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Research Article

Genetic variability, heritability and character association studies in sweet corn (*Zea mays* L. *saccharata*)

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Abstract

An investigation was carried out in sweet corn to evaluate seven lines, seven testers and their 49 crosses during *Kharif* 2017. The study revealed highly significant differences among genotypes, indicating the presence of substantial genetic variability. High heritability coupled with high genetic advance as percent of mean was recorded for the traits *viz.,* green cob yield, green cob weight, 100 seed weight, total sugar, reducing sugar, non-reducing sugar, iron content and zinc content, indicated the importance of these traits for selection. Correlation studies revealed significant positive association of green cob yield with green cob weight, cob breadth, tassel length, plant height, cob length, total chlorophyll content, tassel branches, cob placement height, 100 seed weight and number of kernel rows per cob. Non-significant association between green cob yield and total sugar content indicated the possibility of simultaneous improvement of these traits through further breeding programmes.

Key words
Sweet corn, Variability, Association.

Introduction

Sweet corn (*Zea mays* L. *saccharata*) is a natural mutant from normal corn with high sugar content. It is one of the popular vegetables for the American, Asian and European people, which are characterized by sweet taste, thin pericarp, delicate textured endosperm and high nutritional value. Sweet corn is grown for fresh human consumption and as raw or processed material of food industry throughout the world. In India, this specialty corn has high market value and it is highly suitable for peri-urban agriculture.

Determination of extent of genetic variability is an important for improving the traits of interest using suitable breeding programmes. Heritability is a measure of the phenotypic variance attributable to genetic causes and it predicts the extent to which a particular character can be transmitted to successive generations. Whereas genetic advance shows the degree of gain obtained for the characters under a particular selection pressure. Knowledge about the amount of genetic variability, heritability and genetic advance in selection could assist the breeder to determine the criteria to be used for the improvement of the yield and its contributing traits (Bello *et al.*, 2012). Since grain yield in sweet corn is controlled by polygene, effective yield improvement and simultaneous improvement of yield components are imperative (Reddy *et al.*, 2013). Association studies helps to understand the degree and direction of association between two or more variables. Therefore, the

present study was aimed at obtaining information on genetic parameters and association between yield and yield components of sweet corn genotypes that could be useful in sweet corn breeding programmes aimed at developing inbreds and hybrids with high yield and quality.

Materials and Methods

Fourteen diverse inbred lines of sweet corn were crossed in line x tester mating design (7 lines and 7 testers) during S*ummer* 2017as a resultant 49 hybrids were produced. All the 49 hybrids along with 14 parents and one check (Sugar 75) were evaluated in a Completely Randomized Block Design with three replications during *Kharif* 2017 at the experimental fields of Department of Millets, Centre for Plant Breeding and Genetics (CPBG), Tamil Nadu Agricultural University (TNAU), Coimbatore under irrigated condition. Biometrical data on days to 50% tasseling, days to 50% silking, plant height (cm), tassel length (cm), tassel branches, cob placement height (cm), cob length (cm), cob breadth (cm), number of kernel rows per cob, number of kernels per row, green cob weight (g), green cob yield (t ha^{-1}) and 100 seed weight (g). One physiological parameter *viz.,* total chlorophyll content was measured at the silking stage using a portable Minolta SPAD 502 chlorophyll meter. The average values obtained from the five representative plants in respect of all the characters from each genotype/replication were used for statistical analysis. Quality of the green cob was ascertained by analyzing the quality traits. The immature kernelscollected at milky stage and stored at -20^{0}C was subjected to estimation of quality traits. Total soluble solids was measured using hand refractometer (Olsen *et al.*,1990) by taking juice directly by squeezing a grain at milky stage. Total sugar content was estimated using Anthrone method (Yemm and Willis, 1954), reducing sugar by Nelson Somogyi method (Somogyi, 1952) and non-reducing sugar by subtracting reducing sugar from total sugar. Nutrient estimation was done using Tri-Acid method in the Micronutrient laboratory, Department of Soil Science and Agricultural Chemistry TNAU, Coimbatore. The well dried grain samples were ground into fine powder and this was used for the estimation of iron and zinc content.

Phenotypic and genotypic variances were estimated based on the formula suggested by Chaudhary and Singh (1985). PCV and GCV were calculated according to Burton (1952). Heritability and genetic advance were computed based on Lush (1940) and Johnson *et al.*(1955) respectively. The genotypic correlation coefficient was worked out by using the formula given by Falconer (1967)

Results and Discussion

The genotypes were significantly different for all the traits under study(Table.1). In addition to the phenotypic range of variation, the genetic parameters like genotypic variance (GV), genotypic coefficient of variability (GCV), heritability (broad sense) and genetic advance as percent of mean were also estimated for getting more precise understanding on the extent of genetic variability, which is a prerequisite for selection response (Table.1).

In general, the estimates of phenotypic coefficient of variation (PCV) were higher than the estimates of genotypic coefficient of variation (GCV) for all the traits under study indicating the environmental influence over the traits and the possibility of improvement by phenotypic selection. The high estimates of PCV and GCV were observed for green cob yield,, total sugar, reducing sugar, non-reducing sugar, iron content and zinc content.These results were in accordance with the findings of Dagla *et al.* (2015) and Suhaisini *et al.* (2016).

The genetic components of variation together with heritability estimates would give the best picture of amount of genetic advance to be expected from the selection (Burton, 1952). Heritability indicated the effectiveness with which selection of genotypes would be based on phenotypic performance (Dagla *et al.*, 2015). In the present study, heritability (broad sense) showed a range from 21.55 (tassel branches) to 98.85 (iron content) and it was found to be high for iron content followed by zinc content, reducing sugar, green cob yield, non-reducing sugar, total sugar, green cob weight, number of kernels per row, cob length, total soluble solids, 100 seed weight, plant height, cob placement height, tassel length, days to 50% tasseling and number of kernel rows per cob. Similar findings were reported by Rajesh *et al*. (2014) for plant height, cob placement height, number of kernel rows per ear, number of kernels per row, 100 seed weight and grain yield and Bello *et al*. (2012) for green cob weight, plant height and cob placement height. However, the selection for improvement of such characters may not be useful, because broad sense heritability is based on total genetic variance which includes additive, dominant and epistatic variances. Thus, heritability values coupled with high genetic advance would be more reliable and useful on correlating selection criteria (Reddy *et al.*,2013).

High genetic advance as percent of mean was recorded by reducing sugar followed by zinc content, iron content, green cob yield, non-reducing sugar, total sugar, 100 seed weight and green cob weight. Hemavathy *et al.* (2008) reported similar findings for grain yield and cob length and Dagla *et al.* (2015) for total sugar, reducing sugar and non-reducing sugar.

High heritability coupled with high genetic advance were recorded for characters *viz.*, green cob yield, green cob weight, 100 seed weight, total sugar, reducing sugar, non-reducing sugar, iron content and zinc content, which suggests that these traits are predominantly under the control of additive gene action and selection may be effective. Similar findings were reported by Alake *et al.*(2008) and Gazal *et al.*(2017) for grain yield, Dagla *et al.* (2015) for total sugar, reducing sugar and non-reducing sugar, and Suhaisini *et al.* (2016) for green cob yield, green cob weight, 100 seed weight, total sugar, reducing sugar and non-reducing sugar.

Association analysis provides information on nature and extent of relationships among characters and thereby facilitates simultaneous improvement of two or more characters. Genotypic correlations reveal the existence of real associations, whereas phenotypic correlation involves environmental

influence also (Reddy *et al.*,2013). Therefore, genotypic correlation coefficient is an effective instrument for examining degree of relationships among traits (Table.2).
Since green cob yield is considered as the most important trait, association of other traits with green cob yield was given prime importance. Green cob weight recorded highest significant positive correlation with green cob yield (0.75). Özlem *et al.* (2013) also reported significant positive association of green cob yield and green cob weight. Plant height, tassel length, tassel branches, cob placement height, cob length, cob breadth, number of kernel rows per cob and 100 seed weight were also reported significant positive association with green cob yield. The result was in agreement with the findings of Reddy *et al.*(2013) for plant height, cob placement height, cob length, cob breadth, number of kernel rows per cob and 100 seed weight, Kumari *et al.* (2006) for 100 seed weight and Suhaisini *et al.*(2016) for number of kernels rows per cob, plant height, green cob weight, cob placement height , cob length , cob breadth, 100 seed weight and number of kernels per row. Selvaraj and Nagarajan (2011), Gazal *et al.*(2018) and Sadaiah *et al.*(2013) have also found such positive association of plant height and cob placement height with green cob yield. Total chlorophyll content exhibited significant positive correlation with yield. The finding was in accordance with Gekas *et al.*(2013). Hence, simultaneous improvement can be done in these positively correlated traits through further breeding programmes.

Days to 50% silking showed negatively significant relationship with green cob yield and it indicated the possibility of developing high yielding genotypes with earliness by making simultaneous selection for both the traits. Similar findings were reported by Reddy *et al.*(2013) and Sadaiah *et al.*(2013). Presence of non- significant association between yield and total sugar indicating the scope of development of hybrids with high yield coupled with high sugar content. The results were in accordance with (Khanduri *et al.,* 2010) and Suhaisini *et al.*(2016).

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Table 1. Mean squares of analysis of variance

Characters	Sources of variation				
	Genotypes	Hybrids	Parents	Parents vs hybrids	Error
Days to 50% tasseling	15.28**	14.15**	20.04**	7.20	2.14
Days to 50% silking	7.77**	5.38**	10.55**	86.35**	2.05
Plant height	458.27**	327.97**	145.97**	10772.43**	37.62
Tassel length	27.93**	13.13**	26.98**	750.83**	3.40
Tassel branches	5.20**	3.75	9.48**	18.98*	2.85
Cob placement height	241.98**	211.22**	191.93**	2369.05**	22.51
Green cob yield	14.81**	3.93**	3.65**	681.14**	0.27
Green cob weight	1705.41**	810.29**	1151.25**	51875.94**	61.40
Cob length	4.35**	2.96**	5.39**	57.48**	0.17
Cob breadth	1.25**	0.75**	0.95**	29.02**	0.27
Number of kernel rows per cob	4.93**	5.00**	4.47**	7.91**	0.89
Number of kernels per row	38.72**	36.88**	46.56**	25.55**	1.42
100 seed weight	10.35**	9.61**	11.41**	32.09**	0.98
Total sugar	31.55**	31.64**	32.48**	14.96**	0.90
Reducing sugar	0.48**	0.50**	0.40**	0.89**	0.01
Non reducing sugar	37.30**	37.13**	39.02**	23.20**	0.93
Total soluble solids	2.73**	2.36**	4.30**	0.01	0.13
Total chlorophyll content	28.53**	20.39**	30.39**	395.24**	6.56
Fe content	22.27**	12.82**	11.53**	615.84**	0.09
Zn content	5.89**	5.43**	2.28**	75.06**	0.03

Table 2. Estimates of variability parameters for various traits of sweet corn genotypes

Characters	PV	GV	PCV	GCV	Heritability	GA (%) of mean
Days to 50% tasseling	6.52	4.38	5.20	4.26	67.16	7.19
Days to 50% silking	3.95	1.91	3.83	2.66	48.26	3.81
Plant height	177.83	140.21	7.26	6.45	78.84	11.79
Tassel length	11.77	8.08	9.24	7.66	68.64	13.07
Tassel branches	3.63	0.78	11.22	5.21	21.55	4.98
Cob placement height	95.66	73.15	10.11	8.83	76.47	15.92
Green cob yield	5.12	4.85	25.67	24.98	94.66	50.05
Green cob weight	609.41	548.01	12.39	11.75	89.92	22.94
Cob length	1.56	1.39	6.59	6.22	89.15	12.11
Cob breadth	0.60	0.32	5.10	3.80	54.30	5.70
Number of kernel rows per cob	2.24	1.35	10.38	8.05	60.11	12.86
Number of kernels per row	13.86	12.44	10.43	9.88	89.72	19.28
100 seed weight	4.10	3.13	19.68	17.18	76.20	30.90
Total sugar	11.12	10.21	21.20	20.31	91.86	40.10
Reducing sugar	0.17	0.16	38.03	37.16	95.47	74.80
Non reducing sugar	13.05	12.12	24.64	23.75	92.90	47.15
Total soluble solids	1.00	0.87	6.63	6.18	86.94	11.88
Total chlorophyll content	13.88	7.32	6.88	5.00	52.75	7.48
Fe content	7.84	7.40	27.43	27.27	98.85	55.85
Zn content	1.98	1.95	29.56	29.37	98.73	60.12

Table 3. Genotypic correlation coefficient values for twenty characters in sweet corn

	DFT	DFS	TCC	PH	TL	TB	CPH	CL	CB	RPC	KPR	HSW	TSS	TS	RS	NRS	Fe	Zn	GCW	GCY
DFT	1	0.66**	-0.14	0.02	-0.04	-0.30*	0.02	-0.04	-0.18	0.19	0.00	-0.09	0.00	-0.02	-0.20	0.00	0.00	-0.05	-0.16	-0.22
DFS		1	-0.50**	-0.42**	-0.38**	-0.51**	-0.33**	-0.53**	-0.46**	0.09	-0.15	-0.15	-0.07	-0.04	-0.11	-0.02	0.21	-0.22	-0.58**	-0.74**
TCC			1	0.46**	0.37**	0.54**	0.33**	0.27*	0.42**	0.27*	0.15	0.03	0.13	-0.02	0.04	-0.03	-0.22	0.05	0.39**	0.53**
PH				1	0.53**	0.29*	0.85**	0.46**	0.49**	0.36**	0.06	0.06	0.13	0.07	0.02	0.06	-0.25*	0.22	0.64**	0.64**
TL					1	0.20	0.37**	0.30*	0.29*	-0.03	0.19	0.14	0.10	-0.09	0.21	-0.11	-0.24	0.39**	0.76**	0.67**
TB						1	0.20	0.43**	0.65**	0.20	0.13	-0.11	0.08	0.18	-0.09	0.18	-0.17	0.22	0.39**	0.41**
CPH							1	0.42**	0.42**	0.38**	0.10	-0.08	0.17	0.32**	-0.29	0.33**	-0.22	0.24	0.42**	0.41**
CL								1	0.60**	0.33**	0.19	0.26*	0.05	0.08	0.00	0.08	-0.16	0.17	0.38**	0.55**
CB									1	0.27*	0.22	0.43**	-0.13	0.11	0.05	0.09	-0.40**	0.14	0.45**	0.69**
RPC										1	0.07	-0.10	0.24	0.16	-0.15	0.16	-0.16	0.14	0.13	0.25*
KPR											1	-0.06	0.29*	0.08	-0.03	0.08	0.01	0.15	0.04	0.11
HSW												1	-0.30	-0.01	-0.10	0.10	-0.22	0.10	0.09	0.34**
TSS													1	0.11	-0.07	0.11	-0.02	0.11	0.10	0.07
TS														1	-0.69**	0.91**	0.04	0.19	-0.08	0.01
RS															1	-0.75	0.01	0.10	0.26*	0.16
NRS																1	0.04	0.16	-0.11	-0.01
Fe																	1	-0.18	-0.21	-0.23
Zn																		1	0.19	0.24
GCW																			1	0.75**
GCY																				1

******Significant at 1% * Significant at 5% **DFT**- Days to 50% tasseling, **DFS**-Days to 50% silking**, TCC**-Total chlorophyll content, **PH**- plant height, **TL**-Tassel length, **TB-** Tassel branches, **CPH**- Cob placement height, **CL**- Cob length, **CB**- Cob breadth**, RPC**- number of kernel rows per cob, **KPR**-number of kernels per row, **HSW**-100 seed weight, **TSS**-Total soluble solids, **TS**-Total sugars, **RS**- Reducing sugars, **NRS**- Non reducing sugars**, Fe**- Iron content, **Zn**-Zinc content, **GCW**-Green cob weight, **GCY**- Green cob yield