

positive heterosis was also reported by earlier workers Vaidya *et al.* (1983) and Pethani and Kapoor (1984) Pethani and Dave (1992), suggesting useful exploitation of such potential parents for effective breeding programme. There was differential behaviour of various hybrids to environments for the expression of heterosis. This indicates environmental specificity in the expression of hybrid vigour. However, the study was carried out over three environments and it was remarkable that 732A X PT 1650 maintained its consistent superior performance under all environments. This indicates high stability of

heterosis of the hybrid under varying environments, which can be exploited over wide areas.

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GENETIC DIVERGENCE IN SESAME (*Sesamum indicum*)

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ABSTRACT

Mahalanobis D^2 analysis was employed to study the genetic diversity of 50 sesame genotypes at the Regional Research Station, Vridhachalam during *kharif* 1992. A wide genetic diversity was observed among the 50 genotypes tested. Based on D^2 analysis of Mahalanobis, the genotypes were grouped into four clusters. The clustering pattern indicated that the geographic diversity need not necessarily be related to the genetic diversity. This could be evidenced from the study that genotypes from the same eco-geographic region did scatter in four clusters. Similarly, genotypes from different eco-geographic regions were identified in one cluster. The inter-cluster distance study revealed that cluster IV followed by cluster III were found to be highly divergent from the other two clusters. The genotypes in these two clusters may possibly be utilized for hybridization programme through suitable breeding programmes for the successful exploitation of heterosis in sesame.

KEY WORDS : Sesame, Genetic, Divergence

Sesame (*Sesamum indicum*) has more genetic variability than most of the other self-pollinated crops. A wide range of genetic diversity among parents is an essential feature in any hybridisation programme. Hence, plant breeders are interested to estimate the range of genetic diversity among different genotypes which will help the plant breeders to select parents in the hybridisation programme to achieve the set goals. Mahalanobis D^2 analysis provides a mean to quantitatively estimate the same among crop plants and an attempt of this kind was made in sesame and the results were discussed.

MATERIALS AND METHODS

Fifty eco-geographically different genotypes of sesame (*S. indicum*) were taken for the study from

the germplasm bank maintained at the Regional Research Station, Vridhachalam. The genotypes were raised in randomized block design with three replications in the Research Station during *kharif*, 1992 season. Observations on plant height, number of branches per plant, number of capsules on main stem, number of capsules on branches, total number of capsules per plant, capsule length, number of seeds per capsule and seed yield per plant were recorded in five randomly selected plants of each genotype in each replication.

The data were subjected to multivariate analysis (Rao, 1952). The original mean values were transformed to normalised variables and all possible D^2 values were calculated. For determining group constellations or clusters, a relatively simple criterion suggested by Rao (1952)

Table I. Composition of D² clusters.

Clusternumber	Total number of genotypes	Genotypes	Cluster number	Total number of genotypes	Genotypes
Cluster I	40	IS.20	Cluster II	4	NAL/78/221/B1/1/1
		IS.35			UCR/82/NO/17/NS
		IS.43			Cianno 77/4
		IS.46			Margo-12
		IS.75	Cluster III	5	IS.174
		IS.210			IS.176
		IS.653			IS.178
		ES.2			ES.48
		ES.78	Cluster IV	1	664 Bon of Japan
		ES.176			Cianno 33/8
		ES.655			
		RJS.4			
		RJS.78			
		RJS.194			
		RJS.218			
		KIS.34			
		KIS.77			
		KIS.357			
		INST 15/2/1			
		INST 15/2			
		INST 15/3			
		PDK 31			
		NAL/79/111/9/1			
		NAL/78/111/31/3			
		NAL/78/307/5			
		NAL/78/304/43/18			
		NAL/78/304/44			
		UCR/82/NO/6/NS			
		Cianno 33/1			
		Margo-5			
		Margo-1			
		Cordeborega			
		Cordeborega-1			
		Kanbe white			
		CST-732			
		X 791/1/3			
		C.116			
		TMV.3			
		Co.1			
		SVPR.1			

was followed. After establishing the clusters, the intra-cluster distance was worked out by taking the average of the component genotypes in that cluster. The average inter-cluster divergence was arrived at by taking into consideration all the component D² values possible among the members of the two clusters considered. The value of 'D', the genetic

distance between the clusters, was arrived by taking the square root of the average D² values (Mahalanobis, 1936)

RESULTS AND DISCUSSION

Analysis of variance showed significant differences among the genotypes for all the

Table 2. Inter and intra (diagonal) cluster average of D^2 and D (values in paranthesis) and the extent of diversity among the clusters.

Cluster	I	II	III	IV
I	<u>7.33</u> (2.71)	15.03 (3.88)	15.62 (3.95)	31.71 (5.63)
II		<u>9.04</u> (3.01)	20.92 (4.57)	29.25 (5.41)
III			6.14 (2.48)	33.34 (5.77)
IV				0.00 (0.00)

Figures underlined show intra-cluster average of D^2 and D values.

characters studied. The D^2 values for all possible pairs (1225 D^2 values) ranged from 0.46 to 45.46. By the application of clustering technique, all the fifty genotypes were grouped into four different clusters (Table 1). The number of genotypes included in cluster I, II III and IV were 40, 4, 5 and 1 respectively. In each cluster, the types included were from different geographic origin. Thus, clustering pattern of the genotypes clearly indicated that the geographic diversity need not necessarily be related to the genetic diversity. This finding is in agreement with the earlier reports of Thangavelu and Rajasekaran (1983) in sesame. The largest cluster I included 40 types from different parts of India and also from other different countries. Such grouping of genotypes from different locations might be attributed to the free exchange of breeding materials from one place to another (Verma and Metha, 1976) and/or due to unidirectional selection practiced by breeders of different locations (Singh and Bains, 1968). It was also observed that the type from one geographic region were found to be scattered in different clusters. Such a wide adaptability would be possible due to the factors like heterogeneity, genetic architecture of the populations, past history of selections, development traits and degree of general combining ability (Murthy and Arunachalam, 1966).

The intra and inter-cluster D^2 and D values among four clusters (Table 2) showed that intra-

cluster D^2 D values were zero for cluster IV. The inter-cluster distances were higher for cluster IV followed by cluster III. The highest inter-cluster generalized distance (5.77) was recorded between clusters III and IV while the lowest (3.88) between clusters I and II. From the table, it was evident that cluster IV followed by cluster III were highly divergent from other two clusters. The inter cluster distances were higher than the intra-cluster distances which indicated the existence of substantial diversity among the parents.

Heterosis is of direct relevance for developing hybrids in both cross-pollinated and self-pollinated crops. It is increasingly realized that crosses between divergent parents usually produced greater heterotic effect than those between closely related ones. But, when divergent parents are crossed, heterosis is not found to occur always. It is therefore essential to explore the possible limits to parental divergence within which there are reasonably high chances for occurrence of heterosis (Arunachalam and Bandyopadhyay, 1984). In this study it was found that genotypes fell in cluster IV and cluster III may be chosen for hybridization programme for possible exploitation of heterosis by devising a suitable breeding programme.

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