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Genetic Divergence in Sweet Corn (Zea *mays* L. *saccharata*.)

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ABSTRACT

The genetic divergence among 63 genotypes of sweet corn were estimated by using Mahalanobis D^2 statistic for eleven characters. The genotypes were grouped into eight clusters. Cluster III was the largest having 14 genotypes indicating genetic similarity among them, followed by cluster IV and V (12 genotypes each), cluster I and II (11 genotypes each) and cluster VI, VII and VIII (one genotypes each). The inter-cluster distances were larger than the intra-cluster distances suggesting wider genetic diversity among the genotypes of different groups. The highest inter-cluster distance (586.76) was observed between cluster VI and cluster VIII followed by cluster VI and VII (544.64), cluster V and VIII (523.41), cluster IV and VIII (463.22), cluster IV and VII (396.53), cluster V and VII (352.53), cluster III and VIII (315.22), cluster II and VII (242.25) and cluster I and VIII (216.142) suggesting more variability in genetic makeup of the genotypes included in these clusters. The highest intra cluster distance (103.51) was observed in cluster VIII and lowest in cluster III, IV and VI. The clusters, VI, VII and VIII contained only one genotype and hence, its intra-cluster distance was zero. The cluster VII had highest mean value for grain yield per plant followed by cluster VI, and cluster V. Based on the inter-cluster distances genotypes present in cluster I, II, III, IV, V, VI and VIII can be used as parents for hybridization programme to develop potential hybrids.

Key words: *Genetic diversity, D^2 statistics, Sweet corn, Maize.*

INTRODUCTION

Maize (Zea *mays* L.) is one of the oldest crop and most important food grain in the world as well as in developing countries. It is the highest yielding grain crop having multiple uses. It is one of the most important cereal crop and occupies a prominent position in global agriculture after wheat and rice. In India, maize ranks third next to rice and wheat (Centre for Monitoring Indian Economy, 2010). Sweet corn (*Zea mays* L. *saccharata*) is one of the most popular vegetables in countries like USA and Canada. It is characterized by translucent, horny appearance of kernel when matures and wrinkled appearance when it dries. Sweet corn is consumed in immature stage of the cob. Total sugar content in sweet corn at milky stage ranges from 20-25 % as compared to 2-5 % of normal corn. In any crop improvement programme, assessment of genetic diversity is an essential prerequisite for identifying potential parents for hybridization. Maize acreage and production have shown an increasing trend with the introduction of hybrids due to their high yield potential. Diverse parents are expected to yield higher frequency of heterotic hybrids in addition to generating a broad spectrum of variability in segregating generations. D^2 statistics is a useful multi varietal statistical tool for effective discrimination among various genotypes on the basis of genetic diversity (Murthy and Arunachalam, 1966). The present study was therefore undertaken to analyze the genetic divergence of maize genotypes.

MATERIALS AND METHODS

Sixty three genotypes of Sweet corn (*Zea mays* L. *saccharata*) were grown in randomized block design with three replications at Maize Research Centre, A.R.I, Rajendranagar, Hyderabad, Andhra Pradesh, India, during *rabi*, 2010-2011. Each entry was sown in a single row of 4m length. The spacing between row to row was 75 cm and plant to plant was 25 cm. One plant per hill was maintained. Fertilizers were applied @ 120:60:60 kgha^{-1} of N, P_20_5 and K_2 0 respectively. All the recommended agronomic practices were followed to raise a healthy crop. Observations were recorded on five randomly selected plants in each entry and in each replication for days to 50 per cent tasseling, days to 50 per cent silking, days to maturity, plant height (cm), ear height (cm), cob girth (cm), cob length (cm), number of kernel rows per cob, number of kernels per row, 100- seed fresh weight (cm), sugar content (%) and green cob yield per hectare (Q). The data were subjected to Mahalanobis D^2 analysis. Genetic diversity was estimated as per Mahalanobis D^2 statistics (1936) and clustering of genotypes was done according to Tocher's method as described by Rao (1952).

RESULTS AND DISCUSSION

The analysis of variance revealed highly significant differences among the genotypes for all the twelve characters indicating the existence of genetic variability among the experimental material. The 63 genotypes of sweet corn were grouped into eight clusters, the composition of which is presented in Table 1. Cluster III was the largest having 14 genotypes indicating genetic similarity among them, followed by cluster IV and V (12 genotypes each), cluster I and II (11 genotypes each) and cluster VI, VII and VIII (one genotypes each). Genetic diversity is generally associated with geographical diversity, but the former is not necessarily directly related with geographical distribution. The genotypes with in the same clusters were originated from different geographical regions of the world, which indicated the geographical distribution and genetic divergence did not follow the same trend which might be due to continuous exchange of genetic material among the countries of the world.

The intra and inter-cluster values among the eight clusters are presented in Table 2. The intra-cluster distances were lower than the inter-cluster distances. Thus, the genotypes included with in a cluster had less diversity among them. The maximum intra-cluster distance (103.51) was observed in cluster VIII followed by cluster VII (96.36), cluster I (76.04), cluster II (72.40), cluster IV (69.63), cluster VI (64.69) cluster V (59.79) and cluster III (47.07).

The highest inter-cluster distance (586.76) was observed between cluster VI and cluster VIII followed by cluster VI and VII (544.64), cluster V and VIII (523.41), cluster IV and VIII (463.22), cluster IV and VII (396.53), cluster V and VII (352.53), cluster III and VIII (315.22), cluster II and VII (242.25) and cluster I and VIII (216.142) suggesting more variability in genetic makeup of the genotypes included in these clusters (Fig. 1). The genotypes belonging to the clusters separated by high statistical distance could be used in hybridization programme for obtaining a wide spectrum of variation among the segregates. The genotypes belonging to the clusters separated by high statistical distance could be used in hybridization programme for obtaining a wide spectrum of variation among the segregates. In this context, the genotypes 6019-3 and 6039 from cluster I, 6055-1 from cluster II, 6051-2 from cluster III, 6075-1 from cluster IV, SC-10-3, SC-14-2 and SC-17-4 from cluster V, 6016-2 from cluster VI and 6069-2 from cluster VIII were selected for hybridization programme as they were expected to produce high heterotic crosses. These findings are in conformity with the findings of Singh *et al*. (1999), Khumkar and Singh (2002), Miranda *et al*.(2003), Yin *et al*. (2004), Singh *et al*. (2005), Hemavathy *et al*. (2006), Singh *et al*. (2007), Alam and Alam, (2009), Marker and Krupakar (2009), Ganesan *et al*.(2010) and Azad *et al*. (2012).

The cluster means of twelve characters are presented in Table 3. Greatest range of mean values among the cluster was recorded for different traits. Cluster V recorded highest mean values for green cob yield per hectare (22.06 Q), number of kernels per row (33.40), cob length (15.60 cm) and cob length (16.36 cm), Cluster VI was the second highest for green cob yield per hectare (20.29 Q) with high number of kernel rows per cob (16.72), kernels per row (29.17), cob girth (14.06 cm), ear height (81.00) and plant height (184.00), while the cluster I (17.18 %) had high mean value for sugar content followed by cluster IV (16.87 %).

It is evident based on cluster means, that, wide range of variation observed for green cob yield and its components in sweet maize. Therefore, suggested that most diverse clusters may be used as parents in hybridization programme to develop high yielding hybrids or varieties. It is been well established that more the genetically diverse parents used in hybridization programme, greater will be the chances of obtaining high heterotic hybrids and broad spectrum variability in segregating generations (Arunachalam, 1981). It has also been observed that the most productive hybrids may come from high yielding parents with a high genetic diversity. Therefore, based upon large inter-cluster distances with high grain yield it is advisable to attempt crossing among the genotypes from clusters I, II, III, IV, V, VI and VIII, which may lead to broad spectrum of favorable variability for yield improvement in sweet corn.

Table 1: Grouping of fifty genotypes into different clusters

Cluster	Number of genotypes	Genotypes
Cluster I	11	410-3, **6019-3**, **6039**, 6055-2-1, 6075-1, 6075-2, 6088-3, SC-10, SC-4, SC-6, SC-8-1
Cluster II	11	6051, 6069-5, 6075-1-4-1, SC-12-1, SC-16-2, SC-17-1, SC-17-2, SC-18, 6112-1-3-1, 6112-1-3-2, **6069-2**
Cluster III	14	6075-1-2-1, 6019-1, **6051-2**, 6055-1-2, 6055-2-2, 6075-4, 6088-2, 6091-2-1, 6099-2, 6109-4-1, 6126-5-1, SC-17-4-1, 6112-1-2, 6069-2-1
Cluster IV	12	6045, 6059-1, 6059-2, **6075-1**, 6102, 6075-1-3, 6109-4, SC-10-2, SC-10-1, SC-16-1, SC-16-3, SC-16-4
Cluster V	12	6001-1, **6016-2,** 6019-2, 6036-1, 6051-3, 6051-4, 6122-2, 6109-3, **SC-10-3**, SC-13, **SC-17-4**, 6111-2-1
Cluster VI	1	**SC-14-2**
Cluster VII	1	6111-2-5
Cluster VIII	1	**6055-1**

Note: Values in **Bold** are selected parents

Table 2: Intra and inter cluster distances

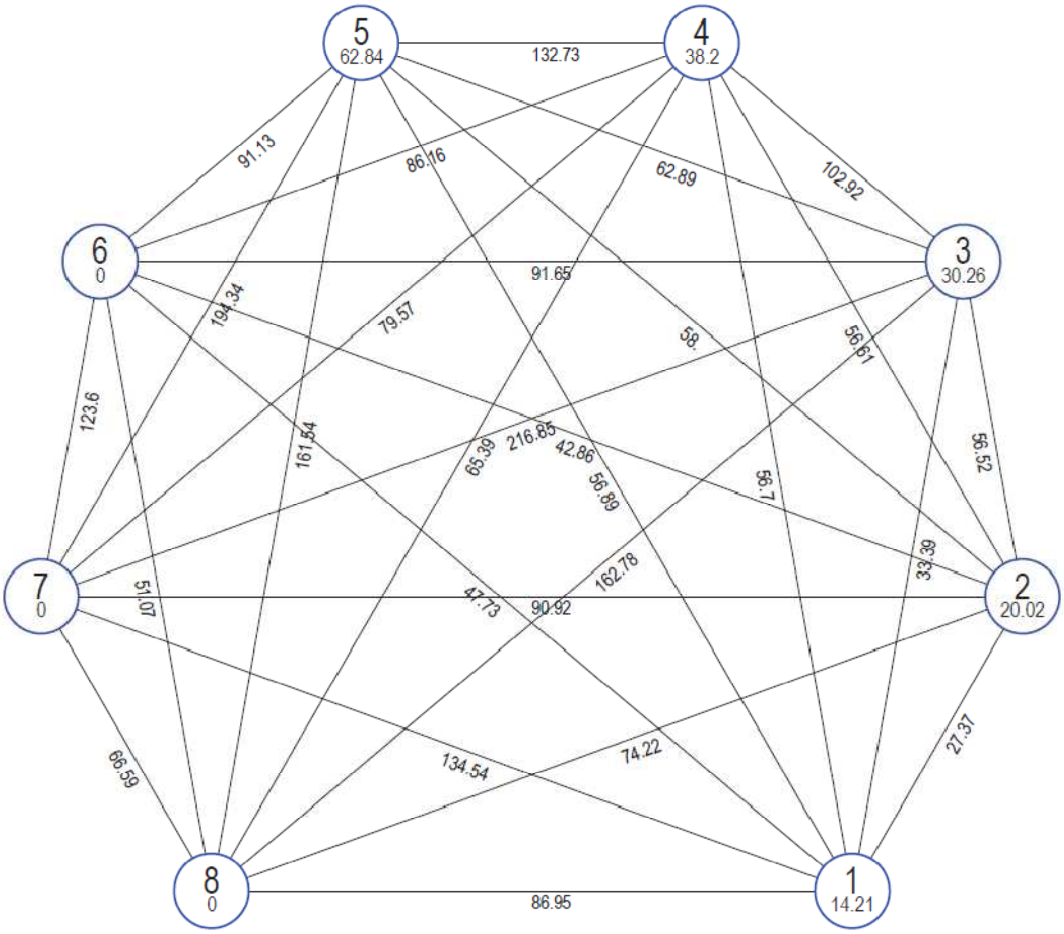
Cluster	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII
Cluster I	**76.04**	105.60	122.93	174.62	184.93	206.76	201.59	216.14
Cluster II		**72.40**	158.10	152.35	226.15	204.11	242.25	213.22
Cluster III			**47.07**	128.55	112.32	229.06	184.75	315.22
Cluster IV				**69.63**	129.43	130.26	396.53	463.22
Cluster V					**59.79**	154.43	352.53	523.41
Cluster VI						**64.69**	544.64	586.76
ClusterVII							**96.36**	160.29
ClusterVIII								**103.51**

Note: Bold values are intra cluster distances

Table 4: Mean performance of different clusters for different quantitative characters in maize

Cluster	Days to 50% tasseling	Days to 50% silking	Days to maturity	Plant height (cm)	Ear height (cm)	Cob girth (cm)	Cob length (cm)	Number of kernel rows per ear	Number of kernels per row	100-seed fresh weight (g)	Sugar content (%)	Green cob yield per hectare (Q)
Cluster I	71.06	73.42	100.619	162.19	64.38	12.13	12.17	14.00	23.71	14.00	17.18	12.67
Cluster II	73.64	76.00	91.833	165.72	61.22	13.47	13.94	13.67	30.50	14.35	14.94	17.83
Cluster III	68.60	70.95	90.714	164.24	63.00	11.29	13.28	14.00	26.10	12.28	15.24	12.98
Cluster IV	76.11	78.53	96.433	163.27	58.63	11.76	13.29	14.00	26.40	12.45	16.87	13.77
Cluster V	70.08	72.42	89.733	179.67	68.07	13.27	16.36	15.60	33.40	15.30	15.58	22.06
Cluster VI	66.33	69.33	98.722	184.00	81.00	14.06	14.54	16.72	29.17	15.77	13.45	20.29
Cluster VII	84.33	86.33	107.963	166.33	69.74	11.84	12.66	15.11	24.00	12.90	14.26	13.80
Cluster VIII	71.33	73.33	98.923	168.54	70.74	12.83	14.81	14.51	29.26	14.50	13.76	16.97

Fig. 1: Cluster diagram



Mahalnobis Euclidean Distance (Not to the Scale)

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