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Research Article

Genetic diversity in sweet corn inbred lines (*Zea mays* L.)

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Abstract
A total of fifty inbred lines of sweet corn were evaluated for eight quantitative characters at the Millet Breeding Station, Department of Millets, Tamil Nadu Agricultural University, Coimbatore during *kharif* 2014 to study the genetic diversity using multivariate (D square) analysis. The fifty inbreds categorized in to ten distinct clusters. The intra-cluster distances in all the ten clusters was low, indicating that the genotypes within the same cluster were closely related. The highest inter-cluster distance was observed between cluster I and cluster X and the lowest between the cluster II and III. The cluster VII and cluster X contained the highest (24) and lowest (1) number of genotypes, respectively. Cluster VI showed the highest mean values for kernel yield and all the yield contributing traits. Cob girth and number of tassel branches expressed maximum contribution towards total divergence among different characters. Development of hybrids utilizing these genotypes has the chance to obtain higher heterosis with high performing crosses.

Keywords
Genetic diversity, cluster analysis, inbred lines, *Zea mays* L.

Introduction

Maize (*Zea mays* L.) has become an important cereal crop of India after rice and wheat and is valued as food, feed, fodder and industrial raw material. In view that maize being produced under diverse ecology in our country, development of high yielding hybrids with in-built resistance and tolerance to disease, pests and various climatic stresses are top priorities. Sweet corn is one of the most popular vegetable in the US and its popularity is growing rapidly throughout the world. Sweet corn is the result of naturally occurring recessive mutation. The productive and diverse inbred lines are very basic requirement for development of hybrids. In Tamil Nadu, maize crop is cultivated in an area of 2.92 lakh ha, with production and productivity of 9.46 lakh ton and 3252 kg/ha respectively. In most parts of the state single cross hybrids are preferred for cultivation. This is the reason for higher productivity to other part of the country.

One important approach to this situation is development of inbred lines which can ultimately give rise to high yielding hybrid varieties. Before hybrid development, prospective parent (inbred line) selection is a pre-requisite. Several studies on maize have shown that inbred lines from diverse stocks tend to be more productive than crosses of inbred lines from same variety Vasal (1998). Saxena *et al.* (1998) also reported that manifestation of heterosis usually depends on the genetic divergence of the two parental lines. The quantification of genetic diversity through biometrical procedure made it possible to choose genetically diverse parents for hybrid production. Genetic diversity is one of the useful tools to select appropriate genotypes/lines for hybridization. The genetic diversity between the genotypes is important as the genetically diverged parents are able to produce high heterotic effects Falconer, (1960); Arunachalam, 1981; Ghaderi *et al.*(1984); Mian and Bahl (1989). Knowledge of genetic diversity among elite breeding materials has a significant impact on the improvement of crop plants Hallauer *et al.(*1988). Maize breeders are consistently emphasizing the importance of diversity among parental genotypes as a significant factor contributing to heterotic hybrids Ahloowalia and Dhawan (1963). Characterization of genetic diversity of maize germplasm is of great importance in hybrid maize breeding Xia *et al.*, (2005). D^2 analysis is a useful tool for quantifying the degree of divergence between biological population at genotypic level and in assessing relative contribution of different components to the total divergence both intra and inter-cluster level Murty and Arunachalam(1966); Ram and Panwar, (1970); Sachan and Sharma(1971). The present investigation was undertaken with a view to estimate the nature and magnitude of genetic diversity in sweet corn inbred lines.

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Materials and Methods

The study was conducted during *kharif* 2014 at Millet Breeding Station and New Area Farm, Department of Millets, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu, India. The fifty inbred lines were outsourced from Winter Nursery Centre, ICAR-Indian Institute of Maize Research. Hyderabad and stabilized at TNAU, Coimbatore for three to five seasons.

Fifty maize inbred lines were grown in a Randomised Block Design with two replications. The seeds of each entry were sown on 4 m long row with spacing of 60 x 25 cm between rows and hills, respectively. One plant was kept per hill after proper thinning. Pre emergence herbicide atrazine was sprayed for weed control. Recommended doses of fertilizers were applied and other intercultural operations were done timely and properly to raise a healthy crop. The following observations were recorded in five randomly selected plants in each replication *viz*., plant height (cm), cob placement height (cm), tassel length (cm), number of tassel branches, number of grains/row, number of kernel rows/ear , cob length (cm) and cob girth (cm). Mahanabolis D^2 was used for the analysis of genetic diversity among the inbreds. Data were subjected to diversity analysis using GENERES software programme.

Results and Discussion

Directional dominance and genetic diversity among the available inbreds has immense value on the development of superior hybrids. The knowledge of genetic diversity among the genotypes is essential for selecting parents for hybridization programme. Mean, maximum, minimum and range variation of eight yield contributing characters in 50 maize inbreds are presented in Table. 1. The ANOVA showed significant differences among inbreds for all characters studied. The D^2 values ranged from 2.09 to 195.08 and principal component scores also indicated a high degree of genetic diversity among the inbred lines. Cluster analysis was done by application of non-hierarchical clustering using co-variance matrix grouped the 50 inbred lines of maize into ten different clusters (Table. 2) It was revealed that cluster VII comprised maximum number (24) of genotypes, followed by cluster VI (7 genotypes) and cluster V (6 genotypes). Cluster X had only a single genotype. Clustering pattern of inbred lines under this study revealed that the inbred lines had considerable genetic diversity among themselves. Chen *et al.* (2007) carried out genetic diversity among 186 maize genotypes and classified these genotypes into ten clusters.

The results of inter cluster and intra cluster distance were presented in Table 3. Intra cluster distance was much lower than the inter cluster one, suggesting, heterogeneous and homogeneous nature between and within groups, respectively. The maximum intra-cluster distance was observed in cluster IX (6.98) and minimum in cluster X (0.0). The maximum inter-cluster distance was observed between the clusters IV and X (13.12). It was minimum between clusters II and V (2.98). Similar results were reported by Singh *et al.* (2005) and Liu *et al.* (2006) in maize. The crosses involving genotypes belonging to the maximum divergent clusters were expected to manifest maximum heterosis and also wide variability in genetic architecture. Thus, crosses between inbred lines of these divergent clusters IV and X would exhibit high heterosis.

The cluster means of eight quantitative traits were presented in Table 4. Mean values of traits varied in different clusters. Cluster II and cluster X recorded highest and lowest mean value for plant height respectively. Cluster X has shorter inbred lines. Cluster I, VIII and IX recorded highest mean values for tassel length, tassel number and cob girth respectively. Cluster X recorded highest mean value for the traits seed number per row, number of rows and cob length. It is always desirable to look for inbred lines having more than one desirable trait as in case of cluster X which is superior for seed number per row, number of rows and cob length. The results were supported by Xia *et al.* (2005) and Chen *et al.* (2007). Therefore crosses involving genotypes falling in these clusters I, VIII, IX and X is likely to manifest maximum heterosis as well as new desirable recombinants.

The contribution of individual characters towards divergence were presented in Table 5. Of the eight quantitative traits studied cob girth (52.57%) and number of tassel branches (11.51%) expressed maximum contribution towards total divergence. Similar results were also reported by Ghaderi *et al*. (1984) and Singh *et al.* (2005) in maize. So these characters should be given weightage, for selecting diverse parents for breeding programme.

Heterosis is a function of directional dominance and diversity between parents utilized for hybridization. So heterosis can be increased by selection of divergent parents. Genetic diversity was studied to find out the more diverse inbred lines in maize which might be used in hybridization programme. Fifty maize inbred lines were grouped into ten different clusters. The crosses involving parents/inbred lines from clusters I, VII, VI, V and X likely to manifest maximum heterosis as well as new desirable recombinants.

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Table 1. Mean and Range of variation for eight quantitative traits

	Plant height (cm)	Cob placement height (cm)	Tassel length (cm)	Tassel no	Seed no/row	No of rows	Cob length (cm)	Cob girth (cm)
Grand Mean	**112.87**	**44.05**	**26.90**	**16.59**	**21.07**	**11.90**	**12.72**	**10.22**
Minimum	75.80	19.80	13.50	8.50	9.50	7.00	8.20	6.80
Maximum	173.45	65.15	36.55	29.00	46.50	16.00	18.05	14.85
Standard deviation	22.20	10.76	4.10	5.17	8.12	2.07	2.72	1.96

Table 2. Cluster formation with critical D-square = 64.32833

Clusters	**Genotypes**
Cluster 1	USC 1207-6-1, USC 1413-6-1
Cluster 2	USC 10-3, USC 1413-5-2-2
Cluster 3	USC 1-2-2, USC 1413-6-2
Cluster 4	USC 3-1-2-2-1, USC 8322-4-2
Cluster 5	USC 1-1-, 1USC 1-2-1, USC 1-2-1-1, USC 1-2-3-1, USC 1207-6-2, 72173-1
Cluster 6	USC 3-1-1-2-2-1, USC 7-1, USC 7-2, USC 10-3-1, USC 10-3-1-1, USC 10-3-2-2, USC 10-3-2-4
Cluster 7	USC 11-2, USC 1107, USC 1378-5-1, USC 1378-5-2, USC 1396-4 USC 1413-6-2-1, USC 1413-6-2-2, USC 1421-11-2, USC 7853, USC 7855-2, USC 7855-3-1, USC 7855-4-1, USC 7855-4-2, USC 7855-10, USC 8229-7-1, PC 8322-4-1, USC 8324-3, USC 72173-3, MMP 1647-7, MMP-1647-11, MMP 9272A (yellow), MMP 927A(red), Red Dent
Cluster 8	Tropical 3, Tropical 8
Cluster 9	Tropical 29, CIMMYT 11
Cluster 10	72173-2

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Table 3. Intra and inter-cluster distance (D^2) of 50 maize inbred lines

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 7	Cluster 8	Cluster 9	Cluster 10
Cluster 1	1.446	5.276	2.993	6.374	6.315	4.816	6.155	7.867	8.164	10.227
Cluster 2		1.787	4.676	2.988	6.092	6.574	5.785	6.434	5.018	12.305
Cluster 3			1.903	5.445	6.123	5.068	6.125	8.419	7.039	11.492
Cluster 4				1.93	7.242	7.055	7.086	7.887	5.013	13.124
Cluster 5					6.711	6.809	6.449	7.559	7.406	10.432
Cluster 6						5.34	6.813	7.934	7.993	9.049
Cluster 7							6.255	6.477	7.444	10.282
Cluster 8								2.737	7.57	9.341
Cluster 9									6.978	13.003
Cluster 10										0

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Table 4. Cluster Means of eight quantitative characters

Cluster No.	Plant height (cm)	Cob placement height (cm)	Tassel length (cm)	Tassel no	Seed no/row	No of rows	Cob length (cm)	Cob girth (cm)
Cluster 1	96.550	36.750	27.250	**20.250**	13.000	12.000	11.625	7.625
Cluster 2	134.675	58.375	26.650	15.750	16.750	12.500	11.475	9.35
Cluster 3	97.875	39.050	27.625	19.500	12.000	9.000	9.375	7.675
Cluster 4	119.925	61.375	25.050	10.500	15.500	10.500	11.325	8.925
Cluster 5	115.008	45.758	28.925	17.250	27.667	12.667	12.017	10.042
Cluster 6	85.443	32.871	23.993	13.143	17.000	10.857	11.436	9.207
Cluster 7	118.877	45.058	27.844	18.396	22.313	11.833	13.406	10.727
Cluster 8	130.550	49.075	27.450	15.250	19.750	15.000	17.250	**14.225**
Cluster 9	127.850	58.275	**28.150**	9.500	20.000	11.500	10.675	11.125
Cluster 10	55.250	19.800	18.300	11.000	34.500	14.000	18.000	13.55

Table 5. Contribution of each character to divergence

Character	No. of first rank	% Contribution
Plant height(cm)	41	3.3469
Cob placement height(cm)	93	7.5918
Tassel length(cm)	55	4.4898
Tassel no	141	11.5102
Seed no/row	114	9.3061
No of rows	98	8.0000
Cob length(cm)	39	3.1837
Cob girth	644	52.5714
Total	**1225**	**100**