general, the dominance effect [h] was predominant in plant height, leaf length, leaf breadth and grain yield. The predominance of dominant effect for these characters was already reported by many workers including Prem Sagar (1970). However, earhead length and earhead breadth, both additive and dominance effects were important. Since for most of the traits including grain yield, the dominance effect was found to be important, heterosis breeding is suggested for improvement of grain yield with its component traits. Among the interaction components, the fixable additive X additive interaction effect [i] was preodminant only for leaf breadth in two crosses. The additive X dominance effect [j] was important for plant height, leaf length, earhead length and grain yield in one cross each. The dominant X dominant effect [l] was predominant in most of the crosses for plant height, leaf length, earhead breadth and grain yield. Hence, among the interaction components the unfixable dominant X dominant effect played a major role in control of most of the traits. Therefore, reciprocal recurrent selection seems to be ideal for developing suitable variety in peatl millet.

In majority of the crosses the [h] and [l] effects had opposite signs for all the traits. These two effects had similar sings in only one cross in different traits. Therefore duplicate kind of epistasis played a major role in governing all the traits than complementary type of interaction.

As a whole, additive, dominance and all the three types of non- allelic interaction effects appeared to govern all the characters studied. However, predominance of dominance and dominance X dominance interaction effects was observed for all the characters. In most of the cases the interaction is of duplicate type. Since the dominance effect is predominant, heterosis breeding is suggested for improvement of grain yield and its component traits. However for establishment of superior varieties, reciprocal recurrent selection is suggested.

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GENETIC DIVERGENCE IN SUNFLOWER

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ABSTRACT

Fifty four genotypes of sunflower were studied for their genetic divergence by D^2 analysis for a set of divergent characters nambely seed yield and five other metric traits. The genotypes were grouped into seven clusters. Based on the intercluster distance and cluster mean for various character, potential parent were identified from clusters VII, VI and V for hybridisation programme. Head diameter, seed yield and days to 50% flowering contributed more towards genetic divergence.

KEY WORDS : Sunflower, Genetic Divergence

Sunflower is one of the potent oil seed corps. Hybrid development programme is much of value for increasing the edible oil production in the country. Asthana and Pandey (1980) reported that the geographic diversity may not necessarily be related with genetic diversity. Therefore, the selection of varieties for hybridisation should be based on genetic diversity rather than geographic diversity. Many sunflower varieties developed for cultivation resulted in poor yield in vertisols under rainfed condition. To get higher yield level, the hybrids are used now-a-days. Since, the hybrid vigour depends upon the parent's divergence, it is necessary to identify diverse parents for hybridisation, multivariate analysis by means of mahalonobis D^2 statistic has been used in several crops. It is a powerful tool in quantifying the degree of genetic divergence among parents.

Table 1. Composition of different clusters

Cluster Number	Number of genotyes	Name of the clutivar
I	13	BSFI. 3, TNAU-SUF. 129, TNAU-SUF.6/222, TNAU- SUF.6/3, Inbred.132, Inbred 289, Co.1/97/11. Co.1/157/9. Co.1/179/1 Modern 178/4 EC 68415/150 No.88/23, Co.2
II	18	BSFI.2, BSFI-3, BSFI-6, BSFI-11, BSFI-16, BSFI-17, BSFI-18, BSFI-21, TNAU-SUL-225, TNAU-SUF-7/309, TNAU-SUL.6/201, Inbred. 184, Modern.13/72, Modern.12/13, EC.68415/139, EC.68415/92, SS.56 B line.
III	4	BSFI.20, Inbred.130, Co.1/186/13, EC.68415/112.
IV	13	Co.2/973/7/6/9, Co.2/838/6/2/16, Co.2/476/2/6/9, Co.2/896/2/3/7, Co.2/1041/7/5, Co.1/144/7, Co.1/147/2, Co.1/91/2, Co.1/179/1, Modern.12/11, Modern.193/4, Modern 193/12, Modern 173/1
V	1	Co.2/2187/3/7.
VI	2	Co.1/97/12. Co.1/155/13
VII	3	EC.68415/126, EC.68415/30, No.61.

However, such information is lacking in sunflower (*Helianthus annus L.*). An attempt was, therefore, made to study the genetic diversity in this crop.

MATERIALS AND METHODS

Fifty four genotypes of sunflower with different origin were raised in randomised block design replicated thrice, during *rabi* 1993 at the Regional Research Station, Kovilangulam, Aruppukottai. Each genotype was sown in the plots of 1.80 x 4 m size and the plants were spaced between 45 x 30 cm. The sowing was taken up after receiving soaking rains in the North east monsoon season. The observation was recorded for six metric traits *viz.*, days to 50% flowering, days to maturity, plant height, head diameter, number of leaves/plant and seed yield. The data were subjected to analysis of variance and multivariate analysis of Mahalanobis' (1928). The genotypes were grouped into different clusters following the Touchers Method (Rao, 1952).

RESULTS AND DISCUSSION

The analysis of variance showed significant difference between genotypes for each character. All the 54 genotypes were grouped into 7 clusters (Table 1). The maximum number of genotypes were included in cluster II (18 genotypes) followed by Cluster I and IV (13 genotypes each) and remaining clusters had one to four genotypes. Cluster I included the genotypes from all sources which indicated that there was no association between clustering pattern and eco-geographical distribution of genotypes. Asthana and Pandey (1980) revealed that geographical diversity is not necessarily related in genetic diversity in linseed.

Though sunflower originated as a cultivable crop in Russia, the present material generated are of Indian origin but from different sources like North Indian States Bangalore and Coimbatore. Hence genotypes from different source genotypes in all the clusters grouped in this study. It is likely

Table 2. Intra and inter cluster average D^2 values

Cluster	I	II	III	IV	V	VI	VII
I	0.0	113.3	168.3	288.1	443.3	566.1	712.8
II		72.9	70.6	182.1	336.9	458.4	605.7
III			57.1	126.2	279.4	400.6	548.0
IV				65.9	158.5	279.3	426.2
V					66.5	124.4	270.5
VI						32.9	151.1
VII							15.2

Table 3. Cluster mean for six characters in sunflower and contribution of each character towards divergence

Cluster	Character					
	Days to 50% flowering	Days to Maturity	Plant height cm.	Head diameter cm.	No. of leaves/ plant	Seed yield (kg/ha)
I	55.0	90.0	138.4	13.4	12.0	403.0
II	49.7	85.2	124.9	12.3	10.1	510.9
III	46.5	81.5	113.9	11.9	9.5	569.0
IV	51.9	87.1	129.3	13.8	10.8	690.4
V	51.4	86.7	125.4	12.8	10.7	846.8
VI	51.0	86.0	119.8	12.7	11.2	968.5
VII	51.6	87.6	150.6	13.0	11.3	1115.6
Ranking	68	49	94	147	185	335
Contribution %	17.15	11.16	11.83	40.46	1.83	17.57

that the genotypes of different places in the countries have some common genes. Since it is an introduced crop to India, the morphological grouping is helpful for broad classification. The intra and intercluster divergence among the materials studied was of varying magnitude (Table 1). The intra cluster D^2 value was found to be zero for the cluster I and it included 13 genotypes. Intra cluster D^2 value 72.9 was maximum in cluster II. The members in the cluster I showed nil D^2 value among them and hence selection of parents for hybridisation within the cluster is not advisable. It is juct opposite in the Cluster II which showed highest D^2 value of 72.9 and selection of parents for hybridisation within this cluster is advisable. This was followed by clusters V, IV, III, VI and VII which have higher intra cluster D^2-value for selection of parents within each cluster. These clusters have more than one genotype in the cluster. The maximum intercluster distance D^2 was observed between I and VII (712.7) followed by II and VII (605.7). Since these clusters have more of interclsuter disance among them, crossing between these clusters will realise higher heterosis. The intercluster D^2 values have been found to be minimum (70.6) between clusters II and III suggesting close relationship between them and the degree of diversity was less in parental lines. The magnitude of heterosis largely depend on the degree of genetic diversity among the parents and so selection of parents in these two cluster is to be avoided.

The comparison of cluster means for six characters under study marked considerable genetic differences between the groups (Table 3). The cluster VII had higher mean values for plant height and seed yield. The cluster I had the highest mean values for days to 50% flowering, days to maturity and number of leaves/plant whereas the cluster IV recorded higher mean values for head diameter only. The other clusters II, V and VI neither exhibited the highest mean nor the lowest for any of the characters taken for the study. Therefore, the contribution of various characters towards the expression of genetic divergence should be taken into account as a criteria for selection of parents for hybridization. The contribution towards genetic difference indicated that head diameter (40.46%), seed yield (17.57%), days to 50% flowering (17.15%) and plant height (11.83%) contributed more to the total genetic divergence in the 54 genotypes of sunflower (Table 3). It was clear from the present study that genotypes showing divergence may be considered for involvement in hybridisation programme, irrespective of geographical considerations.

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