PRINCIPAL COMPONENT, CLUSTERING PATTERN AND ASSOCIATION ANALYSIS OF SWEET CORN (*ZEA SACCHARATA* L.) INBRED LINES

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SUMMARY

In sweet corn, the assessment of morphological and quantitative traits variation contributing towards genetic diversity is of vital importance. This study was conducted using randomized block design with two replications to evaluate 50 sweet corn inbred lines at Tamil Nadu Agricultural University, Coimbatore. The data of nine different morphological and quantitative traits were subjected to simple association between traits, principal component analysis and clustering pattern. The genetic diversity assessed based on plant height, cob placement height, tassel length, number of tassel branches, seed number/row, number of rows/ear, cob length, cob girth and green cob yield. The association analysis showed positive and highly significant correlation of green cob yield with seed number/row (0.82), cob length (0.76), number of rows (0.70), cob girth (0.58), plant height (0.37) and tassel length (0.36). Principal component analysis (PCA) showed that the first 3 PCs had Eigen value >1 explaining 73.80 per cent of total variability among the sweet corn inbred lines for nine quantitative traits. This experiment demonstrated high diversity for the characters studied. The resulting phenotypic dendrogram revealed three main clusters (I, II and III) at 0.93 similarity coefficients. The sweet corn inbred lines in the cluster III were identified as superior for cob yield and its components thereby; it can be used in crop improvement programmes.

Key words : Sweet corn, genetic diversity, association analysis, principal component analysis

The Maydeae tribe contains several genera, including the genus *Zea*, which presents a high economic importance including cultivated species of corn and its probable progenitor teosinte. Among various types of corn, sweet corn has the greatest potential for use as human food and consumed at immature state. It is being used as popular vegetable in the western countries and considered to be a source of fiber and vitamins. The quality of fresh or processed whole-kernels, canned or frozen, is determined by its unique combination of flavour, texture and aroma. Total sugar content in sweet corn at milky stage ranges from 25-30 per cent as compared to 2-5 per cent of normal corn. Sweetness is the most important factor in consumer satisfaction with sweet corn (Evensen and Boyer, 1986). Sweet corn varies from normal corn essentially for gene(s) that affect starch synthesis in the seed endosperm wherein one or more simple recessive alleles in the seed endosperm elevate the level of water-soluble polysaccharides (sugars) and decrease starch (Dinges *et al.,* 2001). Sweet corn is originated through mutation and it is characterized by having at least one of the eight recessive mutant genes. The main genes are : *Shrunken*-2 (sh2) on chromosome 3, *Brittle* (bt) and *Amylose Extender* (ae) on chromosome 5, Sugary Enhancer (se), Sugary (su) and "Brittle-2" (bt2) on chromosome 4; "Dull" (du) on chromosome 10, and Waxy (wx) on chromosome 9 (Tracy *et al.*, 2006). Sweet corn green cob is harvested at physiological maturity stage, then the plant is completely green with photosynthetic state. Hence, the maize stalk is being used as green fodder for cattle population. It harbours most of the essential nutrients, stem sweetness and highly palatable to animals. However, sweet corn improvement highly relies on availability of diversified inbred. In this point of view, it's necessary to quantifying the genetic diversity of sweet corn, which can be used in hybrid production. Manifestation of heterosis highly depends upon diversified inbred lines (Saxena *et al.*, 1998). Knowledge on genetic diversity and characterization of maize germplasm are of great importance in

reference with hybrid production (Xia *et al.*, 2005). The aim of this investigation was to quantifying the nature and magnitude of genetic diversity of 50 sweet corn lines and, therefore, it could be used for crop improvement programme.

MATERIALS AND METHODS

The experiment was carried out at Tamil Nadu Agricultural University, Coimbatore during **kharif** 2014. Fifty sweet corn inbred lines (Table 1) were evaluated under randomized block design (RBD) with two replications. Normal agronomic practices were adopted during this experiment. Quantitative data were observed for plant height (cm), cob placement height (cm), tassel length (cm), number of tassel branches, number of seeds/row, number of kernel rows/ear, cob length (cm), cob girth (cm) and green cob yield per plant (g).

Diversity and Construction of Phenotypic Dendrogram

The data on nine quantitative traits for 50 inbred lines were subjected to association, principal component and multivariate hierarchial cluster analysis performed by Xlstat 2017.01.41659 software. The tree diagram was constructed based on un-weighted paired group of arithmetic mean (UPGMA) method.

RESULTS AND DISCUSSION

In the present study, all inbred lines under consideration showed significant variation for its morphological traits based on the mean performance of a genotype, as it was evident from the range of values (Table 2).

Association Analysis

Understanding the association of other morphological traits with yield and the correlations among themselves is important for any crop improvement programme. A perusal of Table 3 indicates positive and highly significant correlation of green cob yield with seed number/row (0.82), cob length (0.76), number of rows (0.70), cob girth (0.58), plant height (0.37) and tassel length (0.36). So, these parameters exhibited close association with green cob yield. This indicates that high measurement of these traits had direct positive contribution to cob yield.

Therefore, for selection purpose to improve the inbred lines, it was suggested that emphasis should be given on these traits. These findings are substantiated with those of Kashiani *et al.* (2010). Further, plant height had significant correlation with cob yield, indicating that taller plants were better yielding than the shorter ones. This might be attributed to high dry matter accumulation function carried out by the high number of leaves possessed by taller plants (Sujiprihati *et al.*, 2002; Saleh *et al.*, 2002; Kashiani *et al.*, 2008). More importantly taller plants contribute for higher biomass and it can be used for development of dual purpose corn i. e. Sweet corn and fodder. Therefore, these characters should be given utmost consideration for breeding hybrids for higher green cob and stalk yield.

Principal Component Analysis (PCA)

PCA showed that out of nine the first three explained majority of total variation. These three PCs with Eigen value >1 contributed 73.80 per cent of total variability among the sweet corn inbred lines for nine morphological traits (Table 4). However, the remaining six components showed only 27.20 per cent towards the total morphological diversity for this set of inbred lines. The PC I contributed maximum towards the variability (45.20%) followed by PC II (15.20%) and PC III (13.30%). The most important characters in PC I were due to variations among the inbred lines mainly for green cob yield, cob length, seed number/row, cob girth, number of rows and plant height had considerable positive factor loading on PC I. Similarly, the PC II was related to diversity among inbred lines due to tassel number branches and tassel length. The PC III was explained mainly by variation among inbred lines resulting from cob placement height had considerable positive factor loading and tassel number branches had negative loadings. The first two principal components contributing almost 60.45 per cent towards the total variance were plotted to observe the relationships between different clusters with PC I on X-axis and PC II on Y-axis (Fig. 1). Considering a minimum threshold, Eigen value of one, the three principal components (PCs) accounted for whole phenotypic diversity observed among the sweet corn inbred lines. These results are similar with those of Mujaju and Chakuya (2008) on morphological variation traits in sorghum.

The explanation of greater proportion of the entire phenotypic diversity involved in yield related traits (i. e. green cob yield, cob length, seed number/

TABLE 1
Details of inbred/pedigree and source of sweet corn lines

S. No.	Inbred/pedigree	Source
1.	USC 1-1-1	Dept. of Millets, TNAU, Coimbatore
2.	USC 1-2-1	Dept. of Millets, TNAU, Coimbatore
3.	USC 1-2-1-1	Dept. of Millets, TNAU, Coimbatore
4.	USC 1-2-2	Dept. of Millets, TNAU, Coimbatore
5.	USC 1-2-3-1	Dept. of Millets, TNAU, Coimbatore
6.	USC 3-1-1-2-2-1	Dept. of Millets, TNAU, Coimbatore
7.	USC 3-1-2-2-1	Dept. of Millets, TNAU, Coimbatore
8.	USC 7-1	Dept. of Millets, TNAU, Coimbatore
9.	USC 7-2	Dept. of Millets, TNAU, Coimbatore
10.	USC 10-3	Dept. of Millets, TNAU, Coimbatore
11.	USC 10-3-1	Dept. of Millets, TNAU, Coimbatore
12.	USC 10-3-1-1	Dept. of Millets, TNAU, Coimbatore
13.	USC 10-3-2-2	Dept. of Millets, TNAU, Coimbatore
14.	USC 10-3-2-4	Dept. of Millets, TNAU, Coimbatore
15.	USC 11-2	Dept. of Millets, TNAU, Coimbatore
16.	SC 1107	Dept. of Millets, TNAU, Coimbatore
17.	USC 1207-6-1	Dept. of Millets, TNAU, Coimbatore
18.	USC 1207-6-2	Dept. of Millets, TNAU, Coimbatore
19.	USC 1378-5-1	Dept. of Millets, TNAU, Coimbatore
20.	USC 1378-5-2	Dept. of Millets, TNAU, Coimbatore
21.	USC 1396-4	Dept. of Millets, TNAU, Coimbatore
22.	USC 1413-6-1	Dept. of Millets, TNAU, Coimbatore
23.	USC 1413-6-2	Dept. of Millets, TNAU, Coimbatore
24.	USC 1413-6-2-1	Dept. of Millets, TNAU, Coimbatore
25.	USC 1413-6-2-2	Dept. of Millets, TNAU, Coimbatore
26.	USC 1421-5-2-2	Dept. of Millets, TNAU, Coimbatore
27.	USC 1647-11-2	Dept. of Millets, TNAU, Coimbatore
28.	USC 7853	Dept. of Millets, TNAU, Coimbatore
29.	USC 7855-2	Dept. of Millets, TNAU, Coimbatore
30.	USC 7855-3-1	Dept. of Millets, TNAU, Coimbatore
31.	USC 7855-4-1	Dept. of Millets, TNAU, Coimbatore
32.	USC 7855-4-2	Dept. of Millets, TNAU, Coimbatore
33.	USC 7855-10	Dept. of Millets, TNAU, Coimbatore
34.	USC 8229-7-1	Dept. of Millets, TNAU, Coimbatore
35.	PC 8322-4-1	Dept. of Millets, TNAU, Coimbatore
36.	USC 8322-4-2	Dept. of Millets, TNAU, Coimbatore
37.	USC 8324-3	Dept. of Millets, TNAU, Coimbatore
38.	USC 72173-3	Dept. of Millets, TNAU, Coimbatore
39.	MMP 1647-7	Dept. of Millets, TNAU, Coimbatore
40.	MMP 1647-11	Dept. of Millets, TNAU, Coimbatore
41.	MMP 9272A (yellow)	Dept. of Millets, TNAU, Coimbatore
42	MMP 9272A (red)	Dept. of Millets, TNAU, Coimbatore
43.	72173-1	Dept. of Millets, TNAU, Coimbatore
44.	72173-2	Dept. of Millets, TNAU, Coimbatore
45.	Red Dent	Dept. of Millets, TNAU, Coimbatore
46.	Tropical 3	Dept. of Millets, TNAU, Coimbatore
47.	Tropical 8	Dept. of Millets, TNAU, Coimbatore
48.	Tropical 29	Dept. of Millets, TNAU, Coimbatore
49.	CIMMYT 11	Dept. of Millets, TNAU, Coimbatore
50.	USC 1386	Dept. of Millets, TNAU, Coimbatore

row, cob girth, number of rows), tassel traits (tassel number branches and tassel length) and plant phenology trait (plant height). This further confirmed the previous results that also described the importance of these traits in contributing towards the overall diversity of the sweet corn inbred lines.

Cluster Analysis

This clustering was based on their collection site and pedigree relationship. The percentage of similarity between sweet corn inbred lines was 93 per cent (Fig. 2). The resulting phenotypic dendrogram

TABLE 2
Mean and range for nine quantitative traits of sweet corn inbred lines

Characters	Mean	Range	Standard deviation
Plant height (cm)	113.2	75.8-173.5	22.75
Cob placement height (cm)	43.8	19.8-65.2	10.95
Tassel length (cm)	26.8	13.5-36.6	4.13
No. of tassel branches	16.6	8.5-29.0	5.17
Seed number/row	21.1	9.5-46.5	8.13
No. of rows	11.9	7.0-16.0	2.09
Cob length (cm)	12.8	8.2-18.1	2.76
Cob width (cm)	10.2	6.8-14.9	1.97
Green cob yield (g)	241.0	100-389	85.22

TABLE 3
Sweet corn inbred lines association analysis based on nine morphological traits

Characters	CPH	TAL	TAN	SNR	NOR	CBL	CBG	GCY
PHT	**0.44**	**0.40**	0.02	**0.46**	0.28	**0.46**	**0.52**	**0.37**
CPH		0.24	-0.06	0.14	0.12	-0.05	0.12	0.09
TAL			**0.37**	**0.36**	**0.30**	0.26	0.22	**0.36**
TAN				-0.04	0.02	0.02	-0.02	0.00
SNR					**0.43**	**0.66**	**0.51**	**0.83**
NOR						**0.53**	**0.64**	**0.71**
CBL							**0.59**	**0.77**
CBG								**0.59**

Values in bold are different from 0 with a significance level alpha=0.05.
PHT–Plant height, CPH–Cob placement height, TAL–Tassel length, TAN–Number of tassel branches, SNR–Number of seeds/row, NOR–Number of rows, CBL–Cob length, CBG–Cob girth and GCY–Green cob yield.

TABLE 4
Principal component analysis of quantitative traits of sweet corn inbred lines

	PC 1	PC 2	PC 3	PC 4	PC 5	PC 6	PC 7	PC 8	PC 9
Eigen value	4.1	1.4	1.2	0.7	0.6	0.5	0.3	0.2	0.1
Variability (%)	45.2	15.2	13.3	7.7	6.9	5.0	3.4	2.4	0.9
Cumulative (%)	45.2	60.4	73.8	81.5	88.3	93.3	96.7	99.1	100.0
Factor loading by various traits									
PHT	0.66	0.41	-0.34	-0.13	0.44	0.11	0.09	0.25	0.03
CPH	0.24	0.62	-0.62	0.14	-0.22	-0.29	0.05	-0.14	-0.01
TAL	0.51	0.60	0.31	-0.13	-0.25	0.43	-0.02	-0.11	0.00
TAN	0.06	0.52	0.75	0.13	0.18	-0.33	-0.03	0.03	-0.01
SNR	0.82	-0.12	-0.02	-0.41	-0.14	-0.16	-0.27	0.07	-0.14
NOR	0.75	-0.17	0.07	0.53	-0.25	0.06	0.12	0.18	-0.10
CBL	0.82	-0.27	0.13	-0.18	0.18	-0.07	0.35	-0.21	-0.06
CBG	0.78	-0.14	-0.09	0.36	0.33	0.08	-0.29	-0.19	0.03
GCY	0.90	-0.22	0.10	-0.09	-0.24	-0.14	0.01	0.06	0.22

PHT–Plant height, CPH–Cob placement height, TAL–Tassel length, TAN–Number of tassel branches, SNR–Number of seeds/row, NOR–Number of rows, CBL–Cob length, CBG–Cob girth and GCY–Green cob yield.

revealed three main clusters (I, II and III) at a genetic distance of 0.93. Cluster I contained 13 inbred lines at a genetic distance of 0.97 and cluster II contained two inbred lines with varied morphological characters characterized by tassel length, number of rows, cob length and green cob yield. Cluster III contained 35 inbred lines and further these lines were clustered very closely or similar in nature at the genetic similarity of 0.99. These genotypes were characterized by tassel length, tassel number branches, number of rows and green cob yield. Seshu *et al.* (2014) reported that wide range of variation was observed for green cob yield and its components based on higher genetic distance between clusters. Higher the genetically diverse parents used in hybridization programme, greater will be the chances of obtaining high heterotic hybrids and greater
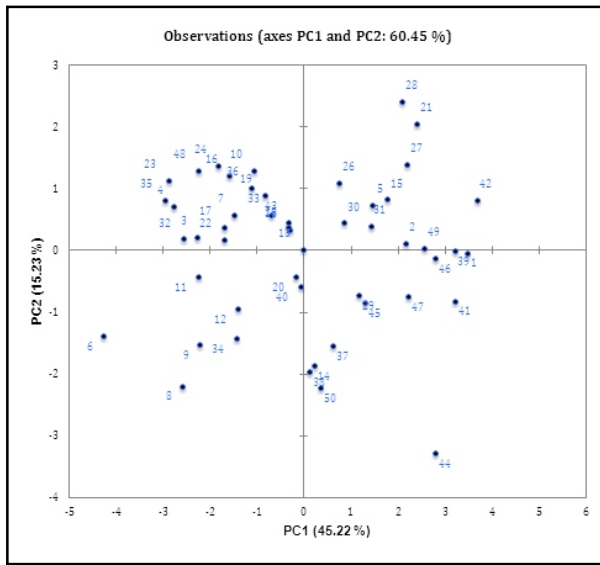
Fig. 1. Scatter plot of sweet corn inbred lines for first two PCs contributing 60.45 per cent to total variability.
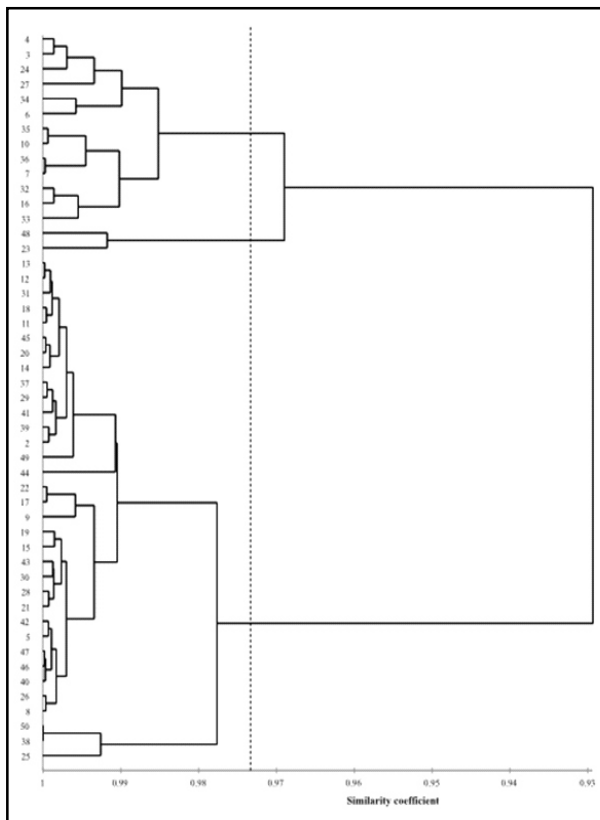

Fig. 2. Phenotypic dendrogram of 50 sweet corn inbred lines based on UPGMA clustering pattern.

variability in segregating generations (Azad *et al.,* 2012). It has also been understood that the most productive hybrids may come from high yielding parents with a high genetic diversity and could be used for yield improvement in sweet corn.Therefore, the clusters III

and I had diversified inbred lines and could be used in hybridization programme to obtain better segregants.

CONCLUSION

The results have implications in selecting parents for use in sweet corn improvement programme by enhanced genetic potential of sweet corn lines. In the present study, the traits like seed number/row, cob length, number of rows and cob girth were highly positively associated with green cob yield. Plant height was also accounted for direct correlation with yield which may offer selection of taller genotypes providing higher green cob and stalk yield. Hence, while selecting lines for high yield, these traits could be considered as useful traits. Further, the inbred lines in clusters I and III were identified as diversified inbred lines. The crosses involving parents/inbred lines from these clusters were expected to manifest maximum heterosis and generate wide variability in genetic architecture and could be used as parental source for breeding programmes with selective objective.

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