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RESEARCH ARTICLE :

Genetic diversity analysis for agro-morphological traits in sunflower (*Helianthus annuus* L.)

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SUMMARY : Genetic diversity analysis was performed on 70 genotypes of sunflower through Mahalanobis D^2 statistics. Based on the results, the genotypes were categorized into 10 clusters connoting the existence of ample genetic diversity in the material evaluated. Cluster I was the largest with 56 genotypes. This was followed by cluster IV with four genotypes; cluster VII with three genotypes and the remaining were monogenotypic clusters. Maximum inter-cluster distance was observed between cluster VI and VIII (19.02) implying that utilization of the genotypes in those clusters might result in desired F_1's upon hybridization.The study also revealed that the traits in the genotypes *viz.*, SCMR (30.31%) followed by hull content (24.39%) contributed more to the total genetic divergence. Five genotypes belonging to monogenotypic clusters *viz*., DRM-342, R-45, CPI-1, NDI-16 and CMS-17B can be utilized in future breeding programme to harness desired heterotic F_1s.

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KEY WORDS :
Sunflower, Genetic diversity, D^2statistics, Clusters

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BACKGROUND AND OBJECTIVES

Sunflower (*Helianthus annuus* L.; 2n=2x=34), a crop of all seasons is an important edible annual oilseed ranking fourth in significanceglobally alongside soybean, rapeseed-mustard and groundnut. Its oil is considered as premium than other vegetable oils owingto its light colour, bland flavour, high smoke point, high level of linoleic acid and absence of linolenic acid. As the modern cultigens of sunflower have reached an yield plateau, there is anurgent need to screen genotypes for genetic divergenceto utilize them in breeding programmes for harnessing higher yields. D^2 analysis, a sort of multivariate technique has been successfully utilized in sunflower to classify genotypes and for determining their inter relationships by many workers (Marinkovic *et al.*, 1992 and Teklewood *et al.*, 2000). In light of the circumstances, the present investigation using D^2 statistics was attempted in 70 genotypes of sunflower to quantify the genetic diversity for identification of potential genotypes in future breeding programmes.

RESOURCES AND METHODS

Seventy sunflower genotypes procured

from IIOR (Hyderabad), RARS Nandyal (Andhra Pradesh) and UAS Bengaluru, Raichur (Karnataka) were utilized for the present study. The field experiment was conducted during *Rabi*, 2016-17at RARS, Nandyal geographically located at $15^0$29' North latitude, $78^0$29' East longitude at an altitude of 211.76 m above mean sea level. The genotypes wereraised as a single row of 0.6m length with a spacing of 60 x 30 cm in Randomized Block Design replicated thrice. All the recommended agronomic practices were adopted to raise a good and healthy crop. In each genotype per replication, five plants were randomly selected and phenotypic data was collected on 15 agro-morphological traits *viz*., days to 50 per cent flowering, days to maturity, plant height, number of leaves per plant, head diameter, 100 achene weight, number of achenes per head, autogamy per cent, volume weight, achene yield per plant, hull content, oil content, SPAD chlorophyll meter reading (SCMR), specific leaf area (SLA) and leaf area index (LAI). After computing means, the data was subjected to Mahalanobis(1936) D^2 analysis as described by Rao (1952). The genotypes were grouped into different clusters according to Tocher's method (Rao, 1952) and inter and intra cluster distances were calculated as per Singh and Choudhary (1977).

OBSERVATIONS AND ANALYSIS

In the present study, the 70 genotypes were categorized into 10 clusters (Table 1 and Fig. 1) implying the existence of ample genetic diversity in the material studied. Cluster I recorded maximum number of genotypes (56) followed by cluster IV with four genotypes, cluster VII with three genotypes and the remaining were monogenotypic clusters *viz*., II, III, V, VI, VIII, IX and X contained only one genotype each. The genotypes NDI-3, NDI-4 are grouped in IV cluster, NDI-16 alone occupied VIII cluster while the remaining NDI lines are grouped in I cluster indicating substantial amount of genetic diversity in the aforesaid three lines. Similarly the genotypes NDLB-2,4 and 8 were grouped into VII, IV and IX clusters and the remaining NDLB lines were grouped in I cluster. CPI-I alone grouped in VI cluster while the remaining lines come under cluster I. In general the genotypes grouped within a cluster exhibit a narrow range of genetic variability, while across clusters shows wider variability. Hence, the genotypes grouped in cluster I are genetically similar and use of lines with in a cluster for developing hybrids may not result in expected heterosis. Similarly the genotypes under cluster IV were having lesser genetic variability and may not exhibit desired heterosis when involved in hybridization programme. Such a narrow range of genetic variability among the lines with in the clusters has been reported by earlier sunflower workers (Teklewold *et al*., 2000, Ramasubrhamanyam *et al.,* 2003 and Srinivas *et al*., 2006). Cluster VII contained three genotypes with maximum intra cluster distance recording significant extent of variability among the genotypes.

Based on the inter cluster distances using D^2 values (Table 2) it was observed that genotypes belonging to clusters VI and VIII (19.02) are more diverse followed by clusters II and VIII (18.86), III and X (18.86) and clusters III and VIII (18.46) suggesting that hybridization between these divergent lines may lead to higher magnitude of heterosis for the characters concerned.

Table 1 : Cluster composition of 70 sunflower genotypes based on Tocher's method

Cluster number	No. of genotypes	Genotypes
I	56	NDI-5, NDI-7, NDI-15, NDI-14, NDI-6, CPI-11, NDLB-5, CPI-6, CPI-12, CPI-5, DRSF-113, NDI-8, GMU-258, NDI-11, NDI-2, GMU-498, R-843, RCR-72, R-853, ARM-249B, GMU-474, GMU-205, RHA-172, RCR-39, RCR-114, GMU-242, NDSI-3, NDI-12, DRSF-108, ARM-248B, RCR-76, CPI-7, NDLB-6, RCR-1296, GMU-53, CPI-8, 150R, R-64, GMU-15, GMU-156, GMU-1134, NDI-13, NDLB-7, RCR-33, NDI-1, CPI-2, GMU-236, CPI-13, GMU-1108, GMU-673, CPI-4, CPI-3, RHA-859, CMS-30B, GMU-152, GMU-42.
II	1	DRM-342
III	1	R-45
IV	4	NDI-4, NDLB-4, NDI-3, RHA-271
V	1	CMS-234B
VI	1	CPI-1
VII	3	NGM-16, NDLB-2, RHA-6D-1
VIII	1	NDI-16
IX	1	NDLB-8
X	1	CMS-17B

Table 2 : Average intra and inter cluster distances for the sunflower genotypes studied

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X
I	8.54	11.47	10.91	11.21	10.62	11.16	11.35	13.18	13.20	15.68
II		0.00	12.47	12.52	15.35	7.93	12.50	18.86	11.59	16.73
III			0.00	12.18	14.61	11.85	8.21	18.46	16.16	18.86
IV				9.29	14.16	11.80	13.89	13.79	14.14	12.76
V					0.00	16.77	13.41	9.52	10.36	13.03
VI						0.00	11.99	19.02	15.90	18.02
VII							9.73	18.23	15.21	18.45
VIII								0.00	14.19	12.98
IX									0.00	12.50
X										0.00

Table 3 : Cluster means with respect to agro-morphological traits among 70 sunflower genotypes

Character Cluster	DF	DM	PH	LP	HD	AW	AH	AU	VW	AY	HC	OC	SCMR	SLA	LAI
1 Cluster	55.33	83.99	119.51	24.23	14.48	5.39	451.42	86.32	32.66	24.08	33.47	34.24	39.34	162.90	3.18
2 Cluster	51.67	80.67	61.00	17.37	12.33	4.73	278.78	108.59	26.00	13.22	45.90	31.82	37.64	142.04	2.80
3 Cluster	60.67	87.33	104.33	21.32	15.33	3.92	348.98	66.69	32.33	13.66	24.78	35.45	34.52	191.60	3.40
4 Cluster	63.75	93.67	119.67	25.74	13.67	4.81	416.60	74.65	34.92	20.21	42.84	32.16	38.28	159.84	3.07
5 Cluster	55.00	84.33	98.33	25.47	12.33	4.78	228.49	88.25	31.67	10.92	26.08	34.66	44.85	166.99	2.43
6 cluster	51.00	79.33	108.33	19.78	13.33	5.87	396.34	74.56	35.00	23.20	45.74	30.76	35.16	267.56	2.73
7 Cluster	54.44	84.00	94.44	17.85	10.78	4.19	273.60	62.08	33.56	11.42	24.79	34.89	36.45	196.36	2.24
8 Cluster	63.67	95.33	135.67	28.86	16.00	7.20	495.24	81.80	36.00	35.66	33.78	33.94	46.16	192.96	3.63
9 Cluster	58.00	86.00	70.00	17.00	10.00	5.30	173.05	55.34	24.67	9.05	41.29	33.46	44.49	136.76	1.53
10 Cluster	64.00	95.00	97.67	26.67	6.67	2.90	116.15	92.51	32.33	3.44	45.24	27.18	44.19	142.27	1.70

DF-Days to 50% flowering, DM-Days to maturity, PH-Plant height, LP-No.of leaves/ plant, HD-Head diameter, AW-100 Achene weight, AH-No. of achenes per head, AU-Autogamy per cent, VW-Volume weight, AY-Achene yield, HC-Hull content, OC-Oil content, SCMR-SPAD chlorophyll meter reading, SLA- Specific leaf area, LAI- Leaf area index.

From the cluster mean values as indicated (Table 3), contrasting genotypes for days to 50% flowering were observed in clusters X and VI, for days to maturity in clusters VI and VIII, plant height in II and VIII, leaves per plant in IX and VIII, head diameter in X and VIII, 100 achene weight in X and VIII, achenes per head in X and VIII, autogamy per cent in IX and II, volume weight in IX and VIII, achene yield in X and VIII, hull content in II and III, oil content in X and III, SPAD chlorophyll meter reading in III and VIII, specific leaf area in VII and VI and leaf area index in X and VIII. From the present study it can be noticed that genotypes under cluster VIII possessed desirable qualities for large number of characters *viz*., plant height, leaves per plant, head diameter, 100 achene weight, achenes per head, volume weight, achene yield and SPAD chlorophyll meter reading. The genotypes under clusters II, III, VI and X recorded desired values for the remaining traits. Hence, inclusion of genotypes under these clusters in hybridization will result in heterosis for yield and

Table 4 : Contribution of agro-morphological traits towards total genetic divergence in 70 genotypes of sunflower

Sr. No.	Character	Times ranked first	Contribution (%)
1.	Days to 50% flowering	349	14.45
2.	Days to maturity	49	2.03
3.	Plant height	102	4.22
4.	Number of leaves per plant	306	12.67
5.	Head diameter	0	0.00
6.	100 achene weight	6	0.25
7.	Number of achenes per head	19	0.79
8.	Autogamy per cent	96	3.98
9.	Volume weight	118	4.89
10.	Achene yield	18	0.75
11.	Hull content	589	24.39
12.	Oil content	25	1.04
13.	SPAD Chlorophyll meter reading (SCMR)	732	30.31
14.	Specific leaf area	0	0.00
15.	Leaf area index	6	0.25

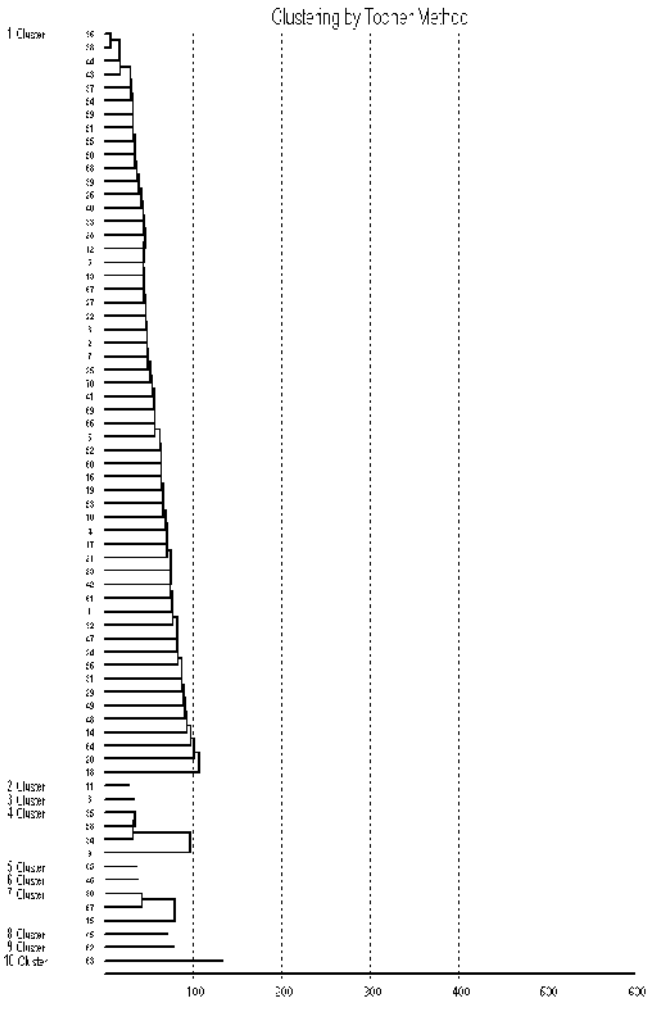

Fig. 1 : Grouping of genotypes into clusters

concerned characters.

The traits SCMR contributed maximum to the total genetic divergence (Table 4). It was closely followed by hull content, days to maturity, leaves per plant, volume weight and plant height are next in the order. Similar results were reported by Sujatha *et al*. (2002) for hull content and plant height, Mohan *et al.* (2007) for days to 50% flowering and Kumar *et al*. (2008) for leaves per plant. Interestingly it was noticed that the traits head diameter and specific leaf area had zero contribution towards total divergence inferring homogeneity for the traits in the genetic material evaluated.

From the foregoing results and discussion it can be inferred that traits *viz*., days to maturity, leaves per plant, hull content, volume weight and plant height can be employed as criterion to classify material for selection of genetically diverse lines. The genotypes DRM-342, R-45, NDI-16 and CMS-17B were identified as promising for majority of the traits and can be deployed as potential parents to harness desired heterotic F_1s in future hybridization programmes.

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