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Research Article

Genetic divergence study in sunflower (*Helianthus annuus* L.)

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Abstract :
An investigation about the genetical diversity among 17 sunflower genotypes using nine agronomic characters was studied at the Department of Oilseeds, Tamil Nadu Agricultural University, Coimbatore. Univariate and multivariate analysis of variance revealed the presence of significant among the genotypes. Mahalanobis D^2 statistics indicated the presence of substantial genetic diversity. The genotypes were grouped into four clusters. Based on the intercluster distance cluster mean for various characters, potential lines were identified from clusters I and III for crossing programme. Among the investigated characters, the seed yield, plant height, oil content and oil yield exhibited high contribution towards genetic divergence. The present study indicates that the inclusion of CSFI 5076, CSFI 5162, CMS 47A, CSFI 5005, CMS 17A, CMS 47A, CSFI 5069, CSFI 5422, CSFI 5109, CSFI 5155, CSFI 5002, COSF 1A , CSFI 5161 and CSFI 5015 in future breeding programs could result in the development of superior sunflower cultivars.

Key words:
D^2, genetic divergence, inbreds, multivariate analysis, seed parameters, sunflower.

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_1 with possibility of broad spectrum of variability in segregating generations. The D^2 statistics (Murty and Arunachalam, 1966) 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; Muppidathi *et al*., 1995).

Materials and methods

The materials used in the present study consisted of 17 genotypes in sunflower (*Helianthus annuus* L.) obtained from Department of Oilseeds, Tamil Nadu Agricultural University, Coimbatore. The genotypes were selected based on diverse pedigree. Seventeen genotypes *viz.,* CSFI 5002, CSFI 5005, CSFI 5015, CSFI 5064, CSFI 5069, CSFI 5076, CSFI 5103, CSFI 5109, CSFI 5154, CSFI 5155, CSFI 5161, CSFI 5162, CSFI 5422, COSF1A, CMS 17 A, CMS 47A and CMS 234 A were used to assess the divergence. All the 17 parents were raised in a randomized block design with two replications in the field during kharif, 2006. A spacing of 60 x 30 cm was adopted, with standard agronomic practices followed throughout the period of crop growth. Each parent was raised in one row, each row consisting of 10 plants. Observations were recorded on five randomly selected competitive plants of each genotype for the two replications from the middle of the row in both the replications were recorded for yield attributing characters such as; days to 50 per cent flowering, days to maturity, plant height, head diameter, volume weight, 100- seed weight, seed yield, oil content and oil yield.

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Results and discussion

In the present investigation, the genetic divergence among 17 sunflower accessions was studied by D^2 statistic of Mahalanobis (1928) followed by clustering of genotypes by Tocher's method. These analyses were carried out to know the extent of divergence in the genotypes, to identify the superior genotypes for utilization in hybridization programme and to find out the contribution of different characters towards genetic divergence in sunflower. The mean values of 17 accessions were tested for significance by univariate ANOVA and wilk's statistic. Significance of these statistics suggested the

existence of considerable divergence and justified further calculation of D^2 clustering resulted in the grouping of 17 accessions into four clusters. The statistical differences among the clusters based on D^2 values are also represented diagramatically in Figure 1.

The square of the distance (D^2 value) between any two entries calculated as sum of the difference between the mean values of all 17 genotypes were obtained for further analysis. Totally 136 combinations of D^2 values were obtained. Group constellation was carried out following Tocher's method (Rao, 1952) which utilizes the D^2 value. The 17 genotypes were grouped into four clusters. The composition of different clusters is given Table 1.

The intra and inter clusters D^2 values are provided in the Table 2. Maximum intra cluster D^2 value of 184.96 was observed for cluster I followed by cluster II (24.81). Cluster III and cluster IV had zero inter-cluster distance since they were represented by a single genotype. The maximum inter-cluster distance D^2 was observed between clusters II and III (887.44) followed by I and IV (691.69), III and IV (608.12) and cluster I and II (463.54). Since these clusters have higher inter-cluster distance among them, crossing between these clusters will result in increased heterosis. The inter-cluster D^2 value was found to be minimum between clusters II and IV (327.25) suggesting a close relationship between them and a low degree of diversity among the lines. The magnitude of heterosis largely depends on the degree of genetic diversity among parents and hence selection of lines from these lines two clusters should be avoided.

Cluster means values of the nine characters are furnished in Table 3. High ranges of mean values among the clusters were noted for the characters. The cluster II had the highest mean values for plant height and low mean values for 100-seed weight and seed yield. Cluster III had the highest mean values for 100-seed weight, seed yield and low mean values for days to 50 per cent flowering, days to maturity and plant height. Cluster IV had the highest mean values for days to 50 per cent flowering, days to maturity and low mean values for head diameter, oil content and oil yield. Considering the mean performance of clusters, the cluster I (CSFI5076, CSFI 5162, CMS 47A, CSFI 5005, CMS 17A, CMS 47A, CSFI 5069, CSFI 5422, CSFI 5109, CSFI 5155, CSFI 5002, COSF 1A and CSFI 5161) had the highest mean values for head diameter, volume weight, oil content and oil yield and it can be used as one of the parents to get higher yield and increased oil content Genotypes of this cluster could be used in crossing programmes for producing heterotic hybrids and for generating variability. To get desirable plant height and highest mean values for 100- seed weight and seed yield the cluster III (CSFI 5015) can be used.

The contribution towards genetic divergence indicated that the seed yield (34.56 %), plant height (22.06 %), oil content (19.85 %) and oil yield (17.65 %) contributed higher to the total genetic divergence in the genotypes of sunflower. The 100- seed weight, volume weight, head diameter, days to 50 per cent flowering and days to maturity contributed least towards the genetic divergence (Table 4). Sasikala (2000), Loganathan (2002), Ravi (2001), Anuradha *et al.* (2004), Mohan and Seetharam (2005) and Loganathan *et al*. (2006) reported that seed yield contributed maximum towards genetic divergence in sunflower.

To conclude, the cluster I (CSFI 5076, CSFI 5162, CMS 47A, CSFI 5005, CMS 17A, CMS 47A, CSFI 5069, CSFI 5422, CSFI 5109, CSFI 5155, CSFI 5002, COSF 1A, CSFI 5161 and cluster III CSFI 5015) are widely divergent and crosses may be effected among the genotypes of these clusters in a line x tester fashion to get more heterosis among the hybrids. The character seed yield was found to be important as the major contributor for genetic divergence.

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Fig. 1. Cluster Diagram of parental lines

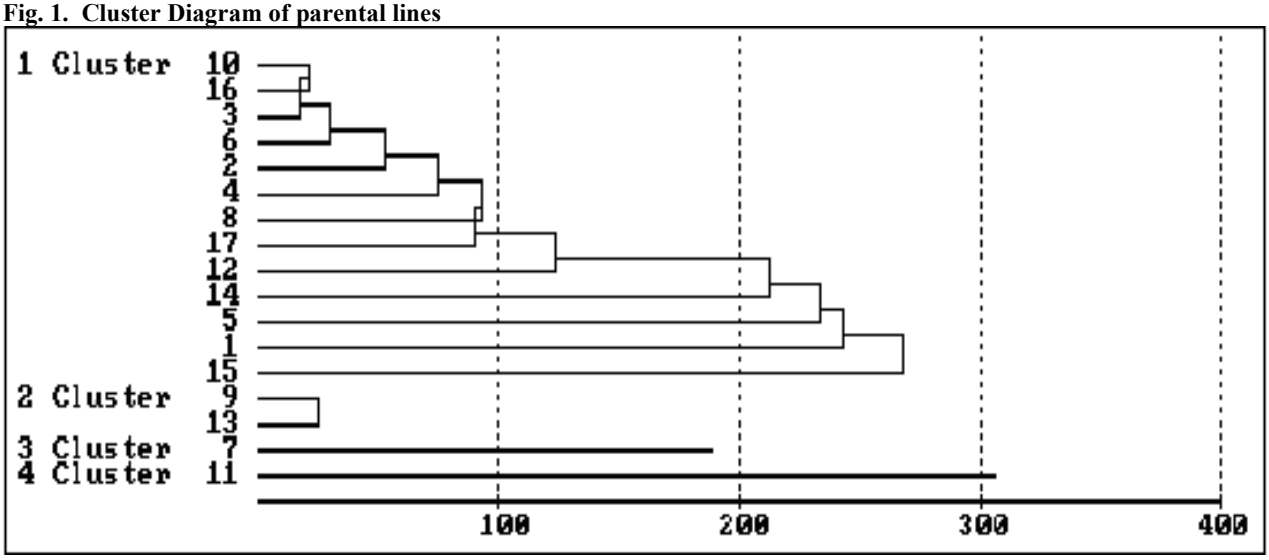

Table 1. Cluster composition of seventeen sunflower accessions

Cluster number	Number of genotypes	Genotypes
I	13	CSFI 5076, CSFI 5162, CMS 47A,CSFI 5005, CMS 17A, CMS 47A, CSFI 5069, CSFI 5422,CSFI 5109, CSFI 5155,CSFI 5002, COSF 1A and CSFI 5161
II	2	CSFI 5064 and CSFI 5154
III	1	CSFI 5015
IV	1	CSFI 5103

Table 2. Intra and inter cluster average of cluster distance

Cluster	I	II	III	IV
I	**184.96** (13.60)	**463.54** (21.53)	**384.16** (19.60)	**691.69** (26.30)
II		**24.81** (4.98)	**887.44** (29.79)	**327.25** (18.09)
III			**0.00** (0.00)	**608.12** (24.66)
IV				**0.00** (0.00)

Table 3. Cluster means for nine different characters

Cluster	Days to 50% flowering (no)	Days to maturity (no)	Plant height (cm)	Head diameter (cm)	Volume weight (g)	100-seed weight (g)	Seed yield (g)	Oil content (%)	Oil yield (g)
I	58.65	89.54	116.73	11.43	38.58	6.16	32.62	26.64	8.70
II	61.50	90.75	120.75	8.25	38.38	5.98	20.73	25.30	5.25
III	56.50	88.00	90.50	11.25	30.75	6.40	33.00	26.10	8.60
IV	62.00	91.50	97.00	8.00	36.25	6.15	22.60	21.30	4.85

Table 4. Contribution of nine characters towards genetic divergence

Character	Number of times ranked first	Percentage of contribution
Days to 50 % flowering (no)	0	0
Days to maturity (no)	0	0
Plant height (cm)	30	22.06
Head diameter (cm)	1	0.74
Volume weight (g)	3	2.21
100-seed weight (g)	4	2.94
Seed yield (g)	47	34.56
Oil content (%)	27	19.85
Oil yield (g)	24	17.65