Cluster analysis of yield traits in sunflower *(Helianthus annuus* L.)

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Abstract : In order to develop improved breeding lines having superior yield and oil content, it is essential to have genetically diverse parental lines. Hence, an attempt was made to find out genetic divergence of twenty four breeding lines for eight traits in sunflower. To assess the genetic divergence among the 24 genotypes in sunflower, Mahalanobis D^2 statistics was applied for eight traits. The genotypes were grouped into ten clusters where cluster I was the largest containing thirteen genotypes followed by cluster IV with three genotypes. The inter-cluster distance was the maximum between cluster VI and cluster VIII followed by cluster IV and cluster VI and cluster VI and cluster IX. Thus, the parents, CSFI 5415 of cluster VI, CSFI 5068 of cluster VIII, 17 A, 47 A and CSFI 5325 of cluster IV, CSFI 5415 of cluster VI, CSFI 5415 of cluster VI and CSFI 5436 of cluster IX should be involved in crosses. They might give high heterotic response and wider segregations after hybridization. The study revealed that plant height contributed maximum divergence (45.29%) which was followed by seed yield per plant (25.72%) and oil content (15.94%). Based on the inter cluster distance and *per se* performance the genotypes *viz.,* 17A, 47A, CSFI 5325, CSFI 5415, CSFI 5436 and CSFI 5013 were identified as suitable parents which could be intercrossed to obtain high heterosis and also to recover desirable transgressive segregants.

Key words : Sunflower, D^2 statistics, genetic divergence.

Introduction

Sunflower is an important edible oilseed crop of the world. The crop is grown under diverse agro-production situations, crossing climatic and geographic boundaries which necessitated the development of more productive hybrids of diverse duration. Development of hybrid is of much value for increasing the production of sunflower. For efficient hybridization programme, selection of genetically diverse parents and superior genotypes are pre-requisites, which ensure high heterosis and exhibit a gamut of transgressive segregants in order to increase the productivity of sunflower. The genetic diversity studies using D^2 statistics of Mahalanobis (1936) is being used for selection of prospective parents for hybrid production. 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 statistic (Murty and Arunachalam, 1966) has been found to be a powerful tool to estimate genetic divergence among population. Genetic divergence and grouping of genotypes into different clusters were already reported (Irene Priyadarshini, (1999); Anuradha *et al.,* (2004); Reddy *et al.* (2004); Loganathan *et al.,* (2006); Mahalaksmi *et al.*, (2006)). The characters head diameter, plant height, seed length, oil content and days to fifty per cent flowering were contributed more towards genetic divergence (Mohan and Seetharam, 2005) and days to first flowering contributed more towards

Table 1. Estimates of average intra and inter cluster distance for *yield* traits in sunflower

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X
I	25.477	34.426	38.947	63.524	33.731	40.646	36.656	64.293	60.841	54.543
II		0.000	56.001	76.092	46.611	41.282	35.515	71.468	83.363	71.526
III			0.000	37.301	38.0751	69.908	37.810	45.691	31.020	32.632
IV				28.111	60.648	94.084	50.574	37.184	39.527	53.499
V					0.000	54.851	33.099	49.964	53.190	35.518
VI						0.000	63.356	95.128	88.813	84.055
VII							0.000	37.648	62.219	49.039
VIII								0.000	53.989	46.544
IX									0.000	37.704
X										0.000

Table 2. Cluster mean values and relative contribution of different characters

Characters	Means Values										Relative Contribution %
	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Cluster IX	Cluster X	
Days to 50 per cent flowering	53.50	50.00	54.00	54.00	53.00	55.00	52.00	50.00	59.00	52.00	0.36
Plant height (cm)	110.49	83.22	159.60	180.23	133.70	72.22	117.04	165.73	198.20	172.40	48.29
Head diameter (cm)	10.21	6.30	9.05	12.08	14.55	7.24	15.32	19.07	11.59	15.80	8.70
Volume weight (g)	25.06	11.55	15.91	29.42	42.17	16.25	32.59	40.56	38.42	45.13	0.00
Hundred seed weight (g)	4.56	5.80	2.80	4.77	9.17	6.20	5.35	8.07	4.80	5.77	3.26
Seed yield (g)	34.45	44.90	34.55	27.46	37.00	29.70	43.25	37.90	23.25	39.70	25.72
Oil content (%)	29.81	39.94	25.86	37.38	24.80	28.68	38.70	38.49	19.50	17.38	18.94
Oil Yield (g)	6.85	4.61	4.12	9.95	10.44	4.66	12.61	15.63	7.51	7.95	0.72

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Fig. 1 Cluster diagram for parental lines
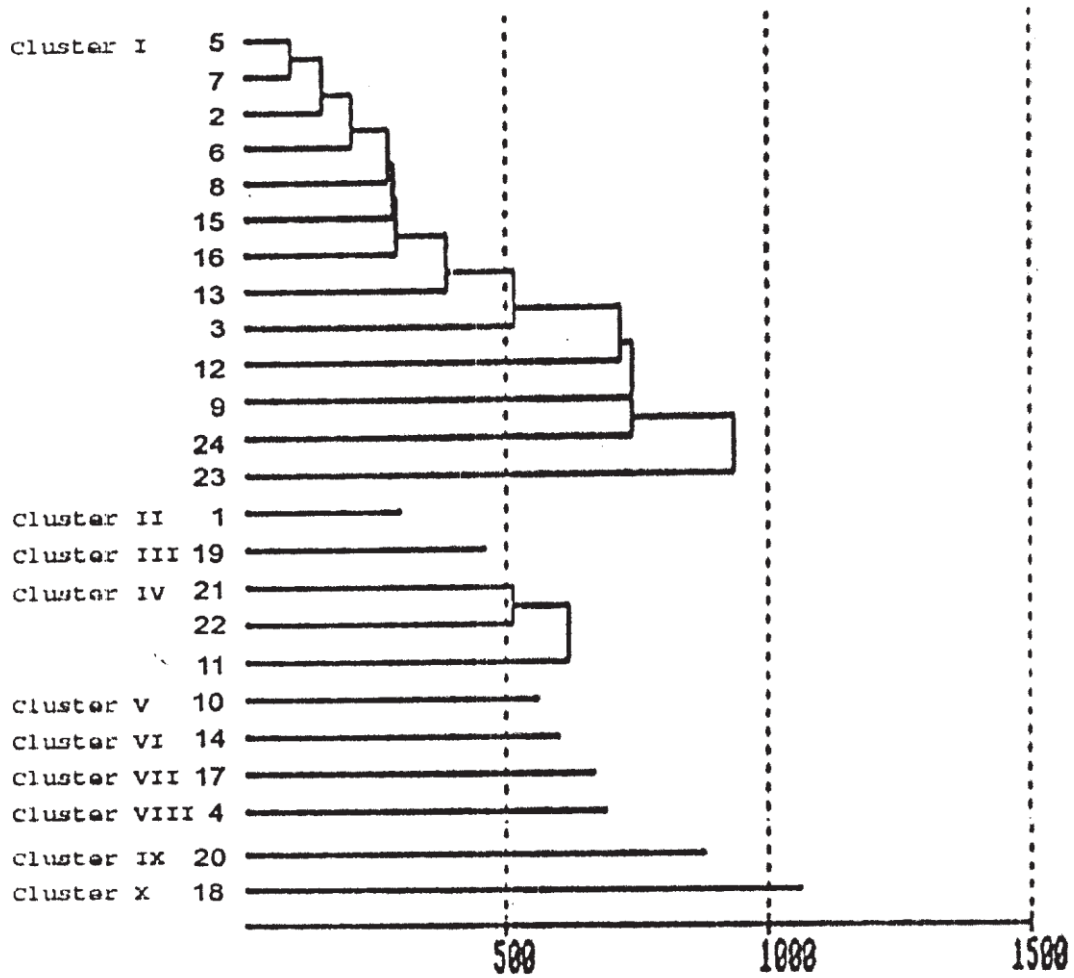
1-CSFI 5013	2-CSFI 5014	3-CSFI 5048	4-CSFI 5068
5-CSFI 5118	6-CSFI 5155	7-CSFI 5156	8-CSFI 5168
9-CSFI 5169	10-CSFI 5274	11-CSFI 5325	12-CSFI 5412
13-CSFI 5414	14-CSFI 5415	15-CSFI 5418	16-CSFI 5419
17-CSFI 5428	18-CSFI 5434	19-CSFI 5435	20-CSFI 5436
21- 17 A	22- 47 A	23- 234 A	24- 851A

genetic divergence (Mahalaksmi *et al.,* 2006). Sridhar *et al.* (2006) grouped 44 genotypes into 9 clusters. Plant height and oil content contributed more towards genetic divergence. Srinivas *et al.* (2006) grouped 45 genotypes into 9 clusters. Days to maturity, hundred seed weight, leaf area index and total dry matter contributed maximum towards genetic divergence. Hence, the present study was an attempt to know magnitude of diversity present in twenty four parental genotypes for yield and yield related component traits in sunflower.

Materials and Methods

The material for the present study consisted of 24 sunflower genotypes. The experiment was conducted at Department of Oil seeds, Centre for Plant Breeding and Genetics, TNAU, Coimbatore during *rabi*/Summer 2005-'06. Each genotype was sown in two rows of 6m length with spacing of 60 cm between rows and 45 cm between plants. The experiment was laid out in a Randomized Block Design with two replications. In each genotype, five plants were randomly selected and used for collection of data on eight characters *viz.,* days to fifty % flowering, plant height (cm), head diameter (cm), volume weight (g), hundred seed weight (g), oil content (%), seed yield per plant and oil yield per plant. The data were subjected to statistical analysis using Mahalanobis D^2 statistic (Mahalanobis, 1936) and Toucher's method as described by Rao (1952) for determining group constellation.

Results and Discussion

Inter crossing of divergent groups would lead to genetic base in the base population and greater opportunities for crossing over to occur, which intern may release hidden variability by breaking close linkage (Thoday, 1960). The progenies derived from such crosses were expected to show wide variability,

providing greater scope for isolating transgressive segregants in the advanced generations. Hence these genotypes may be used repeatedly in the crossing programmes to recover transgressive segregants, which can be either released as variety or can be utilized in the genetic enhancement of sunflower crop.

In the present study, all the twenty-four parental lines were grouped into ten clusters (Fig. 1). Cluster I comprised of thirteen genotypes followed by cluster IV that had three genotypes. The Clusters II, III, V, VI, VII, VIII, IX and X comprised of each only one genotype (Fig.1). The average intra and inter cluster D^2 values are presented (Table 1). Minimum inter cluster D^2 value was observed between cluster V and cluster VII indicating the close relationship among the genotypes included in this cluster. Maximum inter cluster D^2 value was observed between cluster VI and cluster VIII followed by cluster IV and cluster VI and cluster VI and cluster IX. Thus, the parents CSFI 5415 of cluster VI, CSFI 5068 of cluster VIII, 17 A, 47 A, CSFI 5325 of cluster IV, CSFI 5415 of cluster VI, and CSFI 5436 of cluster IX if involved in crosses might give high heterotic response and wider segregations after hybridization. These results are in conformity with Irene Priyadarshini (1999) and Serene Maragatham Isacs (2002). Cluster I exhibited minimum intra-cluster value (25.47) indicating the diversity between the genotypes of cluster I was less, while cluster IV had maximum intra cluster value (28.11) which revealed the existence of diverse nature between 17 A, 47 A and CSFI 5325 (Table 1).

The cluster mean values for different characters are presented (Table 2). Regarding the mean performance of cluster, the genotype CSFI 5013 (cluster II) had the highest mean

for seed yield per plant and oil content with desirable early duration for flowering. A similar result was reported by Serene Maragatham Isacs (2002). The cluster VII and cluster VIII were recorded highest mean values for seed yield per plant, oil content and oil yield with earliness to Slower (Vishnuvardhan Reddy *et al.*, 2005). Hence the genotypes CSFI 5013 (cluster II), CSFI 5428 (cluster VII) and CSFI 5068 (cluster VIII) could be used as one of the parents to get higher yield.

The present study revealed that the selection of parents must be used on the wider inter cluster distance and superior mean performance for yield and yield components. Based on mean performance and genetic divergence, six genotypes *viz.,* 17A, 47A, CSFI 5325, CSFI 5415, CSFI 5436 and CSFI 5013 were identified as desirable parents and could be utilized in hybridization programme to synthesize high yielding hybrids in sunflower.

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