes in these clusters, hence, selection of parents from these two clusters is to be avoided.

The cluster means for different characters under study revealed considerable genetic differences between the groups (Table 3). The cluster IX registered the highest mean value for days to flowering, days to maturity, plant height, number of leaves, leaf area index, total dry matter, and seed yield/plant. Whereas cluster VII recorded high mean values for total number of seeds/head, seed filling (%) and 100-seed weight. Cluster VI recorded high mean values for head diameter and harvest index and low mean value for oil content. Similarly, cluster V recorded high mean values for head diameter and oil content (%), total dry matter and seed yield/plant. Cluster VII recorded low mean values for leaf area index, seed filling (%) and harvest index. Cluster II had the low mean values for days to flowering and days to maturity. Similarly, the genotypes of cluster IV had the lowest number of seeds/head.

The characters contributing maximum to the D^2 values are to be given greater emphasis for deciding

Table 3. Cluster means for 14 characters in sunflower genotypes

Character Cluster Number	Days to Floweing	Days to maturity	Plant height (cm)	No. of leaves	Stem diameter (cm)	Head diameter (cm)	Leaf area index	Total number of seeds/ plant	Seed filling (%)	100-seed weight	Oil content (%)	Total dry matter (g)	Harvest index (%)	Seed yield/ plant (g)
I	58.74	87.76	86.58	19.62	1.32	8.79	1.54	478.01	59.23	3.42	29.57	43.22	22.58	9.80
II	60.57	90.00	100.64	20.19	2.06	12.03	2.10	704.25	64.79	4.61	33.74	65.02	30.50	20.15
III	53.567	81.67	99.78	18.86	1.42	11.86	2.55	340.66	68.00	5.19	23.79	55.67	31.17	12.35
IV	63.67	94.67	94.38	19.53	1.69	11.44	1.54	397.40	67.93	5.31	37.56	62.88	23.06	14.52
V	58.33	85.33	103.13	22.27	2.24	15.06	1.23	670.66	56.35	5.80	42.45	59.67	31.52	17.72
VI	57.33	85.33	87.57	18.00	2.22	15.60	2.55	579.33	59.57	5.96	21.55	58.08	35.99	20.93
VII	62.00	90.00	105.29	20.93	1.40	10.07	0.90	508.33	53.57	5.03	33.76	77.97	16.35	12.80
VIII	55.67	85.67	109.50	20.20	1.97	13.66	1.16	750.00	69.00	7.69	31.67	48.13	35.44	17.02
IX	67.67	97.67	118.54	29.20	2.07	12.33	2.99	7.7.66	68.80	7.03	23.13	86.57	27.12	22.48

the clusters for the purpose of further selection and choice of parents for hybridization (Table 4). The highest contributor in this regard was oil content (24.27%), followed by total number of seeds/head (19.15%) and total dry matter (16.22%). Hence, oil content (%), total number of seeds/head and total dry matter were considered to be important traits contributing towards genetic divergence. The present study suggested that the future hybridization work in sunflower should involve the parents that displayed higher genetic divergence.

Table 4. Relative contribution of 14 characters to genetic diversity in sunflower

Character	Number of times ranked first	% contribution towards divergence
Days to flowering (No.)	75	9.15
Days to maturity (No.)	86	10.49
Plant height (cm)	0	0.00
Number of leaves	3	0.37
Stem diameter (cm)	0	0.00
Head diameter (cm)	0	0.00
Leaf area index	76	9.27
Total no. of seeds/head	157	19.15
Seed filling (%)	8	0.98
100-seed weight (g)	76	9.27
Oil content (%)	199	24.27
Total dry matter (g)	133	16.22
Harvest index (%)	4	0.49
Seed yield/plant	3	0.37

Acknowledgements

The author is very much grateful to Indian Council of Agricultural Research, New Delhi, ANGR Agricultural University, Hyderabad, for providing financial assistance through junior research fellowship and research facilities during the course of research work.

References

Anand IJ and S Chandra (1980) Genetic diversity and inter relationship of oil yielding traits in sunflower. *Sunflower Newslet.* **4:** 5-8.

Haile Kefene (1994) Genetic diversity of introduced sunflower (*Helianthus annuus* L.) varieties and their performance for oil and seed yield in Ethiopia. M.Sc (Ag) Thesis, Alemaya University of Agricultural Sciences, Ethiopia.

Mahalanobis PC (1930) On test and measure of group divergence. *J. Asiatic Soc. Bengal* **26:** 541-588.

Murthy BR and V Arunachalam (1966) The nature of divergence in relation to breeding system in some crop plants. *Indian J. Genet. Plant Breed.* **26(A):** 188-198.

Rao CR (1952) Advanced statistical methods in biometric research. John Wiley and Sons Inc., New York, pp 357-363.

Sankarapandian R, N Muppidathi, S Rajarathinam and S Chidambaram (1996) Genetic divergence in sunflower. *Madras Agric. J.* **83:** 637-639.

Yadava RK, BK Behl and TP Yadava (1988) Assessment of diversity among sunflower collections. *Crop Improv.* **15:** 160-162.

Indian J. Plant Genet. Resour. 15(3): 248-250 (2002)