

## Original Research Article

# **Morphological characterization and genetic diversity analyses of yield and yield attributing traits in sweet corn (*Zea mays var. saccharata*)**

## **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 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.

**Key words :** Genetic variability, Diversity, Correlation, Path coefficient and Clustering

## **INTRODUCTION**

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 (Hannah *et al.*, 1993). 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 (Mahato *et al.*, 2021). The initial stage in the depiction and categorization of germplasm is morphological characterization (Smith and Smith, 1989).

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

(Pena *et al.*, 2012), 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 (Silva *et al.*, 2013). 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 (Singh *et al.*, 2017; Saha *et al.*, 2019). 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 (Roy *et al.*, 2018). 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 (Roy *et al.*, 2018; Rocha *et al.*, 2019). Correlation and path coefficient analyses can be used to discover the specific features that can be improved to enhance the multidimensional character of yield (Rocha *et al.*, 2019). 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 (Singh *et al.*, 2020; Kumari *et al.*, 2017).

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.

## **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).

**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 |

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.

## RESULTS AND DISCUSSION

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.* 2020.

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

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

| G/T    | DFT   | DFS   | CHL   | PH     | EH    | 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  |
| SE     | 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    | 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 <sup>2</sup> (%) | 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; h<sup>2</sup>, Heritability; GAM, Genetic Advance as per cent of mean

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.

A significant difference in grain yield has been reported by Bista *et al.*, 2022; Neupane *et al.*, 2020. 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.

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).

Estimation of Genetic Parameters (**Table 3**) : 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.

High phenotypic and genotypic coefficient of variation values were observed for cob yield per plot, eat 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.*, 2022 for grain yield and Islam *et al.*, 2020 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.*, 2020 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.*, 2022 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.*, 2022 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.*,

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    | <b>-0.003</b> | -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        | <b>-0.008</b> | 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        | <b>-0.065</b> | -0.002       | 0.003         | -0.013       | -0.001       | -0.031        | -0.003       | -0.008       | -0.053        | 0.002        | -0.003       | 0.004        | -0.073       | 0.013        | -0.007        | -0.001        | -0.001        | -0.004       |
| PH     | -0.001        | -0.002        | -0.007        | <b>0.268</b> | -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        | <b>-0.058</b> | -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        | <b>0.214</b> | 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        | <b>0.194</b> | -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       | <b>-0.003</b> | -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        | <b>0.209</b> | -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       | <b>0.131</b> | 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        | <b>-0.073</b> | -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        | <b>0.009</b> | -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       | <b>0.131</b> | -0.137       | -0.031       | -0.073       | 0.087         | 0.096         | 0.081         | -0.111       |
| 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       | <b>0.186</b> | 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        | <b>0.008</b> | -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        | <b>0.213</b> | -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       | <b>-0.073</b> | 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         | <b>-0.076</b> | -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         | <b>-0.068</b> | -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         | <b>0.122</b> |

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

2022 reported high heritability coupled with low GAM for anthesis days, silking days and plant height.

**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.

**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.*, 2020 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**).

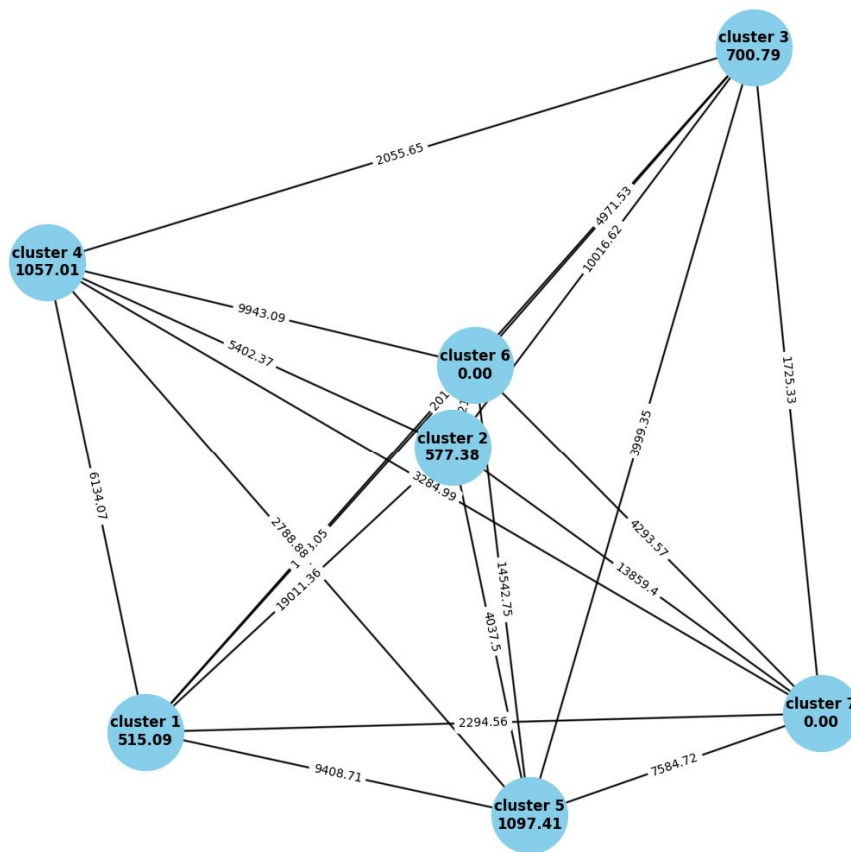
**Cluster analysis :** An initial stage in breeding efforts is often the examination of genotype diversity. The multivariate analysis based on Mahalanobis statistic (1936) is a distinctive approach for evaluating the genetic divergence among biological populations and assessing the contributions of desirable features and agronomic values to the overall divergence. A hierarchical clustering technique was employed to discern the genetic variances among 15 genotypes of sweet corn.

Total 15 genotypes were classified into seven clusters on the basis of their gentic distance (Tocher's method) (**Table 6**). Cluster 1 was contained four genotypes namely G5, G13, G14 and G15. 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.

**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)                |



**Figure 1: Intra and inter cluster distance**

**Figure 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).

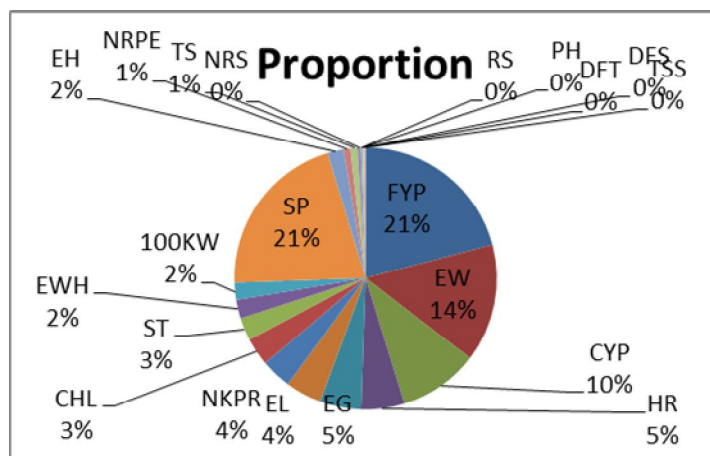
**Table 7: Cluster means for twenty one traits studied in sweet corn genotypes**

| 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

Information on the percentage of divergence of each character under study in relation to total divergence was presented in the **figure 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.



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

**Figure 2: Contribution of individual traits towards divergence**

## CONCLUSION

By the morphological characterization from this study, it can be inferred that to produce high yielding sweet corn hybrids / inbreds along with higher sugar content, G12 and G9 genotypes combinations could be used 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 path coefficient analysis positive direct effect. 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 of identifying potential yield contributing plant traits along with high level of genetic diversity among the genotypes would be beneficial for maize genotype characterization, conservation and planning for further maize breeding program for enhanced yield potential.

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