

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

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Genetic divergence (D2) was studied in 64 genotypes of sunflower during the season Rabi 2009, to quantify the nature and extent of diversity by the Mahalanobis D₂ 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 suprerior. 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, 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.

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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Cluster No.	No. of genotypes	Genotypes
 Cluster-I	9	EC 601609, EC 601610, EC 601612, DRSF 113, EC 601637, EC 601654, EC 601647, EC 601617, EC 601619
Cluster II	5	EC 601627, EC 601701, EC 601695, EC 601628, EC 601699
Cluster III	14	EC 601613, EC 601622, EC 601614, EC 601620, EC 601615, EC 601646, EC 601626, EC 601621, EC 601702, EC 601625, EC 601 629, EC 601635, DRSF 108, EC 601656
Cluster IV	3	EC 601618, EC 601664, EC 601630
Cluster V	8	EC 601662, EC 601680, EC 601682, EC 601671, EC 601 675, EC 601 672, EC 601673, EC 601681,
Cluster VI	10	EC 601660, EC 601693, EC 601688, EC 601689, EC 601665, EC 601694, EC 601696, EC 601697, EC 601661, EC 601691
Cluster VII	5	EC 601657, EC 601684, EC 601685, EC 601687, EC 601676
Cluster VIII	8	EC 601658, EC 601692, EC 601668, EC 601659, EC 601669, EC 601663, EC 601667, EC 601666
Cluster IX	2	EC 601679 EC 601686

Table 1. Distribution of 64 sunflower genotypes in to different clusters



Fig. 1. Cluster diagram representing diveristy for 64 sunflower genotypes

(Table 1) (Fig 1). Out of nine clusters formed, cluster III is the largest group with 14 genotypes, followed by cluster VI with 10 genotypes, cluster I with nine genotypes, while cluster V, VIII had eight genotypes each, cluster II, VII with five genotypes each, cluster IV with three genotypes, and cluster IX with two genotypes. These genotypes were superior for one or fewer characters which made them divergent from the other clusters. It was interesting to note that 64 genotypes of differences in origin were grouped in the same cluster, indicating absence of relationship between genetic diversity and geographic diversity. Similar results have been reported by Thirumala Rao *et al.* (2005) and Srinivas *et al.* (2006).

The average intra and inter cluster distance (Table 2) (Fig 2) revealed that the genetic diversity among the genotypes were generally superior for one or few characters which made them divergent from other clusters. Maximum distance (5616.96) was observed between clusters III and cluster IX followed by cluster II and IX (4627.39) and cluster I and IX (3425.71). On the other hand clusters. VII and VIII (411.68) and V and VIII (413.04) were the closest. Similar results were reported by Mahalakshmi *et al.* (2006) and Ananda Kumar *et al.* (2007).

The cluster means (Table 3) indicated appreciable variation among various clusters, particularly for seed yield/plant, total number of seed/ head and seed filling per cent. However, variations were low for hull content, oil content, 100 seed weight, days to maturity and days to flowering. Based on cluster means, cluster IV include genotypes with high number of filled seeds/head, total number of seeds/head, high seed yield /plant and seed filling

	1 Cluster	2 Cluster	3 Cluster	4 Cluster	5 Cluster	6 Cluster	7 Cluster	8 Cluster	9 Cluster
Cluster1	277.643	426.485	629.044	606.268	786.312	544.664	1526.227	1700.660	3425.717
Cluster2		152.604	440.429	1125.635	1352.28	641.925	2383.233	2562.375	4627.396
Cluster3			292.769	1074.829	1851.33	1162.870	3152.280	3242.218	5616.964
Cluster4				192.596	526.484	654.196	1295.931	1112.059	2617.622
Cluster5					155.559	486.955	493.386	413.048	1391.686
Cluster6						285.756	1170.231	1104.456	2602.170
Cluster7							247.570	411.686	759.364
Cluster8								270.612	705.342
Cluster9									314.786

Table 2. Average intra and inter Euclidean cluster distances

Table 3.	. Cluster means	s for seed yield	and yield con	tributing characte	ers of 64 sunflowe	r genotypes

Cluster	Days to	Days to	Plant	Stem	Head	Filled	Unfilled	Total	Seed	100-seed	Seed	Oil	Hull
No.	50%	maturity	height	diameter	diameter	seeds/	seeds/	seeds/	filling	weight	yield/	content	content
	flowering		(cm)	(cm)	(cm)	head	head	head	(%)	(g)	Plant (g)	(%)	(%)
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





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 D₂ 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	Contribution
	ranked 1st	%
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 601613and 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 programm to develop superior varieties/hybrids in sunflower.

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