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## Genetic divergence in sunflower (*Helianthus annus L.*)

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### Abstract

Genetic divergence was studied for yield component traits for forty eight sunflower genotypes. The analysis of variance revealed presence significant differences among the genotypes for all the characters studied. Based on genetic distance all the forty eight genotypes were grouped under eleven different clusters. The mode of distribution of genotypes from different eco- regions into various clusters was at random indicating that geographical diversity and genetic diversity were not related. The characters like oil content followed by filled seeds per head, 100 seed weight, seeds per head, leaf area, head diameter and stem girth contributed maximum towards genetic diversity. The maximum inter-cluster distance was recorded between cluster VI and X. Selection of genotypes in these clusters which may serve as potential donors for future hybridization programmes to develop potential recombinants with high yield.

**Keywords:** Sunflower, genetic divergence, D<sup>2</sup> analysis

### Introduction

Sunflower has a great potential in bridging the gap between demand and supply of edible oil to a significant extent in the years to come. The choice of suitable parents is of paramount importance for a planned hybridization programme. Hence it is imperative to identify the best parents with wide genetic divergence for characters of economic importance, so that they can be utilized in breeding programmes to produce desirable recombinants. Genetic diversity is of major interest to plant breeders. More diverse the parents, greater are the chances of obtaining heterotic expression in F<sub>1</sub> with possibility of broad spectrum of variability in segregating generations.

The D<sup>2</sup> statistics (Murty and Arunachalam, 1966) [4] has been found to be a powerful tool to estimate genetic divergence among population. It is a powerful tool in quantifying the degree of genetic divergence among parents (Joshi and Singh, 1979; Muppudathi *et al.*, 1995) [1,5].

An attempt was made to classify forty eight genotypes of sunflower to quantify the magnitude of genetic divergence and using them in further breeding to evolve potential transgressive segregants.

### Material and Methods

The experimental material consisted of forty eight sunflower genotypes from different geographical

regions. All the genotypes were evaluated in replicated thrice adopting statistical design RBD during *rabi* 2016-17 at Niger Research Station, Vanarasi, Navsari agricultural university, Navsari. The seeds were sown at 60 cm between rows and 30 cm between plants within the row. The experiment was laid out with one row of 3.6 cm length of each genotype surrounded by two guard rows to avoid damage and border effects. Recommended agronomic practices and need based plant protection measures were taken up. Observations were recorded on thirteen agronomical characters, *viz.*, days to 50% flowering, days to maturity, plant height (cm), head diameter (cm), stem girth (cm), number of leaves per plant, leaf area (cm<sup>2</sup>), seeds per head, filled seeds per head, 100 seed weight (g), oil content (%), harvest index (%) and seed yield per plant (g). Genetic diversity analysis was carried out following D<sup>2</sup> statistics proposed by Mahalanobis (1936) [3].

### Results and Discussion

Based on the relative magnitude values, forty eight genotypes studied were grouped into eleven clusters (Table 1). Cluster I was the largest having sixteen genotypes.

The second largest cluster III had thirteen genotypes and on third position cluster II had eleven genotypes, whereas, clusters IV, V, VI, VII, VIII, IX, X and XI were mono genotypic. The genotypes obtained from different eco-geographical regions were distributed into different clusters was at random, which indicates that geographical distribution and genetic diversity are not related. This suggests that forces other than geographical separation such as exchange of breeding material, genetic drift, natural and artificial selection, environmental variation were also responsible for the genetic diversity. Lack of correlation between genetic and geographic diversity was reported by Subramanyam *et al.* (2003) [8], Kumari and Sheoran (2012) [2] and Reddy *et al.* (2012) [6]. The intra cluster distance ranged from 0.00 to 5.57. The cluster III exhibited maximum intra cluster distance (5.57) followed by the cluster II (5.09) and cluster I (4.56). The intra cluster distance was zero for clusters IV, V, VI, VII, VIII, IX, X and IX indicating limited genetic diversity among genotypes representing this cluster (Table 2).

The relative divergence of each cluster from other inters-cluster indicated greater divergence between cluster VI and cluster X (23.29) followed by VIII and X (20.47), cluster X and XI (19.66), cluster I and X (19.64). The minimum cluster distance was observed between cluster V and VII (5.02) followed by that of clusters VI and VIII (5.45), IV and IX (5.57), I and VI (5.60), I and V (5.65) and I and VIII (6.27).

The inter cluster distance is the criterion used for selection of genotypes as parents in hybridization programme (Singh and Narayanan, 2000) [7]. The hybrids developed from the selected genotypes within the limits of compatibility of these clusters may produce high magnitude of heterosis or desirable segregants.

The average cluster wise mean values for different characters are presented in (Table 3). The cluster mean is another criterion to assess the superiority of clusters, which could be considered in the improvement of various characters through hybridization programme. Cluster I exhibited moderate mean value for almost all the characters, which second highest

mean value for seed yield per plant (34.16 g). The fourth highest mean value for 100 seed weight (5.66 g) was recorded in cluster II. Cluster III exhibited the second highest mean value for oil content (37.52%). Cluster IV revealed lowest value for days to 50 per cent flowering (57.33 days), days to maturity (122.67 days), filled seeds per head (234.00) and seed yield per plant (8.99 g), whereas, second lowest value for number of leaves per plant (24.86), leaf area (93.30 cm<sup>2</sup>), 100 seed weight (4.30 g) and seeds per head (284.33). Cluster V depicted moderate mean value for most of the traits, whereas, second highest mean value for stem girth (6.00 cm) and harvest index (38.33%), whereas lowest value for leaf area (54.72 cm<sup>2</sup>) and plant height (106.17 cm). Cluster VI showed highest mean value for stem girth (6.08 cm), head diameter (17.62 cm) and seeds per head (1327.33). Whereas, second highest mean value was manifested by days to maturity (133.00 days), number of leaves per plant (32.13) and filled seeds per head (1153.67). Lowest value was expressed by oil content (15.90%). Cluster VII exhibited moderate mean values for most of traits in which the highest mean value was expressed by days to 50 percent flowering (75.00 days) and lowest mean values was expressed by number of leaves per plant (23.10). Cluster VIII depicted highest mean value for days to maturity (134.67 days), number of leaves per plant (34.26), 100 seed weight (6.92 g), filled seeds per plant (1166.67), harvest index (43.00%) and seed yield per plant (39.50 g), whereas second highest mean value was recorded for seeds per head (1312.67). Cluster IX depicted second highest mean value for leaf area (136.95 cm<sup>2</sup>) and plant height (181.11 cm). Cluster X exhibited lowest mean value for head diameter (6.53 cm), seeds per head (256.00) and harvest index (25.33%) and highest mean value for oil content (43.97%). Cluster XI depicted highest mean value for leaf area (161.60 cm<sup>2</sup>) and plant height (193.67 cm) and lowest for stem girth (4.42 cm) and 100 seed weight (4.10 g).

Selection of promising genotypes from each of these clusters based on per se of yield and its component characters.

**Table 1:** Composition of cluster based on D<sup>2</sup> values

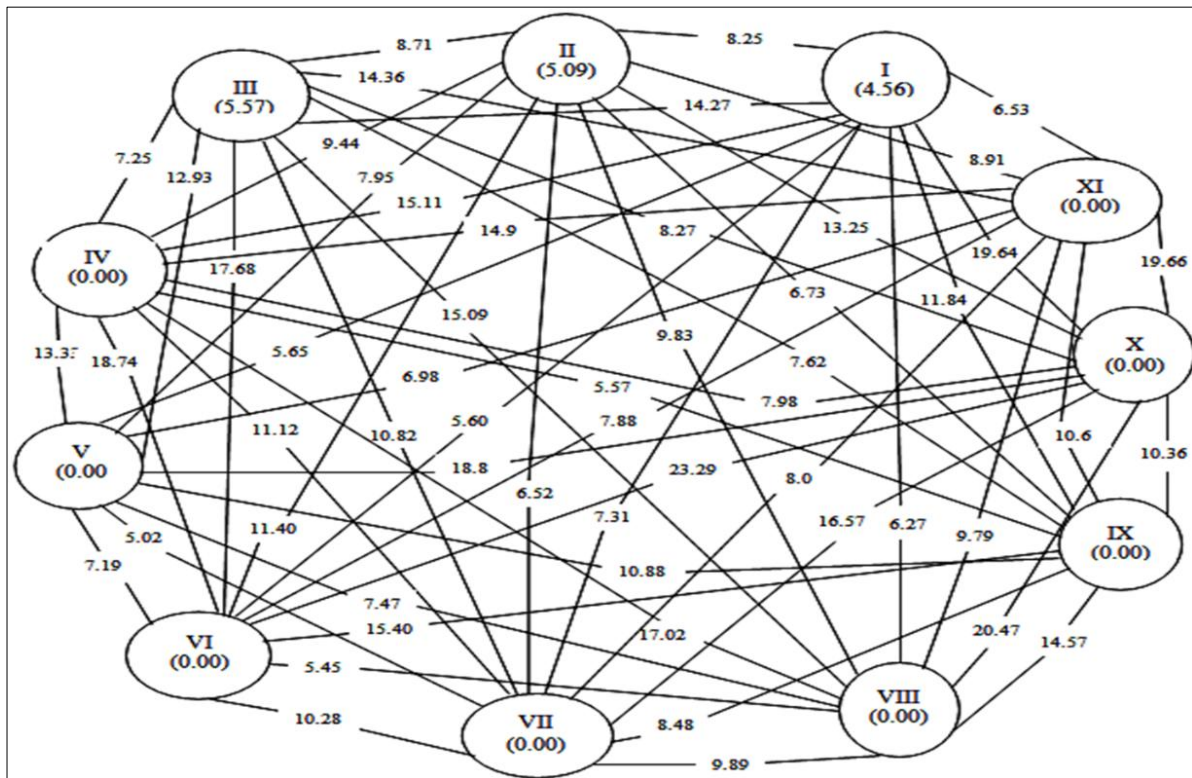
Cluster	No. of genotypes	Genotypes			
I	16	IC-756906	DRSF-113	GMU-355	GMU-1058
		IC-756906	GP6-116	SCG-05	EC-276504
		SCG-78	EC-276320	EC-198054	ID-14
		EC-198066	EC-601713	EC-201831	EC-399512
II	11	IC-302042	EC-276161	EC-75288 M-53	GP6-1116
		EC-279360	IC-306694	EC-201851	EC-399812
		EC-494444	GP6-1254	EC-676365	
III	13	IC-75710	EC-210237	ID-10	EC-201846
		GP6-1436	TSG-68	ID-11	EC-398675
		EC-494366	EC-282338	EC-494422	ID-13
		EC-494377			
IV	1	GMU-1039			
V	1	IC-314193			
VI	1	EC-194430			
VII	1	G6-6-263			
VIII	1	EC-399608			
IX	1	EC-276399			
X	1	EC-625755			
XI	1	SCG-56			

**Table 2:** Intra and inter-cluster distances (D) between eleven clusters

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	4.56	8.25	14.27	15.11	5.65	5.60	7.31	6.27	11.84	19.64	6.53
II		5.09	8.71	9.44	7.95	11.40	6.52	9.83	6.73	13.25	8.91
III			5.57	7.25	12.93	17.68	10.82	15.09	7.62	8.27	14.36
IV				0.00	13.33	18.74	11.12	17.02	5.57	7.98	14.93
V					0.00	7.19	5.02	7.47	10.88	18.80	6.98
VI						0.00	10.28	5.45	15.40	23.29	7.88
VII							0.00	9.89	8.48	16.57	8.00
VIII								0.00	14.57	20.47	9.79
IX									0.00	10.36	10.65
X										0.00	19.66
XI											0.00

**Table 3:** Cluster mean for different characters in sunflower

Clusters	Days to 50 % flowering	Days to maturity	No. of leaves per plant	Stem girth (cm)	Leaf area (cm <sup>2</sup> )	Head diameter (cm)	Oil content (%)	Plant height (cm)	100 seed weight (g)	Seeds per head	Filled seeds per head	Harvest index (%)	Seed yield per plant (g)
I	71.46	128.17	28.57	5.83	120.73	15.45	19.42	144.39	5.74	1018.65	941.15	37.33	34.16
II	69.15	128.33	27.21	5.72	132.47	11.20	27.53	146.57	5.66	734.85	718.15	32.67	21.60
III	67.41	127.31	26.78	5.21	113.57	9.18	37.52	137.43	4.76	669.15	645.79	28.33	16.65
IV	57.33	122.67	24.86	4.88	93.30	6.83	32.39	134.08	4.30	284.33	234.00	36.00	8.99
V	70.33	131.33	29.56	6.00	54.72	14.19	20.29	106.17	4.51	955.33	961.33	38.33	30.30
VI	70.33	133.00	32.13	6.08	106.89	17.62	15.90	127.03	6.01	1327.33	1153.67	40.33	33.35
VII	75.00	131.33	23.10	4.81	109.14	11.20	22.06	121.50	4.62	764.67	795.33	26.67	25.02
VIII	75.00	134.67	34.26	4.69	98.24	17.62	23.70	113.50	6.92	1312.67	1166.67	43.00	39.50
IX	59.67	124.67	27.91	5.82	136.95	6.67	28.05	181.11	4.37	463.33	425.33	25.67	11.90
X	59.67	125.00	30.66	5.36	131.64	6.53	43.97	155.42	5.58	256.00	265.00	25.33	10.00
XI	71.33	131.67	31.11	4.42	161.60	9.75	18.58	193.67	4.10	988.00	859.00	38.00	30.96



**Fig 1:** Intra and Inter- cluster distances (D) between eleven clusters of sunflower  $D = \sqrt{D}$

**Conclusion**

Thus from the present study, it is advisable to attempt crossing of the genotypes from cluster VI with the genotypes of cluster I as well as X and I, VII and III, VIII and I and also between VII and I which may lead to broad spectrum of favourable genetic variability for yield improvement in sunflower.

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