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ANALYSIS OF GENETIC DIVERGENCE OF SUNFLOWER INBRED LINES (*Helianthus annuus* L.)

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Genetic divergence of 77 inbred lines of sunflower for 11 characters were assessed by using Mahalanobis's D^2 statistic. The genotypes were grouped into 10 clusters. No relationship between geographic origin and genetic diversity was observed. Based on inter cluster distance, maximum genetic diversity was observed between genotypes belonging to cluster II and VII. Hence, the genotypes belonging to above clusters will be very useful in the crossing programme and may result high amount of heterosis. Characters viz., plant height, number of filled seeds per head and head diameter contributed more towards genetic divergence.

Key words : Sunflower, genetic divergence

Sunflower is one of the important oilseed crop. Hybrid development is of much value for increasing the production and selection of parents based on the genetic divergence is a pre-requisite in a hybrid programme. Asthana and Pandey (1980) reported that the geographic diversity may not necessarily be related with genetic divergence. Therefore, the selection of lines for breeding should be based on genetic divergence rather than geographical diversity. For the choice of diverse parents, multivariate analysis using Mahalanobis's D^2 statistic has been extensively used as a quantitative measure of genetic divergence. It is a powerful tool in quantifying the degree of genetic divergence among parents. Though sunflower has number of desirable features, the yield is low and unstable in India which necessiates the improvement by adopting suitable breeding strategies. In this direction, the present study deals with genetic divergence in inbred lines for selection of appropriate germplasm material in sunflower breeding programmes.

MATERIALS AND METHODS

The present investigation consisted of 77 inbred lines developed from Directorate of Oilseed Research, Hyderabad were grown in 2 rows of 5 m length with a spacing of 60 × 30 cm in a randomised block design (R.B.D.) with 2 replications at College of Agriculture, Rajendranagar, Hyderabad during *rabi*, 1997. Observations were recorded on 5 random plants on 11 characters viz., plant height, days to 50 per cent flowering, stem girth, no. of leaves per plant, head diameter, days to maturity, no. of filled seeds per head, no. of unfilled seeds per head, test weight, oil per cent and seed yield. To study genetic diversity the data were analysed by using Mahalanobis's D^2 statistic as described by Rao (1952). The genotypes were grouped into different clusters according to Toucher's method (Rao, 1952).

RESULTS AND DISCUSSION

The analysis of variance showed significant differences exists between genotypes for yield, yield component characters. All the 77 genotypes were grouped into 10 clusters (Table 1). The cluster I comprising of 19 genotypes was the longest followed by cluster VII and VIII. Remaining clusters had 3-8 genotypes. These genotypes were

Table 1. Distribution of 77 germplasm stocks of sunflower in different clusters

Cluster	No. of genotypes	Genotypes						
I	19	DRM82	DRM69	DRM59	DRM63	DRM5	DRM6	DRM12
		DRM60	DRM71	DRM86	DRM78	DRM3	VND NB10	DRM77
II	3	DRM7	DRM1	DRM68				
III	7	DRM85	DRM93	DRM11	DRM83	DRM81	DRM91	DRM15
IV	6	GP11949	R-17	R-856	IV55NB-13	VNDNB7	VNDNB2	
V	4	ARM241	ARM249	88-2	GP11937			
VI	3	X-15NB-5	X-15NB-2	P-356-R				
VII	12	R-272-II	234-B	LIB02M-14	GP11669	R-298	RHA271	R- 265
		LIB02M-1	LIB02M-3	LIB02M-6	6D-1	RHA859		
VIII	10	GP1529	GP11288	GP11519	GP1545	GPI3001	GPII499	R-272-1
		88-4	88-9	88-8				
IX	8	GPI255	ARM250	ARM247	ARM244	ARM240	ARM242	ARM245
		ARM238						
X	5	GP12324	ARM239	GPI594	ARM248	ARM246		

Table 2. Average intra and inter cluster distance (D values)

	I	II	III	IV	V	VI	VII	VIII	IX	X
I	23.382	30.313	28.568	36.792	46.024	41.790	45.674	40.107	40.816	48.739
	M	H	M	H	H	H	H	H	H	H
II		33.494	39.762	48.296	59.131	58.039	60.621	47.283	53.244	57.714
		H	H	H	H	H	H	H	H	H
III			25.027	41.548	46.162	41.556	45.334	44.495	43.302	50.441
			M	H	H	H	H	H	H,H	
IV					31.321	40.977	35.822	38.823	44.865	39.631
				H	H	H	H	H	H	H
V					31.109	40.752	35.142	43.617	36.112	41.751
					H	H	H	H	H	H
VI						26.977	35.303	53.455	45.932	58.786
						M	H	H	H	H
VII							30.410	49.100	39.807	51.382
							H	H	H	H
VIII								40.260	36.803	39.915
								H	H	H
IX									26.556	35.546
									M	H
X										30.456
										H

H : Highly divergent (above 30); Moderately divergent (23-30); M generally extraordinary for one or more characters which made them divergent from the other clusters. Maximum distance (60:621) was observed between cluster II and VII (Table 2) followed by II and V (59.131), while the clusters I and II were the lowest (28.568).

The cluster means (Table 3) indicated appreciable variation among various clusters. An examination of cluster means revealed that the clusters VI (6.95) and VII (6.74) were low seed yielders and cluster V recorded maximum seed yield per plant. For plant height (159.62 cm), stem girth (2.00 cm), no. of leaves per plant (26.33) and unfilled seeds per head (151.92) cluster X recorded maximum and cluster V recorded maximum for days to 50% flowering and days to maturity. The genotypes grouped into cluster III recorded maximum test weight (4.98 gm) and cluster VI recorded highest oil per cent (39.60).

Table 3. Mean of cluster from 77 germplasm lines of sunflower for 11 characters

Cluster	Plant height	Days to 50% flowering	Stem girth	No. of leaves per plant	Head diameter	Days to maturity	No. of filled seeds/head	No. of unfilled seeds/head	Test weight	Oil per cent	Seed yield/plant
I	94.984	54.816	1.745	19.592	12.006	77.237	387.984	85.918	4.022	34.656	15.654
II	84.433	55.167	1.793	19.300	14.533	77.167	493.958	98.375	4.053	32.593	20.030
III	92.950	55.429	1.793	18.314	11.429	77.643	279.018	77321	4.988	33409	13.957
IV	99.508	59.500	1.339	19.158	9.105	81.417	358.250	63.000	3.311	36.539	11.577
V	132.150	67.625	1.793	22.988	10.565	89.625	351.063	134.313	3.537	31.300	12.345
VI	93.317	57.333	1.315	19.367	8.297	79.000	195.583	79.292	3.533	39.660	6.952
VII	115.042	60.333	1.645	18.508	8.743	83.917	235.552	66.978	2.882	32.501	6.742
VIII	130.000	62.800	1.775	23.075	12.300	84.950	465.187	107.379	4.228	32.156	19.901
IX	142.400	64.688	1.778	25.163	10.892	86.250	402.234	71.313	3.956	35.122	15.798
X	159.620	64.600	2.005	26.330	13.251	87.000	475.475	151.925	4.461	32.860	21.298

In the present study, maximum inter cluster distance was existed between cluster II and VII. Hence crossing between genotypes belonging to these clusters may result in high heterosis. The characters which contributed maximum genetic divergence (Table 4) are the plant height (23.92%), filled seeds per head (20.78%), head diameter (18.22%). These results are in agreement with the findings of Yadav *et al.* (1980). Among the studies on evolution on understanding the effect of change in breeding system on genetic divergence between populations would be of considerable interest (Murthy and Arunachalam 1996; Singh *et al.*, 1980)

In the present study, it appears that the clusters II, VIII and X had high mean performance of the desirable characters (no. of filled seeds, head diameter and test weight). These clusters were very useful in the crossing programmes of sunflower to develop a good hybrid. Several reports on sunflower path analysis revealed that the characters number of filled seeds per head, head diameter and test weight were directly correlated with seed yield per plant. Hence, breeder should select the parents from these clusters which are having high mean performance of above characters and those parents will be very useful in breeding programmes to develop with yielding hybrids in sunflower.

Selection of genotypes from divergent clusters, might prove to be more useful, if these are also selected with due consideration of *per se* performance. However looking at subjective and arbitrary nature of grouping with D^2 statistic (Singh and Ramanujan, 1981) and depending on breeders interest more than one genotype from a cluster could be selected for hybridization programme.

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