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Genetic parameters for quality traits in sweet corn (*Zea mays* L. Saccharata)

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Abstract

The present study was consists of 26 sweet corn lines to study genetic variability, heritability and genetic advance estimates for quality traits in sweet corn. Analysis of variance for five quality traits *viz.*, total sugar, reducing sugar, sucrose, total carbohydrates and starch revealed that high significant mean sum of squares for all the characters indicating greater diversity among the genotypes. The genotypic coefficients of variation (GCV) for all the characters studied were lesser than the phenotypic coefficients of variation (PCV) indicating the influence of environment under traits. High GCV and PCV values were observed for all the quality traits studied, suggesting that the sufficient variability thus offers scope for genetic improvement through selection. High heritability coupled with high genetic advance as per cent of mean was observed for all the characters studied indicating the role of additive genes in governing the inheritance of these traits which could be improved through simple selection.

Keywords: Sweet corn, genetic variability, heritability, genetic advance

Introduction

Sweet corn is considered a common maize derived vegetable crop through recessive mutation that is characterized by wrinkled and translucent dry grains with high sugar and low starch contents in the endosperm. In the United States sweet corn is economically one of the most important vegetables (Tracy, 1997) [7]. In Brazil the economical potential of the crop consists in fresh consumption, although its production is restricted to southern Brazil. Several factors have contributed to this small expression, including the lack of adapted varieties and the presence of undesirable agronomic traits such as tall plants, lodging susceptibility and poor ear placement (Silva, 1983, Tosello, 1987). The development of superior sweet corn genotypes is crucial to overcome these problems. Improvement of sweet corn yields, while retaining quality is one of the major challenges facing the sweet corn breeders (Hunsperger and Davis, 1987) [5]. Hence, an efforts was made to study the germplasm for different characters and to identify superior sweet corn genotypes that could be further used in the crossing programme to develop high yielding varieties and hybrids.

Materials and Methods

The experiment for the present study was conducted during *kharif*, 2014 at Department of Millets, Tamil Nadu Agricultural University, Coimbatore. The present study was carried out with 26 sweet corn lines (Table 1) and it was laid out in Randomised Block Design with three replications. In every treatment 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) [4] was followed for estimation of total sugar. Determination of reducing sugars by Nelson Somogyi method was followed. The sucrose, total carbohydrates and starch by anthrone method was followed. The genetic parameters *viz*., genotypic and phenotypic coefficient of variation (Burton, 1952), heritability in broad sense and genetic advance as per cent of mean (Johnson *et al*., 1955) [6] were estimated for all the characters.

Results and Discussion

Success of any crop improvement programme depends on the amount of genetic variability present among the characters under consideration for crop improvement. In the present investigation, analysis of variance revealed that, significant differences for all the five quality traits studied which was presented in Table 2. The frequency distribution of quality traits are shown in Fig. 1, 2a-e. The total sugars 2.05(USC 7-2) to 17.14% (USC 8322-4-3)), reducing sugars (0.12 (Madhuri)- 4.01%(USC 1378-5-2)), sucrose (0.91(USC 7855-2) – 16.45% (USC 8322-4-3)), total carbohydrates (16.03 (USC 7-2)– 62.6% (USC 1-2-3-1)) and starch

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(2.59(USC 1-2-3-1)-13.36% (USC 3-1-1-2-2-1)).

In the present investigation, values of phenotypic coefficient of variation were greater than genotypic coefficient of variation for all the traits studied (Table 3). It implied that apparent variation was not only due to genotype but also due to the influence of environment. The values for phenotypic coefficient of variation obtained for various yield and yield attributing characters ranged from 87.40 to 28.64per cent. The phenotypic coefficient of variation was estimated to be high for all the characters *viz.*, reducing sugars (87.40) followed by sucrose (74.73), total sugars (60.43), starch (37.66) and total carbohydrates (28.64). Genotypic coefficient of variance showed a similar trend in all the traits studied and was observed to be high for all the characters studied *viz.*, (86.97) followed by sucrose (74.70), total sugars (60.31), starch (37.63) and total carbohydrates (28.62). All the characters showed narrow differences between phenotypic and genotypic coefficients of variation indicating the very low effect of environment and greater role of genetic factors on the expression of these traits. Therefore, selection on the basis of phenotype alone can be effective for the improvement of these traits. Similar results of high PCV and GCV for total sugar was reported by Devadas Ramgopal (1999) [3] and Corn (2009) [2].

The genotypic and phenotypic coefficients of variation indicated the extent of variation of variability for different traits. For assessing the heritable variation, the magnitude of heritability is the most important aspect in the breeding material which has close bearing on the response to selection with fixable additive gene action. All the five traits studied in the present investigation showed high heritability in broad sense indicating high influence of genetic components.

Nevertheless, the heritability estimates in conjunction with predicted genetic advance will be more reliable (Johnson *et al.*, 1955) [6]. Heritability gives the information on the magnitude of quantitative characters, while genetic advance will be helpful in calculating suitable selection procedures. High heritability along with high genetic advance (% of mean) was observed for all the five quality traits *viz.*, reducing sugars (178.27), sucrose (153.81), total sugars (124.00), starch (77.47) and total carbohydrates (58.93) indicating the role of additive genes in governing the inheritance of these traits which could be improved through simple selection.

Table 1: List of sweet corn entries used for this study

S. No.	Entries	S. No.	Entries
1.	USC 1396-4	14.	USC 1-1-1
2.	USC 1207-6-1	15.	USC 1647-11-2
3.	USC 3-1-2-2-1	16.	USC 1421-5-2-2
4.	USC 7855-2	17.	USC 11-2
5.	USC 7-2	18.	USC 10-3-2-4
6.	USC 1207-6-2	19.	USC 10-3
7.	USC 1378-5-2	20.	229-SC-11-2
8.	USC 8322-4-3	21.	USC 7855-10
9.	USC 1-2-2	22.	USC 72173-3
10.	USC 1413-6-2-1	23.	USC 7-1
11.	USC1-2-3-1	24.	USC 3-1-1-2-2-1
12.	USC 72175-3	25.	USC 1413-6-1
13.	USC 1413-6-2	26.	MADHURI

Table 2: Analysis of variance for different quality characters in sweet corn

S. No.	Parameters	Mean sum of squares		
		Replications (df=2)	Treatments (df=25)	Error (df=50)
1.	Total sugars	0.021	52.98**	0.07
2.	Reducing sugars	0.031	3.304**	0.01
3.	Sucrose	0.029	56.23**	0.02
4.	Total carbohydrates	0.03	499.83**	0.18
5.	Starch	0.05	21.49**	0.01

Table 3: Variability parameters for quality traits in sweet corn

Characters	Mean	Minimum	Maximum	PCV	GCV	Heritability	GA as per cent of mean
Total Sugars (%)	7.00	2.05	17.14	60.43	60.31	99.62	124.00
Reducing sugars (%)	1.19	0.12	4.01	87.40	86.97	99.01	178.27
Sucrose (%)	5.81	0.91	16.45	74.73	74.70	99.91	153.81
Total carbohydrates (%)	45.15	16.03	62.60	28.64	28.62	99.89	58.93
Starch (%)	7.16	2.59	13.36	37.66	37.63	99.87	77.47

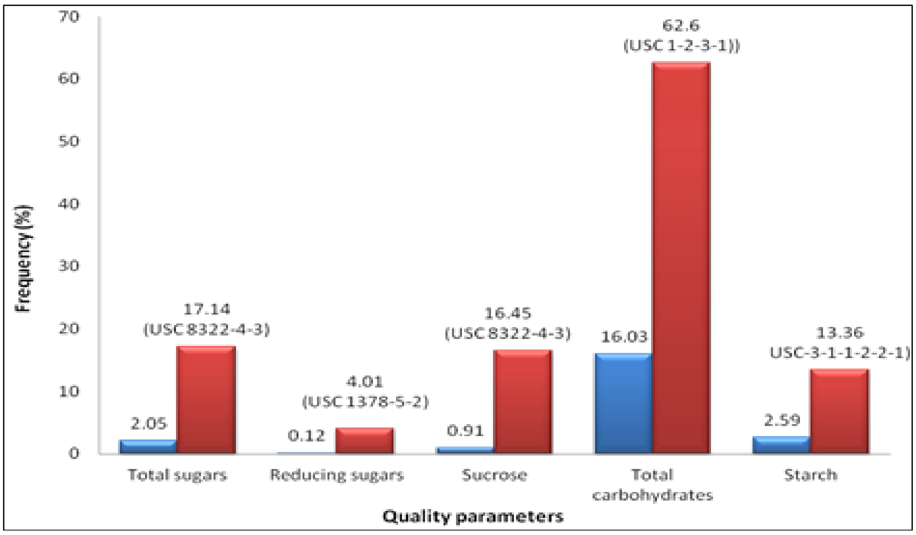

Fig1: Frequency distribution of quality parameters in sweet corn genotypes

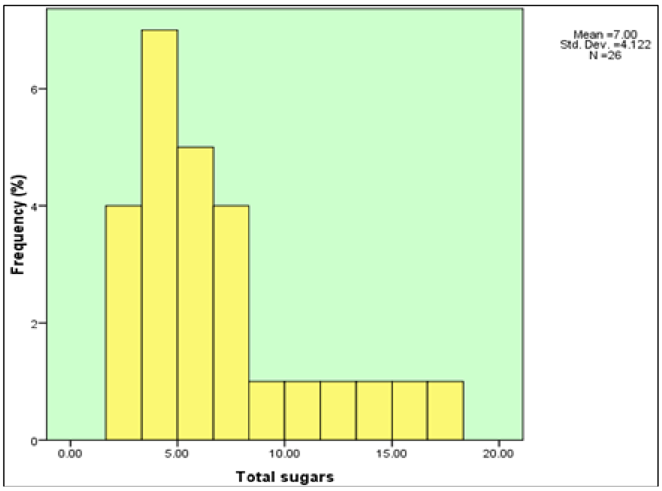

Fig 2a: Frequency distribution of total sugars in sweet corn genotypes

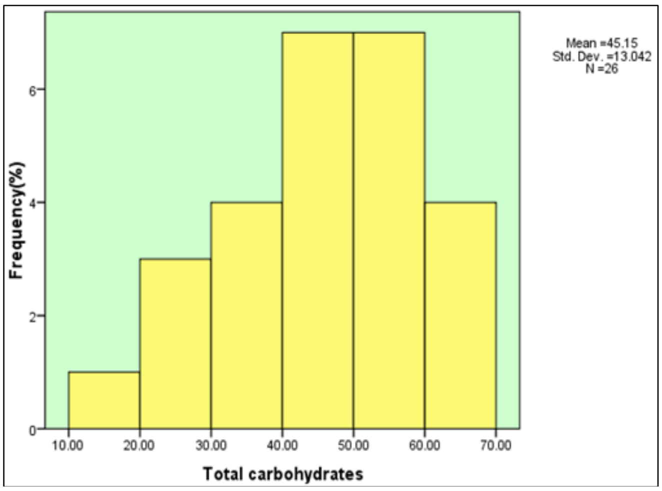

Fig 2c: Frequency distribution of total carbohydrates in sweet corn genotypes

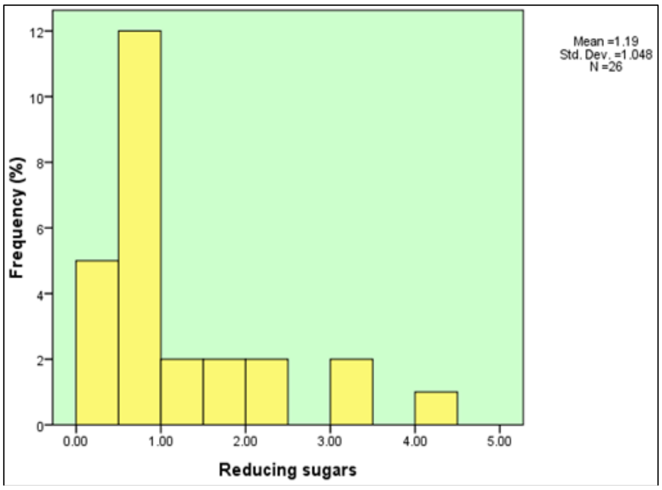

Fig 2b: Frequency distribution of reducing sugars in sweet corn genotypes

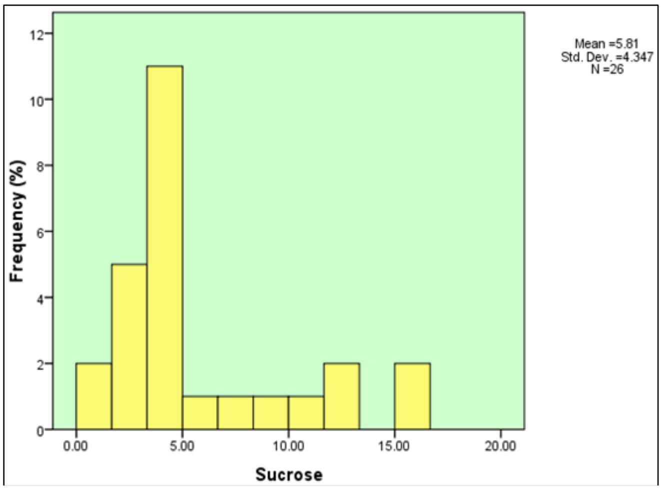

Fig 2d: Frequency distribution of sucrose in sweet corn genotypes

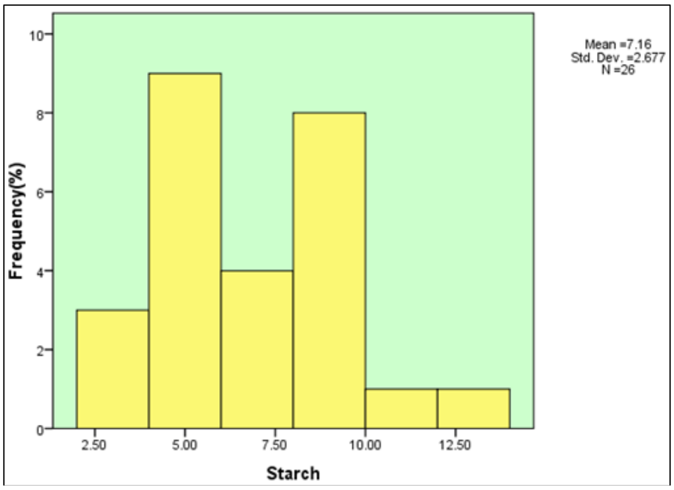

Fig 2e: Frequency distribution of reducing sugars in sweet corn genotypes

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