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Research Article

Genetic diversity analysis of high oleic inbred lines in sunflower (*Helianthus annuus*)

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Abstract
Sunflower hybrids with high oleic acid content have nutritional benefits similar to olive oil. High oleic sunflower hybrids can be obtained by using genetically divergent high oleic parental lines in heterosis breeding. The forty five parental lines with varying oleic acid content including inbred and cms lines were grouped into seven clusters by using Mahalanobis D^2 statistics. Cluster I was found to be the largest with 32 genotypes followed by cluster VI comprising four genotypes, cluster II & VII with three genotypes and Cluster III, IV & V comprising one genotype each. From the ten characters studied Oleic acid content (53.23) contributed maximum to diversity followed by hundred seed weight (20.71). The genotypes within the cluster V and VII shows a maximum inter-cluster distance (56.00), where the restorer line (COSFHO24R) can crossed with the *cms* lines in Cluster VII to exploit high heterosis. Higher genetic divergence for oleic acid content was observed between the clusters III, IV, V & VI thereby the genotypes within the clusters can be used as a parent in hybridization programme to develop hybrids with good vigour for oleic acid content.

Introduction

Sunflower (*Helianthus annuus*) is an annual cross pollinated diploid plant with chromosome number 2n = 34 belonging to the family Compositae. The second most important crop after maize in hybrid breeding is sunflower (Seiler *et al.*, 2017). Sunflower seed oil production makes up around 8% of the total global vegetable oil production. The total production of sunflower is approximately 45 million metric tons. In 2016 the area under its cultivation was 26 million hectares in the world and the average yield of sunflower was 1.78 metric tons per ha. (Konyalı, 2017)**.**The nutritional and functional properties of oil are primarily determined by its fatty acid composition. Sunflower seed contains 35-42% oil. It is rich in linoleic acid (55-70%) and consequently poor in oleic acid (20-25%). Depending on fatty acid composition, sunflower genotypes can be divided into traditional sunflower genotypes with oleic acid content of 14-39% of the oil, mid oleic acid sunflower genotypes with 42-72% oleic acid content and high oleic sunflower genotypes containing 75-91% oleic acid(Alimentarius, 2005). Olive oil is found to be nutritionally beneficial due to the presence of monounsaturated fatty acid (Oleic acid 55 to 83%). It is costlier compared to other oils. Sunflower hybrids with high oleic acid content have nutritional benefits similar to olive oil. High oleic sunflower hybrids can be obtained by using genetically divergent high oleic parental lines in heterosis breeding. Selection of divergent parental material in hybridization programme is an important breeding strategy for the development of superior cultivar(Madhavi Latha, 2017)**.** Mahalanobis D^2 is one of the important statistical techniques used for the study of genetic diversity among the parental lines. The main objective of the present study is to investigate the genetic diversity among the forty five high oleic inbred lines.

Materials and Methods

The present investigation was carried out during *Kharif* 2018 in the experimental fields of Department of Oilseeds, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore. Forty five genotypes comprising maintainer and restorer lines were used as material for the present study. The experiment was laid out in Randomized block design with two replications. In each replication each entry is raised in two row of 4m length with spacing of 60cm between the rows and 30 cm within the row. Recommended agronomic practices and plant protection measures were carried out to raise good crop. Three randomly selected plants from each genotype from every replication were selected and tagged for observing ten biometrical observations. The ten characters observed are plant height, head diameter, volume weight, hundred seed weight, seed yield, oil content, oil yield, oleic acid content and linoleic acid content. The average was worked for each entries in both replications for statistical

computation. Mahalanobis D^2 statistic was utilized to do multivariate analysis (Mahalanobis, 1936) and clustering of genotypes were done following Toucher's method.

Results and Discussion

D^2 statistics was used to measure the genetic diversity among 45 genotypes and they were grouped into seven clusters using Toucher's method (Radhakrishna Rao, 1952). The distribution of each genotypes in cluster is presented in Table 1 and Figure 1. Cluster I was found to be the largest with 32 genotypes followed by cluster VI comprising four genotypes, cluster II & VII with three genotypes and Cluster III, IV & V comprising one genotype each.

The inter-cluster and intra-cluster D^2 values were presented in Table 2. The inter-cluster D^2 value was maximum between the genotypes ofcluster VI with cluster VII (73.92)followed by cluster IV with cluster VII (70.36), cluster III with cluster VII (66.79) and cluster V and VII(56.00). The minimum D^2 distance was (14.81) between cluster III and IV, this indicates the close relationship of genotypes between the two clusters. The intra-cluster distance ranged from 0(cluster III, IV and V) to 22.70(VI). The intra-cluster distance 0 indicates the presence of only one genotype in the cluster III, cluster IV and cluster V. It is desirable to select the genotypes between clusters VI and VII with high inter cluster distance, as parents in hybridization programme for exploiting high heterosis.

Cluster mean of ten biometrical characters were assessed and presented in Table 3. It indicated the uniqueness among the clusters for all the characters. Maximum mean for Days to 50 percent flowering (62.00) was observed in cluster III followed by cluster VI(61.75) while minimum cluster mean for days to 50 percent flowering (56) was observed in cluster VII. The highest mean foe plant plant height (172.33) was observed in cluster V followed by cluster III (158.67) while minimum mean for plant height was observed in cluster VII (121.19).

The highest mean for head diameter (20.90) was observed in cluster V followed by cluster VI (18.22), while lowest mean for head diameter (13.21) was observed in cluster I. The cluster mean of seed yield was highest in cluster V (45.15) followed by cluster III (30.49), while lowest in cluster VI (18.74). Hundred seed weight recorded highest mean of 5.53 in cluster V followed by cluster III (5.45), while lowest mean of 3.83 in cluster II. Cluster II had maximum mean of 39.70 for oil content followed by clusterIII (38.85), while cluster IV had minimum mean of 35.31. Cluster V had maximum mean of 16.60 for oil yield followed by cluster III (11.76), while cluster VI had a minimum mean of 6.70. The highest mean for volume weight (45.13) was observed in cluster V followed by cluster VII (40.42), while lowest mean of 31.76 was observed in cluster VI. Oleic acid content had the highest mean of 91.81in cluster IV followed by cluster VI (87.28), while lowest mean of 47.59 in the cluster VII. Linoleic acidcontent had the maximum mean of 47.41 in cluster VII followed by cluster II(31.81), while minimum mean of 3.19 in cluster IV. Chandirakala and Manivannan (2014), Shamshad *et al.* (2014), Rani (2016),(Reddy *et al.*, 2012) Punitha *et al.* (2010), Naik (2018) and Madhavi Latha (2017) successfully used Mahalanobis D^2 analysis for quantifying divergence in sunflower.

The percent contribution of ten characters towards diversity is given in Table 4. From the ten characters studied Oleic acid content(53.23) contributed maximum to diversity followed by hundred seed weight(20.71), head diameter(12.12), volume weight(7.37), seed yield(3.33), oil content (2.12), plant height(0.61), oil yield(0.40) whereas linoleic acid content and days to fifty percent flowering contribution to divergence is negligible.

The genotypes within the clusters III, IV, V & VI which are genetically diverse has high cluster means for oleic acid content, thereby the genotypes within the clusters can be used as a parent in hybridization programme to develop hybrids with high oleic acid content.

D^2 analysis of 45 high oleic inbred lines in sunflower indicates the presence of lot of diversity in the genotypes which can be further exploited by hybridization programme. The genotypes within the cluster V and VII shows a maximum inter-cluster distance (56.00), where the restorer line (COSFHO24R) can be crossed with the *cms* lines in Cluster VII to exploit high heterosis for oleic acid trait. Higher genetic divergence for oleic acid content was observed between the clusters III, IV, V & VI thereby the genotypes within the clusters can be used as a parent in hybridization programme to exploit heterosis for oleic acid trait.

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Table 1. Clustering pattern of 45 germplasm lines of Sunflower

Cluster	Number of genotypes clustered	Parental lines
I	32	COSF1BHO9,COSF1BHO5,COSFHO5R,COSFHO4R,COSFHO7R, COSFHO1R,COSF1BHO20,COSF1BHO12,COSF1BHO10,COSF1BHO11, COSFHO11R,COSFHO9R,COSFHO20R,COSFHO10R,COSFHO23R, COSFHO6R,COSFHO16R,COSFHO25R,COSF1BHO14,COSFHO8R, COSFHO12R,COSFHO18R,COSFHO21R,COSF1BHO2,COSF1BHO19, COSF1BHO18,COSFHO14R,COSFHO17R,COSFHO19R,COSFHO22R, COSFHO13R,COSFHO15R
II	3	COSF1BHO16,COSFHO2R,COSFHO3R
III	1	COSF1BHO1
IV	1	COSF1BHO4
V	1	COSFHO24R
VI	4	COSF1BHO13,COSF1BHO3,COSF1BHO17,COSF1BHO15
VII	3	COSF1BHO6, COSF1BHO7, COSF1BHO8

Note: COSF1BHO – Coimbatore sunflower 1B high oleic

Table 2. Average inter and intra cluster distance grouped with parental lines in sunflower

	I	II	III	IV	V	VI	VII
I	19.87	30.99	25.66	25.36	28.92	33.32	52.57
II		20.54	43.98	46.94	34.56	55.05	34.41
III			0.00	14.81	35.14	19.90	66.79
IV				0.00	34.04	20.21	70.36
V					0.00	35.55	56.00
VI						22.70	73.92
VII							17.74

Table 3. Cluster mean for ten characters in sunflower

Cluster	Days to 50% flowering	Plant height	Head diameter	Seed yield	Hundred seed weight	Oil content	Oil yield	Volume weight	Oleic acid content	Linoleic acid content
I	59.41	149.56	13.21	29.55	4.32	37.88	11.21	38.14	79.78	15.22
II	60.33	151.50	15.85	28.11	3.83	39.70	11.04	37.80	63.19	31.81
III	62.00	158.67	14.65	30.49	5.45	38.85	11.76	29.97	84.75	10.24
IV	59.00	145.84	13.33	23.76	4.65	35.31	8.39	36.16	91.81	3.19
V	57.00	172.33	20.90	45.15	5.53	36.96	16.60	45.13	80.03	14.97
VI	61.75	148.79	18.22	18.74	5.38	36.90	6.70	31.76	87.28	7.72
VII	56.33	121.19	13.19	25.39	5.16	38.31	9.70	40.42	47.59	47.41

Table 4. Percent contribution of ten characters towards diversity in sunflower

S. No.	Character	Contribution (in percent)
1	Days to 50% flowering	0.00
2	Plant height	0.61
3	Head diameter	12.12
4	Seed yield	3.33
5	Hundred seed weight	20.71
6	Oil content	2.12
7	Oil yield	0.40
8	Volume weight	7.37
9	Oleic acid content	53.23
10	Linoleic acid content	0.10

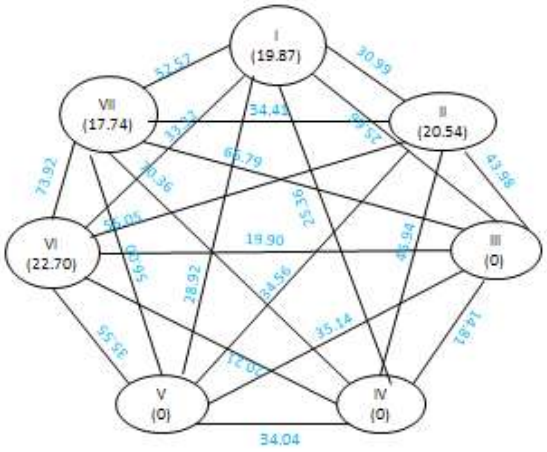

Fig. 1. Intra and inter cluster distances among seven clusters in sunflower genotypes

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