

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

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Fifty-eight sunflower genotypes along with three checks were evaluated for obtaining information regarding genetic divergence through Mahalanobis'  $D^2$  statistic. The analysis of variance revealed significant differences among the genotypes for all the traits. The 61 genotypes were grouped into 19 clusters, where cluster I accommodated maximum number of entries (29). The inter-cluster distance was maximum between cluster XIV and XIX followed by cluster V and XIX and cluster XVIII and XIX. Based on inter-cluster distance and *per se* performance of genotypes, four entries viz., EC 376211, EC 399318, RHA 344 and BLC-P6 were selected which could be intercrossed to obtain high heterotic crosses and also to recover desirable transgressive segregants.

**Key Words:**  $D^2$  Statistic, Genetic Divergence, *Helianthus annuus* L., Sunflower

In order to develop genotypes with desirable traits, the breeder would like to choose genetically distant parents. Genetic diversity plays an important role in plant breeding because hybrids derived from the lines of diverse origin generally display a greater heterosis than those between closely related strains. In addition to the identification of diverse parent material, assessment of genetic divergence also helps in downsizing the core collections to be maintained based on diversity. Several methods have been developed to study the extent of genetic divergence in the genotypes among which Mahalanobis' generalized distance ( $D^2$ ) (Mahalanobis, 1936) is frequently used. In sunflower several inbred lines have been recently developed from different source materials. In order to utilize the material for further improvement, it is imperative to know the extent of diversity among the inbreds. Keeping this in view, the present investigation was carried out to know the magnitude of diversity present in newly developed inbreds and to select diverse parents with an aim to obtain heterotic crosses and wide array of recombinants.

### Materials and Methods

The material for the present study comprised 58 sunflower inbreds and three checks viz., KBSH 1, MSFH 17 and Surya. The experiment was conducted at Directorate of Oilseeds Research, Hyderabad during *khariif*, 1999. Each genotype was sown in two rows of 5 m length spaced at 60 cm with interplant distance of 30 cm. The experiment was laid in Randomized Block Design with three replications. In each entry, five plants were randomly tagged and utilized to collect data on yield and its component characters. The characters considered were days to 50% flowering, days to maturity, plant height (cm), head diameter (cm), 100-seed weight (g), seed

yield plant<sup>-1</sup> (g) and oil content (%). The data were subjected to statistical analysis using Mahalanobis'  $D^2$  statistic (Mahalanobis, 1936). Treating  $D^2$  as a generalized statistical distance, the criterion used by Tocher (Rao, 1952) was applied for determining the group constellation. The character-wise rank totals were used to calculate the percent contribution of each character to the total divergence. Average intra and inter-cluster distances were estimated as per the method given by Singh and Chaudhary (1977).

### Results and Discussion

The analysis of variance revealed significant differences among the genotypes for all the traits studied, indicating the scope for developing high yielding genotypes. Based on  $D^2$  statistic, the 61 genotypes were grouped into 19 clusters with variable number of entries (Table 1) revealing the presence of considerable amount of genetic diversity in the material. Cluster I had the maximum number of 29 genotypes followed by cluster II with 7 genotypes and cluster III with 5 genotypes. These three clusters together accounted for most number of genotypes (41) reflecting narrow genetic diversity among them. The similarity in the base material from which they had been evolved might be the cause of genetic uniformity. Further, clusters IV, XIII and XV had two genotypes in each, while rest of the clusters were solitary entry clusters. However, lines derived from the same source of parentage were grouped in different clusters demonstrating the impact of selection pressure in increasing genetic diversity. The checks Surya, KBSH 1 and MSFH 17 were included in clusters III, X and XI, indicating their distinctness from the inbreds with respect to traits considered. Similar results were reported by Teklewold *et al.* (2000).

Table 1. Grouping of 61 sunflower genotypes into 19 clusters

Cluster	Number of genotypes	Genotypes
I	29	852B, RHA341, RHA348, 345B, ACC1439-1, M924, ACC664-1, NDOL-2, ACC1149, ACC179, ACC916-1, ACC1228-1, ACC914-1, ACC136, ACC1149-1, M1018, ACC916, ACC1139-1, EC399453, ACC1142, ACC 1585, ACC916, ACC1485, ACC64, ACC914, M-1008, ACC1385, M 1017, M1005 and M 1024
II	7	ACC1426, ACC1262, RHA298, 349B, M-1014, M-19-5, RHA345
III	5	ACC1464, M-1001, ACC1439, EC376240, SURYA
IV	2	EC399464, HA341
V	1	343B
VI	1	RHA 346
VII	1	ACC1254
VIII	1	350B
IX	1	ACC1168
X	1	KBSH-1
XI	1	MSFH-17
XII	1	M1026
XIII	2	378B, ACC1376
XIV	1	RHA344
XV	2	No.1874-1, ACC1174
XVI	1	RHA 6D-1
XVII	1	EC399318
XVIII	1	BLC-P <sub>6</sub>
XIX	1	EC376211

The intra and inter-cluster D values are calculated and presented in Table 2. Cluster II recorded maximum intra cluster distance followed by clusters I, indicating similarities among the genotypes in respective clusters for the traits considered together. The members, of clusters XIV and XIX exhibited maximum divergence followed by clusters VI and XIX and clusters XVIII and XIX, indicating greater diversity between genotypes

belonging to respective pairs of clusters, whereas clusters VI and XIV were closest with minimum genetic distance.

The cluster means for all the characters are presented in Table 3. Perusal of the data revealed considerable differences among the clusters for most of the characters studied. The cluster XVII (EC 399318) recorded highest seed yield per plant, days to maturity and low oil content, whereas cluster X (KBSH 1) had highest oil content. However, cluster XIX (EC 376211) had maximum head diameter, days to 50% flowering and 100-seed weight, while cluster XIV (RHA 344) recorded minimum head diameter and 100-seed weight. Further, cluster XVIII (BLC-P<sub>6</sub>) recorded lowest plant height, days to maturity and high oil content. The contribution of each character towards divergence is also presented in Table 2. Among the seven characters studied, 100-seed weight contributed the most to divergence of genotypes, whereas the oil content contributed the least.

The data on inter-cluster distances and *per se* performance of genotypes were used to select genetically diverse and agronomically superior genotypes. The genotypes, exceptionally good with respect to one or more characters were deemed desirable. On this basis, four inbreds *viz.*, EC 376211, EC 399318, RHA 344 and BLC P<sub>6</sub> were selected. Intercrossing of divergent groups would lead to greater opportunity for crossing over, which releases hidden variability by breaking linkage (Thoday, 1960). Progenies derived from such diverse crosses are expected to show wide spectrum of genetic variability, providing a greater scope for isolating transgressive segregants in the advanced

Table 2. Average intra- and inter- cluster D values among the 19 clusters in sunflower

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV	XVI	XVII	XVIII	XIX
I	<b>9.45</b>	14.79	12.94	17.75	14.27	20.26	11.37	12.28	14.38	13.30	17.42	15.13	18.90	24.76	15.26	17.12	17.73	22.91	23.24
II		<b>9.58</b>	22.67	22.90	16.96	13.43	16.84	17.59	17.91	19.19	27.14	15.11	18.92	15.93	14.77	12.20	24.78	17.63	34.34
III			<b>8.02</b>	12.76	19.43	27.67	12.70	12.16	14.62	14.90	11.17	18.16	22.70	32.23	20.29	25.70	17.01	27.97	14.98
IV				<b>9.19</b>	24.35	33.69	19.05	14.20	19.18	23.54	15.90	23.87	27.29	38.32	26.86	30.29	20.02	33.54	13.77
V					<b>0.00</b>	16.29	14.01	21.47	24.37	11.26	25.50	19.80	19.28	23.98	12.23	13.05	25.40	25.08	29.85
VI						<b>0.00</b>	18.49	24.12	24.13	19.13	33.40	15.83	18.07	8.41	10.91	14.16	32.26	13.40	40.59
VII							<b>0.00</b>	11.95	14.72	12.72	19.81	9.92	11.87	23.35	11.90	20.96	22.07	19.94	25.15
VIII								<b>0.00</b>	6.93	19.63	17.20	11.67	19.25	26.92	19.03	24.34	19.74	21.46	22.09
IX									<b>0.00</b>	19.99	17.30	11.45	21.54	25.37	20.04	25.14	20.01	19.83	24.50
X										<b>0.00</b>	18.64	17.96	21.09	24.94	12.79	17.11	21.09	24.05	25.16
XI											<b>0.00</b>	24.40	28.53	36.83	26.05	29.51	10.77	32.58	11.04
XII												<b>0.00</b>	14.11	17.96	12.90	22.36	26.48	12.29	30.92
XIII													<b>8.30</b>	20.91	14.75	23.51	27.61	18.76	34.37
XIV														<b>0.00</b>	16.57	19.02	34.93	10.95	45.18
XV															<b>9.16</b>	16.24	26.36	15.43	32.57
XVI																<b>0.00</b>	26.03	23.99	36.33
XVII																	<b>0.00</b>	32.56	18.82
XVIII																		<b>0.00</b>	40.23
XIX																			<b>0.00</b>

Bold values represent intra cluster D values

Table 3. Cluster means and percent contribution of characters towards divergence in sunflower

Cluster	Days to 50% flowering	Days to maturity	Plant height (cm)	Head diameter (cm)	100 seed weight (g)	Seed yield/plant (g)	Oil content (%)
I	55.87	87.51	129.92	12.41	5.52	20.59	30.20
II	55.05	84.86	103.81	9.18	4.03	12.05	29.92
III	55.47	87.60	145.93	15.01	7.20	27.68	30.05
IV	58.00	91.11	132.67	17.86	7.73	13.16	29.32
V	54.00	87.67	162.67	12.07	3.83	13.80	29.20
VI	49.67	80.00	123.33	8.43	2.93	11.50	24.03
VII	49.67	85.67	135.67	11.97	6.33	18.97	32.17
VIII	54.33	85.33	105.67	13.83	7.10	14.23	29.10
IX	54.67	82.67	100.33	12.30	7.13	24.20	26.03
X	54.00	84.67	168.33	12.30	4.80	34.63	38.93
XI	58.33	89.33	140.33	16.57	7.03	45.67	31.20
XII	49.00	80.33	111.00	10.83	6.25	14.77	32.17
XIII	44.33	86.50	109.17	10.63	5.35	14.63	32.75
XIV	48.33	77.67	95.33	6.83	2.67	15.53	23.17
XV	49.50	82.17	136.17	11.87	3.93	19.13	30.03
XVI	58.00	87.33	130.00	8.77	2.43	15.33	34.33
XVII	59.33	93.33	115.00	15.50	5.37	46.33	28.17
XVIII	46.67	75.67	90.00	11.23	3.93	16.10	34.37
XIX	60.00	92.00	159.33	20.10	8.23	37.07	27.07
Percent contribution	18.96	10.55	14.54	9.45	35.03	11.42	0.05

generations. Hence, these genotypes might be used in a multiple crossing programme to recover transgressive segregants.

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