



Analysis of Genetic Diversity in Germplasm Accessions of Sunflower (*Helianthus annuus* L.)

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Genetic divergence (D_2) was studied in 64 genotypes of sunflower during the season *Rabi* 2009, to quantify the nature and extent of diversity by the Mahalanobis D_2 statistics. Analysis of variance revealed significant difference among the genotypes for all the 13 characters. Sixty two genotypes and two checks *viz.*, DRSF 108, DRSF 113 were grouped into nine clusters. The pattern of distribution of genotypes into various clusters was at random indicating that geographical and genetic diversity were not related. The distinctness of clusters was proven by distance matrix as inter cluster distances than almost cluster distances, genotypes EC 601679, EC 601613, EC 601662, EC 601702, EC 601609, EC 601610, EC 601619 and EC 601654 could be utilized in breeding programme. Based on mean performance the genotypes *viz.*, EC 601618, EC 601619, EC 601621, EC 601664, and EC601702 for seed yield, the genotypes *viz.*, EC 601613, EC 601612, EC 601622, EC 601699 and EC601702 for oil content were identified as superior. Genotypes *viz.*, EC 601618, EC 601621, EC 601629, EC 601630 and EC 601702 for total number of filled seeds, genotypes *viz.*, EC 601613, EC 601614, EC 601618, EC601621 and EC601702 for head diameter, genotypes *viz.*, EC 601610, EC 601617, EC 601619, EC 601621 and EC 601664 for 100 seed weight were identified as superior. These genotypes can be utilized in the breeding programme for improving the respective character, to develop superior varieties/hybrids in sunflower.

Key words: Genetic divergence, sunflower, inter cluster distance.

Sunflower has emerged as a potential oilseed crop in Indian agriculture. Owing to its photo insensitive nature it can be cultivated through out the year. Cultivation of sunflower is mainly for extraction of oil which ranges from 46-54 per cent. Crosses between divergent parents usually produce greater heterosis than those between closely related ones. (Moll and Stuber, 1971). Use of diverse parents in hybridization programme can serve the purpose of combining desirable genes or to obtain recombination. The multivariate D_2 analysis (Mahalanobis, 1936) is one of the important biometrical tools in quantifying the genetic divergence in the germplasm.

An attempt was made to classify 64 genotypes of sunflower to quantify the magnitude of genetic divergence and using them in further breeding to evolve potential transgressive segregants.

Materials and Methods

The material for the present study comprised of 62 germplasm accessions of sunflower and two checks *viz.*, DRSF 108, DRSF 113. The experiment was conducted at Directorate of Oilseeds Research, Hyderabad during *Rabi* 2009. Each accession was sown in two rows of 4m length with a spacing of 60

cm between rows and 30 cm between plants. The experiment was laid out in Simple Lattice Design with two replications. In each accession, five plants were randomly selected and used for collection of data on yield and yield related characters like days to 50 percent flowering, days to maturity, plant height, stem diameter, head diameter, number of filled seeds per head, number of unfilled seeds per head, total number of filled seeds per head, seed filling percent, 100 seed weight, seed yield per plant, hull content and oil content. The data were subjected to multivariate analysis using D_2 statistics (Rao, 1952). The genotypes were further grouped into different clusters based on Euclidean cluster analysis.

$$\text{Seed filling percentage (\%)} = \frac{\text{Number of filled seeds}}{\text{Total number of filled and unfilled seeds}} \times 100$$

Oil content estimation was done by the nuclear magnetic resonance (NMR) technique.

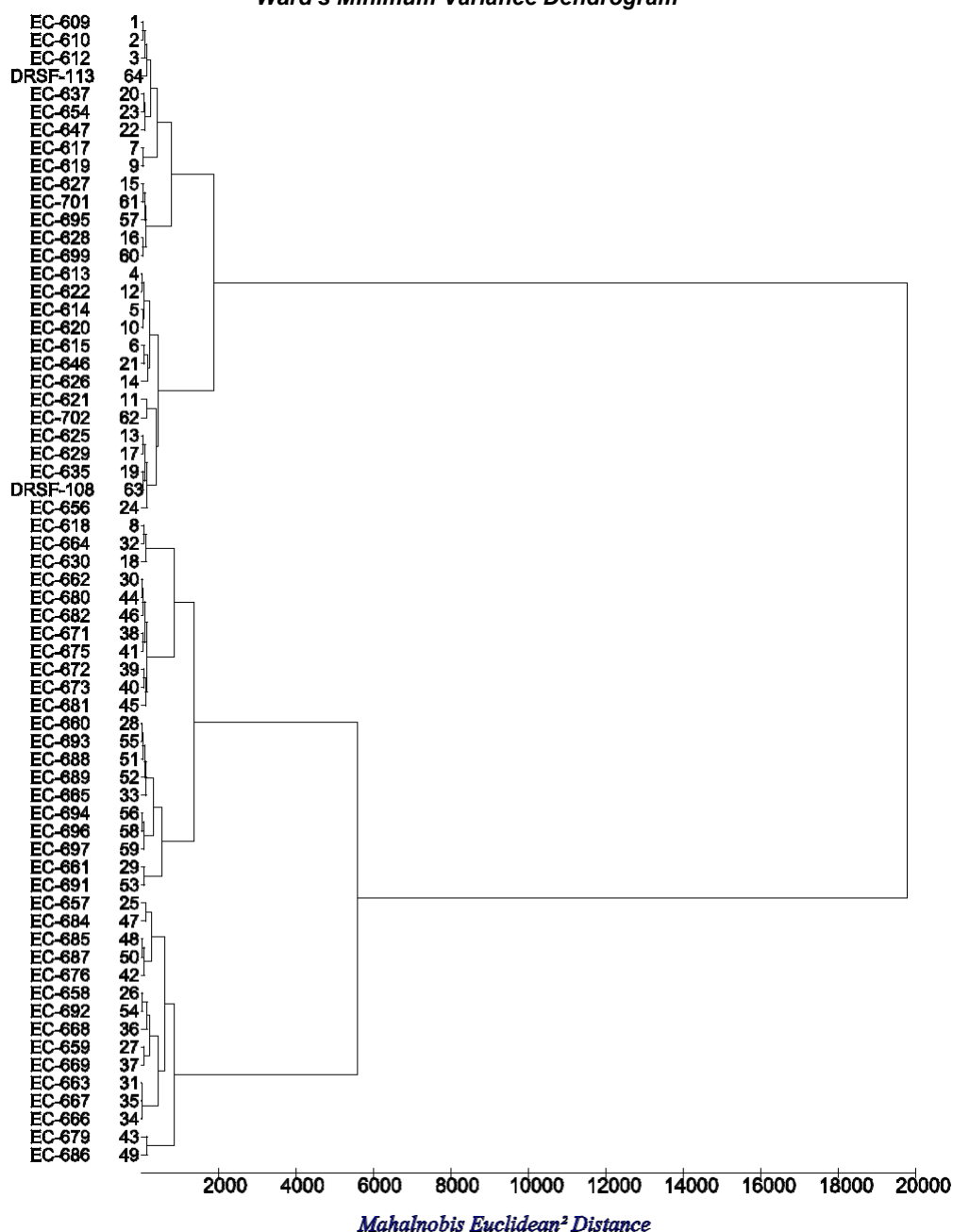
Results and Discussion

Analysis of variance revealed highly significant differences among the genotypes for various characters. Sixty four genotypes were grouped into nine clusters based on D_2 values such that the genotypes belonging to same cluster had smaller D_2 values than those belonging to different clusters

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Table 3. Cluster means for seed yield and yield contributing characters of 64 sunflower genotypes

Cluster No.	Days to 50% flowering	Days to maturity	Plant height (cm)	Stem diameter (cm)	Head diameter (cm)	Filled seeds/head	Unfilled seeds/head	Total seeds/head	Seed filling (%)	100-seed weight (g)	Seed yield/Plant (g)	Oil content (%)	Hull content (%)
1 Cluster	58.172	87.304	133.239	5.205	16.236	557.771	171.115	728.920	76.166	5.509	30.740	34.802	28.087
2 Cluster	60.183	90.553	148.419	5.806	13.621	434.517	195.409	629.926	68.854	4.367	19.194	35.602	27.102
3 Cluster	59.034	89.902	154.488	5.558	18.409	743.299	178.200	921.499	80.333	5.124	38.112	33.466	29.665
4 Cluster	57.513	89.914	125.192	3.418	17.807	823.574	198.113	1021.687	80.533	5.332	43.727	34.960	26.727
5 Cluster	53.309	88.724	113.000	3.632	13.650	434.881	189.102	623.983	69.535	3.929	17.056	34.269	28.856
6 Cluster	61.251	90.103	130.578	4.113	10.982	405.837	188.348	594.185	68.872	4.303	17.603	34.871	26.194
7 Cluster	60.392	87.871	89.903	4.413	11.224	372.958	188.020	560.978	66.720	4.381	16.277	32.963	25.596
8 Cluster	57.013	87.928	97.398	2.876	11.165	376.961	200.495	577.456	64.408	4.660	17.129	34.671	27.933
9 Cluster	52.490	85.261	73.613	3.222	9.174	213.337	241.461	454.461	48.350	4.268	9.191	34.700	25.616
Mean	58.211	88.922	126.021	4.463	14.190	514.281	187.961	702.24	71.665	4.708	24.791	34.361	27.801

Ward's Minimum Variance Dendrogram**Fig. 2. Ward's minimum variance diagram**

per cent, where as cluster III scored for genotypes with high plant height, head diameter and hull content. Selection of genotypes from divergent clusters, might prove more useful and when they are selected with due consideration of *per se* performance. However, looking at subjective and arbitrary nature of grouping with D_2 statistic (Singh and Ramanujam, 1981) and depending on breeder's interest more than one genotypes from a cluster could be selected for breeding programme.

The contribution of individual character towards the divergence (Table 4) indicated plant height (61.26) followed by stem diameter (19.79), head diameter (5.51), filled seed/head (3.22), had major contribution towards divergence, while oil content, days to maturity, days to flowering had negligible contribution. Similar results have been reported by Komaraiah *et al.* (2004)

Table 4. Contribution of different characters towards genetic divergence in sunflower genotypes

Source	Time ranked 1 st	Contribution %
Days to 50% flowering	7	0.35
Days to maturity	1	0.05
Plant height (cm)	1235	61.26
Stem diameter (cm)	399	19.79
Head diameter (cm)	111	5.51
Filled seed / head	98	4.86
Unfilled seeds /head	4	0.20
Total number of seeds/head	48	2.53
Seed filling (%)	43	2.13
100-seed weight (g)	65	3.22
Seed yield/plant (g)	25	1.24
Oil content (%)	10	0.50
Hull content (%)	18	0.89

Plant height, head diameter and stem diameter are the important contribution factors. In that analogy, genotypes superior for one or more characters the

genotypes viz., EC 601618 and EC 601619 for seed yield. The genotypes EC 601613 and EC601612 were identified superior for oil content. The genotypes EC 601618 and EC601621 for total number of filled seeds. The genotypes EC 601613 and EC 601702 for head diameter. The genotypes EC601610 and EC 601 617 for 100 seed weight. These genotypes can be utilized in the breeding program to develop superior varieties/hybrids in sunflower.

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