



Genetic divergence in salicornia (*Salicornia brachiata* Roxb.)

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Genetic diversity of the parental lines is good indicator of progeny performance. Success through hybridization and subsequent selection depends primarily on the selection of parents having high genetic variability for various agronomic traits [1]. The present study is an attempt made to find out the degree and the nature of genetic divergence among the set of 17 select *Salicornia brachiata* (Roxb.) [2] genotypes an annual halophytic species & a unique coastal plant for nutrient rich 'Vegetable salt' [3] and 'Plants bioactives' [4], with sole objectives of selecting genetically divergent parental lines for hybridization and for the development of high yielding salicornia varieties for its' cultivation in saline ingressed soils of India. The above genotypes were collected from different locations of coastal Gujarat (viz., Diu, Diu-tad, Avania, Ghogha, Jafrabad, Kotda, Methla, Newport Bhavnagar, Tarsara and Victor port). These were grown in randomized block design in three replications during Kharif 2001-02 at CSMCRI's saline experimental site at Hathab (India, 20.35 N, 72.16 E). Each genotype was field grown in micro plots (5.0m × 2.5m) maintaining row to row and plant to plant distance at 50 × 25cm. All the necessary cultural practices were followed for raising good stand of salicornia. Observations were recorded on five randomly selected plants to have comparative studies of its height (cm), canopy (cm), number of primary branches, number of segments, length of spike (cm), number of spikes per branches and the seed yield (g/pl). The mean over three replications was used for the statistical analysis. The analysis of genetic divergence was carried out using Mahalanobis's D^2 statistic. Toucher's method [5] was followed for the purpose of clustering of genotypes.

The analysis of variance revealed significant differences amongst the salicornia genotypes for all the phenological characters, (height-379.85**, canopy-19793.4**, mainbranch-1171.2**, segment-539.57**, spike length-10.6*, spike/br-451.27** and seed yield-549.29**) indicating high genetic variability present in the population. All the genotypes were grouped into five clusters, indicating wide diversity in the experimental

material for majority of the characters. Maximum number of genotypes (8) were included in cluster-III.

This was followed by cluster-I (4) and cluster-II (3): Cluster-IV and V each had a solitary genotype (Table 1). Clusters I, II and III included genotypes from different part of India. This pattern of clustering indicated that there was no association between eco-geographical distribution of genotypes and genetic divergence as genotypes selected under diverse locations, get clustered together. On the other hand genotypes from the same geographic region but different breeding programme were distributed in different clusters. This kind of genetic diversity (genotypes belonging to same geographical region) might be due to differential adoption, selection criteria, selection pressure and environment. This indicated that genetic drift and selection in different environments can produce greater diversity than the geographic diversity.

Cluster II contained only three genotypes, but it showed maximum intra-cluster distance, because the genotypes originated from breeding programme is from different location. Thus these three genotypes in cluster II were most heterogeneous and this cluster was best for within group hybridization. Genotypes from this cluster could also be exploited in hybrid development programme, due to their wide intra-cluster within the group genetic distances. On the other hand cluster III contained 8 genotypes but showed minimum intra-cluster distance due to the common origin of many genotypes.

As regards inter-cluster distance (Table 2), cluster IV, showed maximum genetic distance from cluster II (39.98) suggesting wide diversity between these groups. Hybridization between parental lines selected from these clusters are likely to produce most variable progeny. Pradhan and Roy [6] have also pointed out that selection of parents for hybridization should be done from two clusters having wider inter-cluster distance to get maximum variability in *Oriza sativa* L. Cluster I and cluster II had the minimum genetic distance (11.49) between them which showed that these genotypes were

Table 1. Distribution of 17 genotypes of *Salicornia* among five clusters

Cluster	Number of genotypes	Genotypes
I	4	SS-5,SS-13,SS-14,SS-16
II	3	SS-6,SS-11,SS-15
III	8	SS-1,SS-2,SS-3,SS-7,SS-8
IV	1	SS-4
V	1	SS-12

Table 2. Inter- and intra-cluster average D^2 value of 17 genotypes of *Salicornia*

Cluster group	I	II	III	IV	V
I	2.82	11.49	20.70	28.93	26.99
II		8.14	24.03	39.98	18.99
III			0.428	26.57	36.34
IV				0.00	8.32
V					0.00

somewhat similar in genetic constitution and hybridization between these groups may not result in sufficient variability, but could be adopted for cultivations till the varieties are bred.

As far the cluster means are concerned, there was a wide range of variation found for all the characters (Table 3). Cluster IV (SS-4) had high mean values for plant height (35.4), plant canopy (224.25), number of main branches (54.75), number of segments (31.33), length of spike (4.46), number of spikes per branches (28.75), and the seed yield (34.35). This indicated that cluster IV contained genotypes with all the desirable characters which could be directly selected and utilized. The experimental observations further revealed that the plant canopy contributes maximum towards the genetic divergence (36.29%), followed by number of segment per spike (21.48%) and seed yield per plant (14.07%). Thus, an importance to these characters be emphasized as principle contributors to genetic diversity prevalent in such wild non-traditional and seawater tolerant oilseed species.

It is also suggested that for creating variability and developing the varieties a large number of divergent lines, instead of few should be used in the hybridization.

Table 3. Cluster-wise mean values of seven characters in *Salicornia*

Cluster	Characters						
	Plant height (cm)	Plant canopy (cm)	Number of main branches	Number of segments	Spike length (cm)	Number of spikes per branch	Seed yield (g)
I	31.05	162.24	26.65	13.8	2.71	22.89	12.20
II	35.4	145.01	43.91	25.44	3.11	23.14	32.05
III	32.55	150.37	38.62	25.14	3.23	25.14	16.52
IV	35.4	224.25	54.75	31.33	4.46	28.75	34.35
V	22.00	174.40	13.00	4.58	1.28	13.08	24.20

On the basis of observations recorded here on a diverged group of *Salicornia brachiata* genotypes, it is concluded that hybridization between the genotypes of variable clusters specially cluster-IV, I and II may help produce wide spectrum of variation in the segregating progeny to help open up scope of biosaline farming not only to vegetate saline wastelands but also for the industrial farming.

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