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 into 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). D2 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.
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 sourced 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 knowledge 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 D² 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 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 1-1-1, USC 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 10-3-1-1, 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                                                                   |
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         |
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            |