PRINCIPAL COMPONENT ANALYSIS IN SWEET CORN (*ZEA MAYS L. SACCHARATA.*)

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SUMMARY

An experiment was conducted in 26 genotypes of sweet corn to study Principal Component Analysis at Department of Millets, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore during *kharif*, 2014. Eight quantitative and five qualitative characters were taken under observation to estimate substantial variation and relationship among sweet corn genotypes to identify the best performing lines. Analysis of variation for such quantitative traits in diverse line showed considerable and dissimilar level of variability. Green cob yield was highly significant and positively correlated with green cob length (0.410), green cob girth (0.579) and number of kernel rows per cob (0.421) however total sugar, sucrose and starch was non-significant negatively correlated with green cob yield. Principal component analysis showed the amount of variation by principal components as 1 to 6. Clustering analysis based on various morphological traits assorted 26 sweet corn genotypes into eight clusters. Dendrogram based on hierarchal clustering grouped genotypes based on their morphological traits rather than geographic origin. The diverse genotypes will be used for future breeding programme.

Key words : Sweet corn, principal component analysis, clustering, diversity

Maize is third most important crop and it is cultivated for human food, animal feed and fodder and also utilized as raw material for large number of industrial products (Arya *et al.,* 2015).

Sweet corn 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. Correlation studies provide an opportunity to study the magnitude and direction of association of yield with its components and also among various components. In any crop improvement programme genetic diversity is an essential pre-requisite for identifying potential parents for hybridization. Divergence studies indicated that geographical diversity is always not necessarily associated with the genetic diversity. Hence selection of parents for hybridization should be based more on genetic diversity rather than geographic diversity. The divergence analysis by means of principal component analysis and hierarchical cluster analysis have been shown to be useful in selecting genetically distant parents for hybridization. Principal component analysis is used to confirm the diversity pattern brought about by cluster analysis (Chaudhary *et al.,*

2015). Hence the present study was planned to estimate diversity through classification of genotype principal component analysis and hierarchical cluster analysis.

MATERIALS AND METHODS

Genetic evaluation of 26 sweet corn accessions on the basis of agro-morphological traits was evaluated at Department of Millets, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore. Experiment was conducted as per RBD during *Kharif*, 2014. Eight quantitative and five quality characters *viz.,* days to 50 per cent flowering, days to 50 per cent silking, days to green cob harvest, green cob length (cm), green cob girth (cm), number of kernel rows per cob, number of kernals per row, green cob yield (g), total sugars (%), reducing sugars (%), sucrose (%), total carbohydrates (%) and starch (%) for estimating genetic diversity. Mean values of accessions were computed for determining analysis of variance and correlation coefficients. Principal component analysis (PCA) and cluster analysis were also performed to assess genetic diversity among sweet corn accessions.

RESULTS AND DISCUSSION

The entire success of plant breeding programme in any crop largely depends on the range of variability owing to genetic and non genetic causes, present in that crop (Vavilov, 1951). Hence, the present investigation was conducted to assess the variability for all 26 sweet corn accessions and observations were recorded for further analysis. Analysis of variation depicted considerable level of variability among different accessions for most of the traits. Basic descriptive statistics for 13 characters was presented in Table 1. The estimates of phenotypic coefficient of variation (PCV) were higher than those of genotypic coefficient of variation (GCV) for all the traits indicating environmental factors influencing the characters. In case of most of the characters under study the magnitude of genotypic coefficient of variation was closer to the phenotypic coefficient of variation. This indicated that greater role was played by genotype rather than environment.

The characters *viz*., reducing sugar (87.40% and 86.97%), sucrose (74.73% and 74.70%), total sugars (60.43% and 60.31%), starch (37.66% and 37.63%) and total carbohydrates (28.64% and 28.62%) were observed to possess high PCV and GCV estimates indicating that, the selection based on these characters would facilitate easily, the successful isolation of desirable genotypes. Similar findings were earlier reported for these characters in sweet corn by Cartea *et al*., (1996), Hatch kiss et al., (1997), Devadas Ramgopal (1999). Moderate PCV and GCV were recorded for green cob yield, number of kernel rows per cob, number of kernals per row and green cob length. However, narrow difference between genotypic and phenotypic coefficients of variation were observed for all the traits indicated little influence of environment on the expression of these traits and variability was mainly due to genetic constitution. This implied phenotypic variability was a reliable measure of genotypic variability in this study.

The genotypes under study showed high heritability values for all the characters. Since heritability is also influenced by environment, the information on heritability alone may not help in pin pointing characters for enforcing selection. Nevertheless, the heritability estimates in conjunction with predicted genetic advance will be more reliable.

Genetic advance as per cent of mean ranged from 7.91 to 178.27. Reducing sugar (178.27) recorded the highest genetic advance as per cent of mean followed by sucrose (153.81), total sugars (124.00), starch (77.47), total carbohydrates (77.47), number of kernel rows per cob (38.67), green cob yield (38.43), green cob length (22.52) and green cob girth (21.28). This situation indicates that the genotypic variance for these characters is probably owing to their high additive gene effects (Johnson et al., 1955). This also confirms the earlier findings of Singh and Sharma (1970), Debnath (1987), Devadas Rangopal (1999). High heritability along with high genetic advance as per cent of mean were recorded for reducing sugar, sucrose, total sugars, starch, total carbohydrates, number of kernel rows per cob, green cob yield, green cob length and green cob girth. High heritability combined with the lowest genetic advance as per cent of mean was noted for days to green cob harvest revealing little scope for improving these characters through selection and this may be attributed to the non-additive gene effects on these traits (Johnson *et al*., 1955).

TABLE 1

Variation in quantitative traits of sweet corn accessions

Traits	Minimum	Maximum	Range	Mean	Std. deviation	PCV (%)	GCV (%)	Heritability (%)	Genetic advance as per cent of mean
Days to 50% flowering	45.00	63.00	18.00	52.99	4.55	8.57	8.62	98.84	17.54
Days to 50% silking	48.00	68.00	20.00	55.94	4.96	8.85	8.90	98.71	18.10
Days to green cob harvest	68.00	81.00	13.00	74.82	2.93	3.89	3.95	97.34	7.91
Green cob length (cm)	8.75	16.58	7.83	12.08	1.37	11.21	11.49	95.13	22.52
Green cob girth(cm)	8.21	12.98	4.77	10.68	1.15	10.69	11.06	93.38	21.28
No of kernel rows/cob	8.00	18.00	10.00	12.78	2.46	19.14	19.51	96.23	38.67
No of kernels/row	14.21	26.75	12.54	20.59	2.88	13.98	14.03	99.34	28.70
Total Sugar-(9-21%)	2.05	17.87	15.82	6.96	4.20	60.31	60.43	99.62	124.00
Reducing Sugar-(4.0%)	0.12	4.21	4.09	1.21	1.05	86.97	87.40	99.01	178.27
Sucrose- (20%)	0.88	16.58	15.70	5.80	4.33	74.70	74.73	99.91	153.81
Total carbohydrate (%)	15.68	62.60	46.92	45.09	12.91	28.62	28.64	99.89	58.93
Starch (%)	2.48	13.36	10.88	7.11	2.68	37.63	37.66	99.87	77.47
Green cob yield (g)	82.54	187.56	105.02	120.35	22.54	18.71	18.76	99.44	38.43

TABLE 2
Genotypic correlation coefficients for yield and yield components in sweet corn

	DFF	DS	DH	CL	CG	NKR	NK	TS	RS	Su	C	ST	CY
DFF	1.000	0.654**	0.389*	-0.145	-0.028	0.118	-0.201	0.146	0.172	0.097	-0.102	0.479*	-0.336
DS		1.000	0.281	-0.118	-0.088	-0.010	-0.095	0.068	0.107	0.039	-0.238	0.095	-0.164
DH			1.000	-0.351	-0.265	0.232	-0.113	-0.133	-0.120	-0.097	0.032	0.281	-0.350
CL				1.000	0.434*	0.253	0.491*	-0.048	-0.419*	0.055	0.157	-0.145	0.410*
CG					1.000	0.147	0.429*	-0.402*	-0.114	-0.353	-0.095	0.020	0.579**
NKR						1.000	0.441*	0.095	-0.121	0.119	0.086	-0.068	0.101
NK							1.000	-0.143	-0.351	-0.051	-0.133	-0.330	0.421*
TS								1.000	-0.093	0.971**	0.034	-0.159	-0.235
RS									1.000	-0.329	-0.090	0.041	0.165
Su										1.000	0.054	-0.160	-0.263
C											1.000	0.094	0.114
ST												1.000	-0.275
CY													1.000

Correlation coefficient for different quantitative characters was presented in Table 2. Green cob yield was highly significant and positively correlated with green cob length (0.410), green cob girth (0.579) and number of kernel rows per cob (0.421) however total sugar, sucrose and starch was non significant and negatively correlated with green cob yield. These results were in agreement with the findings of Saleh *et al.* (2002). Regarding intercorrelation, days to 50 per cent flowering had positive significant inter correlation with days to silking (0.654), days to green cob maturity (0.389) and starch (0.479). Green cob length had positive inter correlation with green cob girth (0.434), number of kernals per row (0.402). Number of kernel row per cob had positive inter correlation with number of kernels per row (0.441). Total sugar recorded positive significant inter correlation with sucrose (0.971). Hence selection of these traits will be useful for future breeding programme.

The Principal component analysis is a technique which identifies plant traits that contribute the most for the observed variation within a group of genotypes. This tool has a practical application in the selection of best genotypes for breeding purpose. The six principal components of screen plot and three component plot in rotated space on 26 genotypes for 13 traits are depicted in Fig. 1a and 1b.

Principal component analysis showed that the amount of variation by principal components (PCs) 1 to 6 *viz.* 24.61, 17.97, 14.26, 10.41, 8.60 and 7.78% respectively. PCA identified six principal components with eigen values more than one which contributed 83.63 per cent of the cumulative variance. The first Principal Component (PC1) contributed maximum
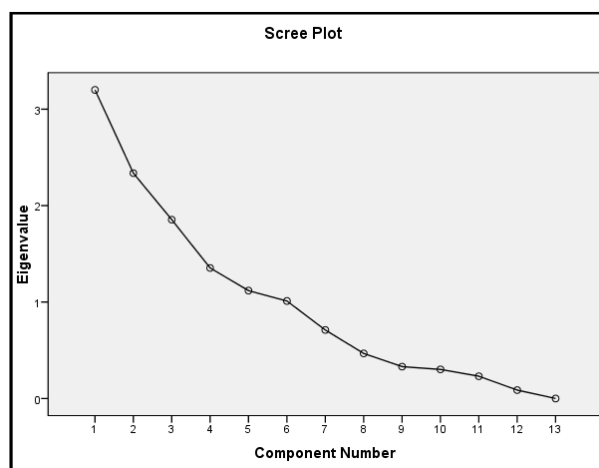

Fig. 1a. Screen plot for 13 traits in 26 sweet corn genotypes.
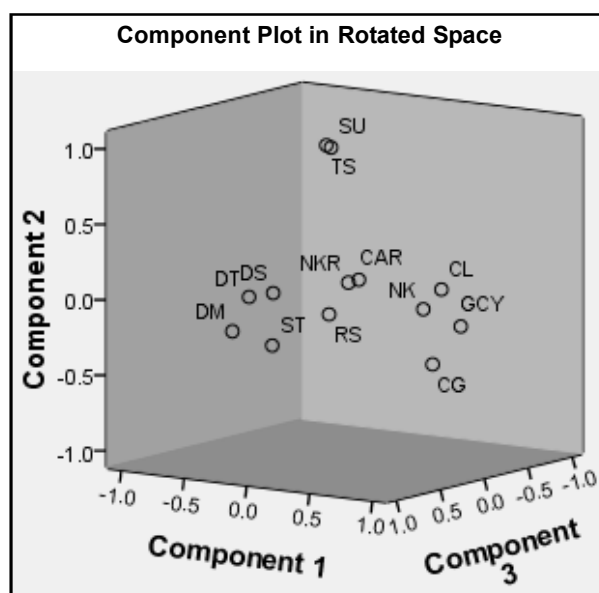

Fig. 1b. Component plots for 13 traits in 26 sweet corn genotypes.

TABLE 3

Eigen vectors, principal components for quantitative traits in sweet corn accessions

Traits	PCA 1	PCA 2	PCA 3	PCA 4	PCA 5	PCA 6
Days to 50% flowering	-0.581	-0.197	0.612	0.213	0.333	0.015
Days to 50% silking	-0.437	-0.165	0.508	0.486	0.07	-0.033
Days to green cob harvest	-0.483	-0.231	0.461	-0.38	-0.388	0.194
Green cob length (cm)	0.665	0.269	0.337	-0.068	0.313	-0.203
Green cob girth(cm)	0.682	-0.309	0.309	0.146	0.257	-0.171
No of kernel rows/cob	0.209	0.219	0.613	-0.138	-0.143	0.557
No of kernels/row	0.687	0.169	0.454	0.097	-0.298	0.038
Green cob yield (g)	0.757	-0.143	-0.042	0.227	0.255	0.296
Total Sugar (%)	-0.372	0.848	-0.02	0.226	0.204	0.107
Reducing Sugar (%)	-0.216	-0.463	-0.366	0.436	0.203	0.545
Sucrose (%)	-0.301	0.916	0.069	0.109	0.145	-0.03
Total carbohydrate (%)	0.07	0.139	-0.114	-0.66	0.469	0.367
Starch (%)	-0.401	-0.403	0.252	-0.363	0.436	-0.241

towards variability (24.61%) was correlated with green cob yield, number of kernals per row, green cob girth, green cob length and number of kernel rows per cob (Table 3). Thus, this component was the weighted average of the characters which determined the yield level. These traits had the largest participation in the divergence and carried the largest portion of its variability. The second Principal Component (PC2) accounted 17.97 per cent of total variance and it reflected positive loading of sucrose, total sugar, green cob length and number of kernel rows per cob. The third PC3 was characterized noticeably by high loading of number of kernel rows per cob, days to 50 per cent flowering, days to 50 per cent silking, number of kernals per row, days to green cob harvest, green cob length and green cob girth. The fourth PC was correlated with days to 50 per cent silking, reducing sugar, green cob yield and days to 50 per cent flowering. The component five PC5 accounted with total carbohydrates, starch, days to 50 per cent flowering, green cob length. The traits number of kernels per row, reducing sugar and total carbohydrates contributed high variation in principal component PC6.
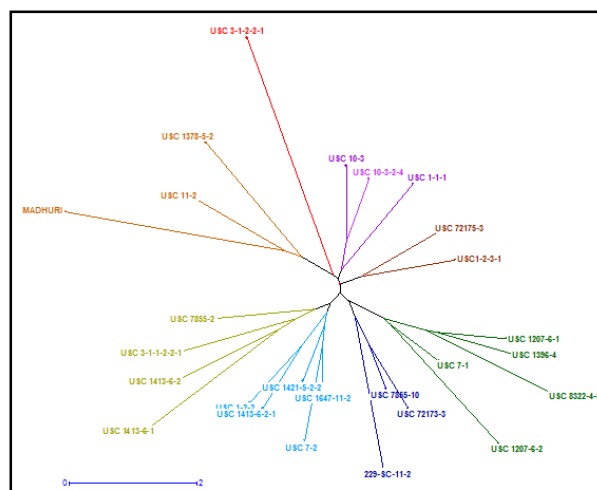

Fig. 2. Cluster diagram for various traits of sweet corn accessions.

Hierarchical cluster analysis based on quantitative traits divided sweet corn genotypes into eight clusters (Table 4 & Fig. 2). Analyses performed by UPGMA divided the 26 genotypes into eight clusters. The distribution of genotypes into various clusters was random, indicating lack of parallelism between genetic and geographic diversities. Among the clusters, cluster VIII and VI contains five genotypes

TABLE 4

Clustering composition of sweet corn genotypes

S. No.	Clusters	Name of genotypes
1.	I	USC 72175-3, USC 1-2-3-1
2.	II	USC 10-3, USC 1-1-1, USC 10-3-2-4
3.	III	USC 3-1-2-2-1
4.	IV	USC 1378-5-2, USC 11-2, Madhuri
5.	V	USC 7855-2, USC 3-1-1-2-2-1, USC 1413-6-2, USC 1413-6-1
6.	VI	USC 1413-6-2-1, USC 1421-5-2-2, USC 1647-11-2, USC 7-2, USC 1-2-2
7.	VII	229-SC-11-2, USC 7855-10, USC 72173-3
8.	VIII	USC 7-1, USC 1297-6-2, USC 8322-4-3, USC 1396-4, USC 1207-6-1

in each. The cluster III forms the solitary cluster with one genotype (USC 3-1-2-2-1) shows that wide diversity exists in this genotypes and it will be used for breeding programme.

The present study showed considerable variability for most of the characteristics that could be exploited for crop improvement. The clustering pattern could be utilized in identifying the best cross combinations for generating variability with respect to various characters under study. The genotypes clubbed in the different clusters if inter crossed may generate wide variability. Clustering pattern indicated no association between geographical distribution of accessions and genetic divergence (Murthy and Arunachalam, 1966). Cluster analysis based on plant morphology suggested that the accessions could be grouped. Such groupings are useful to breeders in identifying possible genotypes that may be used as parents in breeding for any of the morphological traits that were studied. Above all, the information generated will reduce the overall time required by plant breeders to screen large populations for potential breeding stock.

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