



Morphological Characterization and Genetic Diversity Analyses of Yield and Yield Attributing Traits in Sweet Corn (*Zea mays* var. *saccharata*)

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

The genetic diversity among the genotypes were useful resources that enabled breeders to comprehend the performance of attributes or genotypes. This understanding is crucial in selecting appropriate genotypes or traits for hybridization programmes. A total of 15 sweet corn genotypes were utilized to assess the characteristics of genetic diversity, correlation, path coefficient and genetic divergence study. The phenotypic coefficient of variation (PCV) exceeded the genotypic

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coefficient of variation (GCV) for all the traits examined, suggesting certain degree of interaction with the environment. The heritability estimates for all variables examined in this study were found to be high. The genetic advance as per cent of mean (GAM) identified a significant difference between high and low values. The traits ear weight with husk, ear weight without husk, husk ratio, chlorophyll content, ear length, ear girth, number of rows per ear, number of kernels per row, 100 kernel weight, shelling percentage, cob yield per plot and fodder yield per plot exhibited high heritability and high GAM. Furthermore, the correlation analysis revealed a significant and positive association for the aforementioned attributes. Additionally, the path coefficient analysis for these traits indicated a favourable direct influence. A total of 15 genotypes were categorized into seven clusters based on their genetic distance. The features that made the biggest contribution to divergence were fodder yield per plot (21%) and shelling percentage (21%), followed by ear weight (14%) and cob yield per plot (10%). The results of this study would be valuable for identifying the desirable characteristics and genetic makeup that can be used in future breeding programmes aimed at enhancing the production of corn cobs in sweet corn.

Keywords: Genetic variability; diversity; correlation; path coefficient and clustering; sweet corn.

1. INTRODUCTION

“Maize (*Zea mays* L.) is one of the most important grain crops and maximizing its productivity is an essential matter [1,2]. Sweet corn is a type of field corn that has kernels with a higher level of sweetness. It is commonly eaten as a raw vegetable in numerous western countries and its fresh, canned and processed varieties are increasingly gaining favour in India and other Asian countries. During the milk stage, the sweet corn contains starch and sugar in the range of 15-35%, while field corn has more than 50% starch and sugar content [3]. Currently, the primary emphasis in sweet corn breeding is to identify and employ various combinations of endosperm mutations in order to achieve high-yielding hybrids with desirable sugar content and a prolonged time of satisfactory kernel quality [4]. The initial stage in the depiction and categorization of germplasm is morphological characterization [5].

Characterizing morphological diversity is a valuable method for identifying accessions that possess desirable traits, such as early maturity, disease resistance or enhanced ear qualities. The categorization and grouping of germplasm aids breeders in preventing duplication while sampling populations. Sweet corn has unique traits in comparison to regular green corn [6], with limited genetic diversity that can be directly utilized in breeding initiatives. Breeders have faced a challenge due to the limited genetic variability of sweet corn, together with a lack of suitable methods to assess the available genetic variation. The feasibility of a breeding programme is determined by genetic variability, which is enhanced by cross-linking between genotypes that are different from each other [7].

The presence of genetic diversity, variability and heritability in the existing germplasm or varieties is crucial for the success of breeding programmes aimed at improving crops. These factors enable plant breeders to develop advanced or new varieties. Understanding genetic parameters, such as the genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) and heritability estimates, is crucial for gaining insight into genetic advancement and informing selection methods for high-yielding crops [8,9]. The investigation of morphological characteristics has gained utmost significance in plant breeding because it allows for the detection of existing heterogeneity among germplasm and facilitates the selection of superior germplasm of interest [10]. Correlation studies, which can examine phenotypic, genotypic or environmental factors, along with the analysis of genetic parameters, enable breeders to identify meaningful relationships between morphological traits. These studies also assist in developing strategies that increase the likelihood of obtaining superior materials [10,11]. Correlation and path coefficient analyses can be used to discover the specific features that can be improved to enhance the multidimensional character of yield [11]. Quantifying genetic diversity by biometrical procedures, such as cluster analysis and principal component analysis, is valuable for measuring the extent of differentiation between biological populations. In addition, it quantifies the proportional impact of various variables on the overall divergence at both the intra and inter cluster levels [12,13].

The purpose of this study was to gather data on the morphological characteristics of maize lines,

which will assist maize breeders in making informed decisions for future breeding programmes. Thus, the current study attempted to assess the genetic variability, heritability and genetic diversity of plant attributes in different maize genotypes that contribute to grain yield.

2. MATERIALS AND METHODS

This experiment was conducted at the Department of Genetics and Plant Breeding experimental farm, Trihut College of Agriculture, Dholi, Rajendra Prasad Central Agricultural University, Bihar during *Kharif* 2023. A total of 15 sweet corn genotypes were collected from Anand Agricultural University, Godhra were listed in Table 1. The field experiment was carried out in the Randomized Block Design (RBD) with three replications. The entries were cultivated in two rows, each measuring 3 meters in length, with a spacing of 60 x 20 centimeters. This resulted in a plot size of 3.6 square meters. The recommended set of procedures was followed and biometric observations were recorded on ten randomly tagged plants for 16 quantitative traits (days to 50% tasseling, days to 50% silking, chlorophyll concentration measured in SPAD units, plant height measured in centimeters, ear height measured in centimeters, ear weight with husk measured in grammes, ear weight without husk measured in grammes, husk ratio measured as a percentage, ear length measured in centimeters, ear girth measured in centimeters, number of rows per ear, number of kernels per row, 100 kernel weight measured in grammes, shelling percentage measured as a percentage, cob yield per plot measured in kilogrammes and fodder yield per plot measured in kilogrammes) and five quality traits (total soluble solids measured as °Bx, reducing sugar measured as a percentage, non-reducing sugar measured as a percentage, total sugar measured as a percentage and starch measured as a percentage).

The data collected on quantitative attributes were averaged and subjected to basic statistical analyses, including mean, minimum, maximum, standard deviation and coefficient of variation. These analyses were used to assess the level of genetic diversity among the genotypes under study. The TNAU STAT programme was used to conduct diversity analysis (D^2), genetic parameter analyses, correlation and path coefficient analysis.

Table 1. List of sweet corn genotypes used in the study

G. No.	Name of the Genotypes	Source
G1	BSCH 416078	AAU, Godhra
G2	BIO 4043	AAU, Godhra
G3	FSCH 119	AAU, Godhra
G4	MSCH 20	AAU, Godhra
G5	KDM 1263	AAU, Godhra
G6	DMSC 24	AAU, Godhra
G7	MSCH 21	AAU, Godhra
G8	MSCH 22	AAU, Godhra
G9	SC 162	AAU, Godhra
G10	DMSC 37-3	AAU, Godhra
G11	I-07-37-1-5	AAU, Godhra
G12	I-07-62-3-2	AAU, Godhra
G13	BSCH 416086	AAU, Godhra
G14	Hawali Sugar	AAU, Godhra
G15	I-07-37-4-1	AAU, Godhra

3. RESULTS AND DISCUSSION

3.1 Mean Performance

The mean performance and analyses of variance for the different traits recorded are presented in Table 2. In the table, a significant difference were observed for all traits studied. Similar results were found by Neupane et al. [14] The number of days to 50% tasseling was observed between shorter period of 43 days (G4) and longer period of 50 days (G10) with an average of 46 days. The number of days to 50% silking was found between shorter period of 46 days (G4) and longer period of 54 days (G10) with an average of 50 days. So we can use genotype 4 (G4) to produce sweet corn plants with shorter period of time for tasseling and silking. The ear weight of a genotypes were found between 55.80 g (G15) and 128.40 g (G12) with a mean weight of 86.20 g. The range of ear length was observed from 10.14 cm (G1) to 15.38 cm (G4) with an average length of 12.61 cm. The trait ear girth was recorded between 8.13 cm (G1) and 14.19 (G3) with an average girth of 10.85 cm. To produce sweet corn lines with increased ear length and girth, genotypes 3 (G3) and 4 (G4) could be used in the future breeding programme. Total soluble solids brix values were observed between 12.43 (G4) and 16.23 (G6) with an average brix of 13.71. The cob yield per plot was found between 1.56 g (G15) and 3.61 g (G12) with a mean weight of 2.41 g.

Table 2. Mean performance and analysis of variance of the 15 sweet corn genotypes

G/T	DFT	DFS	CHL	PH	EH	EWH	EW	HR	EL	EG	NRPE	NKPR	TSS	100KW	SP	CYP	FYP	RS	NRS	TS	ST
G1	46.00	49.00	35.33	160.02	68.21	74.88	58.50	23.11	10.14	8.13	10.00	14.00	13.30	18.35	43.91	1.64	3.36	2.04	4.23	6.27	10.21
G2	45.00	48.00	41.23	164.34	70.31	81.28	64.00	22.30	11.28	8.30	10.00	16.00	12.89	19.25	48.13	1.79	3.64	2.17	4.56	6.73	11.46
G3	47.00	50.00	48.26	181.23	72.14	115.53	95.48	15.67	13.53	14.19	14.00	16.00	13.24	25.33	59.43	2.67	5.37	2.44	5.04	7.48	11.74
G4	43.00	46.00	49.58	174.38	69.36	138.28	108.43	21.58	15.38	14.12	14.00	19.00	12.43	25.15	61.70	3.03	6.12	2.27	4.83	7.10	12.45
G5	46.00	50.00	46.27	195.17	79.42	103.68	81.00	23.38	12.08	9.53	12.00	15.00	15.21	25.86	57.47	2.27	4.59	2.16	5.32	7.48	12.35
G6	46.00	49.00	56.71	154.19	67.32	153.90	125.12	18.28	14.27	13.25	12.00	19.00	16.23	31.34	57.11	3.50	7.09	2.73	5.13	7.86	13.45
G7	49.00	52.00	48.30	163.28	62.22	126.66	100.52	21.14	12.34	10.10	12.00	20.00	12.68	24.95	59.57	2.81	5.74	2.11	4.46	6.57	12.36
G8	48.00	51.00	45.66	158.26	64.59	90.72	75.60	15.34	14.52	12.60	10.00	18.00	13.86	22.53	53.64	2.12	4.32	2.55	5.33	7.88	12.67
G9	49.00	53.00	48.74	192.21	78.34	120.58	98.84	17.40	13.45	12.05	12.00	18.00	15.12	26.37	57.63	2.77	5.59	2.65	5.42	8.07	12.87
G10	50.00	54.00	47.83	145.22	63.33	122.72	104.00	13.12	12.54	13.19	12.00	19.00	13.16	28.68	62.88	2.91	5.91	2.38	4.68	7.06	11.65
G11	46.00	49.00	45.37	187.13	69.11	102.11	80.40	21.74	12.19	9.45	10.00	16.00	12.78	26.84	53.41	2.25	4.61	2.12	4.42	6.54	11.89
G12	45.00	49.00	52.37	161.31	62.12	157.18	128.84	16.92	13.05	11.89	12.00	20.00	14.25	32.57	60.67	3.61	7.27	2.67	5.34	8.01	12.93
G13	45.00	48.00	47.32	179.15	65.41	77.31	60.40	22.87	11.11	8.57	10.00	15.00	13.12	18.86	46.84	1.69	3.52	2.08	4.23	6.31	10.87
G14	44.00	47.00	47.89	173.28	67.13	70.56	56.00	20.77	11.37	9.14	10.00	13.00	13.21	19.35	44.92	1.57	3.25	2.12	4.51	6.63	12.34
G15	47.00	51.00	42.34	164.44	62.23	71.42	55.80	22.68	11.94	8.24	10.00	15.00	14.11	18.76	50.43	1.56	3.21	2.45	5.27	7.72	13.24
GM	46.00	50.00	46.88	170.24	68.08	107.12	86.2	19.75	12.61	10.85	10.00	17.00	13.71	24.28	54.52	2.41	4.91	2.33	4.85	7.18	12.16
Min.	43.00	46.00	35.33	145.22	62.12	70.56	55.8	13.12	10.14	8.13	10.00	13.00	12.43	18.35	43.91	1.56	3.21	2.04	4.23	6.27	10.21
Max.	50.00	54.00	56.71	195.17	79.42	157.18	128.84	23.38	15.38	14.19	14.00	20.00	16.23	32.57	62.88	3.61	7.27	2.73	5.42	8.07	13.45
CV(%)	2.99	2.70	2.44	2.64	1.95	3.18	3.18	2.77	2.29	2.86	2.27	2.90	2.42	3.30	2.39	2.93	2.73	2.96	2.46	2.87	2.22
S.E	0.80	0.78	0.66	2.6	0.77	1.92	1.59	0.32	0.17	0.18	0.15	0.28	0.19	0.46	0.75	0.04	0.08	0.04	0.07	0.12	0.16
F test	**	**	**	**	**	**	**	**	**	**	**	**	**	**	**	**	**	**	**	**	**

**Significant at 1% level, *Significant at 5% level; GM, Grand Mean; CV, Coefficient of Variance; SE, Standard Error

Table 3. Estimation of variability parameters for morphological traits of 15 sweet corn genotypes

Traits	DFT	DFS	CHL	PH	EH	EWH	EW	HR	EL	EG	NRPE	NKPR	TSS	100KW	SP	CYP	FYP	RS	NRS	TS	ST
PCV(%)	4.87	4.92	10.60	8.78	8.06	27.50	28.75	17.00	11.46	20.99	12.90	13.63	8.18	19.29	11.73	28.72	28.06	10.49	9.18	9.26	7.46
GCV (%)	3.84	4.10	10.31	8.38	7.82	27.33	28.57	16.77	11.23	20.79	12.70	13.32	7.81	19.01	11.49	28.57	27.87	10.07	8.84	8.80	7.11
h ² (%)	62.28	69.8	94.67	90.97	94.12	98.72	98.77	97.33	96.02	98.14	96.80	95.47	91.27	97.07	95.86	98.96	99.05	92.06	92.8	90.41	91.11
GAM (%)	6.25	7.07	20.68	16.46	15.63	55.95	58.50	34.09	22.67	42.44	25.76	26.80	15.38	38.58	23.17	58.55	57.14	19.90	17.55	17.25	13.99

DFT, Days to 50% Tasseling; DFS, Days to 50% Silking; CHL, Chlorophyll content; PH, Plant Height; EH, Ear Height; EWH, Ear Weight with Husk; EW, Ear Weight without Husk, HR, Husk Ratio; EL, Ear Length; EG, Ear Girth; NRPE, Number of Rows Per Ear; NKPR, Number of Kernels per Row; TSS, Total Soluble Solids; 100KW, 100 Kernel Weight, SP, Shelling percentage; CYP, Cob Yield per Plot; FYP, Fodder Yield per Plot; RS, Reducing Sugar; NRS, Non-Reducing Sugar; TS, Total Sugar; ST, Starch; PCV, Phenotypic Coefficient of variation, GCV, Genotypic Coefficient of Variation; h², Heritability; GAM, Genetic Advance as per cent of mean

Table 4. Phenotypic correlation coefficients of different plant traits among 15 sweet corn genotypes

Traits	DFT	DFS	CHL	PH	EH	EWH	EW	HR	EL	EG	NRPE	NKPR	TSS	100KW	SP	FYP	RS	NRS	TS	ST	CYP	
DFT	1.00																					
DFS	0.72**	1.00																				
CHL	-0.01	0.02	1.00																			
PH	-0.19	-0.14	-0.02	1.00																		
EH	-0.07	-0.01	-0.05	0.74**	1.00																	
EWH	0.08	0.11	0.76**	-0.14	-0.02	1.00																
EW	0.14	0.18	0.76**	-0.18	-0.03	0.99**	1.00															
HR	-0.47	-0.49	-0.44	0.38	0.16	-0.47	-0.54*	1.00														
EL	0.05	0.06	0.64**	-0.03	0.06	0.66**	0.67**	-0.52*	1.00													
EG	0.17	0.17	0.64**	-0.14	0.06	0.74**	0.77**	-0.76**	0.86**	1.00												
NRPE	0.04	0.04	0.53*	0.12	0.27	0.74**	0.73**	-0.37	0.63*	0.78**	1.00											
NKPR	0.30	0.31	0.58*	-0.36	-0.26	0.84**	0.85**	-0.53*	0.65**	0.65**	0.53*	1.00										
TSS	0.13	0.20	0.41	0.07	0.31	0.31	0.32	-0.16	0.23	0.16	0.07	0.12	1.00									
100KW	0.17	0.23	0.73**	-0.07	0.04	0.91**	0.92**	-0.56*	0.57*	0.67**	0.58*	0.72**	0.41	1.00								
SP	0.29	0.37	0.61*	-0.05	0.04	0.84**	0.85**	-0.57*	0.70**	0.77**	0.80**	0.79**	0.16	0.80**	1.00							
FYP	0.14	0.17	0.77**	-0.18	-0.04	0.99**	0.99**	-0.54*	0.67**	0.77**	0.72**	0.85**	0.32	0.93**	0.85**	1.00						
RS	0.23	0.30	0.56	-0.24	-0.05	0.57*	0.61*	-0.66**	0.65**	0.62*	0.33	0.55*	0.64**	0.59*	0.49	0.61*	1.00					
NRS	0.17	0.29	0.40	0.12	0.24	0.40	0.41	-0.41	0.59*	0.46	0.34	0.33	0.66**	0.45	0.48	0.41	0.77**	1.00				
TS	0.21	0.30	0.46	0.02	0.16	0.47	0.50	-0.51*	0.62*	0.55*	0.34	0.42	0.66**	0.52*	0.49	0.50	0.85**	0.93**	1.00			
ST	0.05	0.17	0.62	-0.03	-0.04	0.47	0.47	-0.26	0.61*	0.37	0.25	0.44	0.54*	0.48	0.46	0.47	0.67**	0.74**	0.72**	1.00		
CYP	0.14	0.17	0.76**	-0.18	-0.03	0.99**	0.99**	-0.55*	0.67**	0.77**	0.73**	0.85**	0.32	0.93**	0.84**	0.99**	0.61*	0.41	0.51	0.46	1.00	

*significance at 5% level **significance at 1% level

Table 5. Partitioning of phenotypic correlation coefficients into direct and indirect effects on cob yield per plot in sweet corn by path coefficient analysis

Traits	DFT	DFS	CHL	PH	EH	EWH	EW	HR	EL	EG	NRPE	NKPR	TSS	100KW	SP	FYP	RS	NRS	TS	ST
DFT	-0.003	-0.005	0.019	-0.041	0.004	0.091	0.004	-0.001	-0.081	-0.006	-0.063	-0.031	-0.001	0.001	-0.006	0.001	-0.006	-0.005	-0.006	-0.003
DFS	-0.004	-0.008	0.023	-0.011	0.003	0.064	0.008	-0.002	-0.067	-0.005	-0.061	-0.021	-0.003	0.003	-0.003	0.002	-0.003	-0.006	-0.006	-0.002
CHL	-0.001	-0.003	-0.065	-0.002	0.003	-0.013	-0.001	-0.031	-0.008	-0.053	0.002	-0.003	-0.003	0.004	-0.073	0.013	-0.007	-0.001	-0.001	-0.004
PH	-0.001	-0.002	-0.007	0.268	-0.045	0.031	0.109	0.020	0.036	0.022	-0.063	-0.063	-0.001	0.002	-0.063	0.231	-0.034	-0.008	-0.033	-0.013
EH	0.001	-0.003	-0.021	0.011	-0.058	-0.131	-0.091	0.103	0.086	0.153	-0.031	-0.077	-0.001	0.073	-0.073	-0.078	-0.043	-0.009	-0.003	-0.018
EWH	-0.002	-0.004	-0.062	0.143	-0.013	0.214	0.113	-0.006	0.017	0.131	-0.021	0.231	-0.001	0.141	0.053	0.131	-0.081	-0.007	-0.019	-0.021
EW	-0.021	-0.037	-0.062	0.138	0.063	0.171	0.194	-0.008	0.143	0.206	0.090	0.111	-0.003	0.136	0.061	0.111	-0.073	-0.031	-0.016	-0.024
HR	-0.02	-0.043	0.041	0.008	-0.037	-0.084	-0.097	-0.003	-0.091	0.001	-0.036	-0.067	-0.003	0.083	-0.006	-0.091	-0.008	-0.021	-0.006	-0.011
EL	-0.001	-0.001	-0.074	0.073	-0.131	0.081	0.094	-0.006	0.209	-0.057	-0.043	0.143	-0.081	0.031	-0.031	0.031	-0.031	-0.011	-0.008	-0.021
EG	-0.001	-0.006	-0.067	-0.003	-0.066	0.103	0.121	-0.121	-0.219	0.131	0.102	0.114	-0.091	0.121	0.093	0.043	-0.041	-0.006	-0.007	-0.031
NRPE	-0.001	-0.002	-0.002	-0.003	-0.009	-0.008	-0.004	-0.001	-0.118	0.122	-0.073	-0.032	-0.008	0.061	-0.081	-0.063	-0.081	-0.003	-0.004	-0.031
NKPR	-0.031	-0.057	-0.169	0.012	0.231	0.140	0.119	-0.216	0.341	0.126	-0.036	0.009	-0.051	0.246	-0.186	0.009	-0.039	-0.006	-0.003	-0.008
TSS	-0.001	-0.002	-0.023	-0.037	-0.083	-0.101	-0.068	-0.088	0.134	-0.135	-0.008	-0.063	0.131	-0.137	-0.031	-0.073	0.087	0.096	0.081	-0.111

Traits	DFT	DFS	CHL	PH	EH	EW	HR	EL	EG	NRPE	NKPR	TSS	100KW	SP	FYP	RS	NRS	TS	ST	
100KW	-0.021	-0.055	-0.093	0.078	-0.181	0.212	0.246	0.033	0.081	0.213	-0.081	0.107	-0.031	0.186	0.031	0.038	-0.062	-0.006	-0.007	-0.007
SP	-0.032	-0.063	-0.078	-0.007	-0.024	-0.100	-0.081	-0.043	0.061	-0.131	-0.074	-0.010	-0.043	0.123	0.008	-0.074	-0.054	-0.003	-0.004	-0.006
FYP	-0.024	-0.049	-0.199	0.173	0.048	0.168	0.121	0.078	0.073	-0.031	-0.081	-0.051	-0.063	0.121	0.073	0.213	-0.051	-0.004	-0.003	-0.004
RS	-0.001	-0.002	-0.034	-0.034	-0.073	0.017	0.023	-0.061	-0.043	-0.053	-0.081	-0.071	0.063	0.091	-0.036	-0.073	-0.073	0.081	0.076	-0.102
NRS	-0.002	-0.004	-0.087	-0.007	-0.089	0.028	0.069	-0.032	-0.061	-0.063	-0.013	-0.081	0.113	0.093	-0.087	-0.089	0.063	-0.076	-0.063	-0.108
TS	-0.002	-0.005	-0.033	-0.016	-0.036	0.006	0.052	-0.031	-0.054	-0.057	-0.031	-0.093	0.121	0.086	-0.093	-0.061	0.071	0.073	-0.068	-0.100
ST	-0.003	-0.005	-0.011	-0.043	-0.041	0.036	0.125	-0.081	-0.081	-0.091	-0.061	-0.103	0.136	0.099	-0.193	-0.091	0.086	0.093	0.081	0.122

Residual effect = 0.213; DFT, Days to 50% Tasseling; DFS, Days to 50% Silking; CHL, Chlorophyll content; PH, Plant Height; EH, Ear Height; EWH, Ear Weight with Husk; EW, Ear Weight without Husk, HR, Husk Ratio; EL, Ear Length; EG, Ear Girth; NRPE, Number of Rows Per Ear; NKPR, Number of Kernels per Row; TSS, Total Soluble Solids; 100KW, 100 Kernel Weight, SP, Shelling percentage; CYP, Cob Yield per Plot; FYP, Fodder Yield per Plot; RS, Reducing Sugar; NRS, Non-Reducing Sugar; TS, Total Sugar; ST, Starch

A significant difference in grain yield has been reported by Bista et al., [15], Neupane et al., [14], Total sugar percentage of genotypes were recorded between 6.27 (G1) and 8.07 (G9) with an average percentage of 7.18. To produce high yielding sweet corn hybrid / inbred along with higher sugar content, G12 and G9 genotypes combinations could be used in the future breeding programme.

3.2 Estimation of Genetic Parameters

The enhancement of crop output is contingent upon the level of genetic variability within the breeding material and the heritability of the component variables that determine yield across successive generations. Under those circumstances, it is necessary to divide the observed variability between components that can be inherited and those that cannot be inherited. This can be achieved by utilizing genetic factors such as PCV (phenotypic coefficient of variation), GCV (genotypic coefficient of variation), heritability and GAM (genetic advance as per cent of mean). In this present study, the genotypic coefficient of variation (GCV) was less than its corresponding estimates of the phenotypic coefficient of variation (PCV) for all the traits which indicated a significant role of the environment in the expression of these traits (Table 3). High phenotypic and genotypic coefficient of variation values were observed for cob yield per plot, ear weight with husk and ear weight without husk, implying selection for these traits will be effective due to presence of a high amount of variability and thus the phenotypic selection of these traits would be rewarding. This accordance with the findings of Bista et al., [15] for grain yield and Islam et al., [16] for thousand kernel weight and yield per plant. Moderate phenotypic and genotypic coefficient of variation values were observed for 100 kernel weight, ear length, chlorophyll concentration, husk ratio, number of rows per ear, number of kernels per row, shelling percentage and reducing sugar, which is indicating the fair level of scope for phenotypic selection. Similar results was reported by Islam et al., [16] for kernel numbers per row and kernel weight. Low phenotypic and genotypic coefficient of variation were found for the traits viz., days to 50% tasseling, days to 50% silking, total soluble solids, non-reducing sugar, total sugar and starch content. Hence it can be concluded that direct phenotypic selection for these traits may not be rewarding. Similar reports were reported

by Bista et al., [15] for anthesis days, silking days, plant height, number of rows per kernel and cob diameter.

Estimates of heritability should be considered in conjunction with genetic advance to predict the effect of selecting superior crop varieties. In this experiment, all the traits were recorded high heritability whereas genetic advance was varies from high to low. High heritability coupled with high GAM were noticed for the traits, ear weight with husk, ear weight without husk, husk ratio, chlorophyll content, ear length, ear girth, number of rows per ear, number of kernels per row, 100 kernel weight, shelling percentage, cob yield per plot and fodder yield per plot. Bista et al., [15] reported high heritability coupled with high GAM. High heritability and low GAM were noticed for days to 50% tasseling and days to 50% silking. Similarly, Bista et al., [15] reported high heritability coupled with low GAM for anthesis days, silking days and plant height.

3.3 Correlation Coefficient

The phenotypic correlation coefficient of cob yield and yield-attributing characters are shown in both positive and negative correlations were reported in Table 4. Cob yield was found significant and positive correlation with chlorophyll concentration (0.76**), ear weight with husk (0.99**), ear weight without husk (0.99**), ear length (0.67**), ear girth (0.77**), number of rows per ear (0.73**), number of kernels per row (0.85**), 100 kernel weight (0.93**), shelling percentage (0.84**), fodder yield per plot (0.99**) and reducing sugar (0.61**). Similar findings was reported by Islam et al., 2020 for plant height, ear girth, kernel numbers per row, thousand kernel weight and kernel width. Husk ratio was found significant and negative correlation with cob yield. Days to 50% tasseling, days to 50% silking, total soluble solids, non-reducing sugar, total sugar and starch content were recorded positive correlation with cob yield. Whereas the plant height and ear height were found negative correlation with cob yield. For total sugar content significant and positive correlation were observed with ear length, ear girth, total soluble solids, 100 kernel weight, reducing sugar and non-reducing. Ear weight, ear girth and number of kernels per row had significant and positive correlation with chlorophyll content, ear weight with husk, ear length, number of rows per ear, 100 kernel weight, shelling percentage, fodder yield per plot and reducing sugar. Whereas for the same traits

significant and negative correlation were observed with husk ratio.

3.4 Estimation of Path Coefficient

Path coefficient analysis distinguishes between direct and indirect effects of correlation coefficients. Among all the traits, plant height had positive direct effect with cob yield per plot followed by ear weight with husk, ear weight without husk, ear length, ear girth, number of kernel per row, total soluble solids 100 kernel weight, shelling percentage, fodder yield per plot and starch, indicating the selection for these characters is likely to bring about an overall improvement in grain yield directly. Similar result was found by Islam et al., [16] for ear girth, kernel numbers per row, thousand kernel weight, kernel width and kernel thickness. The high positive indirect effect on cob yield per plot was from number of kernels per row via 100 kernel weight followed by ear weight without husk, ear weight with husk and plant height. Selection for these traits would be effective indirectly in enhancing the yield potential of sweet corn hybrids (Table 5).

Table 6. Grouping of 15 genotypes of sweet corn in different clusters based on their agromorphological traits

Clusters	Total Genotypes
Cluster 1	4 (G5, G13, G14, G15)
Cluster 2	2 (G4, G9)
Cluster 3	2 (G11, G3)
Cluster 4	3 (G12, G2, G6)
Cluster 5	2 (G10, G7)
Cluster 6	1 (G1)
Cluster 7	1 (G8)

3.5 Cluster Analysis

An initial stage in breeding efforts is often the examination of genotype diversity. The multivariate analysis based on Mahalanobis statistic [17] is a distinctive approach for evaluating the genetic divergence among biological populations and assessing the contributions of desirable features and agronomic values to the overall divergence. A hierarchical clustering technique was employed to discern the genetic variances among 15

Table 7. Cluster means for twenty one traits studied in sweet corn genotypes

Trait	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 7
DFT	46.00	46.00	47.00	49.00	46.00	45.00	46.00
DFS	48.00	49.00	50.00	52.00	49.00	49.00	50.00
CHL	35.33	48.94	45.52	48.28	54.54	44.70	46.27
PH	160.02	168.83	172.70	172.89	157.75	170.30	195.17
EH	68.21	65.79	66.85	71.27	64.72	66.27	79.42
EWH	74.88	132.47	96.41	119.61	155.54	75.14	103.68
EW	58.50	104.48	78.00	99.44	126.98	59.05	81.00
HR	23.11	21.36	18.54	15.40	17.60	22.15	23.38
EL	10.14	13.86	13.35	13.17	13.66	11.42	12.08
EG	8.13	12.11	11.03	13.14	12.57	8.56	9.53
NRPE	10.00	13.00	10.00	13.00	12.00	10.00	12.00
NKPR	14.00	20.00	17.00	18.00	20.00	15.00	15.00
TSS	13.30	12.56	13.32	13.84	15.24	13.33	15.21
100KW	18.35	25.05	24.69	26.80	31.95	19.06	25.86
SP	43.91	60.64	53.53	59.98	58.89	47.58	57.47
CYP	1.64	2.92	2.18	2.78	3.56	1.65	2.27
FYP	3.36	5.93	4.47	5.63	7.18	3.41	4.59
RS	2.04	2.19	2.34	2.49	2.70	2.21	2.16
NRS	4.23	4.65	4.88	5.05	5.24	4.64	5.32
TS	6.27	6.84	7.21	7.53	7.94	6.85	7.48
ST	10.21	12.40	12.28	12.09	13.19	11.98	12.35

DFT, Days to 50% Tasseling; DFS, Days to 50% Silking; CHL, Chlorophyll content; PH, Plant Height; EH, Ear Height; EWH, Ear Weight with Husk; EW, Ear Weight without Husk, HR, Husk Ratio; EL, Ear Length; EG, Ear Girth; NRPE, Number of Rows Per Ear; NKPR, Number of Kernels per Row; TSS, Total Soluble Solids; 100KW, 100 Kernel Weight, SP, Shelling percentage; CYP, Cob Yield per Plot; FYP, Fodder Yield per Plot; RS, Reducing Sugar; NRS, Non-Reducing Sugar; TS, Total Sugar; ST, Starch

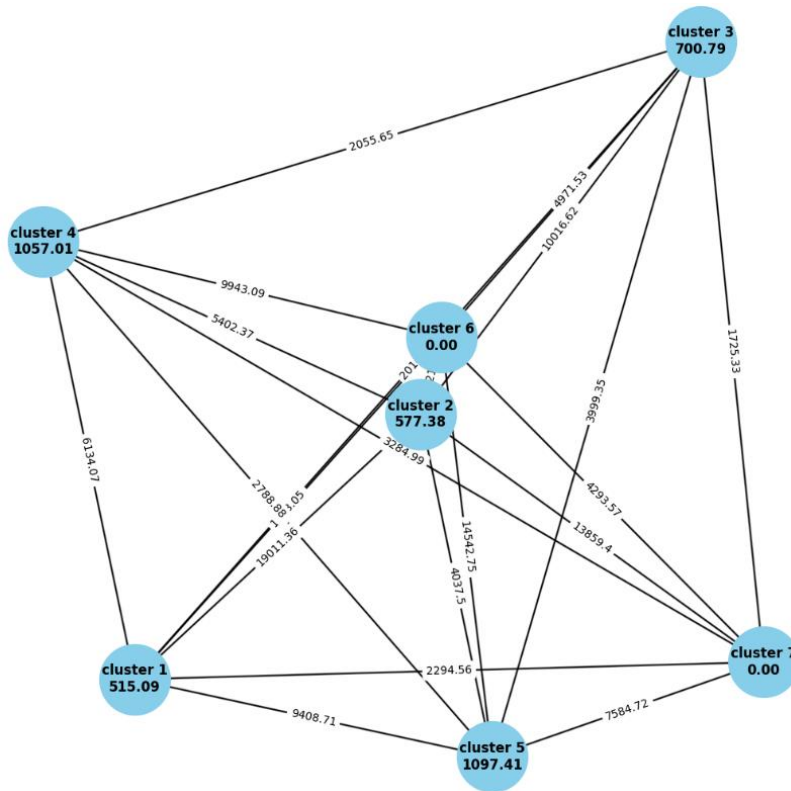


Fig. 1. Intra and inter cluster distance

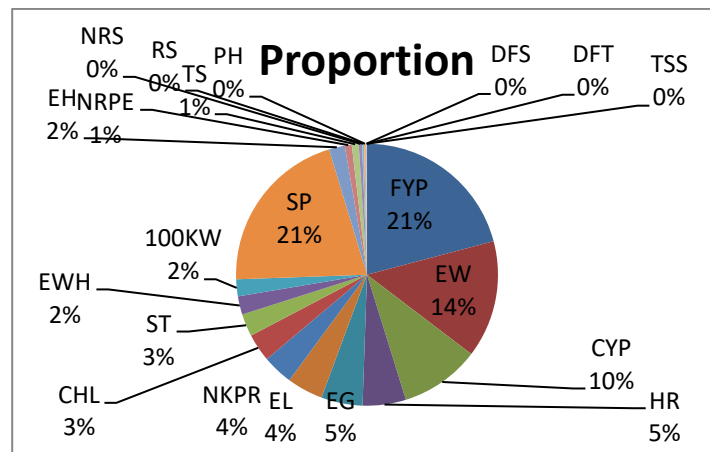


Fig. 2. Contribution of individual traits towards divergence

DFT, Days to 50% Tasseling; DFS, Days to 50% Silking; CHL, Chlorophyll content; PH, Plant Height; EH, Ear Height; EWH, Ear Weight with Husk; EW, Ear Weight without Husk, HR, Husk Ratio; EL, Ear Length; EG, Ear Girth; NRPE, Number of Rows Per Ear; NKPR, Number of Kernels per Row; TSS, Total Soluble Solids; 100KW, 100 Kernel Weight, SP, Shelling percentage; CYP, Cob Yield per Plot; FYP, Fodder Yield per Plot; RS, Reducing Sugar; NRS, Non-Reducing Sugar; TS, Total Sugar; ST, Starch

genotypes of sweet corn. Total 15 genotypes were classified into seven clusters on the basis of their genetic distance (Tocher's method) (Table 6). Cluster 1 was contained four genotypes namely G5, G13, G14 and G15 [18,19]. Since four genotypes from the same cluster are likely

less varied from one another than those in other clusters. So matting between these genotypes won't produce necessary heterotic response. The cluster 4 (G12, G2, G6) had three genotypes. Cluster 2 (G4, G9), cluster 3 (G11, G3) and cluster 5 (G10, G7) had two genotypes each.

Whereas the cluster 6 (G1) and cluster 7 (G8) had only one genotype each. Similarly Islam et al., 2020 reported three clusters of 13 maize genotypes under his study and Shrestha et al., 2013 reported six cluster using 60 maize inbreds. In order to get desired outcome, diverse parents should be chosen from various clusters in the breeding programmes [20].

Fig. 1. displayed distances within and between clusters. The intra cluster distances varies from 1097.41 (cluster 5) to 0.00 (cluster 6, 7). The maximum inter cluster distance (25921.29) was observed between cluster 2 and 6, followed by (19011.36) cluster 1 and 2. Which showed that maximum divergence existed between cluster 2 and 6. The minimum inter cluster distance (1393.05) was found between cluster 1 and 6. According to the cluster means of 21 traits shown in Table 7, cluster 5 showed maximum mean values for almost all the characters viz., chlorophyll concentration (54.54), ear weight with husk (155.54), ear weight without husk (126.98), number of kernels per row (20.00), total soluble solids (15.24), 100 kernel weight (31.95), cob yield per plot (3.56), fodder yield per plot (7.18), reducing sugar (2.70), total sugar (7.94) and starch content (13.19). Followed by cluster 2 for traits ear length (13.86), number of rows per ear (13.00), number of kernels per row (20.00) and shelling percentage (60.64). For earliness traits cluster 6 showed minimum days to 50% tasseling, cluster 1 had showed minimum days to 50% silking and cluster 7 showed minimum husk ratio (23.38).

Information on the percentage of divergence of each character under study in relation to total divergence was presented in the Fig. 2. The highest contribution for divergence was found to the traits fodder yield per plot (21%) and shelling percentage (21%) followed by ear weight (14%) and cob yield per plot (10%). Whereas the remaining 17 traits were given negligible divergence [21,22].

4. CONCLUSION

From the morphological characterization, it can be inferred that to produce high yielding sweet corn hybrids / inbreds along with higher sugar content, G12 and G9 could be used separately / combination in the future breeding programme.

High heritability along with high GAM was observed for ear weight with husk, ear weight without husk, ear length, ear girth, number of kernels per row, 100 kernel weight, shelling percentage and fodder yield per plot. Also for the above mentioned traits correlation analysis showed significant and positive correlation along with positive direct effect in path. These results confirmed the presence of significant relationships between the corresponding plant traits and cob yield. Thereby, direct selection for these traits would result in enhancement of grain yield in the sweet corn breeding programme.

Assessment of genetic diversity also provides the breeder an opportunity to identify the gaps in the collection. Therefore, the present findings showed wider genetic diversity among the genotypes of different groups. Divergence study suggested that genotypes belonging to clusters 5 showed maximum mean values for almost all the traits s, So cluster 5 genotypes may be used as suitable parents to enhance grain yield with enhanced sugar per cent in the future hybridization programme.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

I hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of manuscripts.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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