

GENETIC DIVERSITY STUDIES IN SWEET CORN (*Zea mays* L. SACCHARATA.)

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ABSTRACT

Assessment of genetic diversity is a pre-requisite to broaden the genetic background of cultivated base of sweet corn, an endosperm mutant of field corn that alters starch biosynthesis pathway in endosperm. In the current investigation, genetic divergence among 26 sweet corn inbred lines was assessed on the basis of eight agromorphological traits, five quality parameters. Cluster analysis grouped the sweet corn genotypes into 12 clusters based on the degree of divergence between the genotypes.. Maximum number of five genotypes was grouped under cluster II, while clusters XI and XII forms solitary cluster with one genotype in each cluster and rest of the clusters had two genotypes each. Maximum inter cluster distance was observed between cluster III and cluster IX (162.866) followed by cluster VII and IX (157.555) and cluster IX and XII (153.969). The maximum intra cluster distance (95.812) was observed in cluster II followed by cluster X (81.552), cluster IX (77.475). Among the thirteen traits studied, maximum contribution was made by green cob yield per plant (41.23%) followed by sucrose (22.46%), starch (16.92%) and total carbohydrates (16.62%). The traits viz., green cob yield, sucrose, starch and total carbohydrates contributed 97.23 per cent towards total divergence. Therefore, these characters may be given importance during hybridization programme.

INTRODUCTION

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. Sweet corn differs from dent corn by one recessive gene 'su' on 4th chromosome which prevents the conversion of part of sugars in to starch. Sweet corn has distinct characteristics compared to common green corn (Pena *et al.*, 2012), with reduced genetic variability available for direct use in breeding programs. Crop breeders commonly prefer yield components that indirectly increase yield. Indirect selection of yield components can increase grain yield. Therefore, it is important to know the relationships among yield traits in sweet corn to create higher yields (Kashiani and Saleh, 2010). One of the barriers encountered by breeders has been the relatively low genetic variability of sweet corn, coupled with a lack of appropriate methodologies to evaluate the existing genetic diversity. In any crop improvement programme genetic diversity is an essential pre-requisite for identifying potential parents for hybridization (Prasad *et al.*, 2013). Divergence studies indicated that geographical diversity is always not necessarily associated with the genetic diversity.(Atom Atanasio Ladu Stansluos *et al.*,2019)

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.

(Tirumala *et al.*, 2018). Hence selection of parents for

hybridization should be based on genetic diversity rather than geographic diversity. The divergence analysis has been shown to be useful in selecting genetically distant parents for hybridization. Diverse parents are expected to yield higher frequency of heterotic hybrids in addition to generating a broad spectrum of variability in segregating generations. D2 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 sweet corn genotypes.

MATERIALS AND METHODS

The study was conducted during *khari* 2014 at Millet Breeding Station, new area farm, Department of Millets, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu, India. The twenty six inbred lines were outsourced from Winter Nursery Centre, ICAR-Indian Institute of Maize Research, Hyderabad and stabilized at TNAU, Coimbatore. Twenty six inbred lines were grown in a Randomized Block Design with three replications. The seeds of each entry were sown on 4 m long row with spacing of 60 x 25 cm between rows and plants respectively. One plant was kept per hill after proper thinning. Pre emergence herbicide Atrazine was sprayed for weed control. All the package of practices was taken and the healthy crop was maintained. The following observations were recorded in five randomly selected plants in each replication 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 kernels per row, green cob yield. In

every inbred five plants were allowed for selfing by controlled pollination for the purpose of studying the quality characters viz., total sugar, reducing sugar, sucrose, total carbohydrates and starch. The procedure described by Dubios *et al.* (1956) was followed for estimation of total sugar. Determination of reducing sugars by Nelson Somogyi method, sucrose, total carbohydrates and starch by anthrone method was followed. Mean values of accessions were computed for determining analysis of variance and correlation coefficients. The quantitative measurement of genetic divergence among the genotypes was carried out by Mahalanobis D2 statistic (Rao, 1952). Data were subjected to diversity analysis using GENERES software programme.

RESULTS AND DISCUSSION

The 26 genotypes of sweet corn were grouped into 12 clusters using Mahalanobis D2 analysis, the composition of which is presented in Table 1. Cluster II was the largest having five genotypes indicating genetic similarity among them, followed by clusters I, III, IV, V, VI, VII, VIII, IX and X (two genotypes each) and cluster XI and XII (one genotype each) forms the solitary cluster.

The intra and inter cluster distance are presented in Table 2. Inter cluster distance was higher than intra cluster distance indicating wider genetic diversity among the genotypes. This is in accordance with the earlier report of Seshu *et al.* (2014). The maximum intra cluster distance (95.81) was observed in cluster II followed by cluster X (81.55), cluster IX (77.47), cluster

VIII (59.42), cluster VII (56.93), cluster VI (50.99), cluster IV (50.00), cluster V (44.20), cluster III (39.02) and cluster I (25.42).

The relative divergence of each cluster from other cluster (inter cluster distance) indicated greater divergence between cluster III and cluster IX (162.87) followed by cluster VII and IX (157.56) and cluster IX and XII (153.97). The selection of divergent genotypes from cluster II and IX, VII and IX and IX and XII would produce broad spectrum of variability for yield and yield traits, which may enable further selection and genetic improvement.

The crosses which involve parents from these more divergent clusters will yield relatively potential amount of heterosis in F1 and high frequency of transgressive segregants and genetic variability in subsequent generations. The chance of getting segregants with a higher yield level was quite limited, when one of the clusters had a very low yield level. Hence, if greater diversity was observed between two high yielding clusters, then crossing between those clusters would result in segregants with high seed yield.

The cluster means of 13 characters are presented in Table 3. Greatest range of mean values among the cluster was recorded for different traits. Cluster XII recorded the highest mean values for green cob yield (185.78), number of kernels per row (26.54) and green cob length (16.21). Cluster VIII was the second highest for green cob yield (158.62). This is similar with the results of Seshu *et al.* (2014). Cluster XI recorded the highest mean value for days to 50% flowering, days to 50 % silking, days to green cob harvest, number of kernel rows per cob, total carbohydrate and starch. The results were supported by Xia *et al.* (2005) and Chen *et al.* (2007). The cluster V exhibited high mean for green cob girth, cluster VIII for reducing sugar, cluster IX for total sugars and cluster X for sucrose. It is evident that, based on cluster mean wide range of variation was observed for green cob yield and its components in sweet corn. Therefore, suggested that most diverse clusters may be used as parents in hybridization programme to develop high yielding hybrids or varieties. An analysis of these results also revealed that there was no cluster with at least one genotype with all the desirable traits, which ruled out the possibility of selecting directly one genotype for immediate use. Therefore, judicious combination of all the targeted traits requires hybridization between the selected genotypes from divergent clusters (Saroj *et al.*, 2013).

The contribution of each trait to total divergence is presented in Table 4. Among the traits studied, green cob yield

Table 1 : Cluster composition of 26 sweet corn lines

S.No.	Cluster	No. of number accessions	Accession number
1	I	2	USC 1421-5-2-2, USC 7855-10
2	II	5	USC 1396-4, USC 1207-6-1, USC 3-1-2-2-1, USC 7855-2, USC 72175-3
3	III	2	USC 1-2-3-1, USC 1-1-1
4	IV	3	USC 7-2, USC 1647-11-2
5	V	2	USC1-2-2, USC 1413-6-2-1
6	VI	2	USC 10-3-2-4, USC 10-3
7	VII	2	USC 1413-6-2, USC 3-1-1-2-2-1
8	VIII	2	USC 1378-5-2, USC 11-2
9	IX	2	USC 1207-6-2, USC 72173-3
10	X	2	USC 8322-4-3, USC 7-1
11	XI	1	229-SC-11-2
12	XII	1	Madhuri

Table 2: Intra cluster (diagonal) and inter cluster distances for 12 clusters in sweet corn

	C I	C II	C III	C IV	C V	C VI	C VII	C VIII	C IX	CX	CXI	CXII
CI	25.423	85.576	116.2	53.108	70.575	75.555	90.764	84.114	79.607	109.324	99.826	100.027
CII		95.812	98.158	110.268	84.363	87.027	116.523	114.287	114.737	105.372	108.818	100.502
CIII			39.024	135.67	100.811	68.868	150.841	115.894	162.866	126.23	117.847	73.824
CIV				50.006	84.855	96.09	97.518	91.748	107.875	143.099	113.809	120.836
CV					44.201	78.142	71.339	112.438	112.519	127.334	66.029	98.069
CVI						50.997	114.826	85.635	134.304	128.517	93.15	62.522
CVII							56.933	145.097	114.258	157.555	65.623	144.077
CVIII								59.42	138.259	145.381	151.232	75.77
CIX									77.475	101.475	134.742	153.969
CX										81.552	151.883	140.403
CXI											0	129.807
CXII												0

Table 3: Cluster mean values for thirteen characters in sweet corn

	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII
Days to 50% flowering	54.5	48.53	50.5	54.11	56.67	50.67	57	49.83	59.17	53.83	60.67	47.67
Days to 50% silking	58.5	50.93	54.5	58.89	59.5	54	61.5	51.17	60.67	54.67	64.67	49.33
Days to green cob harvest	76	73.33	72.83	75.56	76.33	78.67	76.17	73	74.67	74	80.33	68.33
Green cob length (cm)	12.88	11.91	11.65	10.84	13.28	11.71	10.8	11.74	11.51	12.69	13.27	16.21
Green cob girth(cm)	10.41	10.19	10.9	10.1	12.48	9.8	9.86	12.37	11.18	10	10.28	12.18
No of kernel rows/cob	14.33	11.4	13.33	10.44	10.17	15.33	11	13	15.83	13.17	17.33	14.33
No of kernels/row	22.28	18.68	21.32	18.42	19.84	23.85	18.02	23.41	21.34	19.82	20.27	26.54
Total Sugar-(9-21%)	7.28	7.97	4.78	3.63	3.58	5.51	5.71	6.4	12.98	14.4	4.4	4.66
Reducing Sugar-(4.0%)	0.9	1.17	1.15	1.74	0.39	1.59	1.86	2.41	0.54	0.76	0.9	0.17
Sucrose- (20%)	6.29	6.85	3.7	1.85	3.49	4.07	3.85	3.99	12.34	13.57	3.7	4.6
Total carbohydrate (%)	32.59	53.08	60.38	25.32	51.65	49.47	52.75	30.15	35.01	47.99	61.34	49.57
Starch (%)	7.27	7.11	2.9	7.13	9.2	5.29	12.55	4.83	9.41	4.84	9.8	5.6
Green cob yield (g)	114.61	121.21	122.74	102.82	128.64	126.11	110.6	158.62	100.25	98.51	108.73	185.78

Table 4: Relative contribution of different characters towards divergence

S. No.	Characters	Contribution percentage (%)
1	Days to 50% flowering	0.31
2	Days to 50% silking	Trace
3	Days to green cob harvest	Trace
4	Green cob length (cm)	Trace
5	Green cob girth(cm)	Trace
6	No of kernel rows/cob	0.31
7	No of kernels/row	1.53
8	Total sugars (%)	Trace
9	Reducing Sugar (%)	0.62
10	Sucrose (%)	22.46
11	Total carbohydrate (%)	16.62
12	Starch (%)	16.92
13	Green cob yield (g)	41.23
	Total	100

contributed maximum divergence (41.23%) followed by sucrose (22.46%), starch (16.92%) and total carbohydrates (16.62%). The minimum percentage of contribution was observed in days to 50 per cent flowering and number of kernel rows per cob (0.31%) followed by reducing sugar (0.62%) and number of kernels per row (1.53%). Similar results were also reported by Tirumala Jawahar Sri Gopi *et al.* (2018). The traits *viz.*, green cob yield, sucrose, starch and total carbohydrates contributed 97.23 per cent towards total divergence. Hence, importance should be given to green cob yield, sucrose, starch and total carbohydrate during hybridization and selection processes of segregating population. Genetic diversity was studied to find out the more diverse inbred lines in sweetcorn which might be used in hybridization programme. The selection of divergent genotypes from cluster II and IX, VII and IX and IX and XII would produce broad spectrum of variability for yield and yield traits, which may enable further selection and genetic improvement.

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