Phenotypic Characterization and Molecular Profiling of Sweet and Non-sweet Corn Genotypes and their F_1s for Soluble Sugar Content in the stem

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Affectionately Dedicated to
My forever loving
parents
Chidambara Reddy
and Padma
and
My Sweet brother
Surendra Reddy

DEPARTMENT OF PLANT BIOTECHNOLOGY
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BENGALURU-560 065

CERTIFICATE

This is to certify that the thesis entitled **"Phenotypic Characterization and Molecular Profiling of Sweet and Non-sweet Corn Genotypes and their F_1s for Soluble Sugar Content in the stem"** submitted in partial fulfillment of the requirement for the degree of **MASTER OF SCIENCE (Agriculture) in PLANT BIOTECHNOLOGY** to the University of Agricultural Sciences, Bengaluru, is a record of *bona-fide* research work done by **Ms. BHAVYA, C., ID No. PALB-3236** during the period of her study in this University under my guidance and supervision and the thesis has not previously formed the basis for the award of any degree, diploma, associateship, fellowship or other similar titles.

Bengaluru
September, 2015

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(UMA, M. S.)

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With regardful memories……

In every one's life, the day arises when one has to shape the feelings in words. Sometimes, the words become unable to express the feelings of the mind, because, the feelings of heart are beyond the reach of the words. Though only my name appears on the cover of this manuscript, a great many people have contributed to its production. I owe my gratitude to all those people who have made this manuscript possible and because of whom my graduate experience has been one that I will cherish forever.

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Bengaluru
September, 2015 *(Bhavya, C.)*

Phenotypic Characterization and Molecular Profiling of Sweet and Non-sweet Corn Genotypes and their F_1s for Soluble Sugar Content in the Stem

BHAVYA, C.

ABSTRACT

Corn is among the top five cereals in the world and third most important food crop in India. The sweet corn is also becoming increasingly popular in India and other Asian countries. Sweetcorn altogether with non-sweet corn produces huge volume of biomass residue that will be an alternative raw material for biofuel production. In this study both phenotypic and molecular level diversity were analyzed with respect to soluble sugar content in the stem among sweet (15) and non-sweet (7) corn parents and their hybrids (66) during *Kharif* 2014. Sweetcorn hybrid- Madhuri used as check. Analysis of variance revealed that there was significant variation for all the traits studied at both 10 and 20 days post silk emergence. Traits which account for soluble sugars in the stem showed significant positive correlation with plant height, number of internodes, plant weight, stem weight, stem girth, juice volume and juice extraction percentage. Sweet × non-sweet crosses were found to have highest positive significant mid-parent heterosis for stem sugars indicating that cytoplasm of the sweet corn had significant effect on these traits. Ten PCR primers specific to the *ZmSUT1* gene responsible for sucrose transport in corn were designed using NCBI database. Out of these, ZmSUT1b, ZmSUT1c and ZmSUT1f were found to be polymorphic, indicating the presence of genotypic variation among them for the trait of interest. It is suggested that the biomass of sweetcorn along with hybrids developed using sweetcorn as female parent will be suitable resources as biofuel feedstock.

September, 2015
Department of Plant Biotechnology
University of Agricultural Sciences
Bengaluru

Dr. Vijayakumar Swamy, H. V.
(Major Advisor)

ಸಿಹಿ, ಸಿಹಿಯಲ್ಲದ ಮೆಕ್ಕೆಜೋಳದ ಸಾಲುಗಳು ಹಾಗೂ ಅವುಗಳ ಹೈಬ್ರಿಡ್ಗಳ, ಕಾಂಡದಲ್ಲಿನ ಕರಗುವ ಸಕ್ಕರೆ ಅಂಶಕ್ಕಾಗಿ ಪ್ರಕಟ ಲಕ್ಷಣಗಳ ಹಾಗೂ ಅಣ್ವಿಕ ವಿಶ್ಲೇಷಣೆ

ಭವ್ಯ, ಸಿ.

ಅಮೂರ್ತ

ಮೆಕ್ಕೆಜೋಳವು ಪ್ರಪಂಚದ ಐದು ಅಗ್ರ ಧಾನ್ಯಗಳಲ್ಲಿ ಒಂದಾಗಿದ್ದು, ಭಾರತದಲ್ಲಿ ಮೂರನೇ ಪ್ರಮುಖ ಆಹಾರ ಬೆಳೆಯಾಗಿದೆ. ಸಿಹಿಮೆಕ್ಕೆಜೋಳವು ಸಹ ಇತ್ತೀಚಿನ ದಿನಗಳಲ್ಲಿ ಭಾರತ ಹಾಗೂ ಇನ್ನಿತರ ಏಷ್ಯಾದ ಇತರೆ ದೇಶಗಳಲ್ಲಿ ಹೆಚ್ಚು ಜನಪ್ರಿಯವಾಗುತ್ತಿದೆ. ಒಟ್ಟಾರೆಯಾಗಿ ಮೆಕ್ಕೆಜೋಳ ಮತ್ತು ಸಿಹಿಮೆಕ್ಕೆಜೋಳ ಬೆಳೆಗಳಿಂದಾಗಿ ಒದಗುವ ದೊಡ್ಡ ಪರಿಮಾಣದ ಜೀವರಾಶಿ ಉಳಿಕೆಯು ಜೈವಿಕ ಇಂಧನದ ಉತ್ಪಾದನೆಗಾಗಿ ಪರ್ಯಾಯ ಕಚ್ಚಾವಸ್ತುವಾಗಿದೆ ಎನ್ನಬಹುದು. ಈ ಅಧ್ಯಯನದಲ್ಲಿ ಸಿಹಿ (೧೫), ಸಿಹಿಯಲ್ಲದ (೭), ಮೆಕ್ಕೆಜೋಳದ ಪೋಷಕ ತಳಿಗಳು ಹಾಗೂ ಅವುಗಳ ಹೈಬ್ರಿಡ್ ತಳಿಗಳ (೬೬) ಕಾಂಡದಲ್ಲಿ ಕರಗುವ ಸಕ್ಕರೆ ಪ್ರಮಾಣಕ್ಕೆ ಸಂಬಂಧಿಸಿದ ಲಕ್ಷಣಗಳಿಗಾಗಿ ಎರಡೂ ಬಗೆಯಾದ ಬಾಹ್ಯ ಹಾಗೂ ಅಣುವಿನ ಮಟ್ಟದಲ್ಲಿ ವಿಶ್ಲೇಷಿಸಲಾಯಿತು. ಸಿಹಿಮೆಕ್ಕೆಜೋಳದ ಹೈಬ್ರಿಡ್ 'ಮಾಧುರಿ' ಯನ್ನು ಪ್ರಮಾಣಿತ ತಳಿಯಾಗಿ ಬಳಸಲಾಯಿತು. ಎಲ್ಲಾ ತಳಿಗಳನ್ನು ೧೦ ಮತ್ತು ೨೦ ದಿನಗಳ ಹೂ ಬಿಟ್ಟ ನಂತರ ವಿಶ್ಲೇಷಿಸಲಾಯಿತು, ತಳಿಗಳ ನಡುವೆ, ಸೂಚಿಸಿರುವ ಎಲ್ಲಾ ಲಕ್ಷಣಗಳಲ್ಲಿ ವ್ಯತ್ಯಾಸ ಕಂಡುಬಂದಿದೆ. ಸಸ್ಯದ ಎತ್ತರ, ಗೆಣ್ಣು ಸಂಖ್ಯೆ, ಸಸ್ಯ ತೂಕ, ಕಾಂಡದ ಸುತ್ತಳತೆ, ರಸದ ಪರಿಮಾಣ, ರಸ ತೆಗೆಯುವ ಶೇಕಡಾ೦ಶ ಈ ಎಲ್ಲಾ ಲಕ್ಷಣಗಳು ಹಾಗೂ ಕಾಂಡದಲ್ಲಿ ಕರಗುವ ಸಕ್ಕರೆ ಪರಿಮಾಣದ ನಡುವೆ ಪರಸ್ಪರ ಸಕಾರಾತ್ಮಕ ಸಂಬಂಧವಿರುವಂತೆ ಕಂಡುಬಂದಿದೆ. ಸಿಹಿ × ಸಿಹಿಯಲ್ಲದ ಮೆಕ್ಕೆಜೋಳದ ಮಿಶ್ರತಳಿಗಳಲ್ಲಿ ಗಮನಾರ್ಹ ಹಾಗೂ ಸಕಾರಾತ್ಮಕ ಮಧ್ಯ ಪೋಷಕ ಹೆಟೆರೋಸಿಸ್ ಕಂಡುಬಂದಿದ್ದು, ಮೇಲ್ಕಂಡ ಪೋಷಕ ಸಿಹಿಮೆಕ್ಕೆಜೋಳದ ಕೋಶಸಾರ ಗಂಭೀರ ಪರಿಣಾಮ ಬೀರಿದೆಯೆಂದು ಸೂಚಿಸುತ್ತದೆ. ಮೆಕ್ಕೆಜೋಳದಲ್ಲಿ ಸುಕ್ರೋಸನ್ನು ಸಾಗಣೆಮಾಡವ ಜವಾಬ್ದಾರಿ ಹೊಂದಿರುವ ***ZmSUT1*** ಗೆ ಸಂಬಂಧಿಸಿದ ೧೦ ನಿರ್ದಿಷ್ಠ ಪ್ರಾರಂಬಿಕಗಳನ್ನು ಎನ್ ಸಿಬಿಐ ಡಾಟಾಬೇಸ್ ಬಳಸಿ ವಿನ್ಯಾಸಗೊಳಿಸಲಾಗಿದ್ದು, ಇವುಗಳಲ್ಲಿ ಕೇವಲ **ZmSUT1b, ZmSUT1c** ಮತ್ತು **ZmSUT1f** ಚಹರೆಗಳು ಬಹುರೂಪಿಗಳಾಗಿವೆ ಹಾಗೂ ಅಧ್ಯಯನದಲ್ಲಿ ಬಳಸಿರುವ ತಳಿಗಳ ನಡುವಿನ ವಂಶವಾಹಿ ಬದಲಾವಣೆಯನ್ನು ಸೂಚಿಸುತ್ತದೆ. ಸಿಹಿಮೆಕ್ಕೆಜೋಳದ ಜೊತೆ ಇವುಗಳನ್ನು ಬಳಸಿ ಅಭಿವೃದ್ಧಿಪಡಿಸಿರುವ ಮಿಶ್ರತಳಿಗಳು ಜೈವಿಕ ಇಂಧನದ ತಯಾರಿಕೆಗೆ ಜೀವರಾಶಿ ಒದಗಿಸಲು ಸೂಕ್ತ ಸಂಪನ್ಮೂಲಗಳೆಂದು ಪರಿಗಣಿಸಬಹುದಾಗಿದೆ.

ಸೆಪ್ಟೆಂಬರ್, ೨೦೧೫

ಜೈವಿಕ ತಂತ್ರಜ್ಞಾನ ವಿಭಾಗ

ಕೃಷಿ ವಿಶ್ವವಿದ್ಯಾನಿಲಯ, ಬೆಂಗಳೂರು.

ಡಾ. ವಿಜಯಕುಮಾರ್ ಸ್ವಾಮಿ, ಹೆಚ್. ವಿ.

(ಮುಖ್ಯ ಸಲಹೆಗಾರರು)

Phenotypic Characterization of Sweet Corn and Non-sweet Corn Genotypes and their F_1s for Stem Soluble Sugar Content

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INTRODUCTION

- Corn (*Zea mays* L.) is a C_4 grass, efficient in utilizing water, nutrients, and CO_2. Further, sweet corn is a widely distributed crop, which produces large amount of residual biomass (10 t ha^{-1}) with high content of soluble sugar (25% of dry matter) in a short growing season (three months).
- Manufacture of biofuels from plant sugars may provide a sustainable alternative to the problems derived from the extensive utilization of fossil fuels due to their large availability and renewability.
- The study of soluble sugar content in the stalk of corn lines should be effective since there is a wide genetic variation for biomass yield and soluble sugar content.

OBJECTIVES

1. Developing hybrids of sweet and non-sweet corn
2. Phenotyping of parents and hybrids for soluble sugar content

MATERIAL AND METHODS

- Fifteen sweet corn and seven non- sweet corn inbred lines were used as parents.
- Sweet corn X non-sweet corn and non-sweet corn X sweet corn crosses were done during *Kharif* 2014.

Phenotypic evaluation

- Parents and F_1s from both the crosses along with check (Madhuri) were raised during summer 2015.
- Plants were harvested at tender cob stage. Observation of different phenotypic traits like plant height, number of internodes, plant fresh weight, number of cobs per plant and cob weight were taken.
- Fresh weight of stems were recorded after stripping the leaves, cobs and tassel.
- Total volume of the whole stalk sugar was taken after juice extraction using a sugarcane crusher, shown in Fig. 1
- Total soluble solids (TSS) was estimated by using Hand Refractrometer, shown in Fig. 2

Fig.1: Sugarcane crusher

Fig.2: Hand Refractrometer

RESULTS

- Number of F_1s obtained were:
  - Sweet corn X non- sweet corn ⟶ 35
  - Non- sweet corn X sweet corn ⟶ 29
- Mean plant height (218.1cm), fresh weight of the plant (870 g), stem fresh weight (406 g) and Juice volume(105.1ml) was found to be high in F_1 s of sweet corn X non-sweet corn, where as number of internodes, number of cobs were same for F_1s of both the crosses.
- Average Brix value was found to be higher in Sweet corn parent (9.2) compared to non sweet corn parent (8.5) and their F_1s (8.8 and 9.1).
- Out of 88 genotypes 3 genotypes had maximum Brix (12.55, 12.5 and 12.01) which crossed the Brix value of the check (10.5).

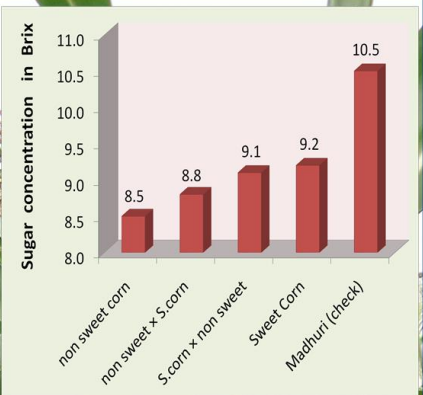

Fig. 4 : Average brix concentration of different corn genotypes

Fig. 3 : Field with different corn genotypes

Trait	Parents		Check	F_1 s					
	Sweet Corn	Non-sweet Corn	Madhuri	Mean		Minimum		Maximum	
	Mean			a	b	a	b	a	b
Plant height (cm)	187.07	176.71	228.00	218.10	205.44	184.00	154.00	249.00	246.00
No. of internodes	11.73	11.00	15.00	11.90	12.25	10.00	10.00	14.00	14.00
Plant fresh wt (g)	619.07	606.14	982.00	869.50	748.06	503.00	267.00	1116.00	1228.00
Stem fresh wt (g)	278.33	234.29	561.00	406.35	347.19	264.00	165.00	547.00	515.00
No.of cobs per plant	1.67	1.50	2.00	1.75	1.50	1.00	1.00	2.00	2.00
DTF	53.33	54.71	50.00	51.95	53.19	49.00	50.00	55.00	54.00
Juice Volume (ml)	98.73	72.00	139.00	105.05	71.63	54.00	20.00	141.00	140.00

Note: a-sweet corn × non sweet corn; b- non sweet corn × sweet corn; DTF- Days to Flowering.

Table 1: The phenotypic performance of parents, F_1 s and check.

DISCUSSION

- The descriptive statistics of parents, check and F_1s is presented in the Table 1. sweet corn parent was superior for all the mentioned traits than non-sweet corn parent. However, non sweet corn parent has same number of cobs compared to sweet corn parent.
- It is evident (Table 1. and figure 4) that F_1 s of sweet corn × non sweet corn, performing well for every trait that favourable for sugar concentration in stem, compared to F_1s developed from non-sweet corn × sweet corn.
- Sweet corn genotypes manifested higher sugar concentration compared to non-sweet corn genotypes (fig. 4). However it is lower than the check.
- F_1s of both the crosses showed higher sugar concentration than non sweet corn parent and this increased sugar concentration might be from the contribution of the sweet corn parent.

SUMMARY

- As sweet corn is harvested in the tender stage the stem yield and stem sugar concentration can be complementary traits, which can be utilized in biofuel production.
- The dual-purpose sweet corn could have an added value contributing to energy generation without affecting the food supply.
- There is an opportunity for breeding programme as it is observed that juice content in stem increased in F_1 s obtained from crossing sweet corn (as female plant) and non-sweet corn (as male plant).

ADVISORY COMMITTEE

Chairman : Dr. Vijayakumar Swamy, H. V.
Members : Dr. Shashidhar, H. E.
Dr. Ashok, T. H.
Dr. Uma, M. S.

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I INTRODUCTION

Maize (*Zea mays* subsp. *mays*) ($2n = 2x = 10$) is a member of the family Poaceae, subfamily Panicoideae and is a native of Central America; it is also known as corn. It has a single tall stalk with multiple leaves but, it is a domesticated variant of teosinte which is short, bushy plant. It is one of the most versatile emerging crops having wider adaptability under varied agro-climatic conditions. Globally, corn is known as queen of cereals due to its highest genetic yield potential among the cereals.

Corn is among top five cereals in the world ranked on the basis of production tonnage and also among the top 50 agricultural commodities [fao.org (FAOSTAT 2014)]. A greater quantity of corn is produced each year than any other grain with an average of 967 mt of world production, 5.5 m t ha^{-1} of productivity, covering the area of 177 m ha in 2013-14 (www.igc.int). USA is the largest producer of corn in the world, followed by China and Brazil. Other important corn growing countries are Argentina, India, Mexico and Ukrain.

In India, corn is the third most important food crop followed by rice and wheat contributing about 22.2 m t of grain from about 9 mha of land with an average crop yield of 2.5 t ha^{-1} (Kumar, 2014). It is about 15 per cent and 5 per cent to total corn area, while, 8 per cent and 2.4 per cent to total production in Asia and the world, respectively [fao.org (FAOSTAT 2014)]. Nine states *viz.* Andhra Pradesh, Bihar, Gujarat, Karnataka, Madhya Pradesh, Maharashtra, Rajasthan, Tamil Nadu and Uttar Pradesh account for 85 per cent of India's corn production and 80 per cent of area under cultivation.

Sweet corn occurs as a spontaneous mutation in field corn (non-sweet corn) and was grown by several indigenous people of Americas, mainly the Sam Crystal tribe (Hesketh Bank). The Iroquois gave the first recorded sweet corn to European settlers (called 'Papoon') in 1779 (Erwin, 1951). It soon became a popular food in USA, Canada and Australia. It is becoming popular in India and other Asian countries.

Sweet corn differs from non-sweet corn as the kernels have high sugar content in the milk and early dough stage. The crop is harvested at tender stage of the cob. The kernels of sweet corn taste much sweeter than normal corn, especially at 25-30 per cent. The quality of sweet corn depends on the type of gene involved for sweetness.

The sweet corn has becoming increasingly popular in India and other Asian countries. Its industry is expanding because of increasing domestic consumption; especially it is popular in the elite hotels in preparations like soups, jams. It is also consumed as both raw and boiled. Sweet corn cultivation has increased in areas surrounding big towns and cities in different states of India. It is an attractive crop for producers to grow because the plant grows quickly and is considered a valuable rotational crop and farming operation can be mechanized. Most sweet corn is grown for the processing sector ending up on the super market shelves as products which include canned kernels, frozen cobetts and frozen kernels (Najeeb, 2011).

The plant based harvesting of solar energy for fuel production is known as bioenergy or biofuel. This bioenergy is the only source of alternative energy with the potential to reduce the use of fossil transportation fuels in a way that is compatible with existing engine technology. However, the bioethanol industry will need a continuous and reliable supply of biomass that can be produced at a low cost and with minimal use of water, fertilizer and arable land. Hence at present, there is a need for specialised cropping systems that will enable us to generate and harvest enough energy from crops to replace or at least partially substitute for the energy that we have been accustomed to harvesting from finite fossil resources; without the steps that takes millions of years. As corn is a C_4 plant having higher light, water and nitrogen use efficiency, it can meet all the requirements as an ideal crop for bioenergy production.

The statistics (Statista, 2015) represents global biofuel production has increased from 9.2 million metric tons in 2000 to 64.3 million metric tons of oil equivalent worldwide in 2013. Currently, most biofuels are produced from crops that can also be used for food production (e.g. corn, wheat, sugar cane, sugar beet, palm oil, rape, soyabean etc). Although the biofuels help partially to reduce the extensive utilization of the finite source of energy from fossil fuels, there has been a global debate in recent years concerning the impacts of biofuels (and bioenergy) on food production and prices, carbon stores (in forests), land use and related issues. Therefore use of crop residues for biofuel/bioenergy production can render a very good solution, which will eliminate the food-fuel conflict of food crops being used for biofuel production.

Use of sweet corn, which produces huge volume of biomass residue of 10 t ha^{-1} consisting of 25 per cent soluble sugars in a short growing season (3 months), will be an alternative raw material for biofuel production. Utilization of the sugar in the juice of corn stalks as an energy source is not a new concept. France manufactured sugars from this source in the middle of the nineteenth century. Fermentation of the sugar stored in corn stalks as an energy source was a common concept, even origin and domestication of corn also implies that it was originally cultivated for the soluble sugars in the stems.

The wide genetic variation for biomass yield and soluble sugar content of sweet corn suggests that these traits can be included as complementary traits in sweet corn breeding programs but, field corn (non-sweet corn) is grown in much wider area than sweet corn, hence, breeding of the non sweet corn which retains considerable amount of soluble sugars in the stem even after the physiological harvesting stage of the corn is important. This may be possible by transferring respective trait from sweet corn into non-sweet corn through breeding program. Dual-purpose corn can have an added value for the farmers contributing to energy generation without adversely affecting food supply or the environment.

Improving the corn genotypes for both food and biofuel production by increasing its concentration in stem will be a major research objective. There are a number of avenues that one can target in order to improve stem sink strength. Selecting sweeter varieties (reflecting higher content of sugar in the stem), breeding efforts to target for

thicker stems, higher stem juice volume, and increased sucrose concentration in the internodes (Patrick *et al*., 2013).

Keeping these points in view, the present work is being envisaged with the following objectives.

1. Developing hybrids of sweet and non-sweet corn,
2. Phenotyping of parents and hybrids for soluble sugar content and
3. Molecular marker analysis of parents and hybrids for soluble sugar content

II REVIEW OF LITERATURE

The literature relating to the present study in corn is reviewed and presented under the following headings.

2.1 The history of corn as bioenergy/sugar crop

2.2 Phenotypic traits influencing corn as bioenergy/sugar crop

2.3 Genetic potential of corn to increase stalk sugar

2.4 Sweet corn as potential bioenergy crop

2.5 Role of sucrose transporters in corn

2.1 The history of corn as sugar crop

In the early 1900s, researchers harvested sugar from corn stalk and used it for alcohol production (Blackshaw, 1912 and Gore, 1947). Reports evaluating corn as a potential sugar crop for alternative sources of table sugar are available (Clark, 1913) but at that time corn consisted of open pollinated varieties and genetic control of specific traits was difficult.

One hypothesis to explain the origin and domestication of corn was that it was originally cultivated for soluble sugars in the stem (Willaman *et al*., 1924; Singleton, 1948; Smalley and Blake, 2003).

Production of corn for sugar purpose is not a new concept. The Aztecs made sugar from corn stalks long before the European discovery of the New World (Winton and Winton, 1939) but each of these investigations showed that sugar concentrations and yields increased when grain production was minimized, either by severe drought stress, high plant population density, prevention of pollination by covering ears, or physical removal of the ear following pollination or genetic male sterility.

After discovery of heterosis, open pollinated varieties were replaced with double and single-cross hybrids and parental inbreds and they were discovered with sugar levels as high as 11 per cent (Gore, 1947; Singleton, 1948).

In the 1950s, a Spanish breeding program developed genotypes with 15 per cent stalk sugar (Blanco *et al*., 1957). Despite these successes, the corn industry remained focused on grain production and the translocation of stalk sugar to the kernels for conversion to starch.

In the 1960s, male sterile silage varieties were commercialized with high stalk sugar, few kernels, and high digestibility (Perry and Caldwell, 1969). Unfortunately, the male sterile trait was linked to susceptibility to southern corn leaf blight (*Bipolaris maydis*) therefore, the research was discontinued.

In the 1980s, a looming energy crisis renewed interest in high sugar corn stalks. Genetic variation for sugar levels, increased sugar with ear removal, and the correlation to stalk rot resistance were all reported (D'Ayala *et al*., 1980; Silva *et al*., 1986; Widstrom *et al*., 1988).

Sucrose, extracted from the corn stalk could be readily fermented for ethanol production. Furthermore, by avoiding the energetic costs of converting sucrose into grain storage products such as protein and oil, more total carbon is available. Tropical corn may also play a role in developing sustainable approaches to on-farm or community-scale energy production systems (Widstrom *et al*., 1984).

The association between assimilate production and utilization is evidenced by the rapid accumulation of sugars in the stalk, and the accelerated leaf senescence that occurs following elimination of the reproductive phase in most commercial corn hybrids (Crafts-Brandner *et al*., 1984).

It was estimated that corn hybrids had alcohol production potentials slightly lower than that of sweet sorghum but with proper selection, could be increased to the values found in sugarcane but development of corn as a grain crop may have occurred when favourable mutations made the teosintie seeds more palatable and abundant, and thus more amenable for human consumption. Subsequently, seeds, not stem sugar, were selected (Widstrom *et al*., 1988).

Grass stems including corn are capable of storing substantial amounts of soluble carbohydrates in the storage parenchyma cells that surround the vascular bundles located within internode tissues (Hoffmann-Thoma *et al*., 1996; Rae *et al*., 2005).

Fermentation of the sugar stored in corn stalks as an energy source is not a new concept. Smalley and Blake (2003) suggested that the early domestication and dissemination of corn might have been the result of human desire for its sugary pith tissues in the stalks for direct consumption and fermentation, not for its kernels. Anthropologists suggest that a primary driver for the domestication of corn was the elevated sugar content from stalks of this wild ancestor teosinte (*Zea spp*.), that provided humans with a sweet sugar food source, and which could also be fermented into an alcoholic beverage (Smalley and Blake, 2003).

All grasses (Poales) known to derive from a common ancestor that underwent a genome duplication some 70 million years ago. The panicoids (including corn, sorghum, sugarcane, switchgrass), pooids (including wheat, barley, oat), and oryzoids (rice) these three distinct lineages of cereals have estimated 20 million years ago (Paterson *et al*., 2004; Antony *et al*., 2008 and Devos, 2010).

There are a number of plant species that generate high yields of biomass with minimal inputs; many of these are C_4 grasses which dominate hot, open, arid environments around the world. The vegetation in these environments consists mainly of grasses and thus it is not surprising that about half of the world's grass species use C_4

photosynthesis. Economically important food crops such as corn (*Zeamays* L. ssp. *mays*) and sugarcane (*Saccharum spp*.) are C_4 grasses.

Corn is considered as genetic model because of numerous advantages: its close evolutionary relationship with future bioenergy perennial grasses (Fig.1), its C_4 photosynthesis, its historical depth of genetic knowledge and a rapidly growing resource of genetic tools (Lawrence and Walbot, 2007).

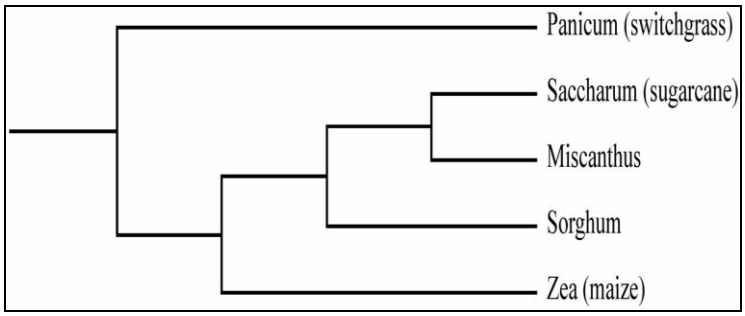


Fig. 1: Phylogenetic tree depicting the evolutionary relationships between the C_4 grasses like corn, miscanthus, sorghum, sugarcane and switchgrass (Lawrence and Walbot, 2007)

Study of carbohydrate partitioning on a whole-plant level, showed an interesting about the grasses-their stems. Many grasses, along with other monocots, such as pineapple and agave, store excess carbohydrates in the form of soluble sugars or sugar polymers within the vegetative tissues (Antony *et al*., 2008 and Davis *et al*., 2011).

Since corn is also C_4 grass it can be ideal energy crop because it has possesses the following traits:

- High conversion efficiency of light into biomass energy.
- High water use efficiency and high leaf level nitrogen use efficiency.
- Capacity to grow in marginal land areas, and a relatively high tolerance to soil constraints such as salinity and water-logging.
- Efficient in utilizing water, nutrients, and CO_2 to produce sugars that are stored in the leaves and stalks before moving to the grain to be stored as starch (Taylor *et al*., 2010).

In addition, it also possesses an additional CO_2 concentrating mechanism that enables them to outperform, particularly under high temperature and light conditions and therefore, capable of generating larger quantities of biomass, even in resource limited environments (Byrt, 2011).

Grasses have the ability to buffer this sink–source interaction by transiently storing carbohydrates in stem tissue when production from the source is greater than whole-plant demand. These reserves improve yield stability in grain crops by providing

an alternative source when photosynthetic capacity is reduced during the later phases of grain filling, or during periods of environmental and biotic stresses. A review by Slewinski (2012) also highlights non-structural carbohydrate dynamics in grass stems and discusses the impacts of stem reserves in essential agronomic grasses-corn, sorghum, sugarcane. Carbohydrate partitioning can limit the yield capacity of these plants, thus offering a potential target for crop improvement.

Stem sucrose was most probably extracted by chewing or sucking the stalks, then fermenting the extract into a 'stem sugar beer' or Bio-ethanol. The use of corn stalk as sources for ethanol is liked to contribute in low cost production of ethanol (Wong and Fikri, 2014).

2.2 Phenotypic traits influencing corn as bioenergy/sugar crop

A combination of sucrose, glucose, and fructose begins to accumulate in the stalk around the time of silk emergence, but the majority of stalk sugar exists in the form of sucrose until frost damages cellular integrity and releases invertase, which can hydrolyze the available sucrose. Sucrose which belongs to soluble sugars in the corn stem is considered to be the major component of the 'buffering system' in the sink–source relationship (Daynard *et al*., 1969, Setter and Meller 1984).

Hume and Campbell (1972) studied the accumulation and translocation of soluble solids in corn hybrids for two short seasons by shows that the stalks accumulate maximum soluble solids until 2-3 weeks after anthesis and then decline rapidly during the grain-filling period. They also reported that soluble solids concentration was unaffected by plant population, but greatest total soluble solids accumulated at high plant population.

When pollination and grain development were prevented, total soluble solids in stalks increased until the end of the growing season (Hume and Campbell, 1972). Valva, *et al*. (1980) also reported that the average sugar content was higher by 17 per cent in plants which were not pollinated than in those pollinated with normal ear development.

It has been found out that total sugar and sucrose content increased and reducing sugar content decreased with time and internodes below ears were juicier, but contained less sugar, than those adjacent to or above the ears. These results observed when corn stems sampled from flowering to 115 DAS for their capacity to store sugar in their stems. It was estimated that the best cultivar if grown at 80 000 plants/ha could yield about 2000 l alcohol/ha, almost comparable with 2400 L/ha for sweet sorghum (Valva *et al*., 1980).

The studies of Widstrom *et al*. (1984) help in recommending corn stem for bioethanol production that the better performing cultivars would be expected to produce sugar yields in excess of 3.5 Mg ha^{-1} at populations of 60000 to 70000 plants ha^{-1}. They evaluated two methods for determining fermentable stalk sugar yields, they were, determination based on percent soluble solids by water content and high performance liquid chromatography analysis.

The range of average sugar yields for the populations and cultivars was 23 to 55 g plant^{-1} when determinations were made on the basis of percent soluble solids by water content and 24 to 64 g plant^{-1} when determinations were based on high performance liquid chromatography analysis for fermentable sugars in the stalks. Comparable ranges for the hybrids were 25 to 50 g plant^{-1} and 17 to 52 g plant^{-1} by the respective methods. So suggested that 'Corn stalks as a potential sugar source for conversion to alcohol fuel', when they assessed stalks in relation with plant height and maturity (Widstrom *et al*., 1984).

Indeed during sugar accumulation within stems, sucrose produced in photosynthetic source, leaves is transported within phloem sieve element – companion cell (SE-CC) complexes to an array of sinks (non-photosynthetic organs) comprising developing vegetative and reproductive organs (growth sinks) as well as the stem storage sink. Within growth sinks carbohydrates are invested primarily into the biosynthesis of cellular structures. In contrast, elongating and mature internodes accumulate sucrose within vacuoles, cytosols and apoplasmic spaces of their storage parenchyma cells (Lingle, 1987 and Shen *et al*., 1999).

Knowledge of possible changes in stalk sugar distribution due to selection for traits such as yield and stalk rot resistance will also be helpful, because the change or difference in pattern of soluble solids gradients was attributed in part to selection for increased resistance to stalk rot, which manifests positive correlation with sugar content (Widstrom *et al*., 1988).

Information on the distribution and amount of sugars and soluble solids found in corn stalks will be important if the corn plant is to be utilized for its total energy production. So in this prospect Widstrom *et al*. (1988), also studied distribution of sugar and soluble solids in the corn stalk and found out that decreased in soluble solids concentration from soil level upward toward the ear node, but increased from the ear node upward.

In contrast to corn grain, Brazil has successfully utilized sugarcane for nearly 30 years to produce ethanol from the readily fermentable sugars, primarily sucrose, extracted from the stalk, whereas, burning the resultant stover, or bagasse to generate electricity (Andrietta *et al*., 2007, Pandey *et al.*, 2000 and Yuan *et al.*, 2008).

Leshem and Wermke (2006) found that dry matter yield increased with density, especially at the early stages of growth. When ear-formation was depressed by increasing plant density, the resulting reduction of ear yield and its quality due to the absence of ear was partly compensated for by the increased yield and quality of the stem. They also studied the effect of plant density and removal of ears on the quality and quantity of forage corn to test the hypothesis that a dense corn stand (320–720 plants ha^{-1}) produced more dry matter of acceptable quality than a stand sown at the density generally advocated (105 plants ha^{-1}).

As grain will likely remain the major product of corn which requires an annual application of high levels of nitrogenous fertilizers for maximum yields, increases the energy balance for using grain as a biofuel feedstock, and can negatively impact water and air quality (Tilman *et al*., 2006 and Mabee *et al*., 2011). So the integration of agro energy crops offers the potential for the development of sustainable biopower and biomaterials that will lead to a new manufacturing paradigm (Ragauskas *et al*., 2006).

Advances in genetics, biotechnology, process chemistry, and engineering are leading to a new manufacturing concept for converting renewable biomass to valuable fuels and products (Ragauskas *et al*., 2006). The growing global consumption of finite fossil fuel resources, the negative climatic consequences and recent concerns about the cost and availability of energy have resulted in efforts to identify and develop alternate renewable sources of fuel for energy that bring the promise of energy security and sustainability (Charles *et al*., 2007).

The potential of tropical corn is to reduce greenhouse gas emissions by combining two of the most effective feedstocks such as stalk sugar and lignocellulosic biomass. In processing the sugar, the biomass itself is co-fired to provide most of the input energy required for distillation. In comparison to gasoline, ethanol made from cellulose and produced with power generated from biomass by-products can result in an 86 per cent reduction in greenhouse gas emissions (Wang *et al*., 2007).

The release of greenhouse gas can be reduced still further if the CO_2 released from fermentation is recaptured photo synthetically into additional feedstock. Brazil and the United States represent approximately 80 per cent of the world supply, mostly using corn or sugarcane China produces bioethanol by fermentation of mostly corn, wheat and cassava as feedstock. In developing economies, food-related feedstock is preferably replaced by non food raw materials, such as sweet sorghum or cassava (Andrietta *et al*., 2007).

Most of the "new renewable energy sources" are still undergoing large-scale commercial development, but some technologies are already well established. These include Brazilian sugarcane ethanol (Goldemberg, 2007), which has always been in the forefront of sugarcane production, also occupies a prominent position as the first country to produce and use biofuel in its automobile fleet.

Recent references about the different generations of bio-ethanol were examined and reveal that the first generation bio-ethanol production will remain the most important production process in the immediate future (Sanchez *et al*., 2008 and Balat, 2011), whilst second and third generation processes still need further development on laboratory and pilot scale to remove major drawbacks, and increase the bio-ethanol yield per input biomass weight (Yu and Tao, 2009).

Manufacture of biofuels from plant sugars may provide a sustainable alternative to the problems derived from the extensive utilization of fossil fuels due to their large

availability, renewability, and the possibility of reduction of CO_2-emissions (Tilman *et al*., 2006 and Fischer *et al*., 2010).

Corn and other cereal crops are being used for the production of first generation biofuels that is starch ethanol production because of their high grain yield and starch accumulation in the grain (Mabee *et al*., 2011). This will bring food- fuel conflict so genetic improvement of corn for bioenergy uses will need to focus on enhancing biomass quantity and quality without impacting grain yield and quality.

For genetic improvement of corn for bioenergy uses plant size, cell wall composition and the distribution of vascular tissue within the plant are the most obvious targets. In addition, optimizing water and nutrient uptake and utilization could improve the sustainability of corn production (Vermerris, 2011).

Total average biomass yields were 24 Mg ha^{-1} for both the of temperate × tropical corn and grain hybrids. However, Temperate × tropical corn partitioned 50 per cent more biomass to the stalk and produced 50 per cent more sugar, and had less than half the grain of the commercial hybrids, indicating inverse relationship between grain production and sugar accumulation (White *et al*., 2011).

When grain formation was prevented by ear shoot bagging, corn hybrids produced an average of 4024 kg ha^{-1} of sugar, without supplemental N fertilizer, which was three to four-folds greater than the non ear shoot-bagged and ear removed hybrid (White *et al*., 2012).

Weijde *et al*. (2013) studied the potential of three important field crops- corn, sugarcane and sorghum and two undomesticated perennial energy grasses-miscanthus and switchgrass. Although all these grasses were high biomass yielding, corn, sorghum, and sugarcane are dual-purpose crops as they produce different products. While, miscanthus and switch grass are exploited exclusively for lignocellulosic biomass.

With the global increasing demand for energy, bioethanol is considered as an important renewable fuel to partly replace fossil-derived fuels. The world production of bioethanol increased from 50 million m^3 in 2007 to over 100 million m^3 in 2012 (Chen *et al*., 2013 and Kang *et al*., 2014b)

The current literature specifies a conversion of biomass to bioethanol of 30 to ~50 per cent only. Novel processes increase the conversion yield to about 92 per cent of the theoretical yield. New combined processes reduce both the number of operational steps and the production of inhibitors. Recent advances in genetically engineered microorganisms are promising for higher alcohol tolerance and conversion efficiency. By combining advanced systems and by intensive additional research to eliminate current bottlenecks, second generation bioethanol could surpass the traditional first generation processes (Kang *et al*., 2014a).

2.3 Genetic Potential of Corn to Increase Stalk Sugar

Few studies of sugar content in corn stalk have focused primarily on the distribution of sugar content (Welton *et al*., 1930; Li *et al*., 2007; Bian *et al*., 2009). When coupled with reductions in grain formation, due to reproductive asynchrony, the sugar from photosynthesis is not translocated to the grain and converted to starch, but is instead retained in the stalk as sugar, primarily sucrose with small amounts of glucose and fructose (Van Reen and Singleton, 1952).

One study by King *et al.* (1972) included a tropical line among the temperate-adapted varieties reported that corn varieties adapted to the tropics and grown in a temperate environment exhibit several changes associated with sensitivity to photoperiod, including a slower rate of shoot maturation, more vegetative leaves, thicker stalks, (Stevenson and Goodman, 1972), Each of these physiological responses to photoperiod provides the benefit of prolonged photosynthesis and carbon fixation.

Marten and Westerberg (1972) confirmed the hypothesis that preventing grain formation in corn reduces its efficiency in producing fodder dry matter by studying the relative yield potential and quality of high-sugar, male-sterile (barren) vs. normal, male-fertile (fruited) corn for silage crops. Corn breeders are likely to produce higher yielding, high quality silage cultivars by developing male-fertile, fruited genotypes instead of male-sterile, high-sugar genotypes.

A study by Valva *et al*. (1980) reported that sugar yield did not differ between sterile male and fertile male cultivar. They have also reported that sugar yield was higher in single cross than in double cross and open pollinated cultivars cultivar.

Hybrid means of percent soluble solids by water content and fermentable sugars in the stalks reported to be significantly correlated, while, that of population and cultivar means were not significantly correlated because of the greater genetic heterogeneity within cultivars and populations compared to hybrids. The average sugar yields of cultivars and populations on a per plant basis were comparable to the hybrids, and large differences within both groups suggested that selection progress for improved yield is a reasonable expectation, genetic variability resulting from crosses also extends to the sugar concentration in the stalks and through inbred selection for better hybrids, sugar yields can be increased (Widstrom *et al*., 1984).

Genetic correlations of sugar traits assist in sugarcane selection (Milligan *et al*., 1990). Bertolini *et al*. (1993), studied soluble solids content in the stalk of corn (*Zea mays* L.) lines and hybrids, by evaluating a total of 218 entries. Results showed a high level of variability (from 5 to 16 % °Brix), suggesting that breeding for this trait should be effective. Correlation analysis demonstrated the absence of strong negative relationships between soluble solids content and relevant yield components.

Some disadvantages of tropical corn cultivars are that they exhibit weak stalks and roots and greater disease susceptibility when grown in a temperate climate (Holland and Goodman, 1995).

Ethanol within Brazil is produced largely from sugar cane. While, sugar cane production is unsuitable for temperate climates, recent studies have focused on sweet sorghum (Laopaiboon and Laopaiboon, 2012), which also accumulates soluble sugars in its stalks, as an alternative to grain corn for ethanol production. Grain corn is the major feedstock for ethanol production in the United States (Wang *et al*., 2005).

Pordesimo *et al.* (2005) made research on variation in corn stover composition and energy content with crop maturity using two almost identical corn cultivars - Pioneer 32K61 and 32K64 Bt. They Studied Compositional analysis of corn stover fractions from an estimated two weeks before corn kernel physiological maturity until 4 weeks after the grain had already reached a moisture content suitable for combine harvesting. The energy content of corn stover anatomical fractions is shown to remain fairly constant over time and from one plant to another (16.7–20.9 kJ g^{-1}).

The stalk sugar content in corn may be improved by modifying sugar-related traits, in that perspective screening and evaluation of germplasm (Bai *et al*., 2007; Bai *et al*., 2009; Li *et al*., 2007; Bian *et al*., 2010), effects of environmental factors and genotypes on water-soluble carbohydrate content (Kruse *et al*., 2008; Zsubori *et al*., 2013) were reported.

Biotechnology has also been a valuable means of improving corn and more biotechnology traits have been commercialized for corn than any other crop species. Through a combination of breeding and biotechnology approaches, genes can be identified and modified to enhance biomass and sugar production in corn or provide benefits to the downstream saccharification and fermentation processes or other conversion routes (Vermerris *et al*., 2007).

°Brix had a high positive correlation with sugar content (Ritter *et al*., 2008). The genetic mapping of QTLs for sugar-related traits (°Brix, glucose, sucrose, flowering time, PHT, stem diameter, stem and leaf fresh weight, juice weight, total dry matter and grain yield) was also reported in sorghum (Ritter *et al*., 2008; Guan *et al*., 2011; Shiringani *et al*., 2010).

By crossing temperate and tropical parental germplasm of corn, the temperate parent can potentially impart improved agronomic traits to the hybrid such as better disease and pest resistance, decreased lodging, and abiotic stress tolerance (Nelson and Goodman, 2008).

The release of the genome sequence of inbredline B73 (Schnable *et al*., 2009) added to its rich history as a genetic model organism gives corn a major role in the bioenergy research portfolio: Despite the historic focus on grain yield, evidence is emerging that stover yield and stover composition could be incorporated as selection criteria as part of a grain breeding program, since these traits do not necessarily conflict with each other (Lewis *et al*., 2010).

When corn varieties adapted to tropical latitudes are grown in temperate environments such as the US Corn Belt, they flower later and produce little or no grain, but have higher total biomass yields compared to modern commercial corn grain hybrids, tropical corn is a hybrid bred by crossing tropical and temperate-adapted cultivars, when grown in middle latitudes, it accumulates large amounts of extractable sugars (sucrose, glucose and fructose), produces larger amounts of plant cell wall biomass, and generates little or no grain and this kind of utilizing tropical corn stem syrup for bioethanol production that helped in tropical corn breeding and development for use as another feedstock for the biofuel industry (White *et al*., 2011).

A study showed that there is a significant correlation between plant height (PHT), days to silking (DTS), three ear leaves area (TELA) and °Brix in corn (Bian *et al*., 2011).

Hybrids derived from crossing temperate-adapted and tropical parents successfully combine the high biomass potential of tropical corn with the genetic improvements from the past century of corn breeding for high grain yields in temperate environments. Named "tropical corn," these tropical x temperate hybrids produce greater biomass and sugar compared to current US corn hybrids (Hegyi *et al*., 2011; White *et al*., 2012).

Studies of White *et al*. (2012) to evaluate biological potential, genetic variability and impact of nitrogen (N) on biomass, stalk sugar, and biofuel potential of temperate × tropical corn (TTM) hybrids shows 40 per cent taller, exhibited later reproductive maturity, greater flowering asynchrony, and remained green longer. All hybrids responded to supplemental N by producing more biomass and grain, a lower percent of biomass partitioned to stalk and leaf, whereas, TTM also had a decreased concentration of sugar.

Genetic analysis of stalk sugar content was done using major gene and polygene mixed models (Bian *et al*., 2012, 2013), but still there is a notable lack of information in the literature regarding QTL for corn stalk sugar content. Breeding programs are heavily based on the exploitation of genetic mechanisms for the target traits. Therefore, a study on QTL and stalk sugar content is a prerequisite for breeding corn hybrids with high stalk sugar content.

Studies of Chen *et al*. (2013) suggest that the tropical corn is an alternative energy crop being considered as a feedstock for bioethanol production in the North Central and Midwest United States. Further, tropical corn also accumulates high amounts of extractable stalk sugar (sucrose, glucose, and fructose) because of reduced grain formation. Although offering potential benefits as a feedstock for biofuels, the direct use of tropical corn germplasm in temperate environments is hampered by greater lodging, less stress tolerance, and susceptibility to disease and insect pests – traits that have been greatly improved in modern US corn grain hybrids.

Bian *et al*. (2014) investigated QTLs associated with stalk sugar traits including °Brix, plant height (PHT), TELA and DTS. Seven QTLs controlling °Brix were mapped

on chromosomes 1, 2, 6 and 9 in the combined environments. These QTLs could explain 2.69-13.08 per cent of the phenotypic variance. One major QTL for °Brix on chromosome 2 located between the markers bnlg1909 and umc1635 explained 13.08 per cent of the phenotypic variance. One major QTLs controlling PHT on chromosome 1 and TELA on chromosome 4 were also identified and accounted for 13.68 and 12.49 per cent of the phenotypic variance, respectively. QTL alleles for increased DTS were located on chromosomes 1 and 5. Significant epistatic effects were identified in four traits, but no significant QTL and environment interactions were observed.

One of the most energy efficient systems of biofuel production uses the sugar extracted from corn said in a study by Reid *et al*. (2015), also suggested that stem sucrose content could reach values found in sugar cane if selection was for sugar and not for grain production, but there were marked differences between cultivars. Mean stalk sucrose concentration was significantly higher in plants where pollination was prevented. This study evaluated 39 genotypes from diverse backgrounds to determine if there was corn germplasm, adapted to the short-season regions of Canada, with high stalk sugar content. The evaluation for stalk sucrose accumulation and associated traits (juice percentage, plant height, weight, and moisture) in field trials from 2007 to 2009 shows genotypic differences for stalk sucrose and juice percentage, and were highly significant.

Mean stalk sucrose ranged from 5.1 to 16.4 °Brix (°Bx) and fresh biomass from 45 to 135 Mg ha^{-1} suggesting the presence of exploitable genetic variation. Calculated sucrose yield of experimental hybrids ranged from 4.3 to 6.0 Mg ha^{-1}. At the current conversion efficiency, the products of sucrose and fresh biomass can be translated into 3600 L ha^{-1} ethanol plus 47 Mg ha^{-1} silage, indicating that this high stalk sugar corn (or "sugarcorn") would be a valuable and an economically viable crop for Canada and elsewhere (Reid *et al*., 2015).

2.4 Sweet corn as potential bioenergy crop:

The shorter growing season, like the season of sweet corn (3 months), might enable more efficient use of the capacity of stover for fuel ethanol production because a higher concentration of soluble sugars (25 % of dry matter) may be expected (Hume and Campbell, 1972; Pordesimo *et al*., 2005).

Advantage of sweet corn to use as potential bioenergy crop is that, it would be harvested when tassels were beginning to expand because it may be that more carbohydrates in a more easily extractable form, liquid expressed from cells, would be available before sugar moved to the seed. Sweet corn stalk internode tissue senesces with age, the senescence increases as ears develop and mature (Russo and Pappelis, 1994).

The use of food crops for first-generation bioethanol production generates a direct competition between energy and food uses. Similarly, dedicated energy crops like switchgrass or giant miscanthus could also compete indirectly with food production if they were to be grown on agricultural land (Walsh *et al*., 2003).

In contrast to field corn that is harvested 150–180 days after planting (DAP), sweet corn is harvested when the concentration of free sugars in the endosperm is highest (21 days after flowering or 90 DAP). The biomass collection at early stages of development could explain the high concentration of soluble sugars observed in sweet corn stover which later on will be probably polymerized into carbohydrates (Jung, 2003). At difference of field corn, the biomass may be harvested early in sweet corn because the grain is adequate for human consumption at 21–23 days after flowering (Pordesimo *et al*., 2005; Fred, 2007).

Sweet corn mutation occurred in field corn as a natural spontaneous mutation in the genes that control conversion of sugar to starch inside the endosperm of the corn kernel. There are several mutations responsible for the various types of sweet corn. The sugary1 (*su1*) mutant has been traditionally used since pre-Columbus times and contains about 5-10 per cent sugar by weight. The shrunken2 (*sh2*) mutant replaced *su1* in processed sweet corn because it has a longer harvest season that allows better response to market demands (Marshall and Tracy, 2003).

Biofuels production using biomass residues of food crops seems an appealing alternative because it does not compete with food and does not require new inputs for cultivation (Pordesimo *et al*., 2005).

Sweet corn is a widely distributed crop in both temperate and tropical zones that generates large amounts of residual biomass (10 t ha^{-1}) without significant commercial value. As senescence progresses it may be that extractable liquids would not be as they are more tightly held in the senescent cells in the stalks or moved to the seed and converted to starch. Additional chemical methods will be needed to make carbohydrates in senescent cells available for conversion to bioethanol. The potential ethanol production from structural and soluble sugars extracted from sweet corn stover reached up to 4400 l ha^{-1} in the most productive hybrids, 33 per cent of which (1500 L ha^{-1}) were obtained by direct fermentation of free sugars (Barros-rios *et al*., 2015).

There is a wide genetic variation for biomass yield and soluble sugar content in various above mentioned studies, suggesting that those traits could be included as complementary traits in sweet corn breeding programs. Dual-purpose sweet corn hybrids can have an added value for the farmers contributing to energy generation without affecting food supply or the environment.

2.5 Role of Sucrose transporters in corn:

Sucrose (Suc) is the predominant form of sugar transported through the phloem from source to sink organs and is also a prominent sugar for short-distance transport. Whether from photosynthesis or storage reserves, it is the principal form of assimilated carbon transported throughout plants and its distribution follows a diversity of routes includes movement through the symplast and transport across plasma membranes for intercellular transport via the apoplast and across endomembranes for intracellular compartmentation (Riesmeier *et al*., 1994; Hackel *et al*., 2006; Srivastava *et al*., 2008; Ayre, 2011).

Sucrose transporters (*SUTs*) are essential for the export and efficient movement of sucrose from source leaves to sink organs in plants. It has been reported that reducing the activities of *SUTs* involved in phloem loading by mutation or transcript reduction strategies results in dramatically stunted plants and carbohydrate accumulation in source leaves (Kuhn *et al*., 1996; Gottwald *et al*., 2000; Slewinski *et al*., 2009). These findings are similar to those reported in dicot plants containing mutations in *SUT* genes that are responsible for phloem loading (Burkle *et al*., 1998; Lemoine, 1999; Eckardt, 2003).

Sucrose transporter of corn *ZmSUT1* is the first that works in both directions under physiological conditions. Based on its expression pattern and biochemical activity, it has been proposed that *ZmSUT1* functions in phloem loading in source tissues (Aoki *et al*., 1999; Carpaneto *et al*., 2005).

It has been shown that *ZmSUT1* is capable of transporting Suc across the plasma membrane. It is highly expressed in photosynthetic tissues, with maximal expression in leaf blades at the end of the day and minimal expression during the night (Aoki *et al*., 1999).

Barker *et al*. (2000) and Barth *et al*. (2003) reported that among the classes of *SUTs* the type IIA *SUTs* are more enigmatic and they are found in all land plants, have lower affinity for sucrose, and have been postulated to be sucrose sensors rather than functional *SUTs*).

More carbohydrate would be sent to sink organs for growth and/or storage, and there would be more primary productivity because enhanced sucrose transport would help remove Suc-mediated product inhibition on photosynthesis (Paul and Foyer, 2001; Stitt *et al*., 2010; Stitt, 2013; Ainsworth and Bush, 2011).

Different research groups divide the *SUT* family into three to five clades and use different nomenclature for those subdivisions, but the basic structures of the trees are similar (Aoki *et al*., 2003; Sauer, 2007; Braun and Slewinski, 2009; Kuhn and Grof, 2010). The *SUT* clades analyzed in the context of land-plant evolution are designated as types I, IIA, IIB, and III; with dicot-specific Type I and monocot-specific Type IIB functioning in phloem loading. Earliest land plants had type II transporters localizing to the plasma membrane and type III transporters localizing to the tonoplast (Aoki *et al*., 2003; Reinders *et al*., 2012).

A detailed biophysical study of *ZmSUT1* revealed that this carrier is working like a perfect thermodynamic machine by which the proton gradient drives sucrose transport. As a matter of fact it is capable to mediate sucrose loading and unloading of the phloem under physiological condition and capable of mediating both the sucrose uptake into the phloem in mature leaves (source) as well as the desorption of sugar from the phloem vessels into heterotrophic tissues (sink). As predicted from a perfect molecular machine, the *ZmSUT1*- mediated sucrose-coupled proton current was reversible and depended on the direction of the sucrose and pH gradient as well as the membrane potential across the transporter (Carpaneto *et al*., 2005).

The physiological and biochemical functions of *SUTs* have been regularly reviewed (Sauer, 2007; Braun and Slewinski, 2009; Kühn and Grof, 2010; Ayre, 2011). In all species studied, SUTs form small families whose members have distinct gene expression patterns, and the encoded proteins have distinct kinetic properties and subcellular localizations.

Findings of Qiu *et al*. (2007) says that the content and activity of sucrose (Suc) synthase (*SUS*) protein is high in sink organs but low in source organs. They examined that light and metabolic signals regulating SUS protein degradation in corn (*Zea mays*) leaves during deetiolation.

SUTs are best characterized for their role in apoplastic phloem loading in which Suc, after release into the apoplast from photosynthetic cells, is actively accumulated to high concentrations in phloem companion cells in preparation for long-distance transport to heterotrophic tissues (Braun and Slewinski, 2009; Kuhn and Grof, 2010).

A study by Slewinski *et al*. (2009) determined that *ZmSUT1* functions in phloem loading by characterizing a knockout mutation which resulted in reduction of assimilates delivered to sink tissues due to the failure to export Suc from source leaves. Hence, it appears, at least in corn, that *SUT1* function is essential for phloem loading of Suc. Determining the biological functions of the five additional *SUT*s in corn will require characterizing plants that harbor mutations in each gene (Braun and Slewinksi, 2009).

Altering phloem transport of Suc by manipulating the *SUTs* involved in phloem loading has been put forward as a means to improve plant productivity. As one example, Suc loading is modified in response to the physiological and environmental needs of the plant to maintain phloem hydrostatic pressure and coordinate source output with sink demand (Ayre, 2011; Dasgupta *et al*., 2014), and it was proposed that heterologous promoters that are uncoupled from this natural regulation may be useful to keep loading rates constantly high (Srivastava *et al*., 2011).

Increased Suc transport from source leaves to sink organs was proposed to be an effective method to enhance crop productivity (Ainsworth and Bush, 2011), especially in conditions where carbohydrate is in excess (Stitt, 2012). As a relatively large and polar molecule, Suc movement across membranes requires facilitators, which may be passive or energized. *SWEETs* are a recently described family of transporters participating in passive movement (Chen *et al*., 2012), while, Suc/H+ symporters, alternatively called sucrose transporters (*SUTs*) or sucrose carriers (*SUCs*), couple the movement of Suc to the proton motive force to allow energized Suc accumulation.

Among angiosperms, eudicots adapted type III *SUTs* for phloem loading and other high-affinity uptake processes across plasma membranes, probably by losing the tonoplast localization signals, to form the type I clade, while, monocots recruited type II *SUTs* for similar high-affinity uptake processes to form the type IIB branch (Reinders *et al*., 2012).

Four phylogenetic ally and structurally distinct *SUT* subfamilies originated from two ancient *g*roups (AG1 and AG2) that diverged early during terrestrial colonization. Tonoplastic Type III and plasma lemmal Type II represent evolutionarily conserved descendants of AG1 and AG2, respectively (Peng *et al*., 2014).

Type I and Type IIB were previously thought to evolve after the dicot-monocot split. However, that divergence of Type I from Type III *SUT* predated basal angiosperms, likely associated with evolution of vascular cambium and phloem transport. Type I *SUT* was subsequently lost in monocots along with vascular cambium. *SUTs* are also found throughout the plant, and their regulation and role in carbohydrate distribution remain active research areas (Peng *et al*., 2014).

III MATERIAL AND METHODS

The details of material used, methods and protocols followed and statistical tools employed for analysis are presented under the respective experiments in this chapter.

3.1 Developing hybrids of sweet and non-sweet corn

3.2 Evaluation of parents and hybrids for soluble sugar percentage and its attributing traits in the corn stem

3.3 Combining ability analysis and heterosis

3.4 Molecular marker analysis of parents and hybrids using *ZmSUT1* gene specific markers

3.1 Developing hybrids of sweet and non-sweet corn

3.1.1 Experimental material

Fifteen sweet corn genotypes were collected from Zonal Agricultural Research Station, V.C. farm, Mandya, India and seven non-sweet corn genotypes were collected from Department of Genetics and Plant Breeding, University of Agricultural Sciences, Bengaluru, India. As presented in the Table 1 fifteen sweet corn and seven non-sweet corn parents were selected for the current study.

Table 1: List of sweet corn and non-sweet corn germplasm used in the crossing study

Sl. No.	Sweet corn Genotypes			Sl. No.	Non-sweet corn Genotypes
1	MAI-14	9	MAI-289	1	M-65
2	MAI-102	10	MAI-292	2	MAI-7
3	MAI-282	11	MAI-325	3	MAI-308
4	MAI-283	12	K-4356-1	4	BGUDI-10
5	MAI-284	13	K-4366-1	5	BGUDI-13
6	MAI-285	14	K-4571	6	BGUDI-80
7	MAI-286	15	K-4673-1	7	BGUDI-81
8	MAI-287	-	-	-	-

3.1.2 Experimental details – *Kharif* 2014

The experiment was carried out during *Kharif* 2014 at Department of Plant Biotechnology, University of Agricultural Sciences, Bengaluru, India located at 12° 58' North; longitude 77° 35' East and altitude of 930 meters above mean sea level (MSL).

Selected genotypes were grown in the field with the spacing of 60 cm between rows and 30 cm between plants. Total area used for the experiment was 104 sq. m (four blocks of 26 sq. m area), each block had all 22 genotypes of both sweet corn and non-sweet corn. Total four staggered sowing of all the genotypes selected for crossing has been followed to synchronize the flowering in one week interval each.

The field management was followed with the recommended package of UAS, Bengaluru to raise healthy crop. Fertilizers (NPK) were applied in the ratio of 135:62.5:50 kg ha^{-1} along with 12.5 t ha^{-1} of FYM. N was provided in the form of urea at basal, 30 and 60 DAS at 50 per cent, 25 per cent and 25 per cent respectively. P and K were provided as single super phosphate (16 % P_2O_5) and Murite of potash (60 % K_2O) respectively at 100 per cent as basal dose. Zn was also applied as basal dose, in the form of $ZnSo_4$ at the rate of 37.5 kg ha^{-1}. Irrigation was done once in five days. All necessary measures were taken to control pest and disease infestation.

3.1.3 Crossing programme

Reciprocal crosses were done, which involved 15 sweet corn and seven non-sweet corn inbred lines highly diverse for stem sugar content. The details of crossing work as follows

- The tassels were covered with brown paper bags when blooming started near the tip of the central axil and it proceeded downward. Simultaneously covered plants were tagged and labelled with date of bagging.
- Ear shoots of all the female plants which were emerged from the leaf sheath *i.e.*, before silk emergence were bagged with butter paper.
- Regular examination was done to confirm whether the silk emerged from the female plant was two-three inch long.
- Crossing was done in the morning hours either by dusting the pollen from tassel bag of selected male plant, over the silk of the female cob/ear or by placing the entire pollen bag over the cob/ear.
- Care was taken to avoid contamination of silk with foreign pollens by covering the pollinated cob/ear and covering the cobs was ensured until the seed set was confirmed.
- Staggered sowing helped to achieve both direct reciprocal crosses, as due to it, there was enough viable pollen availability to cross even early flowering genotype and late flowering genotype.

3.1.4 Harvesting and storage

The matured cobs from respective crosses were harvested at physiological maturity stage, dehusked and oven dried. Seeds were separated from the cobs and stored in labelled paper bags.

Plate 1: View of crossing block *Kharif* 2014

Plate 2: Field view of both parents and F_1 corn genotypes for phenotypic characterization in Summer 2015

3.2 Phenotyping of parents and hybrids for soluble sugar percentage and its attributing traits in the stem

3.2.1 Plant materials

The plant material in this study consists of sixty six F_1 s of sweet corn and non-sweet corn genotypes developed during *Kharif* 2014, which contains both direct and reciprocal crosses. The study also includes sweet corn parents and non-sweet corn parents along with one sweet corn hybrid- Mhadhuri as a check. The detailed list has been presented in the Table 2.

Table 2: Crosses obtained from sweet corn and non-sweet corn inbred parents

		Non-sweet corn (♂)						
	Parents	M-65	MAI-7	MAI-308	BGUDI-10	BGUDI-13	BGUDI-80	BGUDI-81
Sweet corn (♀)	MAI-14		*	*				
	MAI-102		*			*		
	MAI-282						#	
	MAI-283			✓		*		
	MAI-284	✓	✓	✓		✓	*	
	MAI-285		✓	✓		✓		
	MAI-286		✓	✓				
	MAI-287		✓	✓	#			
	MAI289		*	*	#			#
	MAI-292		*	✓	*			*
	MAI-325		*					
	K-4356-1	*	*		✓			
	K-4366-1	✓	✓	#	✓	#		#
	K-4571	✓	*	#	✓	✓		*
	K-4673-1				*	#		

✓ both direct and reciprocal hybrids; * Sweet corn × non-sweet corn;
 # non-sweet corn × sweet corn;

3.2.2 Experimental site-Summer 2015

The experiment was carried out during summer 2015 in a Randomized Complete Block Design (RCBD) at same location as mentioned in 3.1.2

3.2.3 Cultural operations

Selected genotypes were grown in the field with the spacing of 60 cm between rows and 30 cm between plants. The field management was followed as accordance with 3.1.3.

3.2.4 Method of sampling and recording of observations

Plants were sampled at two stages of plant growth, one at 10 days post silk emergence (DPSE) and another at 20 DPSE. The border row at the beginning and the end of the blocks and the first and last plant of each row were excluded from sampling for controlling competition. Harvesting date varied among plots according to the particular flowering date of each plot. Plants from each replication were taken for recording the observations. The mean of the observations recorded on these plants were considered for analysis. The details regarding recording the observations for characters are presented below:

3.2.4.1. Plant height (cm)

The height of the plant was measured from base of the plant (ground level) to the tip of the tassel.

3.2.4.2 Days to 50 per cent flowering

Total number of days taken by each genotype from sowing to emergence of tassel in 50 per cent of the plants was recorded.

3.2.4.3 Number of internodes

The number of distinguishable nodes above the ground level was counted at the time of harvest.

3.2.4.4. Stem girth (cm)

This was measured at the middle of the first internode above the ground level with the help of verniercalipers.

3.2.4.5 Whole plant weight (g)

The fresh weight of the whole plant of all genotypes was recorded after harvesting.

3.2.4.6 Stem weight (g/plant)

The fresh weight of each stem (from base of the stem to upper most node) at physiological maturity after removal of leaves and leaf sheath was recorded.

3.2.4.7 Number of cobs

Total number of cobs of each plant was recorded.

3.2.4.8 Fresh cob weight (g)

Fresh weight of all the cobs of individual plant was recorded in grams.

3.2.4.9 Juice volume (mL)

Total quantity of juice obtained by crushing the cane, which harvested at 10 and 20 DPSE using roller crusher, was collected in a measuring jar and the volume was recorded.

3.2.4.10 Juice extraction percent (JEP)

Weight of the stem residue remained after juice extraction was recorded and juice extraction percent was calculated using the formula:

$$JEP = \frac{(\text{stem weight before extraction} - \text{stalk weight after extraction})}{(\text{stalk weight})} \times 100$$

3.2.4.11 Total soluble solids (°Brix)

°Brix was measured by adding a drop of the extracted cane juice on to the space provided for the same in digital refractrometer (ATAGO Pocket Refractrometer PAL-1) having a capacity to measure 0 to 53 per cent °brix.

3.2.4.12 Estimation of total sugars by phenol-sulphuric acid method

Procedure

1. One mL of extracted juice was diluted into 200 mL of distilled water.
2. One mL of diluted sample was taken in a test tube and 0.5 mL of phenol reagent and 5 mL of conc. H_2SO_4 was added.
3. The test tubes were incubated at room temperature for 10 min and shaken well.
4. Later the test tubes were incubated in a water bath at temperature 25-30 $^{\circ}$C for 20 minutes.
5. The incubated samples were analyzed by checking the O.D. at 510 nm.
6. A graph was plotted against standard to get the total sugars.

3.2.4.13 Estimation of total reducing sugars (TRS): by the Shaffer-somgyi method

Principle

Reducing sugars containing a free or potentially free aldehyde or ketone group reduce cupric ions to cuprous ions in alkaline medium. This property was made use of in the estimation of reducing sugars by the Shaffer-somgyi method.

The reducing sugar was heated with Shaffer-somgyi method copper reagent when part of the cupric ions were reduced to cuprous oxide which was dissolved in acid and KI reagent was added to the reaction mixture when iodine was liberated. The liberated iodine

reoxidizes cuprous ions to cupric ions. The excess iodine was titrated against standard against standard thiosulphate.

Procedure

1. Five ml of solution containing 0.5 to 2.5 mg of glucose was pipetted out into test tubes. Five ml of copper reagent was added and mixed well.

2. A blank was prepared using 5 mL of water and 5 mL of reagent.

3. The tubes were capped with bulbs or funnels and incubated in boiling water bath for 15 min. The caps were removed without shaking and cooled under running water for min. 2 mL of potassium iodide-potassium oxalate solution and 3 mL of 2 N H_2SO_4 were added through the sides of the tubes.

4. The solution in test tube was mixed well so that all the cuprous oxide which was dissolved and allowed to stand in cold water for 5 min with intermittent mixing.

5. The solution was titrated against 0.005 N sodium thiosulphate using starch as indicator.

6. The titer value was subtracted from the blank and determined the amount of reducing sugars in 5 mL of solution from the equation.

3.2.4.14 Estimation of Sucrose content by Reo's method

Sucrose content determined in test tubes containing 500 µL, 6 per cent KOH and 500 µl test extract. Tubes were boiled in a water bath for 20 minutes. Cooled at room temperature, 10 mL of 0.1 per cent Resorcinol solution and 3 ml of 30 per cent HCl added to each tube, following by incubation at 80 ˚C for 10 minutes. OD (Optical Density) of the solution was taken at 490 nm and values were compared to standard absorption curves.

3.2.5 Test of normality

3.2.5.1 Normal distribution

The normal distribution (the term first used by Galton, 1989) function is determined by the following formula:

$$f(x) = 1/[(2*\pi)^{1/2}*\sigma]*e^{**}\{-1/2*(x-\mu)/\sigma^2\} \quad -\infty \text{ to } \infty$$

Where,

'μ' is the mean

'σ' is the standard deviation

'e' is Euler's constant (2.71)

'π' is the constant Pi (3.14)

3.2.5.2 Skewness

Skewness is a measure of the extent to which the distribution of the respective variable is skewed to the left (negative value) or right (positive value), relative to the standard normal distribution (for which the skewness is 0). Genetic expectations of skewness reveal the nature of genetic control of the traits (Fisher *et al*., 1932). The adjusted mean values of each genotype for quantitative traits were used to estimate coefficient of skewness using "SPSS 16.0" software program. The skewness is calculated with the formula:

$$\text{Skewness} = n * M_3 / [(n-1) * (n-2) * \sigma^3]$$

Where,

'M_3' is equal to Σ (Xi – mean X) **3

'N' is the valid number of cases

'σ^3' is the standard deviation (sigma) raise to the third power.

3.2.5.3 Kurtosis

Kurtosis is a measure of how "wide" or skinny ("flat" or "peaked") the distribution is for the respective variable, relative to the standard normal distribution (for which the kurtosis is equal to 3). Kurtosis indicates the relative number of genes controlling the traits (Robson, 1956). The kurtosis is calculated with the formula:

$$\text{Kurtosis} = [n* (n+1) * M_4 - 3 * M_2 * M_2 * (n-1)] / [(n-1)* (n-2)* (n-3)* \sigma^4]$$

Where,

'M_j' is equal to Σ (Xj – mean X)**j

'N' is the valid number of cases

'σ^4' is the standard deviation (sigma) raise to the fourth power

3.2.6 Statistical analysis

Mean values of five plants used for recording the observations were computed for different plant characters for each of the genotypes. The phenotypic data for all the genotypes for each character were subjected to statistical analysis.

3.2.6.1 ANOVA due to different sources of variance

The analysis of variance for different characters was used to partition the variance due to different sources following the method given by Panse and Sukhatme (1964). The significance was tested by comparing with the table values as given by Yates (1965). Standard error of means (SE_M) and Critical difference (CD) were worked out using appropriate formula for comparing mean of the individual lines.

Source of variation	df	Mean sum of squares	F-value
Replication	(r-1)	M_r	M_r/M_e
Genotypes	(g-1) (r-1)	M_t	M_g/M_e
10 DPSE	(a-1)	M_a	M_a/M_e
20 DPSE	(b-1)	M_b	M_b/M_e
(10 vs 20) DPSE	1	M_{ab}	M_{ab}/M_e
Error	(g-1) (r-1)	M_e	
Total	(gr-1)		

Wherein,

r = Number of Replications

g = a+b

a = b= Number of genotypes

Source of variation	df	Mean sum of squares	F-value
Replication	(r-1)	M_r	M_r/M_e
Parents	(p-1)	M_p	M_p/M_e
Sweet corn	(s-1)	M_s	M_s/M_e
Non- sweet corn	(n-1)	M_n	M_n/M_e
Sweet vs non-sweet corn	1	M_{sn}	M_{sn}/M_e
Error	(p-1) (r-1)	M_e	
Total	(pr-1)		

Wherein,

r = Number of Replications

p = Number of parents

s = Number of sweet corn parents

n = Number of non-sweet corn parents

Source of variation	df	Mean sum of squares	F-value
Replication	(r-1)	M_r	M_r/M_e
Hybrids	(h-1)	M_h	M_h/M_e
S × NS	(s-1)	M_s	M_s/M_e
NS × S	(n-1)	M_n	M_n/M_e
(S × NS) vs (NS × S)	1	M_{sn}	M_{sn}/M_e
Error	(h-1) (r-1)	M_e	
Total	(hr-1)		

Wherein,

r = Number of Replications

h = Number of hybrids

s = Number of crosses (sweet × non-sweet corn)

n = Number of crosses (non-sweet × sweet corn)

Source of variation	df	Mean sum of squares	F-value
Replication	(r-1)	Mr	Mr/Me
Genotypes	(g-1)	Mg	Mg/Me
Parents	(p-1)	Mp	Mp/Me
Hybrids	(h-1)	Mh	Mh/Me
P vs H	1	Mph	Mph/Me
Error	(g-1) (r-1)	Me	
Total	(gr-1)		

Wherein,

r = Number of Replications

g = Number of genotypes

p = Number of parents

h = Number of crosses

3.2.6.2 Phenotypic and Genotypic coefficient of variation (PCV and GCV)

The phenotypic and genotypic coefficient of variation was computed as per Burton and Dewane (1953) for low moisture stress.

$$PCV = \frac{P}{X} \times 100 \qquad GCV = \frac{G}{X} \times 100$$

Wherein,

P = Phenotypic standard deviation

G = Genotypic standard deviation

X = Grand mean of character

PCV = Phenotypic coefficient of variation

GCV = Genotypic coefficient of variation

PCV and GCV were classified according to Robinson *et al.* (1949). 0-10 per cent was considered as low, 10-20 per cent as moderate and 20 per cent and above as high.

3.2.6.3 Heritability (h^2)

Broad Sense Heritability was calculated using the formula (Hanson *et al.,* 1956).

$$h^2(\%) = \frac{Vg}{Vp} \times 100$$

Wherein,

h^2 (%) =Heritability percentage

Vg= Genotypic variance

Vp= Phenotypic variance

Heritability percentage was categorized as follows (Robinson *et al.,* 1949).

0-30 per cent was considered as low,

30-60 per cent was considered as moderate

60 per cent and above as high

3.2.6.4 Genetic advance (GA)

Genetic advance was calculated by using formula given by Johnson *et al.,* (1955).

$$GA = h^2 \times \sigma_p \times K$$

Wherein,

h^2 = Heritability (Broad sense)

σ_p = Phenotypic standard deviation

K = Selection differential which is 2.06 at 5 per cent intensity of selection (Lush, 1949).

3.2.6.5 Genetic advance as per cent mean

$$\text{GA as per cent mean} = \frac{GA}{X} \times 100$$

Wherein,

GA = Genetic advance and

X =Treatment mean for the character.

The GA as per cent mean was classified (Johnson *et al.,* 1955) as given below.

0-10 per cent Low

10-20 per cent Moderate

20 per cent and above as high

3.2.6.6 Correlation analysis

To estimate the degree of association between the traits studied, phenotypic correlation was computed by using the formula given by Webber and Moorthy (1952).

$$r_p = \frac{COV(X, Y)}{[V(X).\ V(Y)]^{1/2}}$$

Wherein,

r_p = phenotypic correlation co-efficient.

COV (X, Y) = Phenotypic covariance.

V(X) and V(Y) = Phenotypic variances of the traits X and Y

3.2.6.7 Path-coefficient analysis

Path-coefficient analysis was carried out using phenotypic correlation values of different characters as suggested by Wright (1921) and as illustrated by Dewey and Lu (1959) was carried out to know the direct and indirect effect of the morphological traits and grain Zn content on yield. Standard path-coefficients which are the standardized partial regression coefficients were obtained using statistical software package Genres 1. These values were obtained by solving the following set of 'P' simultaneous equations by using the above package.

$$P_{01} + P_{02}\, r_{12} + \text{----------} + P_{0P}\, r_{1P} = r_{01}$$

$$P_{01} + P_{12}\, r_{02} + \text{----------} + P_{0P}\, r_{2P} = r_{02}$$

$$\downarrow$$

$$P_{01} + r_{1P} + P_{02}\, r_{2P} \text{ ---------- } + P_{0P} = r_{0P}$$

Wherein, P_{01}, P_{02}, ------- P_{0P} are the direct effects of variables 1, 2, -------- p on the dependent variable 0 and r_{12}, r_{13} ,---------- r_{1P} -------- $r_{P\,(P-1)}$ are the possible correlation coefficients between various independent variables and r_{01}, r_{02}, r_{03} ------- r_{0P} are the correlations between dependent and independent variables. The indirect effect of the i^{th} variable *via* j^{th} variable is attained as ($P_{oj} \times r_{ij}$). The contribution of remaining unknown factor is measured as the residual factor, which is calculated and given below.

$$P^2ox = 1 - [P^2_{01} + 2P_{01}\, P_{02}\, r_{12} + 2\, P_{01}\, P_{03}\, r_{13} + \text{-------} + P^2_{02} + 2P_{02}\, P_{03}\, r_{13} + \text{-----} + P^2_{0P}]$$

$$\text{Residual factor} = (P^2_{ox})^{½}.$$

3.3 Combining ability analysis

Analysis was done according to line × tester analysis for 14 crosses involving seven sweet corn parents as lines and two non-sweet corn parents as testers. The mean sum of squares due to crosses was partitioned into lines, tester and line by tester effects.

The mean values computed from the observations recorded for 14 quantitative characters in each genotype and replication on five randomly selected plants were

subjected to line × tester analysis (Kempthrone, 1957), keeping in view the caution given by Arunachalam (1974). Statistical analysis of the data was carried out using statistical program TNAU 2.0 for combining ability analysis. The structure of ANOVA for line × tester analysis is as follows:

3.3.1 Structure of ANOVA for combining ability

Source	df	MSS	Components of expected MSS
Replication	(r – 1)		
Crosses	(mf – 1)		
Lines	(f – 1)	M_1	$\sigma_e^2 + r\sigma^2_{sca} + r.m.\sigma^2_{gca}$
Testers	(m – 1)	M_2	$\sigma_e^2 + r\sigma^2_{sca} + r.f.\sigma^2_{gca}$
Line × Tester	(f – 1) (m – 1)	M_3	$\sigma_e^2 + r[Cov.(F.S.) - 2\,Cov.(HS)]$
Error	(r – 1) (g – 1)	M_4	σ_e^2
Total	(gr – 1)		

Wherein,

g = (m + f + mf)

HS=Half sibs

FS=Full sibs

σ^2_{gca} = Covariance HS

σ^2_{sca} = [Covariance (FS) – 2 Cov (HS)]

From the mean sum of squares, covariance of full sibs and covariance of half sibs were estimated as per King *et al.,* (1961)

$$\text{Covariance of FS} = \frac{M_1 + M_2 + M_3 - 3M_4 + 6r.Cov(HS) - r(m+f).Cov(HS)}{3r}$$

$$\text{Covariance of half sibs (average)} = \frac{M_1 + M_2 - 2M_3}{r(m+f)}$$

Variance due to gca effects ($\sigma^2 gca$) = ½ Cov (HS) (average)

Variance due to sca effects ($\sigma^2 sca$) = [Cov (FS) – 2 Cov. (HS)]

$$\sigma^2_{gca} \text{ for females} = \frac{M_1 - M_3}{r.m.}$$

$$\sigma^2_{gca} \text{ for males} = \frac{M_2 - M_3}{r.f.}$$

$$\sigma^2_{sca} = \frac{M_3 - M_4}{r}$$

Wherein,

M_1 = Mean sum of squares due to females

M_2 = Mean sum of squares due to males

M_3 = Mean sum of squares due to female x males

M_4 = Mean sum of squares due to error.

3.3.2 Estimation of general and specific combining ability effects:

The following linear model was used to estimate general combining ability (gca) and specific combining ability (sca) effects.

$$X_{ij} = \mu + g_i + g_j + S_{ij} + e_{ijk}$$

Wherein,

μ = population mean

g_i = gca effect of i^{th} female parent

g_j = gca effect of j^{th} male parent

S_{ij} = sca effect of ij^{th} combination

e_{ijk} = Error associated with the observation X_{ijk}

i = Number of female parents

j = Number of male parents

k = Number of replications

The individual effects were estimated as follows:

(i) General combining ability effects

a) **Lines**: $\hat{g}_i = \frac{x_{i..}}{mr} - \frac{x...}{mfr}$

Where,

$x_{i..}$ = Total of i^{th} female parent over all male parents and replications.

x... = Total of all hybrids over female and male parents

$\hat{g}_i$ = General combining ability effects of i^{th} line

b) **Tester:** $\hat{g}_j = \frac{x_{.j.}}{fr} - \frac{x...}{mfr}$

Where,

x... = Total of all hybrids over female and male parents

$x_{.j.}$ = Total of j^{th} male parent over all the female parents and replications

$\hat{g}_j$ = General combining ability effects of j^{th} tester

(ii) Specific combining ability effects

$$S_{ij} = \frac{x_{ij.}}{r} - \frac{x_{i..}}{mr} - \frac{x_{.j.}}{fr} + \frac{x...}{mfr}$$

Where,

S_{ij} = Specific combining ability effect of ij^{th} combination

X_{ij} = Total of ij^{th} combination over all the replications

The standard errors for testing the significance of gca and sca effects were estimated using the following formulae:

$$\text{Standard error (SE) of } g_i\text{'s} = \sqrt{\frac{m_4}{mr}}$$

$$\text{Standard error (SE) of } g_j\text{'s} = \sqrt{\frac{m_4}{fr}}$$

$$\text{Standard error (SE) of } S_{ij}\text{'s} = \sqrt{\frac{m_4}{r}}$$

The estimates of g_i's and S_{ij}'s were tested for their statistical significance by means of 't' test.

$$t_{g_i} = \frac{g_i - 0}{SE\,(g_i)}; \qquad tg_j = \frac{g_j - 0}{SE\,(g_j)}; \qquad ts_{ij} = \frac{s_{ij} - 0}{SE\,(s_{ij})}$$

3.3.3 Standard errors for testing the significance of gca and sca effects

The standard errors for testing the significance of gca and sca effects were estimated using the following formulae.

Standard error (SE) for gca effects of lines = SE $g_i = (Me/tr)^{½}$

Standard error (SE) for gca effects of testers = SE $g_j = (Me/lr)^{½}$

Standard error (SE) for sca effects of hybrids = SE $s_{ij} = (Me/r)^{½}$

The estimates of g_i and s_{ij} were tested for their statistical significance by't' test. For testing the significance of difference between gca effects of two lines (or two testers) and sca effects of hybrids, the standard errors are computed as follows

$$\text{Standard error of } (g_i - g_j) \text{ for lines} = (2M_e/\ tr)^{½}$$

$$\text{Standard error of } (g_i - g_j) \text{ for testers} = (2M_e/\ lr)^{½}$$

$$\text{Standard error of } (s_{ij} - s_{kl}) \text{ for crosses} = (2M_e/\ r)^{½}$$

The corresponding critical difference (CD) values were computed by multiplying SE value with $(2)^{½}$ and table't' value at 5 per cent and 1 per cent respectively.

CD = $(2)^{½}$ (SE) (table 't' value for error degrees of freedom) at 5 and 1 per cent, respectively

3.3.5 Estimation of Heterosis

The treatment mean values for each trait were used for the estimation of heterosis. Heterosis over mid-parent (MP) was computed by the method suggested by Turner (1953) and Hayes *et al*. (1955).

$$\text{Heterosis per cent over mid parent (\%)} = \frac{F1 - MP}{MP} \times 100$$

To compute the standard error (SE) of estimates of heterosis, mean squares due to error (Me) was considered.

$$\text{SE for heterosis over mid-parent (MP)} = (3\ Me / 2\ r)^{½}$$

Where,

Me = Error MSS in general ANOVA table

r = Number of replications

MP = Mean value of hybrid over two replication

C D = S.E. × table't' value at error df. × $\sqrt{2}$

Further,'t' value is calculated to test the significance for heterosis

$$\text{'t' value for mid parent heterosis} = \frac{F1 - MP}{SE\ (MP)}$$

The calculated't' value was compared with table't' value at error degrees of freedom.

3.3.6 Detection of cytoplasmic effects

As analysis of variance of sweet × non-sweet and non-sweet × sweet corn was carried out separately, the error mean sum of squares of individual analysis were pooled after testing their homogeneity (Bartlett, 1937). The polled error mean sum of squares was used for estimating critical difference (CD) to compare sweet × non-sweet and non-sweet × sweet corn hybrids in terms of mid-parent heterosis.

CD = SE(mph) × 't' table value at error df at P = 0.05 and p = 0.01 × sqrt (2)

Significance of differences among sweet × non-sweet and non-sweet × sweet corn hybrids for mid-parent heterosis was considered as an evidence for the presence of cytoplasmic effects on mid-parent heterosis.

3.4 Molecular marker analysis of parents and hybrids for sugar content

3.4.1 Isolation of genomic DNA

DNA extraction for twenty genotypes was done using CTAB method from young leaves tissues as the protocol described by Doyle and Doyle (1990) as below.

Requirements

- Leaf samples were collected from 15 days old seedlings and stored immediately at -70 °C.
- Cetyl trimethyl ammonium bromide (CTAB) extraction (100 mL)

CTAB	2 % (w/v)
Tris HCl (pH 8.0)	100 mM
Sodium Chloride	4 M
EDTA	20 mM

(Tris, sodium Chloride and EDTA were autoclaved and 2 per cent CTAB was added after autoclaving and preheated before using the buffer).

0.2 per cent β - Mercaptoethanol (added freshly).

- Tris EDTA (TE) buffer

Tris HCl (pH 8.0)	10 mM
EDTA (pH 8.0)	1 mM

(This was dissolved and made up to 100ml, autoclaved and stored at 4 °C)

- 2 per cent Polyvinyl poly pyrrolidone (PVP)
- Ice cold Isopropanol
- Chloroform: Isoamyl alcohol 24:1 (v/v)
- Sodium acetate (3.0 M, pH 7.0) (pH adjusted using glacial acetic acid)

- Absolute ethanol and 76 per cent ethanol (stored at -20 °C)
- RNase A: 10 mg/mL (RNase A was dissolved in TE buffer and stored at -20 °C).

Protocol for extraction of genomic DNA

- Leaf samples (approximately 2 g) were cut into small bits with sterile scissors and transferred to prechilled mortar.
- The leaf tissues were frozen using liquid nitrogen and ground to fine powder.
- The fine powder was allowed to thaw in 10ml of preheated extraction buffer in polypropylene centrifuge tubes and incubated for 30 minutes at 65 ^{o}C in water bath with occasional mixing.
- The tubes were removed from the water bath and equal volume of chloroform: Isoamyl alcohol mixture (24:1 v/v) was added and mixed by inversions for 15 minutes.
- The contents of polypropylene centrifuges tubes were centrifuged at 10000 rpm for 10 minutes at room temperature.
- The clear aqueous phase was transferred to a new sterile tube and equal volume of ice cold isopropanol was added and mixed gently by inversion and then kept in the freezer at 4 ^{o}C for the precipitation of DNA.
- Using blunt end tips, the precipitate was pooled out into a microcentrifuge tube and air dried after removing the supernatant by brief spin.
- 500 µL of chloroform: Isoamyl alcohol mixture was added and centrifuged at 10000 rpm for 10 minutes at room temperature.
- Aqueous phase was transferred to another microcentrifuge tube without disturbing the inner phase.
- To this, 2.5 volume of absolute alcohol and 1/10 volume of sodium acetate were added and kept for incubation overnight.
- It was centrifuged and the supernatant was discarded. To this 500 µl of each 70 per cent and 100 per cent ethanol was used subsequently to wash the DNA by centrifugation.
- The alcohol was discarded and DNA was completely air dried and DNA pellet was dissolved in 250 µl of TE and stored at 4 °C.

3.4.2 DNA quality assay using agarose gel electrophoresis

Materials

- 3X loading dye

5 M NaOH	200 µL
95 per cent formamide (v/v)	95 mL
50 per cent bromophenol blue (w/v)	50 mg
0.5 per cent xylene cyanol (w/v)	50 mg

(Dissolved in sterile double distilled water and made up the volume to 100 mL)

- 10X Tris Borate EDTA buffer (TBE)

Tris base	107.8 g
Boric acid	55.2 g
EDTA ($Na_2.2H_2O$)	9.2 g

(Dissolved in 800 ml of sterile double distilled water and made up to 1000 mL)

- 50X Tris Acetate EDTA buffer (TAE)

Tris base	242 g
Glacial acetic acid	57.1 mL
EDTA ($Na_2.2H_2O$) (0.5M, pH 8.0)	18.6 g in 100 mL of double distilled water

(Dissolved in 800 ml of sterile water and made up to 1000 mL)

- 100bp Ladder

  40 µL loading dye

  10 µL 100 bp ladder

  120 µL sterilized double distilled water

  (Total volume made up to 170 µL)

Protocol

- The pyrex gel casting plate's open ends were sealed with cello tape and the comb was placed properly in casting plate kept on a perfectly horizontal platform

- 0.8 per cent (0.8 g/100 mL) agarose was added to 1X TBE, boiled until the agarose dissolved completely and then allowed to cool. Ethidium bromide (DNA intercalating agent) was added when temperature reaches to 55 – 60 $^{\circ}$C as the staining agent.

- Then it was poured into the gel mould with combs placed and allowed to solidify. The comb and the cello tape were removed carefully after solidification of the agarose.

- The casted gel was placed in the electrophoresis unit with wells towards the cathode and submerged with 1X TBE to a depth of about 1 cm.

3.4.3 Loading the DNA samples

- 1 µl of the crude DNA sample was pipetted onto a parafilm and mixed well with 3 µl of 3X loading dye by pipetting up and down gently several times.

- The mixed contents were transferred to the wells of agarose gel placed inside the 1X TBE buffer.

3.4.4 Quantification of DNA

The genomic DNA was quantified spectrophotometrically both at 260 nm and 280 nm wavelengths. The absorbance at 260 nm allows the calculation of DNA concentration in the sample. An OD of 1 at 260 nm corresponds to 50 µg of double stranded DNA. A pure sample of DNA shows the ratio of OD 260/280 as 1.8. Ratios less than 1.8 indicate contamination in the isolation either with phenol or with proteins. The values higher than this indicate the presence of RNA in the isolation.

3.4.5 Normalization of the DNA concentration

Normalization of the DNA concentration was done to bring all the DNA concentrations to a relatively equal level (50 ng/µL) by appropriate dilutions for PCR reaction. Dilution was done with double distilled sterile water.

Primer design

3.4.6 Exploring the genes associated with sucrose transportation in corn

Gene reported to be associated with sucrose transport in *Zea mays* had been explored.

3.4.7 Downloading the sequence of candidate genes

The genomic sequences of the explored candidate genes were downloaded by using the NCBI website (www.ncbi.nlm.nih.gov). Nucleotide database of NCBI (http://www.ncbi.nlm.nih.gov/nuccore) was used to download the sequence of the gene reported to be associated with sucrose transport. Genomic DNA sequence of the target gene was downloaded.

3.4.8 Primer design

Primers specific to gene associated with sucrose transport on corn were designed by using the "pick primer" tool of NCBI in collaboration with Primer 3 (Ye *et al.*, 2012).

The whole sequence of the downloaded gene was uploaded into NCBI database. Then pick primer tools was used and some of the criteria considered were 50 per cent optimum GC content, less difference (0.5 $^{\circ}$C) in melting temperature of forward and

reverse primers, optimum length of 20 base pairs. The step wise procedure followed to design gene specific primers is shown in the Plate 3.

3.4.9 PCR reaction mixture

PCR for candidate markers was performed in a total volume of 20 µl containing 1X PCR buffer (contains 10 mM Tris-HCl, pH 8.0 at 25 °C, 50 mM KCl, 1.5 mM $MgCl_2$), 0.25 µM of each forward and reverse primers (Sigma Aldrich, USA), 50 ng rice genomic DNA, 0.5 mM dNTPs mix and 1.2 units of *Taq* polymerase (Bangalore Genei, India).

3.4.10 Amplification condition

The amplification profile is given below

Table 3: PCR amplification conditions

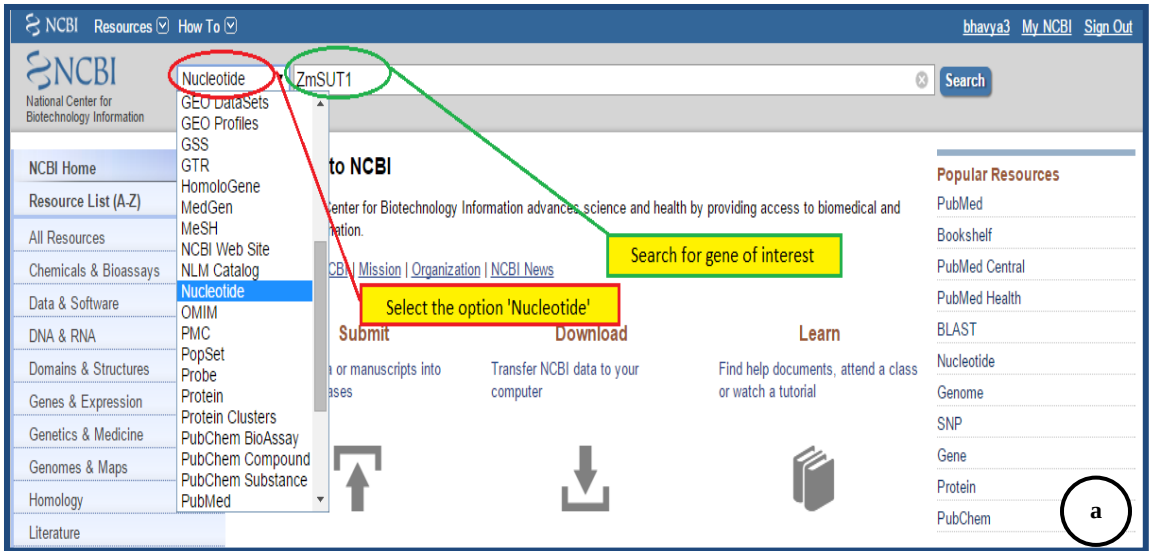
Sl. No.	Step	Temperature (°C)	Time	
1	Initial denaturation	94	5 min	
2	Denaturation	94	30 sec	35 cycles
3	Primer annealing	Depends on the primers	1 min	
4	Primer extension	72	1 min	
5	Final extension	72	7 min	
6	Final hold	04	Till removal	

3.4.11 Agarose gel electrophoresis

Agarose gel (3.0 %) was prepared using electrophoresis grade agarose (Bangalore Genei, India) in a volume of electrophoresis buffer (1X TAE) sufficient for constructing a gel (220 ml for 20 X 20 cm gel). Ethidium bromide was added at concentration of 10 mg/ml of gel. The gel was allowed to solidify fully before removing the combs and loading the sample. 7 µl of 3X loading dye was added to 20 µl of PCR products, and mixed well before loading into the well. Care was taken to prevent mixing of samples between the wells. A voltage of 5 V/cm was given for a time period of three hours for separation of PCR fragments. The gel was viewed under UV trans-illuminator and the DNA banding pattern was recorded directly and later with Alpha Innotech gel documentation instrument.

3.4.12 Screening of candidate markers for polymorphism

A total of 10 candidate gene markers (Table 4) designed based on the strategy described earlier, were screened to discern their amplification profiles.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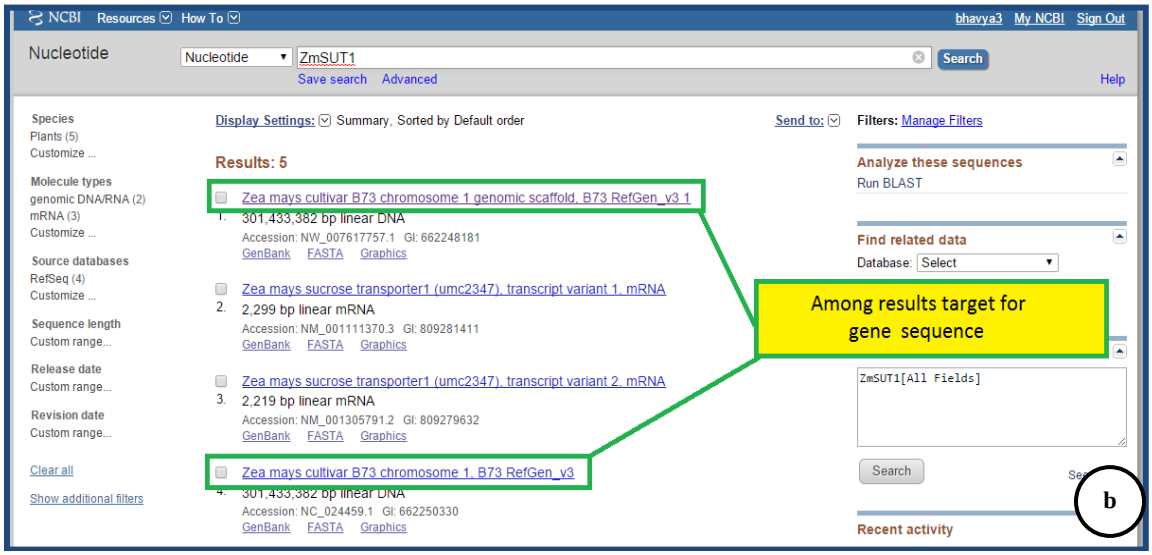
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Analyze these sequences
Run BLAST
Find related data
Database: Select
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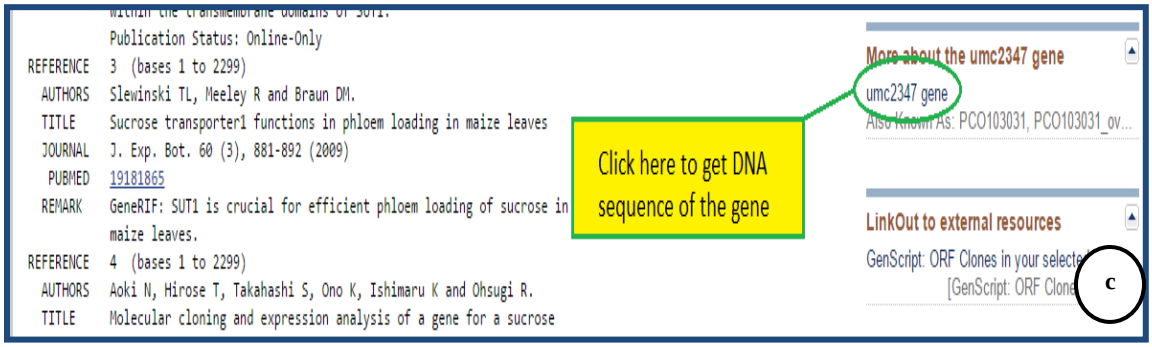
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AUTHORS Slewinski TL, Meeley R and Braun DM.
TITLE Sucrose transporter1 functions in phloem loading in maize leaves
JOURNAL J. Exp. Bot. 60 (3), 881-892 (2009)
PUBMED 19181865
REMARK GeneRIF: SUT1 is crucial for efficient phloem loading of sucrose in maize leaves.
REFERENCE 4 (bases 1 to 2299)
AUTHORS Aoki N, Hirose T, Takahashi S, Ono K, Ishimaru K and Ohsugi R.
TITLE Molecular cloning and expression analysis of a gene for a sucrose
Click here to get DNA sequence of the gene
More about the umc2347 gene
umc2347 gene
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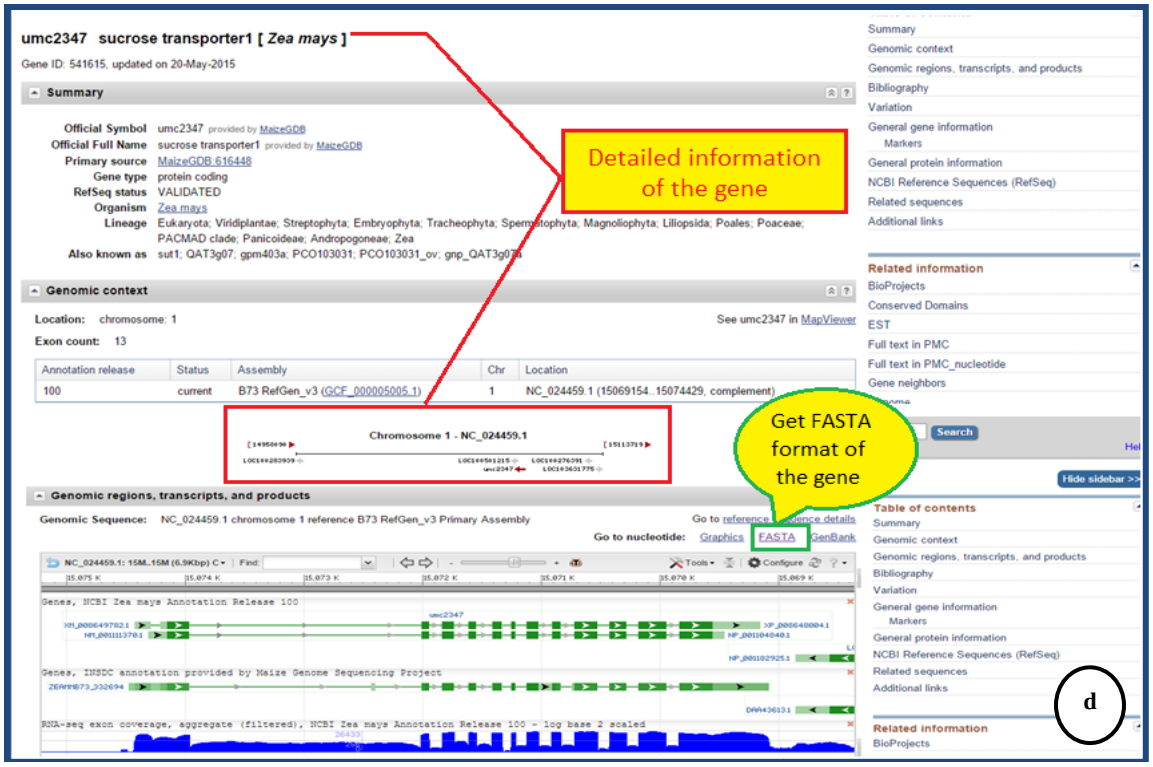
umc2347 sucrose transporter1 [Zea mays]
Gene ID: 541615, updated on 20-May-2015
Summary
Official Symbol umc2347 provided by MaizeGDB
Official Full Name sucrose transporter1 provided by MaizeGDB
Primary source MaizeGDB:616448
Gene type protein coding
RefSeq status VALIDATED
Organism Zea mays
Lineage Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACMAD clade; Panicoideae; Andropogoneae; Zea
Also known as sut1; QAT3g07; gpm403a; PCO103031; PCO103031_ov; gnp_QAT3g07
Detailed information of the gene
Genomic context
Location: chromosome: 1
Exon count: 13
See umc2347 in MapViewer
Annotation release | Status | Assembly | Chr | Location
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Chromosome 1 - NC_024459.1
Get FASTA format of the gene
Genomic regions, transcripts, and products
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Summary
Genomic context
Genomic regions, transcripts, and products
Bibliography
Variation
General gene information
Markers
General protein information
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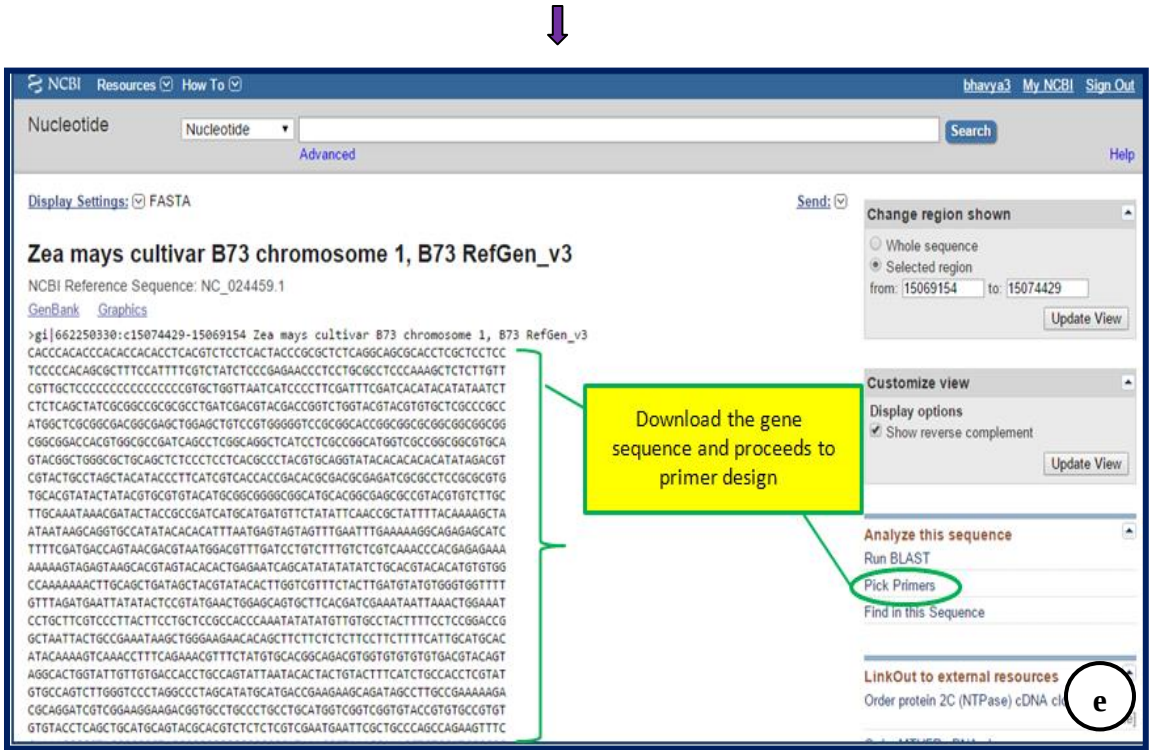
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Analyze this sequence
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Pick Primers
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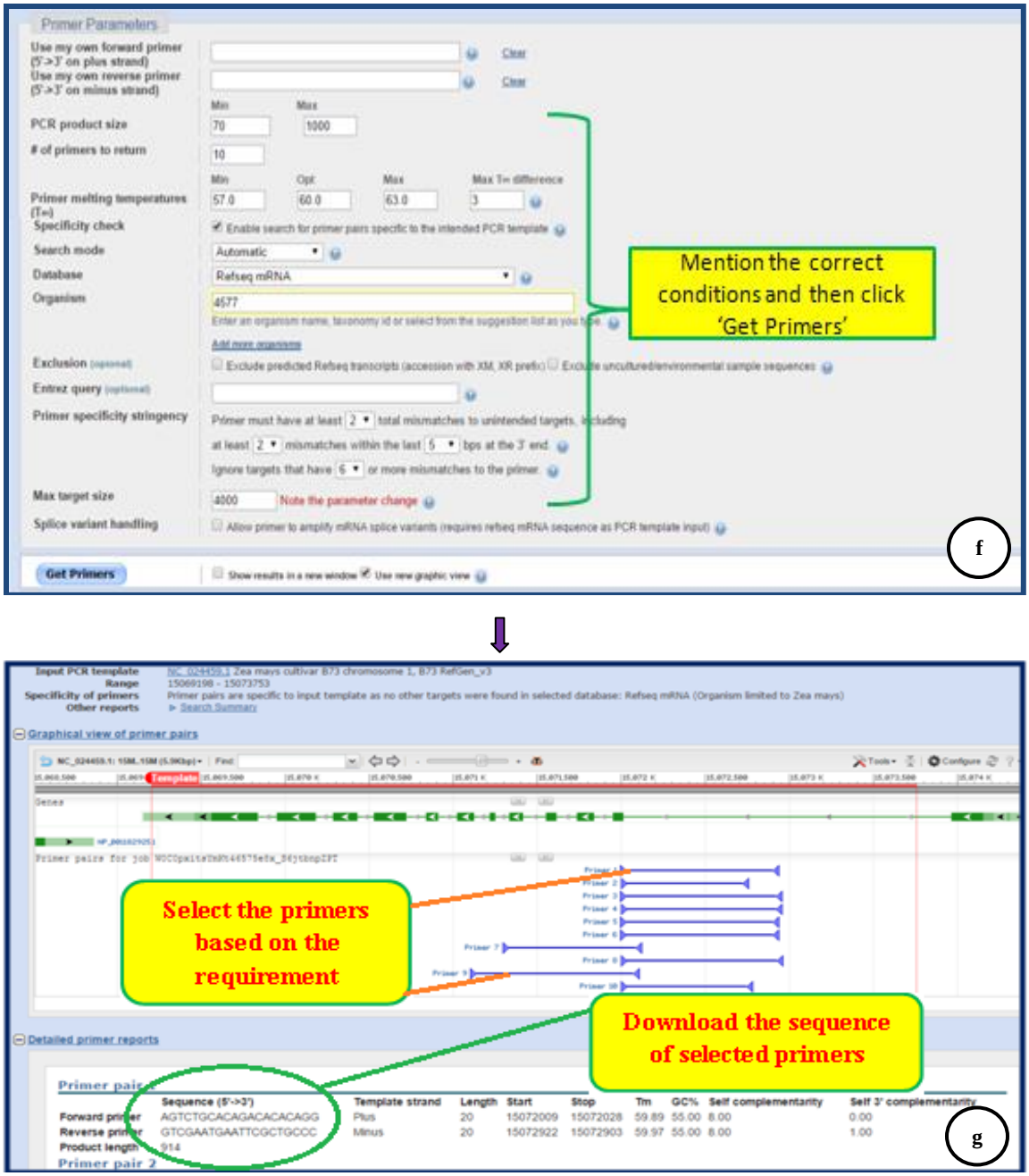


Plate 3: Steps involved in designing gene specific primers

a) Step-I in designing gene specific primers
b) Step-II in designing gene specific primers
c) Step-III in designing gene specific primers
d) Step-IV in designing gene specific primers
e) Step-V in designing gene specific primers
f) Step-VI in designing gene specific primers
g) Step-VII in designing gene specific primers

3.4.13 Scoring of generated bands

The bands generated by gene specific primers were scored as '1' for bands of higher size bands, '3' for lower size, '2' for those showing both the bands, 5 for unusual single size band and 7 for those showing unusual double bands.

Table 4: Details of the gene specific primers designed

Sl. No.	Primer name	Primer Sequence 5' to 3' Direction.	bp	Annealing temperature (°C)	Expected product size (bp)
1	ZmSUT1a-01F	AACGGCGGACAATACACAGT	20	53.1	744
	ZmSUT1a-01R	TGTCCTGATCGACCCATCTCT	21		
2	ZmSUT1b-02F	GTGGTAGTCCTTGAGCGACC	20	54.85	405
	ZmSUT1b-02R	TCGTCCATGCAGCTCTCTTG	20		
3	ZmSUT1c-03F	GGGAACCAAGAGAGCTGCAT	20	53.8	362
	ZmSUT1c-03R	TTACTATTCCCCAGTGCCGC	20		
4	ZmSUT1d-04F	TCTGCACAGACACACAGGTAA	21	52.1	531
	ZmSUT1d-04R	TCGTCGTGCACCTTTTGGAT	20		
5	ZmSUT1e-05F	TACCGCACAGATCAGCCATC	20	54.85	731
	ZmSUT1e-05R	GTAAGCACGGGACCCAATCG	20		
6	ZmSUT1f-06F	CTGTATTTTGCGGCACTGGG	20	53.8	490
	ZmSUT1f-06R	ATGATGGCTGATCTGTGCGG	20		
7	ZmSUT1g-07F	AAACCTGCCAGATACGCCTG	20	54.85	533
	ZmSUT1g-07R	GTACGCACGTCTCTCTCGTC	20		
8	ZmSUT1h-08F	ATTCGACGAGAGAGACGTGC	20	53.8	241
	ZmSUT1h-08R	GTTGTGACCACCTGCCAGTA	20		
9	ZmSUT1i-09F	CCCAAGACTGGCACATACGA	20	52.8	205
	ZmSUT1i-09R	AGCTGGGAAGAACACAGCTT	20		
10	ZmSUT1j-10F	TGCATGATCGGCGGTAGTATC	21	54.4	647
	ZmSUT1j-10R	ACACCTCACGTCTCCTCACTA	21		

IV EXPERIMENTAL RESULTS

The results obtained from the present investigation are presented under the following sub-headings.

4.1 Developing hybrids of sweet and non-sweet corn

4.2 Phenotyping of parents and hybrids for soluble sugar content of the stem

4.3 Molecular profiling of parents and hybrids using *ZmSUT1* gene specific markers

4.1 Developing hybrids of sweet and non-sweet corn

Out of 66 crosses of 15 sweet corn and seven non-sweet corn inbred lines, both direct and reciprocal hybrids obtained were 40, sweet corn × non-sweet corn hybrids were 17 and nine were the crosses of non-sweet corn × sweet corn. The hybrid seeds showed reciprocal difference in appearance (Plate 4-6). All the 66 F_1s along with their parents were evaluated during Summer 2015 to study the soluble sugar content in the stem and its attributing traits.

4.2 Phenotyping of parents and hybrids for soluble sugar content of the stem

4.2.1 Analysis of variance

4.2.2 Phenotypic mean performance of genotypes

4.2.3 Test for normality

4.2.4 Correlation and path-coefficient studies

4.2.5 Heterosis and combining ability analysis

4.2.1 Analysis of variance

The mean sum of squares due to different sources of variation for 14 characters of both parent and hybrid corn genotypes at two different reproductive phases *i.e.*, at 10 DPSE and 20 DPSE are represented in Table 5 -11.

It was observed that, there were high significant differences ($P < 0.01$ and 0.05) at both sampling phases for soluble sugars in the stalk and related traits among parents and hybrids. Further, the interaction studies of 10 vs 20 DPSE, sweet vs non-sweet corn parents, direct vs reciprocal crosses and parents vs hybrids were all found to be highly significant for all the traits in the study. These results indicated that, there was wide exploitable genetic variation for stem sugar and other biomass components among the genotypes studied.

Table 5: Analysis of variance for phenotypic traits recorded at two harvesting stages of selected corn genotypes

Source	df	Mean sum of squares										
		PH	NOI	PW	SW	SG	JV	JEP	°Bx	TS	SP	RS
Genotypes	177	640.01*	2.41*	86198.02*	34142.86*	24.37*	2057*	654.59*	6.15*	8.02*	2.61*	2.62*
10 DPSE	88	642.70*	2.42*	84468.57*	34291.01*	23.86*	2056.57*	813.41*	6.26*	6.81*	1.47*	1.75*
20 DPSE	88	644.59*	2.42*	88901.40*	34382.12*	25.16*	2080.67*	500.99*	6.09*	7.98*	3.7*	1.57*
(10 vs 20) DPSE	1	0.1	0.03	493.15	51.95	0.42	11.51	195.16	442.27*	117.95*	6.62*	170.42*
Error	177	31.72	0.54	3827.05	841.43	2.79	59.96	73.8	0.31	0.11	0.05	0.07

DPSE: days post silk emergence; **df**: degrees of freedom; **PH**: Plant height; **NOI**: Number of internodes; **PW**: Plant weight; **SW**: Stem weight; **SG**: Stem girth; **JV**: Juice volume; **JEP**: Juice extraction percentage; °**Bx**: °brix value; **TS**: Total sugars; **SP**: Sucrose per cent; **RS**: Reducing sugars.

Table 6: Analysis of variance for phenotypic traits recorded in parents at 10 DPSE

Source of Variation	df	Mean sum of squares													
		DTF	PH	NOI	PW	NOC	CW	SW	SG	JV	JXP	°Bx	TS	SP	RS
Parents	21	58.47	626.46*	1.45*	89839.52*	0.65*	17642.49*	54200.70*	26.75*	1853.79*	417.31*	4.74*	5.36*	1.46*	1.05*
S	14	73.32	230.84*	1.19*	52334.34*	0.8*	21831.83*	24820.53*	30.63*	1584.94*	235.38*	4.49*	5.09*	1.27*	1.05*
NS	6	2.24	146.64*	1.4*	25027.80*	0.17	10399.28*	3118.45*	5.76*	844.40*	297.83*	2.80*	3.11*	0.65*	0.82*
S vs NS	1	188.01	9044*	5.54*	1003782.2*	1.52*	2450.91	772016.72*	98.24*	11674.09*	3681.29*	19.97*	22.75*	9.10*	2.49*
Error	21	54.5	40.12	0.44	2491.45	0.28	2142.41	697.84	0.28	42.18	49.17	0.16	0.18	0.06	0.07

S: Sweet corn parents; **NS**: Non-sweet corn parents; **df**: degrees of freedom; **DTF**: Days to flowering; **PH**: Plant height; **NOI**: Number of internodes; **PW**: Plant weight; **SW**: Stem weight; **SG**: Stem girth; **JV**: Juice volume; **JEP**: Juice extraction percentage; °**Bx**: °brix value; **TS**: Total sugars; **SP**: Sucrose per cent; **RS**: Reducing sugars.

Plate 4: Direct and corresponding reciprocal hybrid seeds obtained from sweet corn and non-sweet corn parents

Plate 4: contd.....

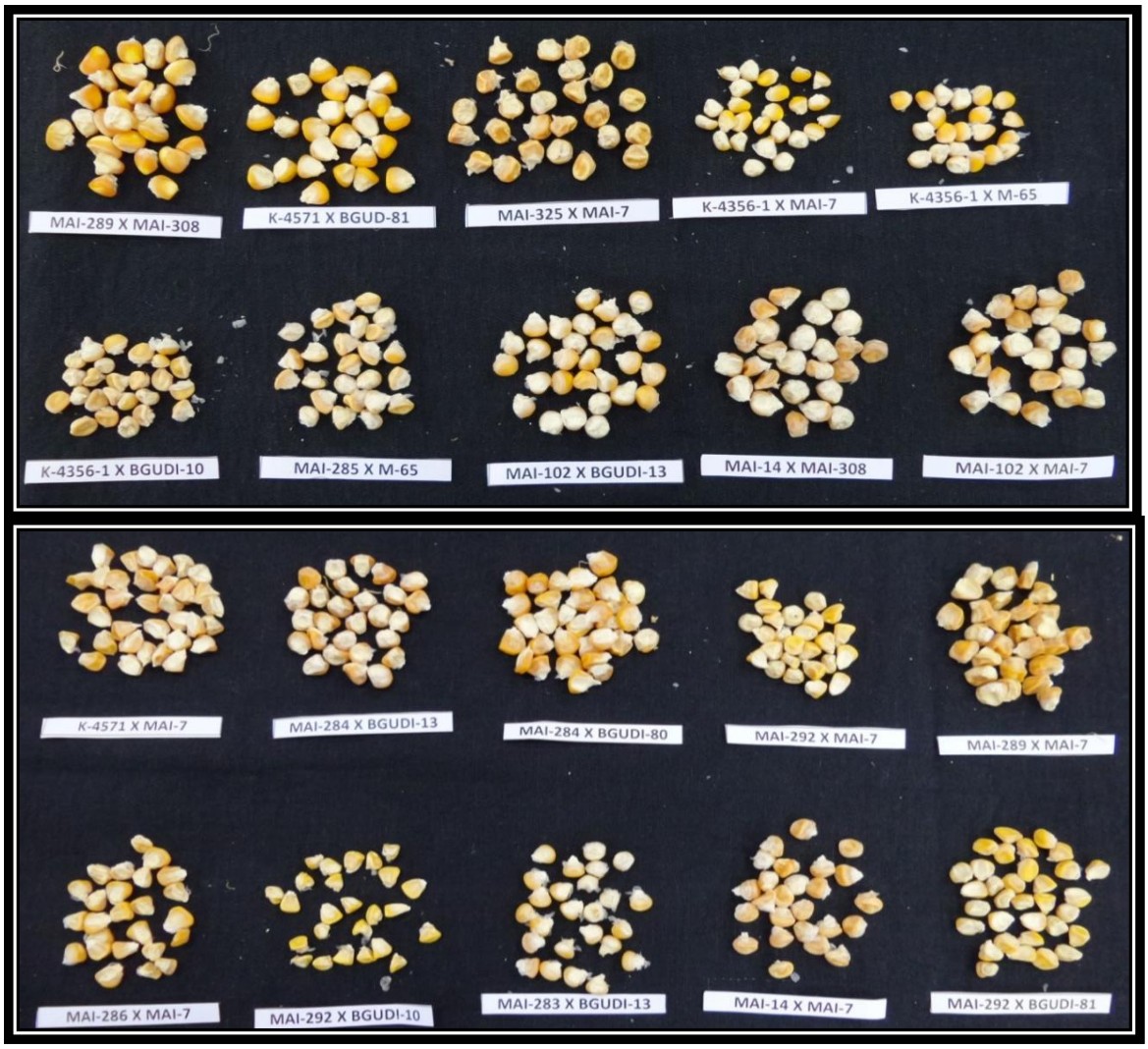


Plate 5: Sweet corn × non-sweet corn hybrid seeds

Plate 6: Hybrid seeds obtained from the crosses non-sweet × sweet corn

Table 7: Analysis of variance for phenotypic traits recorded in hybrids at 10 DPSE

Source of variance	df	Mean sum of squares													
		DTF	PH	NOI	PW	NOC	CW	SW	SG	JV	JXP	°Bx	TS	SP	RS
Hybrids	65	5.47*	631.12*	2.52*	80832*	0.55*	40057.79*	26218.73*	20.82*	2063.46*	321.69*	5.35*	6.47*	1.33*	1.75*
S ×NS	36	4.90*	403.96*	2.79*	57275*	0.40*	54724.90*	23998.71*	18.96*	1447.41*	306.08*	5.67*	6.29*	1.24*	1.75*
NS × S	28	4.09*	593.31*	1.98*	49269*	0.75*	20603.73*	15410.63*	15.75*	1038.34*	347.18*	3.80*	4.04*	0.76*	1.24*
S × NS vs NS × S	1	64.73*	9867.28*	7.87*	1812638*	0.4	56755.35*	408766.55*	229.68*	52944.64*	170.28*	36.99*	80.68*	20.74*	16.29*
Error	65	0.15	24.45	0.57	4434.09	0.24	5365.56	910.66	3.68	68.93	0.02	1.28	0.12	0.03	0.04
Sem±		0.28	3.5	3.5	47.09	0.34	51.8	21.34	1.36	5.87	0.1	0.8	0.24	0.13	0.15
CD @5 %		0.78	9.88	9.88	132.99	0.97	146.29	60.27	3.83	16.58	0.29	2.26	0.68	0.35	0.42
CV (%)		0.74	2.38	2.38	8.05	27.6	28.28	7.77	7.11	10.1	0.3	13.76	3.86	2.94	7.9

S: Sweet corn parents; **NS**: Non-sweet corn parents; **df**: degrees of freedom; **PH**: Plant height; **NOI**: Number of internodes; **PW**: Plant weight; **SW**: Stem weight; **SG**: Stem girth; **JV**: Juice volume; **JEP**: Juice extraction percentage; °**Bx**: °brix value; **TS**: Total sugars; **SP**: Sucrose per cent; **RS**: Reducing sugars.

Table 8: Analysis of variance for phenotypic traits recorded in both parents and hybrids at 10 DPSE

Source of variance	df	Mean sum squares													
		DTF	PH	NOI	PW	NOC	CW	SW	SG	JV	JEP	°Bx	TS	SP	RS
Genotypes	87	18.54	624.14*	2.30*	84728.04*	0.57*	36924.23*	34026.14*	23.69*	2027.29*	818.41*	5.69*	6.53*	1.44*	1.69*
P	21	58.47*	626.46*	1.45*	89839.52*	0.65*	17642.49*	54200.70*	26.75*	1853.79*	1880.31*	4.74*	5.36*	1.46*	1.05*
H	65	5.48	631.12*	2.52*	80832.04*	0.55*	40057.79*	26218.73*	20.82*	2063.46*	454.11*	5.35*	6.47*	1.33*	1.75*
P vs H	1	29.12	122.19	5.52*	230627.32*	0.01	238159.44*	117841.93*	146.45*	3320.03*	2197.78*	48.24*	34.96*	7.51*	11.33*
Error	87	13.77	31.94	0.55	3916.89	0.25	4555.98	853.63	2.85	63.41	232.39	0.85	0.13	0.04	0.05
Sem±		2.62	4	0.52	44.25	0.35	47.73	20.66	1.19	5.63	10.78	0.65	0.25	0.14	0.16
CD@P=0.05*		7.38	11.23	1.47	124.39	0.98	134.16	58.07	3.36	15.83	30.3	1.83	0.72	0.38	0.44
CV (%)		7.04	2.72	6.23	7.76	28.04	28.39	7.25	6.38	9.4	30.61	10.79	3.98	3.13	7.98

P: Parents; **H**: Hybrids; **df**: degrees of freedom; **PH**: Plant height; **NOI**: Number of internodes; **PW**: Plant weight; **SW**: Stem weight; **SG**: Stem girth; **JV**: Juice volume; **JEP**: Juice extraction percentage; °**Bx**: °brix value; **TS**: Total sugars; **SP**: Sucrose per cent; **RS**: Reducing sugars

Table 9: Analysis of variance for phenotypic traits recorded in parents at 20 DPSE

Source of variance	df	Mean sum of squares													
		PH	NOI	PW	NOC	CW	SW	SG	JV	JXP	°Bx	TS	SP	RS	CB
Parents	21	696.35**	3.42**	138383.96**	0.58*	46943.54**	20991.42**	24.71**	1577.24**	147.54**	4.80**	6.96**	4.04**	0.64**	0.86**
S	14	298.22**	3.37**	115947.89**	0.50*	42251.31**	13081.09**	18.10**	257.60**	139.10**	4.30**	5.75**	3.70**	0.56**	0.50**
NS	6	244.73**	2.14**	86032.61**	0.57*	41587.47**	32569.88**	23.01**	1783.64**	186.67**	2.73**	2.65**	0.90**	0.68**	0.75**
S vs NS	1	8979.75**	11.85**	766597.00**	1.75*	144771.22**	62265.22**	127.54**	18813.89**	30.96**	24.29**	49.69**	27.63**	1.52	6.69**
Error	21	17.62	0.19	491.37	0.22	17.42	60.3	0.29	4.75	0.73	0.06	0.11	0.01	0	0.060159
Sem±		2.97	0.31	15.67	0.33	2.95	5.49	0.38	1.54	0.38	0.18	0.24	0.05	0.05	0.173434
CD@P=0.05*		8.73	0.91	46.1	0.98	8.68	16.15	1.11	4.53	1.11	0.54	0.69	0.15	0.14	0.510074
CV (%)		1.95	3.62	2.46	25.21	1.55	1.99	2.01	2.55	2.01	2.78	3.11	1.16	1.63	1.699987

S: Sweet corn parents; **NS**: Non-sweet corn parents; **df**: degrees of freedom; **PH**: Plant height; **NOI**: Number of internodes; **PW**: Plant weight; **SW**: Stem weight; **SG**: Stem girth; **JV**: Juice volume; **JEP**: Juice extraction percentage; °**Bx**: °brix value; **TS**: Total sugars; **SP**: Sucrose per cent; **RS**: Reducing sugars; **CB**: cob °brix value.

Table 10: Analysis of variance for phenotypic traits recorded in hybrids at 20 DPSE

Source of variance	df	Mean sum of squares													
		PH	NOI	PW	NOC	CW	SW	SG	JV	JXP	°Bx	TS	SP	RS	CB
Hybrids	65	539.71**	3.18**	103262.08**	0.59**	36837.76**	17348.67**	19.61**	896.80**	164.47**	5.97**	8.08**	3.48**	1.91**	0.99**
S × NS	36	445.52**	3.52**	91033.24**	0.80**	38592.08**	20212.63**	26.19**	883.26**	214.53**	5.52**	6.78**	2.71**	2.49**	0.98**
NS × S	28	455.06**	2.32**	93930.10**	0.35**	35067.33**	12083.37**	9.80**	632.17**	89.42**	3.83**	4.23**	1.27**	0.88**	1.04**
S × NS vs NS × S	1	6300.63**	15.07**	804795.88**	0.02	23254.06**	61674.50**	57.51**	8794.11**	463.57**	82.32**	163.10**	92.99**	9.98**	0.05
Error	65	10.5	0.09	689.2	0.17	55.89	35.26	0.17	5.44	1.41	0.1	0.08	0.09	0.11	0.03
Sem±		2.29	0.22	18.56	0.29	5.29	4.2	0.29	1.65	0.84	0.22	0.2	0.21	0.24	0.11
CD@P=0.05*		6.47	0.63	52.43	0.82	14.93	11.86	0.83	4.66	2.37	0.64	0.56	0.6	0.67	0.32
CV (%)		1.53	2.68	2.51	19.04	1.75	1.59	1.54	2.76	2.43	3.73	2.77	5.22	8.01	1.17

S: Sweet corn parents; **NS**: Non-sweet corn parents; **df**: degrees of freedom; **PH**: Plant height; **NOI**: Number of internodes; **PW**: Plant weight; **SW**: Stem weight; **SG**: Stem girth; **JV**: Juice volume; **JEP**: Juice extraction percentage; °**Bx**: °brix value; **TS**: Total sugars; **SP**: Sucrose per cent; **RS**: Reducing sugars; **CB**: cob °brix value.

Table 11: Analysis of variance for phenotypic traits recorded in both parents and hybrids at 20 DPSE

Source of variance	df	Mean sum of squares												
		PH	NOI	PW	NOC	CW	SW	SG	JV	JXP	°Bx	TS	SP	RS
Genotypes	87	576.24*	3.2*	118299.33*	0.61*	48382.79*	18141.13*	20.64*	1044.41*	158.91*	5.76*	7.89*	3.67*	1.59*
S vs S × NS	1	1121.58*	1.99*	317017.04*	0.56	366689.24*	12080.66*	2.02*	1245.40*	30.21*	3.80*	3.58*	1.78*	0.02
S vs NS × S	1	8860.65*	19.23*	24862.61*	0.38	215192.24*	89667.43*	53.06*	11727.80*	132.24*	80.13*	138.81*	77.54*	5.46*
NS vs S × NS	1	6458.83*	7.70*	1933465.23*	4.10*	760834.46*	38217.01*	131.89*	15906.24*	4.4	16.20*	41.25*	23.47*	2.14*
NS vs NS × S	1	1018.34*	0.19	693238.97*	3.61*	583569.10*	2032.15*	45.89*	4529.82*	217.08*	1.97*	1.52*	0.87*	0.18
Error	87	12.15	0.12	644.65	0.19	46.18	40.9	0.2	3.6	1.23	0.1	0.09	0.07	0.08
Sem±		2.46	0.25	17.95	4.81	4.81	4.52	0.31	1.34	0.78	0.22	0.21	0.19	0.21
CD@P=0.05*		6.93	0.69	50.47	13.51	13.51	12.71	0.88	3.77	2.2	0.61	0.58	0.52	0.58
CV (%)		1.64	2.93	2.52	1.75	1.75	1.69	1.66	2.24	2.26	3.51	2.87	4.47	6.94

S: Sweet corn; **NS**: Non-sweet corn; **df**: degrees of freedom; **PH**: Plant height; **NOI**: Number of internodes; **PW**: Plant weight; **SW**: Stem weight; **SG**: Stem girth; **JV**: Juice volume; **JEP**: Juice extraction percentage; °**Bx**: °brix value; **TS**: Total sugars; **SP**: Sucrose per cent; **RS**: Reducing sugars.

4.2.2 Performance of genotypes

The genetic variability parameters *viz*., minimum, maximum, mean, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability in broad sense (h^2) and genetic advance as per cent mean (GAM) for soluble sugar content in the stalk and related traits of all the genotypes grown in summer-2015 are presented in Tables 12, 13 and 14.

The phenotypic performance of individual genotypes with respect to juice content, juice extraction percentage and soluble sugars of the stem are represented in the fig. 2-8.

4.2.2.1 Days to 50 per cent anthesis

The range of variation for days to 50 per cent anthesis was varied among different category of corn genotypes taken for the study. The range of days to 50 per cent anthesis in sweet corn parents was 49.5 (MAI-289) to 55.5 (MAI-286) with an average of 51.97 days, while, that of non-sweet corn parents ranged from 53.5 (BGUDI-81) to 56.5 (BGUDI-80), with an average of 55.07 days. For crosses of above mentioned parents *viz*. sweet × non-sweet corn, it was ranged from 48 (K-4571 × BGUDI-13) to 57 (MAI-325 × MAI-7) with an average of 52.36 days and for non-sweet corn × sweet corn from 51 (BGIDI-13 × MAI-285) to 57 (BGUDI-10 × K-4356-1) with an average of 53.78 days.

Phenotypic coefficient of variation (PCV) of 2.91 per cent, genotypic coefficient of variation (GCV) of 7.58 per cent, broad sense heritability of 14.71 per cent and genetic advance as per cent of mean (GAM) of 2.30 per cent was recorded for this trait.

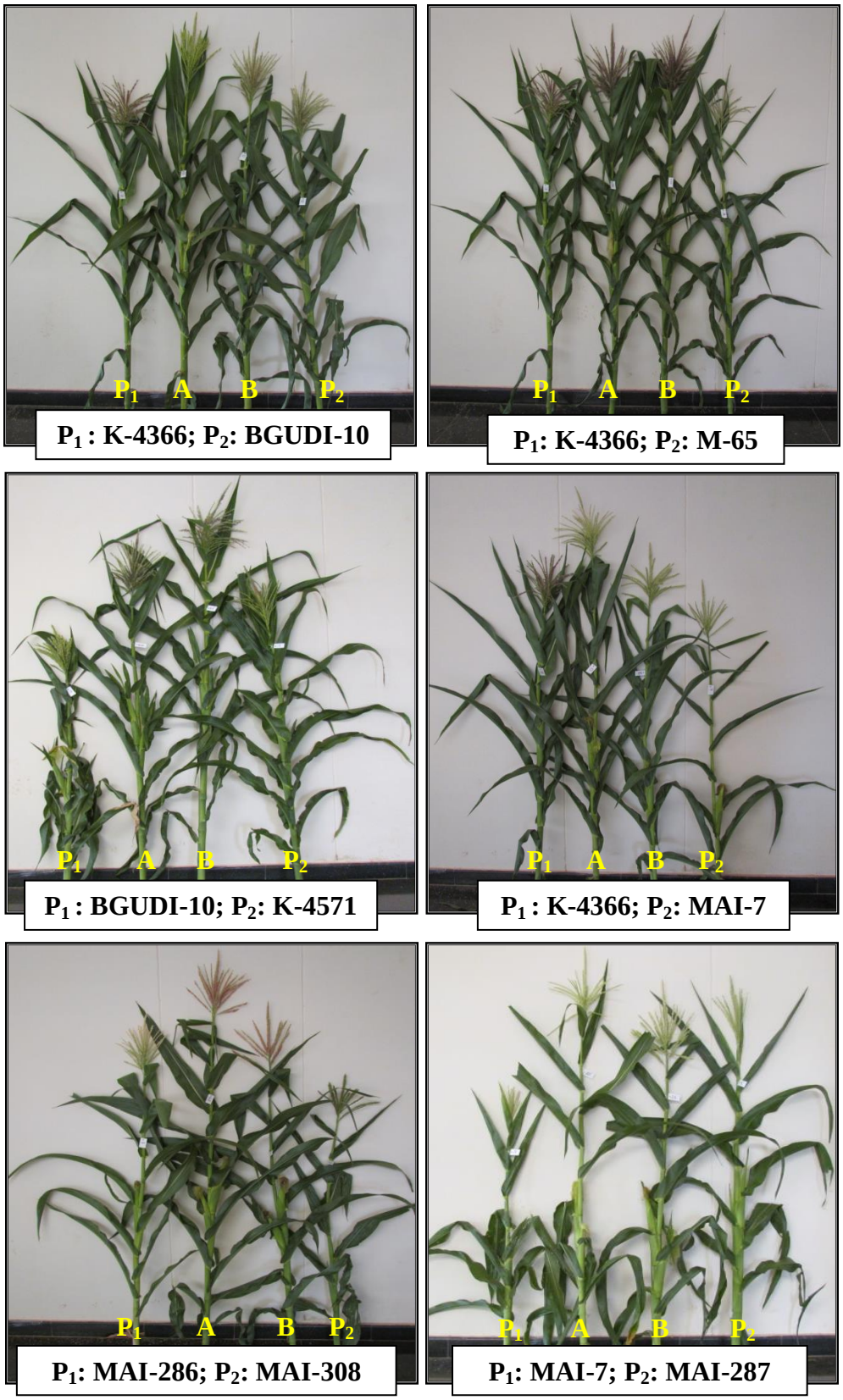
4.2.2.2 Plant height (cm)

Plant height at 10 DPSE ranged from 172.5 (K-4673-1) to 238.00 (MAI-102) across the 89 genotypes studied, with an average of 216.07, 185.29, 215.85 and 198.43 cm for sweet corn, non-sweet corn, sweet × non-sweet corn and non-sweet corn × sweet corn genotypes respectively. While, average plant height of sweet corn, non-sweet corn, sweet × non-sweet corn and non-sweet corn × sweet corn at 20d PSE was 224.60, 195.86, 217.53 and 200.66 respectively, with the range of 180.50 (BGUDI-10) to 245.00 (MAI-284 × M-65) among all the genotypes.

GCV and PCV of 8.4 and 8.83 respectively, high h^2 of 90.55 and moderate GAM of 16.46 was recorded at 10 DPSE. At 20 DPSE 8.02, 8.18, 95.92 and 16.17 per cent of GCV, PCV, h^2 and GAM respectively was observed.

4.2.2.3 Number of internodes

Number of internodes at 10 DPSE ranged from 9.50 (BGUDI-10) to 14.50 (MAI-285 × MAI-7) among all the genotypes studied, with an average of 11.83, 11.07, 11.78 and 12.28 for sweet corn, non-sweet corn, sweet × non-sweet corn and non-sweet corn × sweet corn genotypes respectively. While, average number of internodes of sweet corn, non-sweet corn, sweet × non-sweet corn and non-sweet corn × sweet corn at 20d PSE

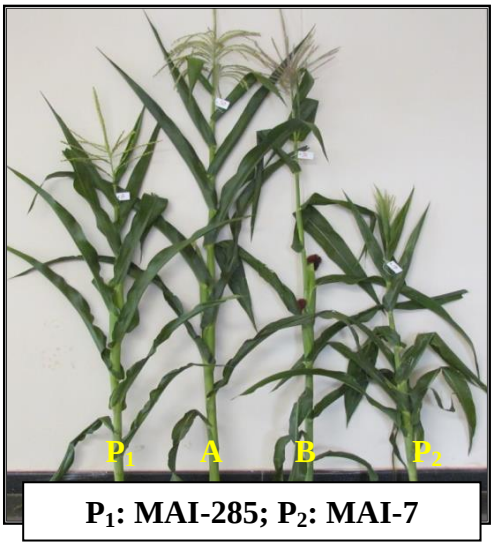


A: P_1× P_2; B: P_2 × P_1

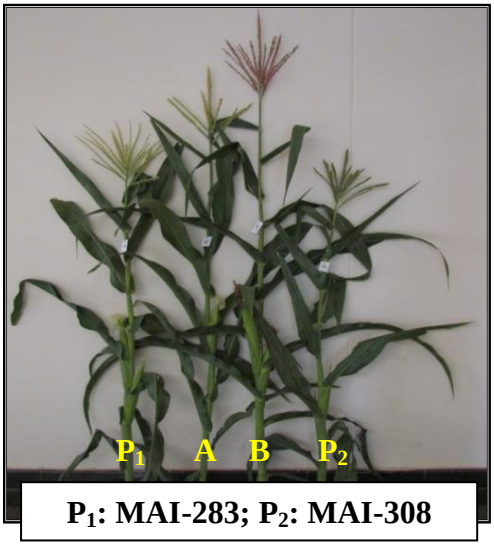
Plate 7: A view of direct and reciprocal F_1 plants with their parents

P_1: K-4571; P_2: M-65

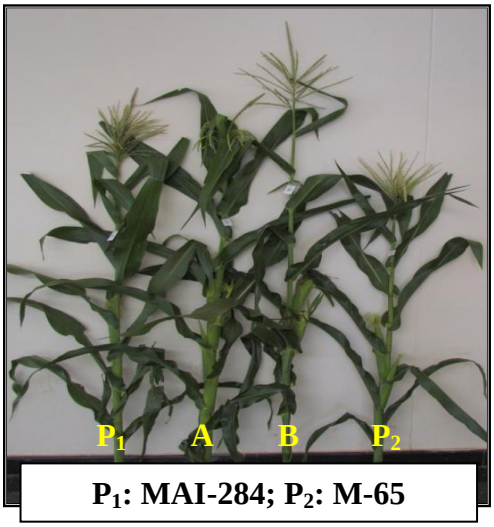
P_1: MAI-285; P_2: BGUDI-13



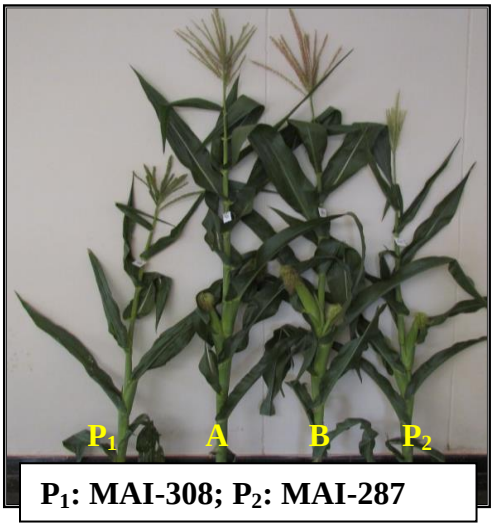
P_1: MAI-285; P_2: MAI-7



P_1: MAI-283; P_2: MAI-308



P_1: MAI-284; P_2: M-65



P_1: MAI-308; P_2: MAI-287

A: $P_1 \times P_2$; B: $P_2 \times P_1$

Plate 7: contd…..

Table 12: Phenotypic performance of parents and hybrids at 10 DPSE

Traits	Sweet corn			Non-sweet corn			Sweet × Non-sweet corn			Non-sweet corn × sweet corn		
	Min	Max	Mean±Sem	Min	Max	Mean±Sem	Min	Max	Mean±Sem	Min	Max	Mean±Sem
DTF	49.50	55.50	51.97±6.32	53.50	56.50	55.07±0.35	48.00	57.00	52.36±0.38	51.00	57.00	53.78±0.20
PH (cm)	203.50	236.00	216.07±4.67	173.50	199.50	185.29±4.38	172.50	238.00	215.85±2.63	158.00	229.50	198.43±4.01
NOI	10.50	13.00	11.83±0.49	9.50	12.00	11.07±0.45	9.50	14.50	11.78±0.47	10.00	14.00	12.28±0.53
PW (g)	538.00	1228.50	847.07±38.65	372.00	662.50	522.79±19.72	612.00	1239.00	931.23±36.23	426.50	959.00	695.12±54.20
NOC	1.00	3.50	1.9±0.34	1.00	2.00	1.5±0.45	1.00	2.50	1.72±.038	1.00	3.50	1.83±0.30
CW (g)	55.50	453.00	179.17±32.30	51.00	242.50	163.14±33.13	50.50	992.50	277.38±54.26	96.00	460.50	235.6±38.24
SW (g)	335.50	704.00	538.53±20.61	209.00	327.00	254.14±13.13	307.00	620.25	466.47±22.80	213.75	481.25	348.47±19.02
SG (mm)	19.80	30.88	25.88±0.41	21.19	26.25	22.67±0.31	21.95	35.36	28.14±0.92	19.58	31.83	25.48±1.52
JV (mL)	56.50	153.00	103.4±4.62	41.00	92.00	68.43±4.16	40.50	170.50	99.97±5.89	25.00	129.50	59.62±5.50
JXP	40.36	82.76	68.26±4.61	38.89	69.58	48.62±5.32	34.48	79.45	49.79±0.03	13.24	74.80	47.5±0.12
˚Bx	8.05	12.55	9.9±0.21	7.50	10.50	8.45±0.41	6.20	12.75	9.01±0.66	4.75	11.00	7.63±0.21
RS (%)	2.45	4.76	3.39±0.23	2.20	3.86	2.88±0.44	1.59	4.94	2.96±0.14	0.51	4.08	2.25±0.11
SP	5.77	8.28	6.81±0.19	5.07	6.69	5.83±0.07	5.24	7.87	0.02±0.09	4.27	7.02	5.57±0.13
TS (%)	8.36	13.25	10.31±0.20	7.77	10.93	8.77±0.14	7.12	13.27	9.49±0.20	4.90	11.34	7.91±0.23

DTF: Days to 50 per cent flowering; **PH**: Plant height; **NOI**: Number of internodes; **PW**: Plant weight; **SW**: Stem weight; **SG**: Stem girth; **JV**: Juice volume; **JEP**: Juice extraction percentage; °**Bx**: °brix value; **TS**: Total sugar; **SP**: Sucrose per cent; **RS**: Reducing sugars.

Table 13: Phenotypic performance of parents and hybrids at 20 DPSE

Traits	Sweet corn			Non-sweet corn			Sweet × Non-sweet corn			Non-sweet corn × sweet corn		
	Min	Max	Mean±Sem	Min	Max	Mean±Sem	Min	Max	Mean±Sem	Min	Max	Mean±Sem
PH (cm)	205.50	243.00	224.6±2.27	180.50	214.00	195.86±4.06	182.50	245.00	217.53±1.49	164.50	217.50	200.66±1.14
NOI	9.50	14.00	12.4±0.27	9.50	12.50	11.29±0.41	9.50	14.00	11.88±0.18	10.00	14.00	12.03±0.21
PW (g)	106.25	1147.00	185.6±16.15	100.25	115.00	107.43±13.10	700.91	1495.33	1113.4±8.76	537.82	1449.07	956.07±22.69
NOC	1.00	3.00	2±0.33	1.00	2.50	1.57±0.27	1.00	3.50	1.97±0.26	1.00	3.50	1.98±0.31
CW (g)	74.00	547.00	308.87±3.09	51.50	477.50	185.71±2.29	0.11	748.50	421.91±3.68	177.00	674.00	413.19±2.61
SW (g)	254.12	507.26	416.36±4.51	138.36	526.11	335.6±6.95	131.64	565.52	392.57±2.63	209.42	533.45	349.02±2.35
SG (mm)	21.75	32.16	27.74±0.32	18.96	28.70	24.09±0.48	21.95	35.36	28±0.20	23.05	29.57	25.45±0.18
JV (ml)	48.85	120.50	96.45±1.59	21.50	103.00	55.21±1.55	46.30	134.00	96.19±2.04	19.00	129.50	59.86±0.54
JXP	31.22	96.30	52.41±0.07	38.54	64.01	51.05±1.06	8.64	73.27	50.44±0.73	24.14	61.78	46.66±0.74
˚Bx	8.05	12.55	9.77±0.19	6.85	10.50	8.17±0.17	7.05	13.35	9.34±0.15	4.75	10.15	7.75±0.29
TS (%)	9.42	14.56	11.45±0.06	8.06	11.27	9.16±0.03	7.91	13.91	11.04±0.07	6.05	11.98	8.8±0.05
RS (%)	3.25	5.38	4.39±0.06	3.43	5.02	3.99±0.04	2.06	6.23	4.41±0.16	2.62	5.29	3.86±0.19
SP	4.92	9.16	6.77±0.22	4.21	6.18	5.07±0.23	3.81	8.32	6.48±0.22	3.30	6.51	4.79±0.21
CB	13.7	15.4	14.69±0.17	12.95	14.70	13.86±0.18	12.30	15.30	13.92±0.12	12.45	15.60	13.96±0.09

PH: Plant height; **NOI**: Number of internodes; **PW**: Plant weight; **SW**: Stem weight; **SG**: Stem girth; **JV**: Juice volume; **JEP**: Juice extraction percentage; **˚Bx**:˚brix value; **TS**: Total sugar; **SP**: Sucrose per cent; **RS**: Reducing sugar percent; **CB**: cob °brix value.

Table 14: Estimates of genetic parameters for phenotypic traits at two phases of harvest

At 10 DPSE					At 20 DPSE				
Traits	**GCV (%)**	**PCV (%)**	**h^2 (%)**	**GAM (%)**	**Traits**	**GCV (%)**	**PCV (%)**	**h^2 (%)**	**GAM (%)**
DTF	2.91	7.58	14.71	2.3	**PH**	8.02	8.18	95.92	16.17
PH	8.4	8.83	90.55	16.46	**NOI**	10.61	11	93.02	21.07
NOI	8.13	10.2	63.47	13.34	**PW**	24.43	24.56	98.95	50.07
PW	24.83	25.99	91.23	48.85	**NOC**	22.13	30.46	52.82	33.14
NOC	22.73	36.23	39.36	29.37	**CW**	39.82	39.85	99.81	81.94
CW	53.59	60.65	78.06	97.53	**SW**	25.59	25.65	99.55	52.6
SW	31.92	32.72	95.17	64.14	**SG**	11.91	12.03	98.07	24.29
SG	12.24	13.79	78.85	22.4	**JV**	26.95	27.09	98.99	55.24
JV	37.01	38.17	94.02	73.93	**JXP**	18.07	18.13	99.31	37.09
JXP	26.83	27.64	94.21	53.65	**°Bx**	19.43	19.74	96.89	39.4
°Bx	19.94	20.29	96.56	40.37	**SP**	22.9	23.34	96.35	46.31
SP	13.8	14.14	95.18	27.73	**RS**	23.38	24.35	92.17	46.23
RS	32.89	33.82	94.57	65.88	**CB**	5.05	5.24	92.79	10.02
TS	20.1	20.49	96.3	40.64	**TS**	19.51	19.71	97.91	39.76

GCV: Genetic co-efficient of variation; **PCV**: Phenotypic co-efficient of variation; **h^2**: Heritability; **GAM**: Genetic advance for mean; **PH**: Plant height; **NOI**: Number of internodes; **PW**: Plant weight; **SW**: Stem weight; **SG**: Stem girth; **JV**: Juice volume; **JEP**: Juice extraction percentage; **°Bx**: °brix value; **TS**: Total sugar; **SP**: Sucrose per cent; **RS**: Reducing sugars; **CB**: cob °brix value.

were 12.40, 11.29, 11.88 and 12.03 respectively, with the range of 9.5 (MAI-7, BGUDI-10) to 14.5 (MAI-286 × MAI-308) among all the genotypes.

GCV and PCV of 8.13 and 10.20 respectively and h^2 of 63.47 with the moderate GAM of 13.34 was recorded at 10 DPSE. At 20 DPSE 10.61, 11.00, 93.02 and 21.07 per cent of GCV, PCV, h^2 and GAM respectively was observed.

4.2.2.4 Plant weight (g)

Plant weight ranged from 372.00 (MAI-7) to 1239.00 (MAI-284 × M-65) at 10 DPSE with an average of 847.07, 522.79, 931.23 and 695.12 for sweet corn, non-sweet corn, sweet × non-sweet corn and non-sweet × sweet corn genotypes respectively. While, average plant weight of sweet corn, non-sweet corn, sweet × non-sweet corn and non-sweet corn × sweet corn at 20 DPSE were 991.53, 708.14, 1113.40 and 956.07 respectively, with the range of 378.5 (MAI-7) to 1495.33 (K-4571 × BGUDI-81) among all the genotypes.

At 10 DPSE the GCV, PCV, h^2 and GAM recorded were 24.83, 25.99, 91.23 and 48.85 respectively. At 20 DPSE GCV of 24.43 per cent, PCV of 24.56 per cent, h^2 of 98.95 per cent and GAM of 50.07 per cent were observed.

4.2.2.5 Number of cobs

Number of cobs at 10 DPSE ranged from 1.00 (MAI-14) to 3.50 (MAI-285) among all the genotypes studied, with an average of 1.90, 1.50, 1.72 and 1.83 for sweet corn, non-sweet corn, sweet × non-sweet corn and non-sweet corn × sweet corn genotypes respectively. While, average number of cobs of sweet corn, non-sweet corn, sweet × non-sweet corn and non-sweet corn × sweet corn at 20 DPSE were 2.00, 1.57, 1.97 and 1.98 respectively, with the range of 1.00 (MAI-308 × MAI-284) to 3.50 (MAI-287 × MAI-308) among all the genotypes.

GCV and PCV of 22.73 and 36.23 respectively, h^2 of 39.36 and GAM of 29.37 were recorded at 10 DPSE. At 20 DPSE 22.13, 30.46, 52.82 and 33.14 per cent of GCV, PCV, h^2 and GAM respectively was observed.

4.2.2.6 Cob weight (g)

Cob weight of individual plants ranged from 50.50 (MAI-285 × MAI-7) to 992.50 (MAI-283 × MAI-308) at 10 DPSE with an average of 179.17, 163.14, 277.38 and 235.60 for sweet corn, non-sweet corn, sweet × non-sweet corn and non-sweet × sweet corn genotypes respectively. While, average cob weight of sweet corn, non-sweet corn, sweet × non-sweet corn and non-sweet corn × sweet corn at 20 DPSE were 308.87, 185.71, 421.91 and 413.19 respectively, with the range of 51.50 (M-65) to 748.50 (MAI-287 × MAI-308) among all the genotypes.

At 10 DPSE the GCV, PCV, h^2 and GAM per cent recorded were 53.59, 60.65, 78.06 and 97.53 per cent respectively. At 20 DPSE GCV of 39.82 per cent, PCV of 39.85 per cent, h^2 of 99.81 per cent and GAM of 81.94 per cent were recorded.

4.2.2.7 Stem weight (g)

Stem weight ranged from 209.00 (BGUDI-81) to 704.00 (K-4356-1) at 10 DPSE with an average 538.53, 254.14, 466.47 and 348.47 for sweet corn, non-sweet corn, sweet × non-sweet corn and non-sweet × sweet corn genotypes respectively. While, average stem weight of sweet corn, non-sweet corn, sweet × non-sweet corn and non-sweet corn × sweet corn at 20 DPSE were 416.36, 335.60, 392.57 and 349.02 respectively, with the range of 131.64 (MAI-289 × MAI-7) to 565.52 (K-4571 × BGUDI-13) among all the genotypes.

At 10 DPSE the GCV, PCV, h^2 and GAM recorded were high as 31.92, 32.72 95.17 and 64.14 per cent respectively. At 20 DPSE GCV of 25.59 per cent, PCV of 25.65 per cent, h^2 of 99.55 per cent and GAM of 52.60 per cent were observed.

4.2.2.8 Stem girth (mm)

Stem girth at 10 DPSE ranged from 19.80 (MAI-289) to 35.36 (MAI-14 × MAI-308) among all the genotypes studied, with an average of 25.88, 22.67, 28.14 and 25.48 for sweet corn, non-sweet corn, sweet × non-sweet corn and non-sweet corn × sweet corn genotypes respectively. While, average stem girth of sweet corn, non-sweet corn, sweet × non-sweet corn and non-sweet corn × sweet corn at 20 DPSE were 27.74, 24.09, 28.00 and 25.45 respectively, with the range of 18.96 (M-65) to 35.36 (MAI-14 × MAI-308) among all the genotypes.

Moderate GCV and PCV of 12.24 and 13.79 per cent respectively, high h^2 and GAM of 78.85 and 22.4 per cent were recorded at 10 DPSE. At 20 DPSE 11.91, 12.03, 98.07 and 24.29 per cent of GCV, PCV, h^2 and GAM respectively were observed.

4.2.2.9 Juice volume (mL)

Juice volume ranged from 25.00 (MAI-308 × MAI-286) to 170.50 (MAI-284 × M-65) at 10 DPSE with an average 103.40, 68.43, 99.97 and 59.62 for sweet corn, non-sweet corn, sweet × non-sweet corn and non-sweet × sweet corn genotypes respectively. While, average juice volume of sweet corn, non-sweet corn, sweet × non-sweet corn and non-sweet corn × sweet corn at 20 DPSE were 96.45, 55.21, 96.19, 59.86 respectively, with the range of 19.00 (MAI-308 × MAI-286) to 134.00 (MAI-283 × BGUDI-13) among all the genotypes.

At 10 DPSE the GCV, PCV, h^2 and GAM recorded were high as 37.01, 38.17, 94.02 and 73.93 per cent respectively. At 20 DPSE GCV of 26.95 per cent, PCV of 27.09 per cent, h^2 of 98.99 per cent and GAM of 55.24 per cent recorded were all high in range.

4.2.2.10 Juice extraction percentage

Juice extraction percentage ranged from 13.24 (M-65 × K-4571) to 82.76 (MAI-102) at 10 DPSE with an average 68.26, 48.6, 49.79 and 47.50 for sweet corn, non-sweet corn, sweet × non-sweet corn and non-sweet × sweet corn genotypes respectively. While, average juice extraction percentage of sweet corn, non-sweet corn, sweet × non-sweet corn and non-sweet corn × sweet corn at 20 DPSE were 52.41, 51.05, 50.44 and 46.66

correspondingly, with the range of 8.64 (MAI-102 × MAI-7) to 96.30 (MAI-14) among all the genotypes.

At 10 DPSE the GCV, PCV, h^2 and GAM recorded were as high as 26.83, 27.64, 94.21 and 53.65 per cent respectively. At 20 DPSE moderate GCV and PCV of 18.07 and 18.13 per cent respectively, high h^2 and GAM of 99.31 and 37.09 per cent correspondingly were observed.

4.2.2.11 °Brix

°Brix at 10 DPSE ranged from 4.75 (MAI-308 × MAI-287) to 12.75 (MAI-283 × BGUDI-13) among all the genotypes studied, with an average of 9.90, 8.45, 9.01 and 7.63 for sweet corn, non-sweet corn, sweet × non-sweet corn and non-sweet corn × sweet corn genotypes respectively. While, average °brix of sweet corn, non-sweet corn, sweet × non-sweet corn and non-sweet corn × sweet corn at 20 DPSE were 9.77, 8.17, 9.34 and 7.75 respectively, with the range of 4.75 (MAI-308 × MAI-287) to 13.35 (MAI-289 × MAI-7) among all the genotypes.

It was observed that, moderate GCV of 19.94 and high PCV, h^2 and GAM of 20.29, 96.56 and 40.37 per cent respectively were recorded at 10 DPSE. At 20 DPSE 19.43 and 19.74 per cent of moderate GCV and PCV, 96.89 and 39.40 per cent of high h^2 and GAM correspondingly were observed.

4.2.2.12 Total sugars

Total sugar percentage ranged from 4.90 (MAI-308 × MAI-287) to 13.27 (MAI-283 × BGUDI-13) at 10 DPSE with an average 10.31, 8.77,9.49 and 7.91 for sweet corn, non-sweet corn, sweet × non-sweet corn and non-sweet × sweet corn genotypes respectively. While, average total sugars of sweet corn, non-sweet corn, sweet × non-sweet corn and non-sweet corn × sweet corn at 20 DPSE were 11.45, 9.16, 11.04 and 8.80 respectively, with the range of 6.05 (MAI-308 × MAI-287) to 14.56 (K-4673-1) among all the genotypes.

At 10 DPSE the GCV, PCV, h^2 and GAM recorded were as high as 20.10, 20.49, 96.30 and 40.64 per cent respectively and were high in range. At 20 DPSE moderate GCV and PCV of 19.51 and 19.71 per cent, high h^2 and GAM of 97.91 and 39.76 per cent recorded were high in range.

4.2.2.13 Sucrose percentage

Sucrose percentage ranged from 0.51 (MAI-308 × MAI-287) to 4.94 (MAI-283 × BGUDI-13) at 10 DPSE with an average 3.39, 2.88, 2.96 and 2.25 for sweet corn, non-sweet corn, sweet × non-sweet corn and non-sweet × sweet corn genotypes respectively. While, average sucrose percentage of sweet corn, non-sweet corn, sweet × non-sweet corn and non-sweet corn × sweet corn at 20 DPSE were 6.77, 5.07, 6.48 and 4.79 respectively, with the range of 3.30 (MAI-308 × MAI-287) to 9.16 (K-4673-1) among all the genotypes.

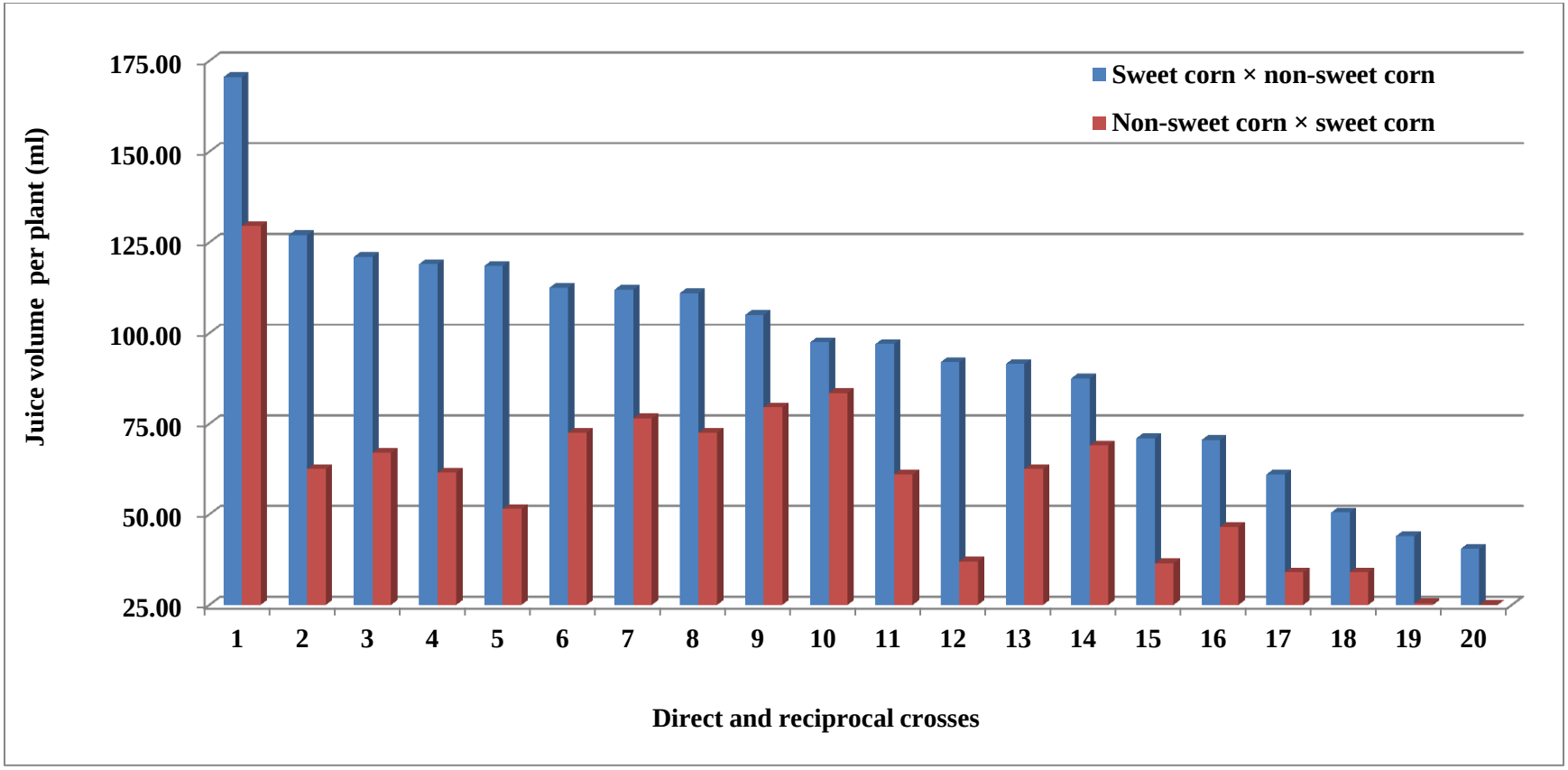


Fig. 2: Stem juice content of both direct and reciprocal hybrids of corn

	1	2	3	4	5	6	7	8	9	10
Sweet corn	MAI-284	K-4571	K-4356-1	MAI-286	MAI-285	MAI-284	K-4366-1	K-4571	MAI-292	K-4571
Non-sweet corn	M-65	BGUDI-13	BGUDI-10	MAI-7	MAI308	BGIDI-13	M-65	BGUDI-10	MAI-308	M-65
	11	12	13	14	15	16	17	18	19	20
Sweet corn	MAI-285	K-4366-1	MAI-285	K-4366-1	MAI-284	MAI-283	MAI -287	MAI -287	MAI-284	MAI-286
Non-sweet corn	BGUDI-13	MAI-7	MAI-7	BGUDI-10	MAI-308	MAI-308	MAI -7	MAI-308	MAI-7	MAI-308

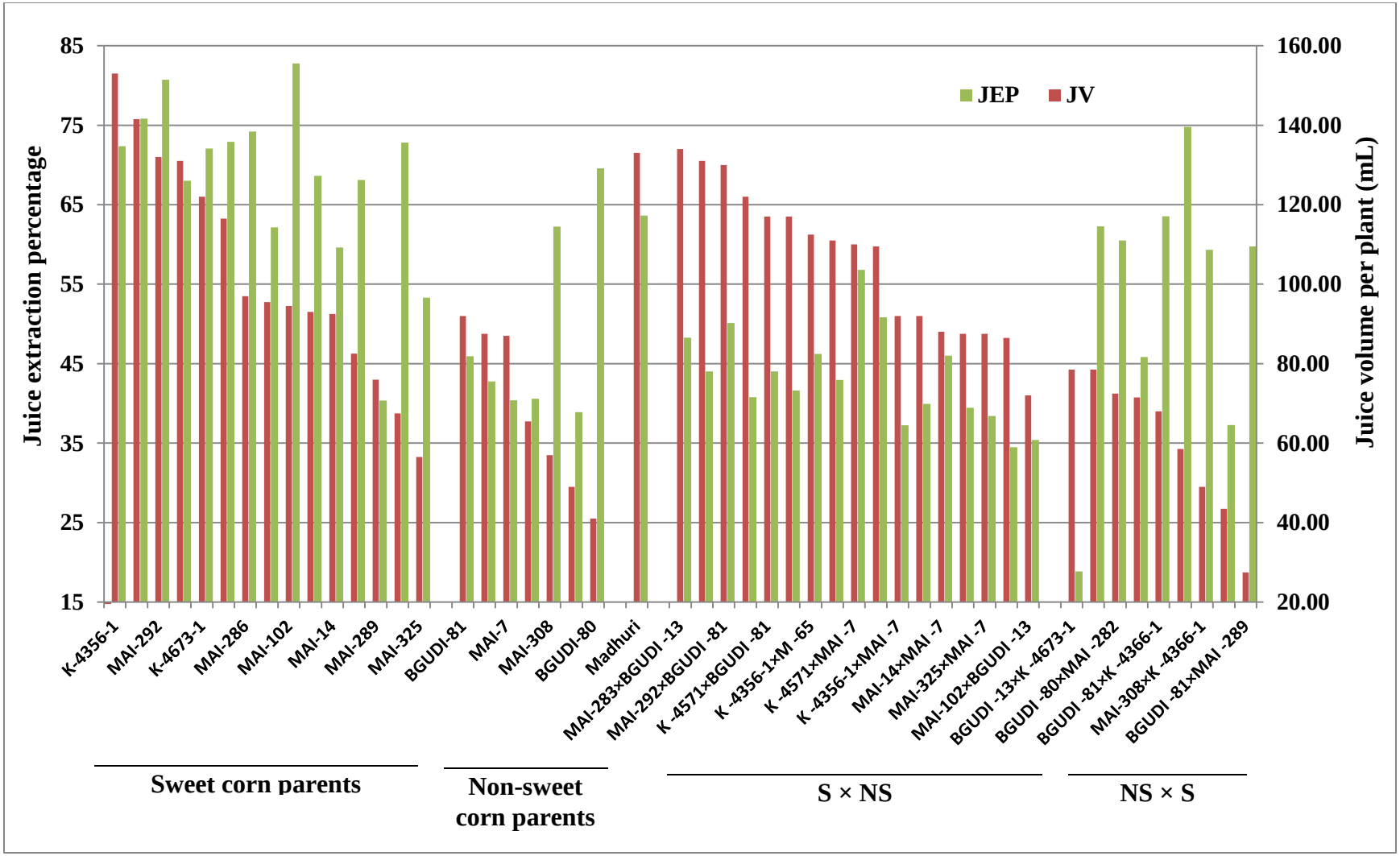


Fig. 3: Juice volume and juice extraction percentage of both parents and crosses along with check

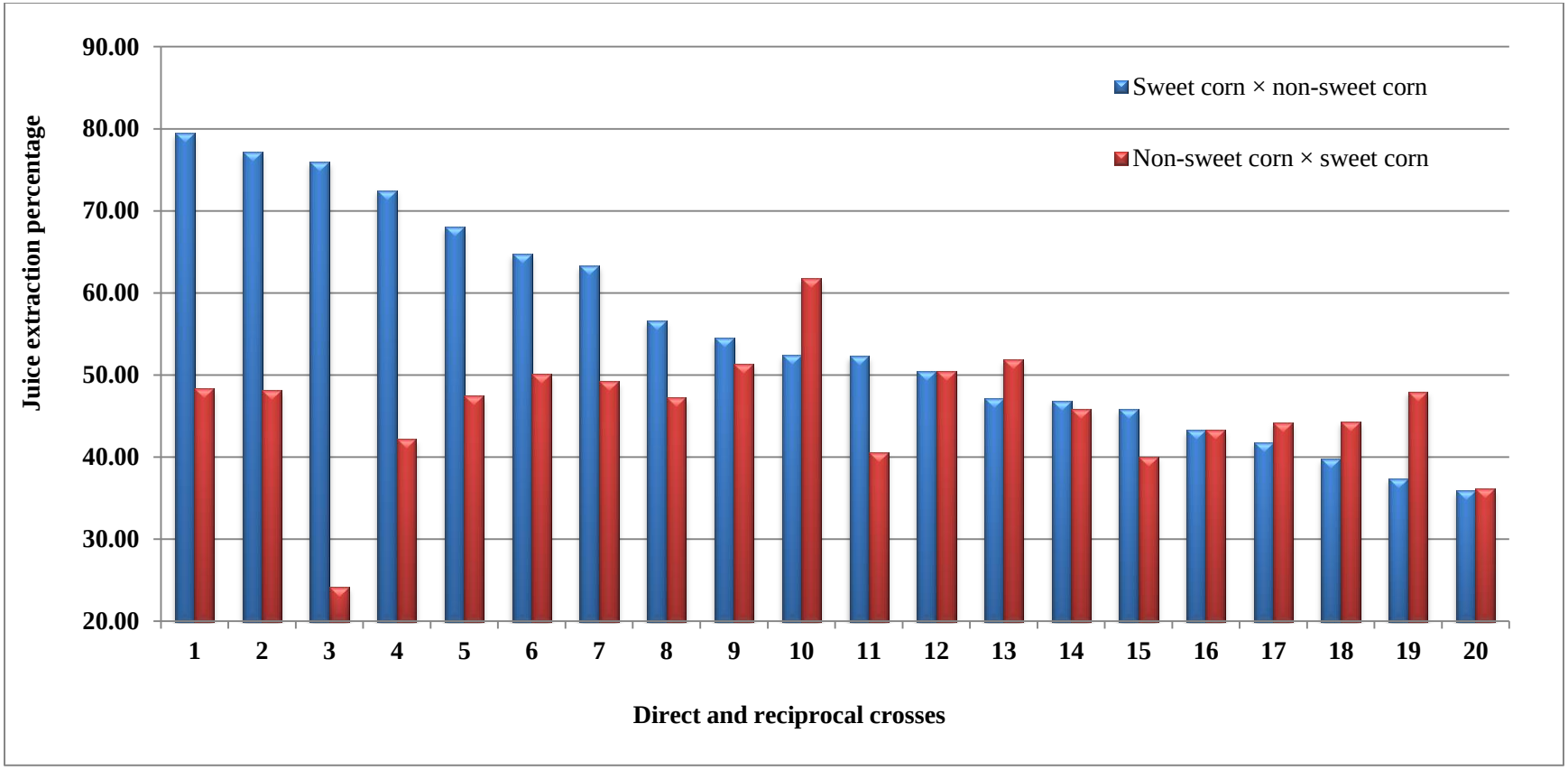


Fig. 4: Juice extraction percentage of both direct and reciprocal hybrids

	1	2	3	4	5	6	7	8	9	10
Sweet corn	MAI-283	K-4571	K-4356-1	MAI-284	K-4571	MAI-287	K-4366-1	MAI-284	MAI-286	MAI -287
Non-sweet corn	MAI-308	M-65	BGUDI-10	MAI-308	BGUDI-10	MAI-308	M-65	M-65	MAI-308	MAI -7
	11	**12**	**13**	**14**	**15**	**16**	**17**	**18**	**19**	**20**
Sweet corn	K-4366-1	K-4366-1	MAI-285	MAI-285	MAI-284	MAI-284	MAI-286	K-4571	MAI-285	MAI-292
Non-sweet corn	MAI-7	BGUDI-10	BGUDI-13	MAI308	MAI-7	BGIDI-13	MAI-7	BGUDI-13	MAI-7	MAI-308

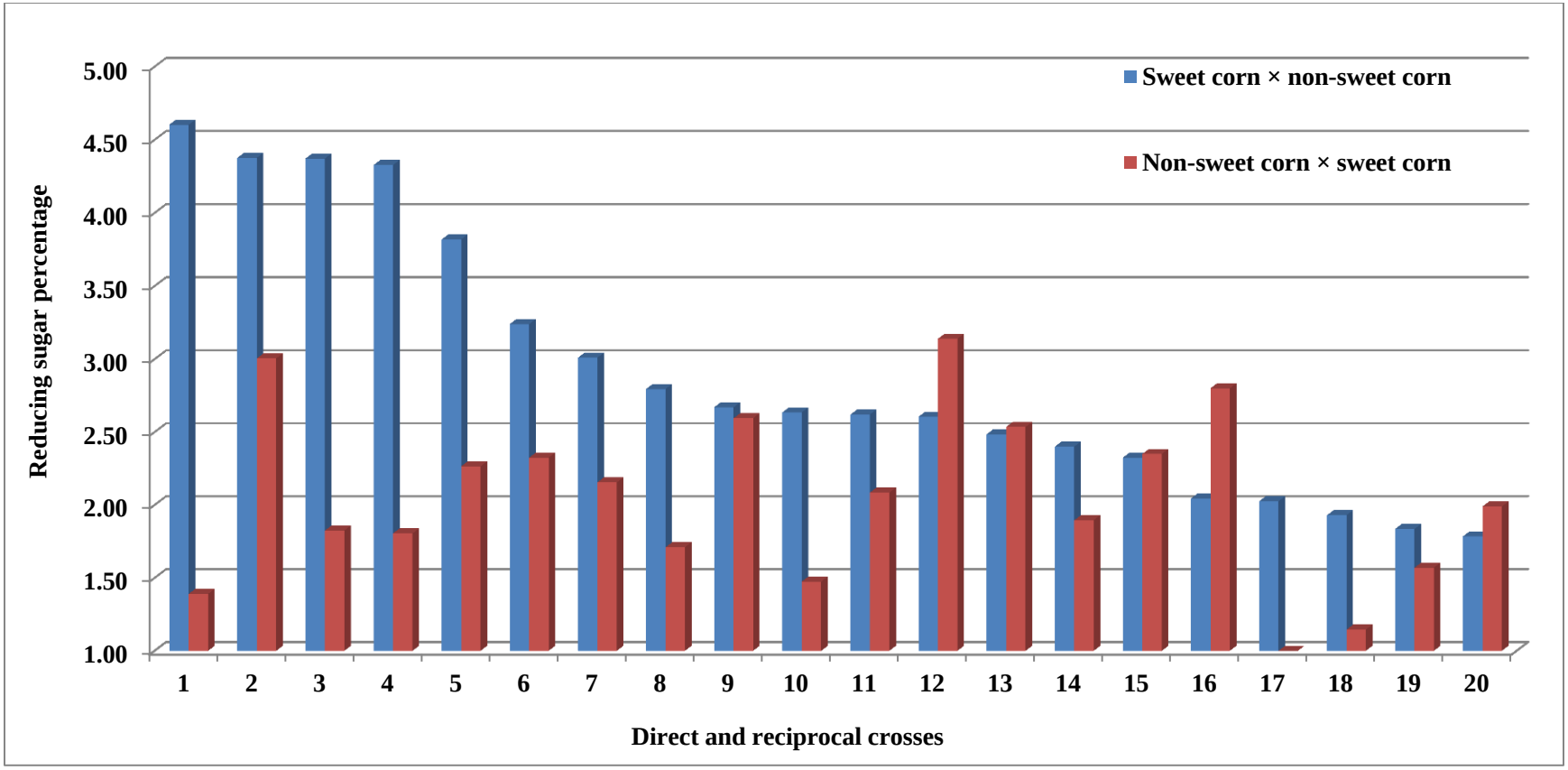


Fig. 5: Reducing sugar percentage of both direct and reciprocal hybrids

	1	2	3	4	5	6	7	8	9	10
Sweet corn	MAI-284	MAI-284	MAI-285	MAI-285	MAI-284	K-4571	K-4366-1	MAI -287	K-4366-1	K-4356-1
Non-sweet corn	M-65	BGIDI-13	MAI-7	BGUDI-13	MAI-7	M-65	BGUDI-10	MAI -7	MAI-7	BGUDI-10
	11	12	13	14	15	16	17	18	19	20
Sweet corn	MAI-286	MAI-286	MAI-292	MAI-283	MAI-285	MAI-284	MAI-287	K-4571	K-4366-1	K-4571
Non-sweet corn	MAI-7	MAI-308	MAI-308	MAI-308	MAI308	MAI-308	MAI-308	BGUDI-10	M-65	BGUDI-13

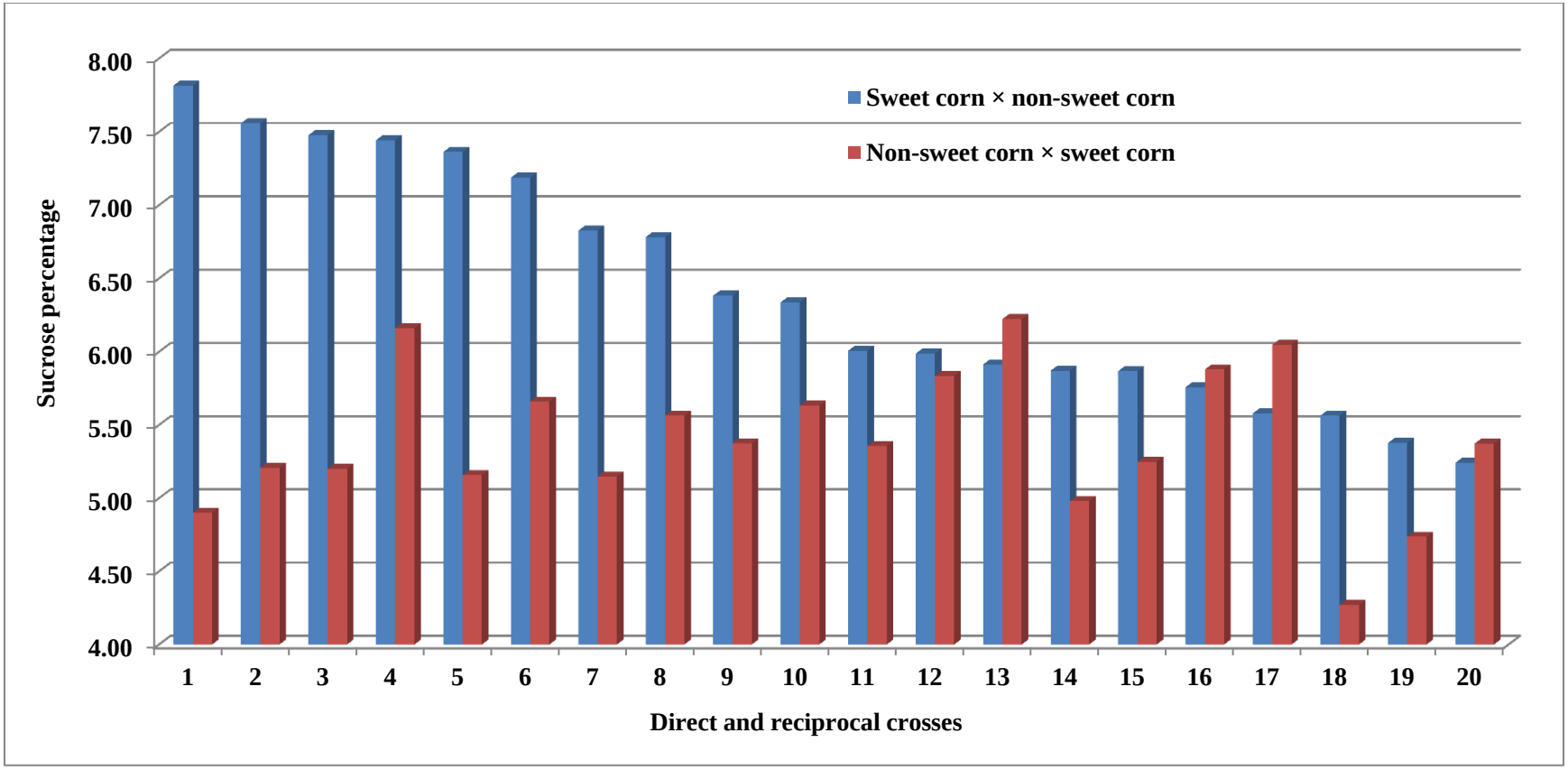


Fig. 6: Sucrose percentage of both direct and reciprocal hybrids

	1	2	3	4	5	6	7	8	9	10
Sweet corn	MAI-284	MAI-285	MAI-285	MAI-284	MAI -287	MAI-285	K-4366-1	MAI-284	K-4366-1	K-4571
Non-sweet corn	M-65	BGUDI-13	MAI-7	BGIDI-13	MAI -7	MAI308	M-65	MAI-7	BGUDI-10	M-65
	11	12	13	14	15	16	17	18	19	20
Sweet corn	MAI-283	K-4366-1	MAI-286	K-4356-1	MAI-286	MAI-292	MAI-284	MAI-287	K-4571	K-4571
Non-sweet corn	MAI-308	MAI-7	MAI-308	BGUDI-10	MAI-7	MAI-308	MAI-308	MAI-308	BGUDI-10	BGUDI-13

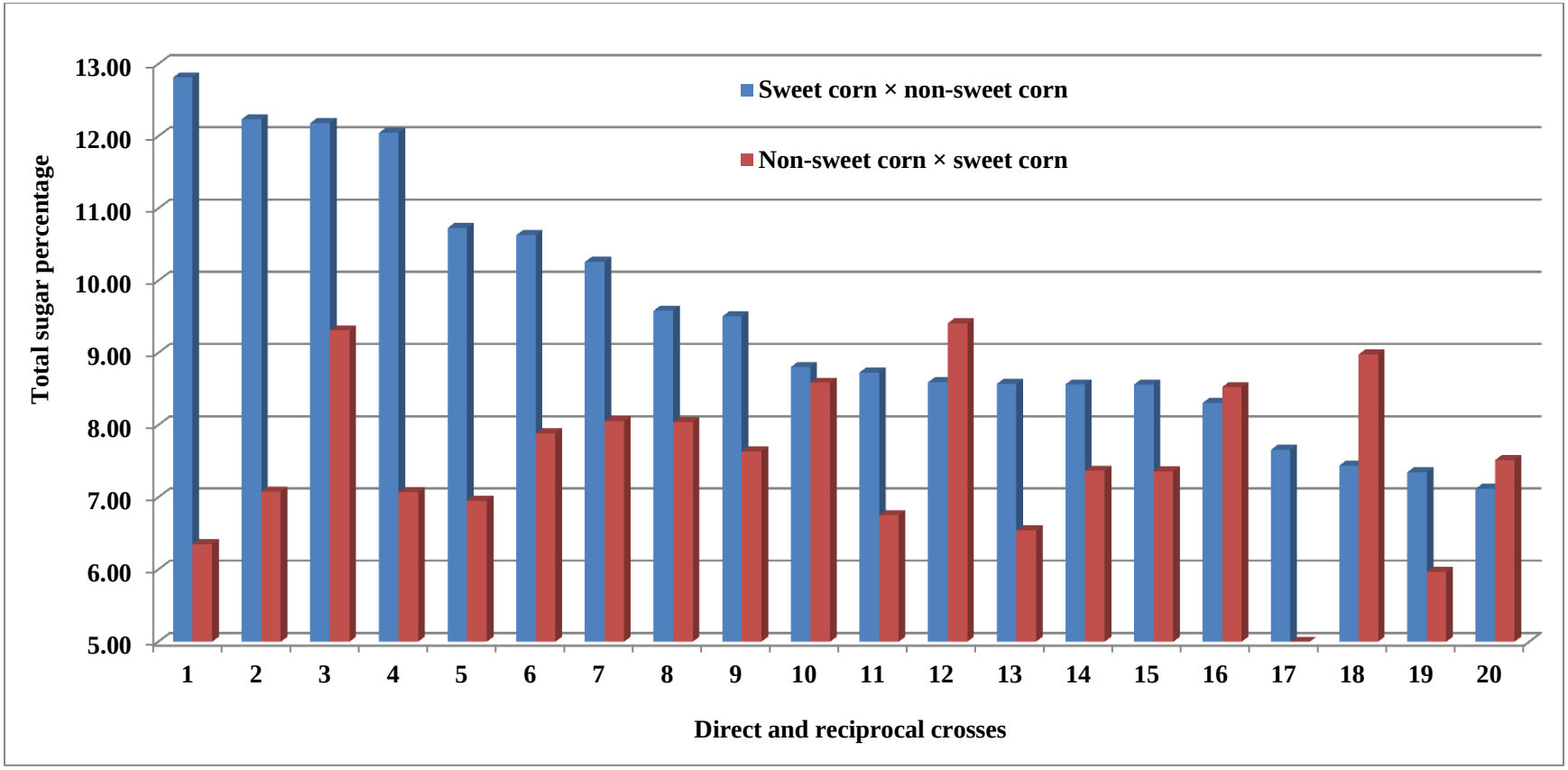


Fig. 7: Total sugars of both direct and reciprocal hybrids

	1	2	3	4	5	6	7	8	9	10
Sweet corn	MAI-284	MAI-285	MAI-284	MAI-285	MAI -287	MAI-284	MAI-285	K-4571	K-4366-1	K-4366-1
Non-sweet corn	M-65	MAI-7	BGIDI-13	BGUDI-13	MAI -7	MAI-7	MAI-308	M-65	BGUDI-10	MAI-7
	11	12	13	14	15	16	17	18	19	20
Sweet corn	K-4366-1	MAI-286	K-4356-1	MAI-283	MAI-286	MAI-292	MAI-287	MAI-284	K-4571	K-4571
Non-sweet corn	M-65	MAI-308	BGUDI-10	MAI-308	MAI-7	MAI-308	MAI-308	MAI-308	BGUDI-10	BGUDI-13

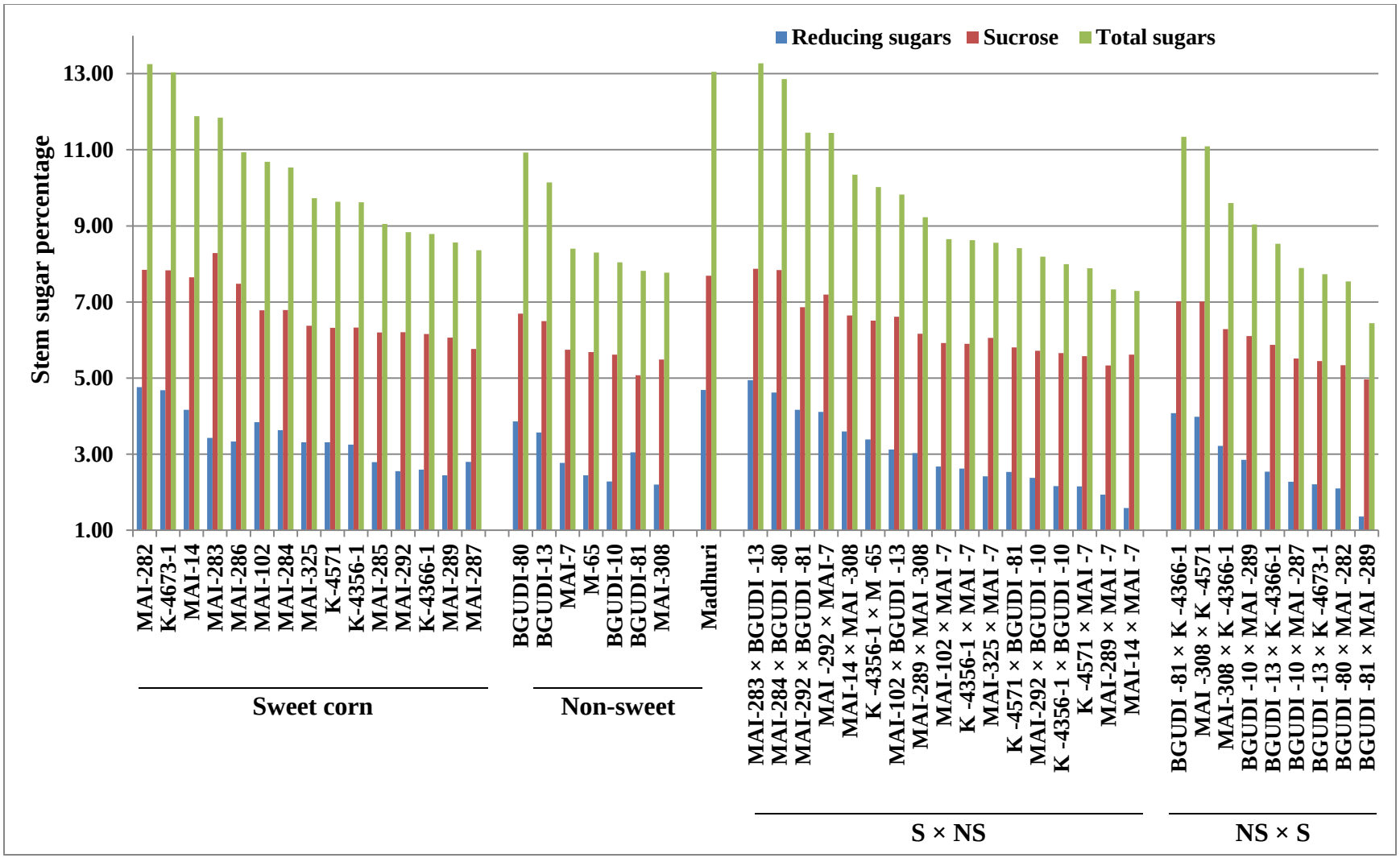


Fig. 8: Stem soluble sugars of both parents and crosses along with check

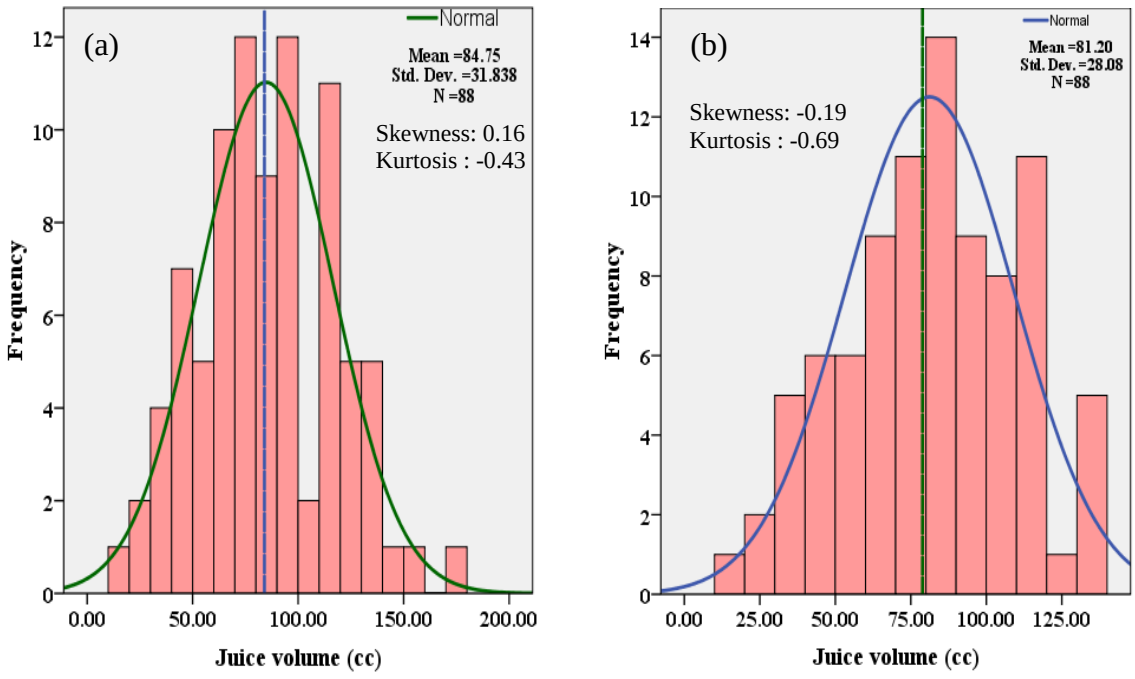


Fig. 9: Frequency distribution for juice content among corn accessions used in the study (a) 10 DPSE and (b) 20 DPSE

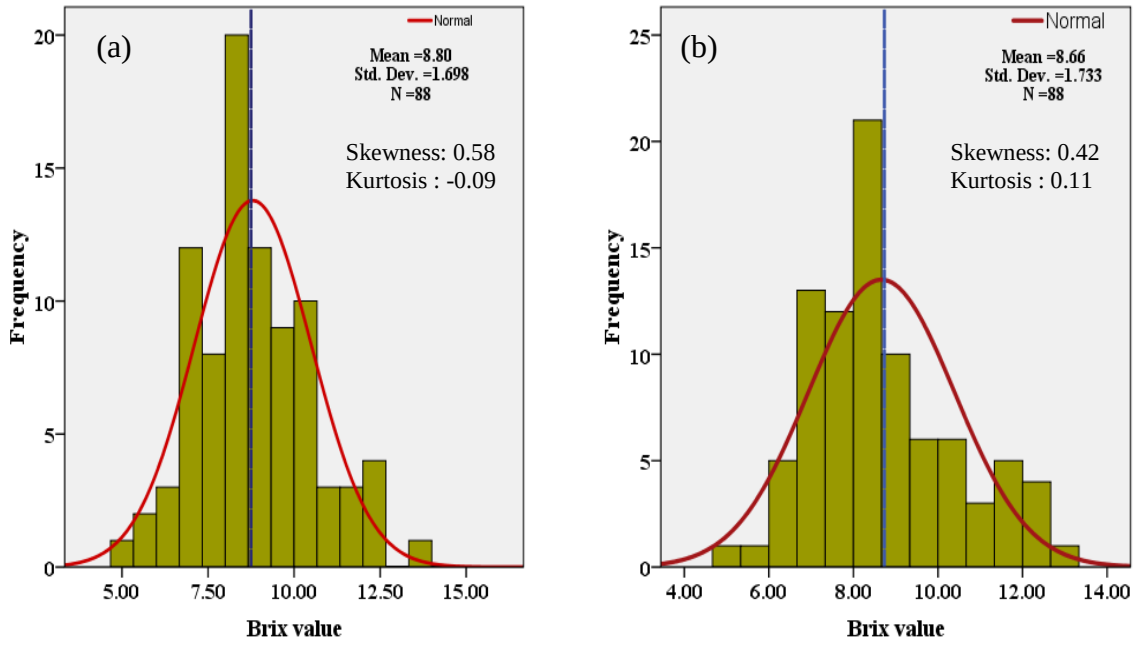


Fig. 10: Frequency distribution for Brix content among corn accessions used in the study (a) 10 DPSE and (b) 20 DPSE

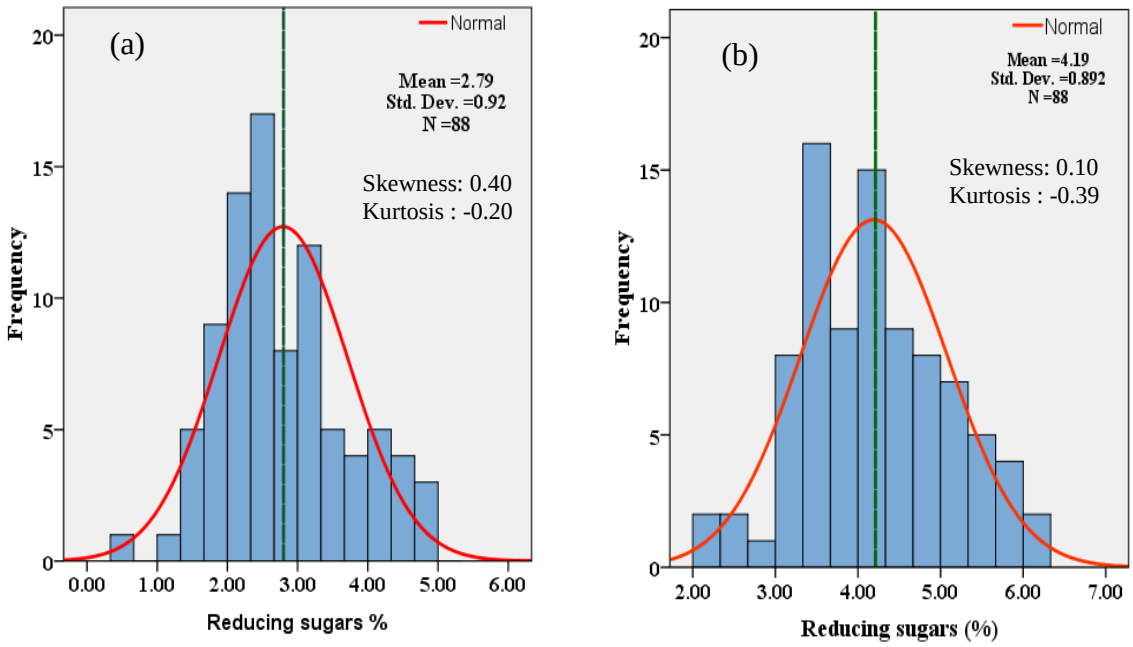


Fig. 11: Frequency distribution for reducing sugars among corn accessions used in the study (a) 10 DPSE and (b) 20 DPSE

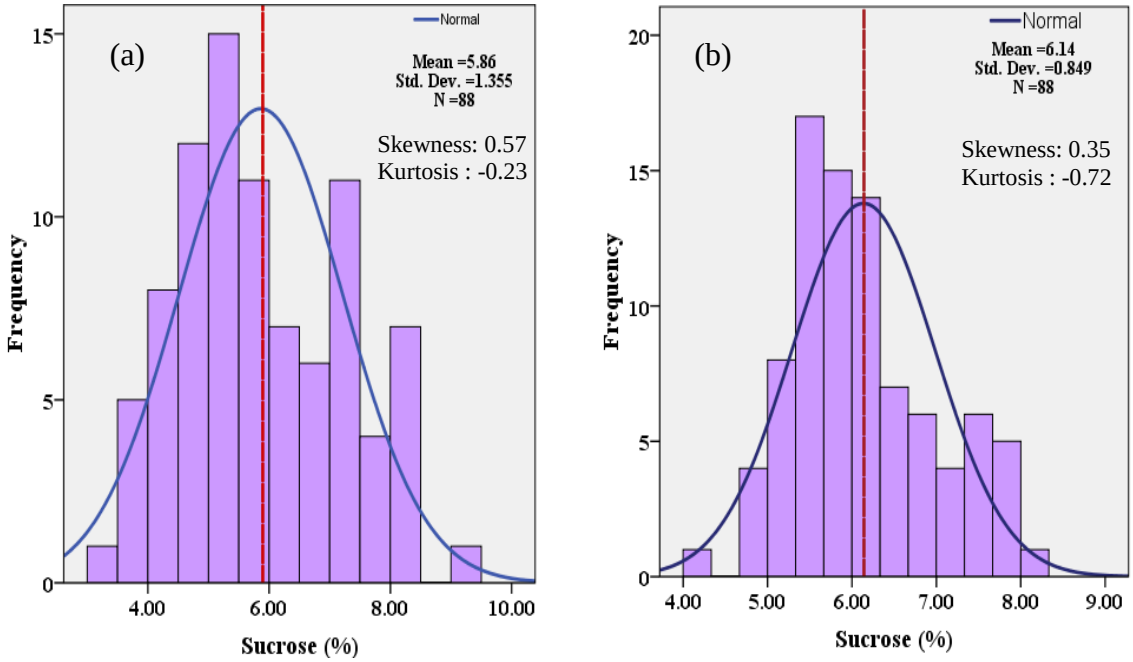


Fig. 12: Frequency distribution for sucrose percentage among corn accessions used in the study (a) 10 DPSE and (b) 20 DPSE

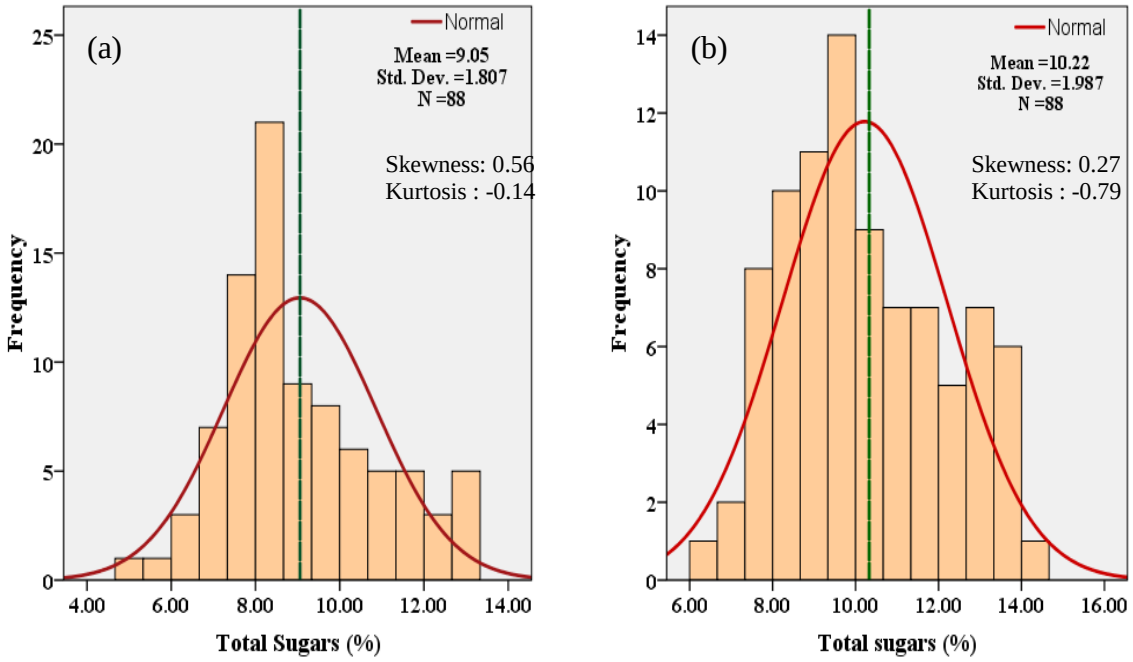


Fig. 13: Frequency distribution for total sugars among corn accessions used in the study (a) 10 DPSE and (b) 20 DPSE

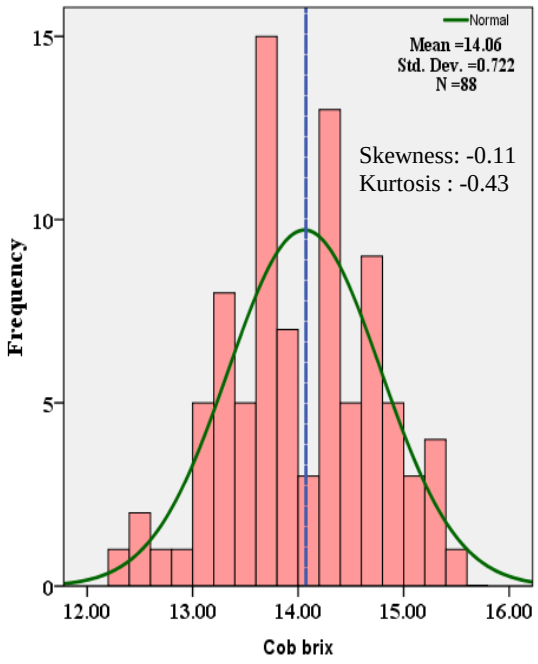


Fig. 14: Frequency distribution for cob brix among corn accessions at 20 DPSE

It was observed that, moderate GCV and PCV of 13.80 and 14.14 respectively, high, h^2 and GAM of 95.18 and 27.73 per cent respectively were recorded at 10 DPSE. At 20 DPSE 22.90, 23.34, 96.35 and 46.31 per cent of high GCV, PCV, h^2 and GAM correspondingly were observed.

4.2.2.14 Reducing sugars

Reducing sugar percentage ranged from 4.27 (MAI-308 × MAI-287) to 8.28 (MAI-282) at 10 DPSE with an average 6.81, 5.83, 6.37 and 5.57 for sweet corn, non-sweet corn, sweet × non-sweet corn and non-sweet × sweet corn genotypes respectively. While, average reducing sugars of sweet corn, non-sweet corn, sweet × non-sweet corn and non-sweet corn × sweet corn at 20 DPSE were 4.39, 3.99, 4.41 and 3.86 respectively, with the range of 2.06 (MAI-289 × MAI-7) to 6.23 (K-4356-1 × M-65) among all the genotypes.

At 10 DPSE the GCV, PCV, h^2 and GAM recorded were high as 32.89, 33.82, 94.57 and 65.88 per cent respectively were high in range. At 20 DPSE high GCV and PCV of 23.38 and 24.35 per cent, high h^2 and GAM of 92.17 and 46.23 per cent recorded were high in range.

4.2.3 Test of normality

4.2.3.1 Skewness

Among characters taken for normal distribution study, the traits *viz*., juice volume (only at 10 DPSE), °brix, total sugars, reducing sugars and sucrose percentage except juice volume and cob °brix at 20 DPSE, showed the skewness more than zero indicating the right skewed distribution and most values are concentrated on left of the mean, with extreme values to the right (Fig. 9-14).

4.2.3.2 Kurtosis

The distribution curves for all the traits taken for normal distribution study *viz*., juice volume, °brix, total sugars, reducing sugars and sucrose percentage and cob °brix found to be platykurtic with a kurtosis value less than three at both 10 and 20 DPSE (Fig. 9-14). Platykurtic distribution explains the probability for extreme values was less than for a normal distribution, and the values were widely spread around the mean.

4.2.4 Correlation and path coefficient studies

4.2.4.1 Correlation studies

The results of the correlation analysis are presented in Table 15 for both 10 and 20 DPSE. The trait of interest, soluble sugar percentage in the stem showed positive correlation with most of the associated traits such as plant height, plant weight, stem weight, stem girth, juice volume and juice extraction percentage at both stages of harvest.

In the 89 genotypes selected for the study, days to 50 per cent anthesis has showed significant negative correlation with juice volume (-0.26), juice extraction

Table 15: Phenotypic correlation coefficients for traits recorded in corn genotypes at 10 and 20 DPSE (n = 89)

Trait	DTF	PH	NOI	PW	NOC	CW	SW	SG	JV	JEP	°Bx	RS	SP	TS	CB
PH	-0.16	1	-0.68**	0.62**	-0.70**	0.26*	0.59**	-0.67**	0.57**	-0.10	-0.58**	0.39**	0.38**	0.29**	0.51**
NOI	0.14	0.23*	1	-0.38**	0.99**	-0.23*	-0.25*	0.99**	-0.185	0.23*	0.95**	-0.06	-0.13	0.03	-0.57**
PW	-0.09	0.68**	0.12	1	-0.40**	0.70**	0.66**	-0.35**	0.49**	0.011	-0.33**	0.21	0.22*	0.15	0.20
NOC	0.01	0.05	-0.09	0.16	1	-0.23*	-0.28**	0.10**	-0.26	0.23*	0.95**	-0.066	-0.14	0.02	-0.57**
CW	-0.05	0.11	-0.24*	0.27*	0.24*	1	0.39**	-0.2	0.12	0.03	-0.23*	-0.01	0.11	-0.09	-0.01
SW	-0.16	0.66**	0.09	0.90**	0.18	0.12	1	-0.23*	0.60**	0.17	-0.20	0.25*	0.30**	0.17	0.30**
SG	-0.08	0.40**	0.11	0.58**	0.05	0.16	0.51**	1	-0.17	0.24*	0.95**	-0.04	-0.12	0.04	-0.58**
JV	-0.26*	0.54**	0.03	0.59**	0.14	-0.07	0.63**	0.37**	1	0.01	-0.12	0.36**	0.31**	0.31**	0.25*
JEP	-0.22*	0.27*	-0.01	0.17	0	0.01	0.36**	0.08	0.16	1	0.24*	0.10	-0.01	0.17	-0.08
°Bx	-0.31**	0.36**	-0.02	0.27*	-0.18	-0.09	0.34**	0.23*	0.36**	0.23*	1	0.19	0.07	0.29*	-0.54**
RS	-0.26*	0.34**	0	0.19	-0.22*	-0.15	0.26*	0.15	0.37**	0.21	0.92**	1	0.81**	0.92**	0.17
SP	-0.29**	0.40**	0	0.33**	-0.13	-0.05	0.39**	0.29*	0.40**	0.26*	0.95**	0.89**	1	0.57**	0.14
TS	-0.28**	0.37**	0.01	0.26*	-0.16	-0.09	0.33**	0.19	0.40**	0.23*	0.96**	0.97**	0.97**	1	0.07

Values below the diagonal: 10 DPSE; values above the diagonal: 20 DPSE

DTF: Days to flowering; **PH**: Plant height; **NOI**: Number of internodes; **PW**: Plant weight; **SW**: Stem weight; **SG**: Stem girth; **JV**: Juice volume; **JEP**: Juice extraction percentage; **°Bx**: °brix value; **TS**: Total sugar; **SP**: Sucrose percentage; **RS**: Reducing sugar, **CB**: Cob °brix.

percentage (-0.22) and reducing sugar percentage (-0.26) at P > 0.01 and with °brix (0.31), sucrose percentage (-0.29) and total sugar percentage (-0.28) at P > 0.05.

Plant height has showed only positive influence on plant weight (0.68), stem weight (0.66), stem girth (0.40), juice volume (0.54), °brix (0.36), reducing sugar per cent (0.34), sucrose per cent (0.40) and total sugars (0.37) at P > 0.01 and number of leaves (0.23) and juice extraction percentage (0.27) at P > 0.05.

Plant weight has showed only significant positive correlation with cob weight (0.27), stem weight (0.90), stem girth (0.58), juice volume (0.59), °brix (0.27), sucrose percentage (0.33) and total sugar percentage (0.26).

There was a significant positive correlation between number of cobs and cob weight (0.27). However, number of cobs showed significantly negative correlation with reducing sugar percentage (-0.22) in the stalks. Cob weight has no significant correlation with any of the trait.

Stem weight has showed significant positive correlation with stem girth (0.51), juice volume (0.63), juice extraction percentage (0.36), °brix (0.34), reducing sugar percentage (0.26), sucrose percentage (0.39) and total sugar percentage (0.33).

Stem girth has showed significant positive influence on juice volume (0.37), °brix (0.23) and sucrose percentage (0.33).

Juice volume has showed significant positive correlation with °brix (0.36), reducing sugar percentage (0.37), sucrose percentage (0.40) and total sugar percentage (0.40) in the stem. Juice extraction percentage has significant positive correlation with °brix (0.23), sucrose percentage (0.26) and total sugar percentage (0.23) in the stem.

Juice extraction percentage has showed significant positive correlation with °brix (0.23), sucrose percentage (0.26) and total sugar percentage (0.23).

°Brix has showed significant positive correlation with reducing sugar percentage (0.92), sucrose percentage (0.95) and total sugar percentage (0.96). Reducing sugar percentage has showed significant positive correlation with sucrose percentage (0.89) and total sugar percentage (0.97). There was a significant positive correlation between sucrose percentage and total sugar percentage (0.97).

4.2.4.2 Path-coefficient analysis

The path-coefficient analysis was carried out to discern direct and indirect effects of yield attributing traits on grain yield. Results are presented in Table 16.

Among the traits included in the study, sucrose percentage had the highest positive direct effect of 0.57 on total soluble sugar percentage in the stem whereas, plant height had lowest positive direct effect of 0.02 on total soluble sugar percentage.

Table 16: Estimates of direct and indirect effects of different traits on total soluble sugar percentage in the stem (n=89)

Traits	PH	NOI	PW	NOC	CW	SW	SG	JV	JXP	°Bx	SP	RS	CB
PH	**0.02**	0.03	0.02	0.07	-0.07	-0.04	-0.06	0.05	-0.01	0.04	0.22	0.24	-0.02
NOI	0.01	**0.06**	0.01	-0.02	-0.02	-0.03	-0.05	0.04	-0.01	0.02	0.12	0.20	0.00
PW	0.01	0.01	**0.04**	0.33	-0.31	-0.04	-0.10	0.05	-0.01	0.02	0.09	0.14	0.00
NOC	0.00	0.00	0.03	**0.48**	-0.41	-0.02	-0.09	0.02	-0.01	-0.01	-0.01	0.00	0.00
CW	0.00	0.00	0.03	0.46	**-0.43**	-0.02	-0.08	0.02	0.00	0.00	-0.04	0.03	0.01
SW	0.01	0.03	0.02	0.17	-0.13	**-0.06**	-0.09	0.06	-0.01	0.03	0.09	0.18	-0.01
SG	0.01	0.02	0.03	0.31	-0.24	-0.04	**-0.14**	0.04	0.00	0.02	0.07	0.11	0.00
JV	0.01	0.03	0.02	0.11	-0.10	-0.05	-0.08	**0.07**	-0.01	0.02	0.12	0.13	-0.02
JXP	0.00	0.01	0.00	0.09	-0.04	-0.02	-0.01	0.02	**-0.05**	0.00	0.05	0.03	-0.01
°Bx	0.01	0.01	0.01	-0.03	0.00	-0.02	-0.03	0.02	0.00	**0.10**	0.44	0.34	0.00
SP	0.01	0.01	0.01	-0.01	0.03	-0.01	-0.02	0.02	0.00	0.08	**0.57**	0.23	-0.01
RS	0.01	0.02	0.01	0.00	-0.03	-0.02	-0.03	0.02	0.00	0.07	0.27	**0.50**	-0.01
CB	0.00	0.00	0.00	-0.03	0.08	-0.01	0.01	0.02	0.00	0.01	0.05	0.06	**-0.07**
RESIDUAL EFFECT= 0.059													

DTF: Days to 50 per cent flowering; **PH**: Plant height; **NOI**: Number of internodes; **PW**: Plant weight; **SW**: Stem weight; **SG**: Stem girth; **JV**: Juice volume; **JEP**: Juice extraction percentage;°**Bx**: brix value; **TS**: Total sugars; **SP**: Sucrose percentage; **RS**: Reducing sugars, **CB**: Cob brix.

Among all the characters studied, cob weight had highest negative direct effect of -0.43 on total soluble sugar percentage in the stem while, juice extraction percentage had lowest negative direct effect of -0.05 on total soluble sugar percentage in the stem.

In the selected characters for the study, °brix had the highest positive indirect effect of 0.44 *via*., sucrose percentage towards total soluble sugar percentage in the stem. Whereas, plant height, number of internodes and plant weight had lowest positive indirect effect of 0.01 *via*., °brix content towards total soluble sugar percentage in the stem.

Among the selected traits, cob weight had highest negative indirect effect of -0.41 *via*., number cobs towards total soluble sugar percentage in the stem whereas, plant weight, number of internodes, plant weight, number of cobs, stem weight and juice volume had lowest negative indirect effect of -0.01 *via*., juice extraction percentage towards total soluble sugar percentage in the stem.

4.2.5 Heterosis and combining ability analysis

4.2.5.1 Cytoplasmic effects on mid-parent heterosis

The present study focuses on the differences between sweet × non-sweet and non-sweet × sweet corn hybrids with respect to mid patent heterosis to highlight the presence or absence of cytoplasmic effect.

At 10 DPSE, out of all traits under study, the significant mid-parent heterosis was observed only for four traits such as number of cobs per plant, °brix, total sugar, reducing sugar and sucrose percentage in the stalk. However all the traits recorded of sweet × non-sweet and non-sweet corn showed significant differences for mid-parent heterosis and presented in the Table 17.

With respect to days to 50 per cent flowering, sweet × non-sweet (S × NS) and non-sweet × sweet corn (NS × S) hybrids expressed significant difference between them for mid-parent heterosis in six nuclear genetic backgrounds with majority (five) favouring sweet corn cytoplasm.

Difference in mid-parent heterosis between S × NS and NS × S hybrids for plant height was significant in 10 genetic backgrounds all favouring sweet corn cytoplasm. For number of leaves, except four crosses all S × NS and NS × S hybrids showed significant differences for mid-parent heterosis with nine crosses favoured sweet corn cytoplasm.

With respect to plant weight, significant differences between S × NS and NS × S hybrids for mid-parent heterosis was noticed in only one nuclear genetic background, which was in favour of sweet corn cytoplasm. With respect to number of cobs, all the crosses showed significant differences between S × NS and NS × S hybrids for mid-parent heterosis except two crosses with majority (11) favouring non-sweet corn cytoplasm.

Table 17: Comparison of mid-parent heterosis of sweet × non-sweet corn and non-sweet corn × sweet corn hybrids at 10 DPSE

Sweet corn	Non-sweet corn	DTF		Diff	Plant height		Diff	Number of leaves		Diff	Plant weight		Diff	Number of cobs		Diff
		a	b		a	b		a	b		a	b		a	b	
MAI -287	MAI -7	-2.35	7.39	-9.74	-10.51	-15.96	5.45	-2.44	-13.73	11.29**	44.76	-37.14	81.9	66.67**	100.00**	-33.33**
MAI -287	MAI-308	-4.27	9.27	-13.54*	16.25	-0.8	17.05*	11.63	11.63	0	62.54	-12.42	74.96	14.29	0	14.29**
MAI-283	MAI-308	-2.37	4.95	-7.32	7.81	-6.01	13.82	-6.67	-4	-2.67*	3.95	-43.92	47.87	-42.86	-25	-17.86**
MAI-285	MAI-7	-3.7	5.37	-9.07	11.66	0	11.66	12.2	-5.66	17.86**	25.82	-26.17	51.99	-33.33	14.29	-47.62**
MAI-285	MAI308	-0.93	-1.89	0.96	22.43	-1.08	23.51**	16.28	14.29	1.99*	51.23	-25.6	76.83	0	0	0
MAI-285	BGUDI-13	-3.77	-4.67	0.9	7.75	-7.51	15.26*	15.56	0	15.56**	22.94	21.02	1.92	-40	50	-90**
MAI-284	M-65	-4.07	6.67	-10.74*	24.18	-10.83	35.01**	0	3.7	-3.7*	85.48	0.63	84.85	-33.33	133.33**	-166.63**
MAI-284	MAI-7	-3.7	0	-3.7	8.91	-0.39	9.3	4.55	6.98	-2.43*	-2.47	-39.54	37.07	60.00*	-42.86	102.86**
MAI-284	MAI-308	-1.85	1.41	-3.26	11.67	-12.13	23.8**	13.64	22.73	-9.09**	60.24	3.32	56.92	20	-42.86	62.86**
MAI-286	MAI-308	-3.17	-1.42	-1.75	16.34	-13.21	29.55**	31.82	-20	51.82**	31.06	-11.98	43.04	-33.33	33.33	-66.66
K-4571	BGUDI-10	-4.63	-4.23	-0.4	11.34	1.68	9.66	-8.7	16.28	-24.98**	17.81	-37.49	55.3	0	-20	20
K-4571	M-65	-3.26	5.26	-8.52	9.81	-11.09	20.9*	-17.39	8.33	-25.72**	55.7	-30.29	85.99	0	-14.29	14.29**
K-4356-1	BGUDI-10	-5.94	8.06	-14	9.14	-2.21	11.35	10.64	10.64	0	19.06	-0.43	19.49	-14.29	100.00**	-114.29**
K-4366-1	M-65	-1.85	0.47	-2.32	11.52	-1.42	12.94	10.2	6.38	3.82**	119.06	-8.97	128.03	-33.33	-11.11	-22.22**
K-4366-1	MAI-7	-5.99	8.74	-14.73**	1.5	-14.04	15.54*	19.05	4.17	14.88**	18.32	-46.07	64.39	-20	0	-20**
K-4366-1	BGUDI-10	17.16	3.32	13.84**	14.59	-4.9	19.49	9.52	8.33	1.19	77.93	5.39	72.54	14.29	60	-45.71**
K-4571	BGUDI-13	-13.12	1.41	-14.53**	17.72	-17.04	34.76**	8.7	17.39	-8.69**	124.78	-44.86	169.64*	33.33	-14.29	47.62**
MAI-286	MAI-7	-8.18	2.91	-11.09*	2.58	-2.47	5.05	23.81	22.73	1.08	40.55	-13.47	54.02	20	14.29	5.71**
MAI-292	MAI-308	-4.93	-2.78	-2.15	22.16	-4.31	26.47**	-6.98	-16	9.02**	106.26	8.85	97.41	14.29	14.29	0
MAI-284	BGIDI-13	1.92	0.95	0.97	19.33	-7.97	27.3**	25.58	0	25.58**	5.87	-14.71	20.58	-50	-25	-25**
SEm±		0.38	0.2	3.21	2.63	4.01	4.89	0.47	0.53	0.64	36.23	54.2	54.2	0.38	0.3	0.43
CD @ P=0.05		1.12	0.58	9.86	7.78	11.87	15.01	1.4	1.58	1.97	107.24	160.43	166.2	1.12	0.9	1.32
CD @ P=0.01		1.54	0.8	13.76	10.63	16.22	20.95	1.91	2.16	2.75	146.59	219.3	232.05	1.54	1.22	1.84

a: Sweet × non-sweet corn; b: Non-sweet × sweet corn

Table 17 contd.....

Sweet corn	Non-sweet corn	Cob weight		Diff	Stem weight		Diff	Stem girth		Diff	Juice volume		Diff	Juice extraction percentage		Diff
		a	b		a	b		a	b		a	b		a	b	
MAI -287	MAI -7	54.35	103.89	-49.54	25.37	-36.92	62.29**	21.08	-4.03	25.11**	-28.02	-67.77	39.75**	-3.35	-8.22	4.87
MAI -287	MAI-308	58.15	10.77	47.38	48.05	-12.39	60.44**	21.83	-12	33.83**	-27.6	-64.68	37.08**	-0.64	27.66	-28.3
MAI-283	MAI-308	189.15	14.8	174.35	0.53	-43.88	44.41*	2.77	-20.46	23.23**	-7.54	-60.68	53.14**	27.74	13.53	14.21
MAI-285	MAI-7	-50.73	-11.03	-39.7	-3.35	-26.09	22.74	22.48	-16.67	39.15**	-19.91	-48.13	28.22*	-35.65	-8.67	-26.98
MAI-285	MAI308	148	-34.32	182.32*	22.29	-25.56	47.85*	10.58	14.13	-3.55	19.4	-41.81	61.21**	-32.13	12.43	-44.56*
MAI-285	BGUDI-13	16.22	139.53	-123.31	13.9	21.1	-7.2	6.56	-8.81	15.37**	1.84	-44.42	46.26**	-17.77	-35.78	18.01
MAI-284	M-65	68.39	23.63	44.76	54.77	0.84	53.93**	30.14	-11.58	41.72**	121.43	10.45	110.98**	-17.08	-14.34	-2.74
MAI-284	MAI-7	84.44	-37.62	122.06	-26.11	-39.55	13.44	8.36	-2.62	10.98**	-51.11	-67.82	16.71	-15.98	11.07	-27.05
MAI-284	MAI-308	117.39	-25.86	143.25	21.18	3.22	17.96	17	-3.19	20.19**	-21.11	-70.08	48.97**	33.02	-7.55	40.57*
MAI-286	MAI-308	30.45	75	-44.55	9.42	-11.9	21.32	7.96	-22.79	30.75**	-47.4	-83	35.6**	-20.12	6.24	-26.36
K-4571	BGUDI-10	44.35	-55.28	99.63	-2.07	-37.43	35.36*	28.34	-8.88	37.22**	1.6	-16.91	18.51	22.79	24.2	-1.41
K-4571	M-65	29.08	-46.75	75.83	13.99	-30.26	44.25*	-8.91	-15.61	6.7**	-0.76	-36.98	36.22**	42.18	-71.32	113.5
K-4356-1	BGUDI-10	210.99	103.49	107.5	13.31	-0.25	13.56	13.73	-16.21	29.94**	0.62	-33.99	34.61**	32	7.25	24.75
K-4366-1	M-65	65.63	-53.23	118.86	72.33	-8.97	81.3**	7.54	-3.05	10.59**	68.42	-25.37	93.79**	11.7	23.1	-11.4
K-4366-1	MAI-7	15.63	27.82	-12.19	-13.68	-45.98	32.3	0.14	-4.85	4.99*	-15.6	-69.61	54.01**	-3.44	-8.66	5.22
K-4366-1	BGUDI-10	-10.17	78.79	-88.96	51.38	5.47	45.91*	32.83	-2.98	35.81**	-2.23	-23.12	20.89	-24.96	56.92	-81.88**
K-4571	BGUDI-13	86.24	-60.32	146.56	124.85	-44.81	169.66**	31.15	-15.74	46.89**	66.01	-40.19	106.2**	-4.58	0.89	-5.47
MAI-286	MAI-7	58.16	-25.55	83.71	55.66	-13.42	69.08**	28.25	-8.51	36.76**	75	-46.41	121.41**	5.53	7.92	-2.39
MAI-292	MAI-308	153.84	104.7	49.14	92.53	8.86	83.67**	23.64	-1.1	24.74**	114.29	-26.9	141.19**	-45.51	18.03	-63.54**
MAI-284	BGIDI-13	-18.37	-64.28	45.91	5.74	-14.73	20.47	12.42	7.46	4.96*	47.54	48.72	-1.18	-3.58	40.12	-43.7
SEm±		54.26	38.24	58.45	22.80	19.02	25.30	0.92	1.52	1.46	5.89	5.50	6.90	0.03	0.12	13.20
CD @ P=0.05		160.61	113.18	179.24	67.48	56.29	34.59	2.73	4.50	4.48	17.42	16.27	21.15	0.09	0.36	40.48
CD @ P=0.01		219.54	154.71	250.27	92.23	76.94	51.33	3.73	6.15	6.26	23.82	22.24	29.53	0.12	0.49	56.52

a: Sweet × non-sweet corn; b: Non-sweet × sweet corn

Table 17 contd....

Sweet corn	Non-sweet corn	°Brix		Diff	Total sugar		Diff	Reducing sugar		Diff	Sucrose percentage		Diff
		a	b		a	b		a	b		a	b	
MAI -287	MAI -7	26.93	-20	46.93**	27.98	-19.92	47.9**	0.38	-35.35**	35.63**	27.92**	-13	40.92**
MAI -287	MAI-308	-5.47	-44.61	39.14**	-5.06	-45.02**	-50.08**	-19.01	-81.62**	62.61**	-1.12	-29.66**	12.71**
MAI-283	MAI-308	-12.47	-21.11	8.64**	-12.66	-20.64	7.98**	-14.67	-35.73**	21.06**	-12.74	-13.83	1.09**
MAI-285	MAI-7	39.88	-34.47	74.35**	40.16*	-33.92	40.16**	57.30**	-49.58**	106.88**	25.25**	-24.09**	49.34**
MAI-285	MAI308	19.14	-11.17	30.31**	21.97	-11.19	33.16**	-6.81	-16.18	9.37**	23.04*	-8.49	31.53**
MAI-285	BGUDI-13	27.37	-27.47	54.84**	25.5	-26.88	52.38**	36.09**	-42.40**	78.49**	19.07	-18.44	37.51**
MAI-284	M-65	37.78	-48.86	86.64**	37.02	-49.29**	-12.27**	66.35**	-69.10**	135.45**	20.56	-35.85**	56.41**
MAI-284	MAI-7	12.64	-7.88	20.52**	12.23	-8.1	20.33**	19.37	-10.51	29.88**	8.26	-6.8	15.06**
MAI-284	MAI-308	-21.43	-14.99	-6.44**	-21.48	-15.13	-6.35**	-36.08**	-21.12	-14.96**	-10.92	-10.09	-0.83**
MAI-286	MAI-308	-7.22	-7.65	0.43	-8.09	-7.64	-0.45	-5.86	-7.05	1.19**	-8.79	-5.44	-3.35**
K-4571	BGUDI-10	-16.47	-18.44	1.97	-16.86	-18.44	1.58**	-31.01*	-35.04**	4.03**	-9.92	-13.48	3.56**
K-4571	M-65	7.25	-24.21	31.46**	6.89	-24.42	31.31**	12.6	-34.55**	-21.95**	5.56	-16.74	22.3**
K-4356-1	BGUDI-10	-2.94	-22.46	19.52**	-2.96	-22.23	19.27**	-4.79	-41.00**	36.21**	-1.72	-14.29	12.57**
K-4366-1	M-65	2.74	-12.21	14.95**	2.18	-14	16.18**	-27.18*	-23.69	-3.49**	15.23	-9.92	25.15**
K-4366-1	MAI-7	-2.02	-4.9	2.88*	-2.39	-4.68	2.29**	-12.15	-6.49	-5.66**	-0.73	-4.11	3.38**
K-4366-1	BGUDI-10	-8.5	-15.94	7.44**	-8.64	-14.48	5.84**	-12.53	-23.65	11.12**	-4.17	-10.9	6.73**
K-4571	BGUDI-13	-13.02	-11.85	-1.17	-12.88	-11.92	-0.96	-24.52	-23.54	-0.98**	-7.27	-8.35	1.08**
MAI-286	MAI-7	-7.56	-28.57	21.01**	-7.67	-27.74	20.07**	-17.33	-40.30**	22.97**	-4.14	-20.24	16.1**
MAI-292	MAI-308	-11.11	9.27	-20.38**	-11.15	-17.52	6.37**	-17.97	-29.52**	11.55**	-5.45	-9.73	4.28**
MAI-284	BGIDI-13	6.36	16.5	-10.14**	6.1	16.04	-9.94**	22.14	30.51**	-8.37**	0.31	9.49	-9.18**
SEm±		0.66	0.21	0.80	0.20	0.23	0.31	0.09	0.13	0.19	0.14	0.11	0.17
CD @ P=0.05		1.96	0.61	2.44	0.58	0.67	0.96	0.27	0.40	0.59	0.41	0.34	0.51
CD @ P=0.01		2.68	0.83	3.41	0.79	0.91	1.34	0.37	0.54	0.83	0.56	0.46	0.71

a: Sweet × non-sweet corn; b: Non-sweet × sweet corn

Significant differences between S × NS and NS × S hybrids for mid-parent heterosis was noticed in only one and two nuclear genetic backgrounds, which were in favour of sweet corn cytoplasm with respect to cob weight and stem weight respectively.

Significant differences between S × NS and NS × S hybrids for mid-parent heterosis was noticed in all the crosses except only one and four nuclear genetic backgrounds, which were in favour of sweet corn cytoplasm with respect to cob stem girth and juice volume respectively.

With respect to juice extraction percentage, S × NS and NS × S hybrids expressed significant difference between them for mid-parent heterosis in five nuclear genetic backgrounds with majority (four) favouring non-sweet corn cytoplasm.

Five of the total crosses showed significant mid-parent heterosis for number of cobs, of which, sweet × non-sweet corn hybrid MAI-287 × MAI-7 and its corresponding reciprocal hybrid MAI-7 × MAI-287, both showed positive heterosis of 66.67 and 100.00 per cent respectively. M-65 × MAI-284 (133.33 %) showed the highest positive mid-parent heterosis. Difference in mid-parent heterosis between S × NS and NS × S hybrids was significant in all the crosses except three crosses with majority (14) favouring sweet corn cytoplasm.

With respect to total sugar percentage in the stem, only three hybrids showed significant mid-parent heterosis, of which, sweet × non-sweet corn hybrid MAI-285 × MAI-7 (40.16 %) showed positive heterosis. Whereas, non-sweet × sweet corn hybrid M65 × MAI-284 (-49.29 %) showed highest negative heterosis followed by MAI-308 × MAI-287 (-45.02 %).

For reducing sugar percentage in the stem, eighteen of the total crosses showed significant mid-parent heterosis, of which, sweet × non-sweet corn hybrid MAI-284 × M-65 (66.35 %) showed highest positive heterosis while its corresponding reciprocal hybrid M-65 × MAI -284 (-69.10 %) showed negative mid-parent heterosis, whereas, non-sweet × sweet corn MAI -308 × MAI -287 showed highest negative heterosis of -81.62 per cent.

With respect to sucrose percentage in the stalk, five crosses showed significant mid-parent heterosis, of which, sweet × non-sweet corn hybrid MAI-287 × MAI-7 (27.92 %) showed highest positive heterosis while, non-sweet × sweet corn hybrid M-65 × MAI-284 (-35.85 %) showed highest negative heterosis. MAI-285 × MAI-7 (25.25 %) showed positive heterosis, whereas, its corresponding reciprocal hybrid MAI -7 × MAI -285 showed negative heterosis of -24.09 per cent.

Significant differences between S × NS and NS × S hybrids for mid-parent heterosis was noticed in all nuclear genetic backgrounds, in which majority were in favour of sweet corn cytoplasm with respect to total sugar, reducing sugar and sucrose percentage in the corm stalk.

At 20 DPSE (Table 18), for all the traits significant differences between S × NS and NS × S hybrids for mid-parent heterosis was noticed in all nuclear genetic backgrounds, in which majority were in favour of sweet corn cytoplasm except cob °brix, which showed significant differences between S × NS and NS × S hybrids for mid-parent heterosis with majority favouring non-sweet corn cytoplasm.

Eight of sweet × non-sweet corn hybrids manifested significant mid-parent heterosis for number of cobs per plant, of which, five hybrids showed positive mid-parent heterosis while, three hybrids showed negative heterosis. MAI-284 × MAI-7 and K-4571 × BGUDI-13 showed highest positive heterosis of 143.00 per cent followed by MAI-285 × MAI-7,which showed mid-parent heterosis of 100.00 per cent while, MAI-284 × BGUDI-13 showed highest negative heterosis 0f -55.56 per cent followed by K-4571 × BGUDI-10 which showed -50.00 per cent negative heterosis. Among non-sweet × sweet corn reciprocal hybrids, only four hybrids showed significant mid-parent heterosis for number of cobs per plant, of which M-65 × MAI-284 showed the highest positive mid-parent heterosis of 133.33 per cent.

With respect to °brix content, among the crosses obtained, sweet × non-sweet corn hybrids *viz*., K-4571 × BGUDI-13, MAI-285 × MAI-308 and K-4571 × BGUDI-10 showed highest significant positive mid-parent heterosis of 42.77, 42.99 and 41.04 per cent respectively. Whereas, non-sweet × sweet corn hybrids, MAI-308 × MAI-287 (-48.37 %), M-65 × MAI-284 (-40.87 %) and MAI-7 × MAI-286 (-34.88 %) showed highly significant negative mid-parent heterosis.

Eight crosses out of 40 manifested significant heterosis for total soluble sugar content which includes, both positive and negative mid-parent heterosis, of which sweet × non-sweet corn hybrids, K-4571 × BGUDI-13 (49.70 %) showed highest positive mid-parent heterosis. The cross MAI-285 × MAI-7 and its corresponding reciprocal hybrid MAI-7 × MAI-285 had showed significant positive and negative heterosis of 47.53 per cent and -35.43 per cent respectively, which clearly indicates the effect of sweet corn cytoplasm towards increasing the total sugar content in the stem, while, the cross non-sweet × sweet corn M-65 × MAI- 284 (-45.88 %) showed highest negative heterosis.

With respect to reducing sugar percentage in the stalk, four of sweet × non-sweet corn hybrids showed only positive significant mid-parent heterosis, of which MAI-285 × MAI-7 showed the highest positive heterosis of 66.35 per cent. Whereas, non-sweet × sweet corn hybrids showed both positive and negative significant heterosis, of which MAI-7 × MAI-287 (33.40 %) positive heterosis while, BGUDI-13 × MAI-285 showed highest negative mid-parent heterosis of -35.62 per cent.

For sucrose percentage in the corn stalk, eleven crosses showed significant mid-parent heterosis, of which sweet × non sweet corn hybrids MAI-287 × MAI-7 (57.83 %), MAI-285 × MAI -7 (34.06 %) and their corresponding reciprocal hybrids MAI -7 × MAI -287 (-37.71 %), MAI -7 × MAI-285 (-47.35 %) showed positive and negative mid-parent heterosis respectively. sweet × non sweet corn hybrid K-4571 × BGUDI-13 showed highest positive heterosis of 60.24 per cent while, non-sweet × sweet corn hybrid M-65 × MAI-284 showed highest negative mid-parent heterosis of -52.66 per cent.

Table 18: Comparison of mid-parent heterosis of sweet × non-sweet corn and non-sweet corn × sweet corn hybrids at 20 DPSE

Sweet corn	Non-sweet corn	Plant height		Diff	Number of Internodes		Diff	Plant weight		Diff	Number of cobs		Diff	Cob °brix		Diff
		a	b		a	b		a	b		a	b		a	b	
MAI -287	MAI -7	-13.3	-14.77	1.47	-14.29	-6.38	-7.91**	46.12	-29.32	75.44*	33.33	66.67**	-33.34**	-0.53	17.96	-18.49**
MAI -287	MAI-308	9.81	-1.48	11.29	-10.64	6.67	-17.31**	64.23	-3.92	68.15*	75.00**	-20	100**	-3.41	-3.83	0.42
MAI-283	MAI-308	2.22	-7.32	9.54	-22.45	-2.04	-20.41**	36.89	-40.54	77.43*	-25	-40	15**	1.42	10	-8.58**
MAI-285	MAI-7	8.6	1.31	7.29	16.67	2.04	14.63**	134.59	71.12	63.47	100.00**	0	100**	3.51	11.28	-7.77**
MAI-285	MAI308	13	-1.78	14.78*	13.04	9.09	3.95**	63.69	-9.26	72.95*	14.29	-25	39.29**	-1.41	4.35	-5.76**
MAI-285	BGUDI-13	5.29	-8.48	13.77*	2.13	0	2.13**	39.74	6.28	33.46	33.33	50.00*	-16.67**	7.36	3.76	3.6**
MAI-284	M-65	25.32	-10.83	36.15**	20	3.7	16.3**	84.37	0.69	83.68*	0	133.33**	-133.33**	-1.59	3.76	-5.35**
MAI-284	MAI-7	-3.28	-0.39	-2.89	-2.22	6.98	-9.2**	26.44	0.66	25.78	140.00**	-42.86	182.86**	-5.34	7.52	-12.86**
MAI-284	MAI-308	5.32	-12.13	17.45*	15.56	22.73	-7.17**	14.57	-14.07	28.64	60.00**	-42.86	102.86**	-4.99	-1.72	-3.27**
MAI-286	MAI-308	14.07	-13.21	27.28**	30	-20	50**	80.1	-30.66	110.76**	25	33.33	-8.33**	-9.45	-1.85	-7.6**
K-4571	BGUDI-10	8.51	1.68	6.83	30.23	16.28	13.95**	-5.77	10.02	-15.79	-50.00*	-20	-30**	1.41	3.18	-1.77**
K-4571	M-65	-0.11	-11.09	10.98	0	8.33	-8.33**	29.56	-14.82	44.38	14.29	-14.29	28.58**	-4.19	-7.23	3.04**
K-4356-1	BGUDI-10	9.99	-2.21	12.2	15.56	10.64	4.92**	39.66	-24.08	63.74	33.33	100.00**	-66.67**	5.92	7.94	-2.02**
K-4366-1	M-65	3.37	-1.42	4.79	0	6.38	-6.38**	2.3	-25.67	27.97	-33.33	-11.11	-22.22**	0.17	14.29	-14.12**
K-4366-1	MAI-7	-9.09	-14.04	4.95	6.38	4.17	2.21**	5.63	-40.59	46.22	-42.86	0	-42.86**	-10.85	2.96	-13.81**
K-4366-1	BGUDI-10	4.47	-4.9	9.37	2.22	8.33	-6.11**	31.04	26.91	4.13	-11.11	60	-71.11**	0.17	1.77	-1.6**
K-4571	BGUDI-13	13.27	-17.04	30.31**	11.63	17.39	-5.76**	108.86	-29.55	138.41**	140.00**	-14.29	154.29**	-5.55	-0.74	-4.81**
MAI-286	MAI-7	-4.55	-2.47	-2.08	-2.22	22.73	-24.95**	39.97	-25.95	65.92	60.00*	14.29	45.71**	-5.17	-3.93	-1.24**
MAI-292	MAI-308	14.03	-4.31	18.34**	-2.22	-16	13.78**	61.88	23.84	38.04	33.33	14.29	19.04**	0.89	-12.01	12.9**
MAI-284	BGIDI-13	11.3	-11.83	23.13**	10.2	-20	30.2**	7.25	-12.05	19.3	-55.56*	-25	-30.56**	-7.32	6.41	-13.73**
SEm±		1.49	1.41	4.17	0.18	0.21	0.3	8.76	22.69	21.99	0.26	0.31	0.38	0.12	0.09	0.17
CD @ P=0.05		1.12	4.19	12.77	7.78	0.61	0.92	1.4	67.17	67.42	107.24	0.91	1.16	0.09	0.26	0.52
CD @ P=0.01		1.54	5.72	17.83	10.63	0.83	1.29	1.91	91.81	94.14	146.59	1.25	1.62	0.12	0.36	0.73

a: Sweet × non-sweet corn; b: Non-sweet × sweet corn

Table 18: contd.....

Sweet corn	Non-sweet corn	Cob wt		Diff	Stem wt		Diff	Stem girth		Diff	Juice volume		Diff	JEP		Diff
		a	b		a	b		a	b		a	b		a	b	
MAI-287	MAI-7	172.17	50.48	121.69**	-19.31	21.8	-41.11**	7.95	3.69	4.26**	19.34	-50.83	70.17**	-4.76	36.7	-41.46**
	MAI-308	197.61	109.74	87.87**	12.07	-18.42	30.49**	10.82	-20.25	31.07**	29.96	-52.28	82.24**	12.65	-1.46	14.11**
MAI-283	MAI-308	20.32	-5.37	25.69**	-7.6	-27.94	20.34**	-8.01	-21.19	13.18**	6.14	-54.59	60.73**	-4.04	-2.34	-1.7
MAI-285	MAI-7	235.55	95.36	140.19**	108.23	57.59	50.64**	32.31	-1.34	33.65**	99	4.58	94.42**	6.25	-2.79	9.04**
MAI-285	MAI308	127.77	9.19	118.58**	46.09	9.63	36.46**	-2.53	2.14	-4.67**	50.32	-18.9	69.22**	5.33	4.52	0.81
MAI-285	BGUDI-13	221.11	28.18	192.93**	-7.16	2.15	-9.31*	-10.33	-13.46	3.13**	4.36	-34.12	38.48**	5.3	17.91	-12.61**
MAI-284	M-65	27.92	2.29	25.63**	16.27	9.57	6.7*	20.81	-3.6	24.41**	49.67	39.45	10.22**	-4.23	-4.54	0.31
MAI-284	MAI-7	251.05	74.17	176.88**	57.55	37.15	20.4**	34.94	-2.62	37.56**	30.99	-67.82	98.81**	65.15	-14.83	79.98**
MAI-284	MAI-308	189.1	-11.48	200.58**	79.26	1.04	78.22**	34.58	-3.19	37.77**	63.84	-70.08	133.92**	17.99	-18.03	36.02**
MAI-286	MAI-308	103.96	-9.83	113.79**	-5.5	-45.22	39.72**	15.85	-22.79	38.64**	18.51	-83	101.51**	37.97	4.71	33.26**
K-4571	BGUDI-10	-66.07	52.81	-118.88**	24.16	65.61	-41.45**	-6.24	-8.88	2.64**	55.06	-16.91	71.97**	34.86	-2.73	37.59**
K-4571	M-65	102.81	-19.94	122.75**	1.03	-27.65	28.68**	-2.91	-15.61	12.7**	23.31	-36.98	60.29**	1.43	-8.08	9.51**
K-4356-1	BGUDI-10	75.65	-32.86	108.51**	20.98	-23.43	44.41**	7.87	-16.21	24.08**	34.16	-33.99	68.15**	-20.19	-57.21	37.02**
K-4366-1	M-65	36.9	-46.61	83.51**	-18.81	-8.24	-10.57**	-10.19	-3.05	-7.14**	-8.81	-25.37	16.56**	-5.61	5.93	-11.54**
K-4366-1	MAI-7	-99.96	-32.5	-67.46**	-6.73	-42.95	36.22**	4.77	-4.85	9.62**	48.39	-69.61	118**	19.34	-14.36	33.7**
K-4366-1	BGUDI-10	-99.94	5.85	-105.79**	45.27	31.61	13.66*	7.49	-2.98	10.47**	37.8	-23.12	60.92**	5.89	-21.28	27.17**
K-4571	BGUDI-13	513.5	-19.72	533.22**	40.54	-40.57	81.11**	15.06	-15.74	30.8**	100.95	-40.19	141.14**	-11.79	46.42	-58.21**
MAI-286	MAI-7	248.95	-49.01	297.96**	-16.11	-9.04	-7.07*	19.62	-8.51	28.13**	24.29	-46.41	70.7**	12.83	-11.86	24.69**
MAI-292	MAI-308	57.6	32.45	25.15**	56.95	4.34	52.61**	37.08	-1.1	38.18**	37.5	-26.9	64.4**	0.28	-38.75	39.03**
MAI-284	BGIDI-13	-22.44	-23.37	0.93**	36.73	-26.64	63.37**	7.79	3	4.79**	18.66	24.1	-5.44**	-3.92	4.02	-7.94**
SEm±		3.68	2.61	5.89	2.63	2.35	5.54	0.20	0.18	0.39	2.04	0.54	0.96	0.73	0.74	1.64
CD @ P=0.05		1.12	7.72	18.05	160.61	6.96	16.98	67.48	0.53	1.18	17.42	1.60	2.95	2.73	2.19	5.04
CD @ P=0.01		1.54	10.55	25.20	219.54	9.52	23.71	92.23	0.72	1.65	23.82	2.18	4.11	3.73	2.99	7.04

a: Sweet × non-sweet corn; b: Non-sweet × sweet corn, JEP: Juice extraction percentage

Table 18: Contd.....

Sweet corn	Non-sweet corn	°Bx		Diff	Total sugar (%)		Diff	Reducing sugars (%)		Diff	Sucrose (%)		Diff
		a	b		a	b		a	b		a	b	
MAI-287	MAI-7	26.93	-34.11	61.04**	21.59	-20.54	42.13**	-22.77	33.40*	-56.17**	57.83**	-37.71**	95.64
MAI-287	MAI-308	-5.47	-48.37**	1.37**	-9.27	-39.44**	30.17**	-23.59	-28.22*	4.63**	5.42	-47.26**	52.68
MAI-283	MAI-308	32.71	-20.36	53.07**	4.57	-29.29	33.86**	8.38	-27.12	35.5**	7.62	-30.18	37.8
MAI-285	MAI-7	12.5	-18.18	30.68**	47.53**	-35.43*	82.96**	66.35**	-12.81	79.16**	34.06**	-47.35**	81.41
MAI-285	MAI-308	42.59**	-22.89	65.48**	37.89**	-21.95	59.84**	49.53**	-15.24	64.77**	32.65*	-26.45	59.1
MAI-285	BGUDI-13	-15.52	-27.85	12.33**	31.35	-33.04	64.39**	43.97**	-35.62	79.59**	21.85	-33.14	54.99
MAI-284	M-65	7.78	-40.87**	48.65**	24.35	-45.88**	70.23**	36.77**	-36.37**	73.14**	17.73	-52.66**	70.39
MAI-284	MAI-7	12.64	-0.27	12.91**	10.91	-4.08	14.99**	22.81	7.18	15.63**	3.28	-11.1	14.38
MAI-284	MAI-308	23.63	1.76	21.87**	25.03	-9.1	34.13**	32.31*	-3.31	35.62**	20.44	-14.71	35.15
MAI-286	MAI-308	16.67	-17.92	34.59**	9.34	-13.78	23.12**	-12.3	-23.02	10.72	25.21	-5.32	30.53
K-4571	BGUDI-10	41.04**	-19.86	60.9**	39.52**	-15.96	55.48**	24	15.43	8.57	56.87**	-30.49	87.36
K-4571	M-65	6.63	-6.34	12.97**	23.96	-13.99	37.95**	26.95	-2.13	29.08	20.7	-19.37	40.07
K-4356-1	BGUDI-10	-4.35	-25.88	21.53**	0.74	-20.41	21.15**	-16.33	-30.71	14.38	18.38	-12.82	31.2
K-4366-1	M-65	18.77	-12.99	31.76**	6.98	-14.1	21.08**	15.48	-2.05	17.53	-4.63	-20.68	16.05
K-4366-1	MAI-7	0.85	-19.51	20.36**	-0.44	-16.39	15.95**	-41.88	-14.12	-27.76	32.08**	-16.66	48.74
K-4366-1	BGUDI-10	-8.5	-7.05	-1.45**	-14.16	-24.32	10.16**	-17.07	-21.43	4.36	-9.53	-26.17	16.64
K-4571	BGUDI-13	42.77**	-12.91	55.66**	49.70**	-6.46	56.16**	29.12*	7.67	36.79	60.24**	-9.31	69.55
MAI-286	MAI-7	-1.79	-34.88*	33.09**	-5.6	-34.81*	40.41**	46.57**	-35.27**	81.84	25.6	-35.48*	61.087
MAI-292	MAI-308	2.78	18.75	-15.97**	0.7	-13.94	14.64**	-16.69	-13.5	-3.19	16.58	-15.4	31.98
MAI-284	BGIDI-13	27.41	16.5	10.91**	7.37	17.23	-9.86**	15.91	27.41	-11.5	4.74	11.91	-7.17
SEm±		0.15	0.29	0.27	0.22	0.21	0.25	0.16	0.19	0.23	0.07	0.05	0.25
CD @ P=0.05		1.96	0.87	0.82	0.58	0.62	0.78	0.27	0.56	0.70	0.41	0.14	0.77
CD @ P=0.01		2.68	1.18	1.15	0.79	0.85	1.09	0.37	0.76	0.97	0.56	0.19	1.08

a: Sweet × non-sweet corn; b: Non-sweet × sweet corn

4.2.5.2 Mid-parent heterosis of sweet × non-sweet corn hybrids

At 10 DPSE (Table 19), among sweet × non sweet corn hybrids, only K-4571 × MAI-7 showed significant positive mid-parent heterosis of 60.00 per cent for number of cobs per plant. For total sugar percentage in the stem, only hybrid showed significant heterosis was MAI-292 × MAI-7 (44.32 %).

With respect to reducing sugar percentage, eleven out of eighteen hybrids showed significant mid-parent heterosis, of which MAI -292 × MAI-7 showed highest positive heterosis of 54.28 per cent while, MAI-14 × MAI-7 showed highest negative mid-parent heterosis of -48.4 per cent.

For sucrose percentage in the stem, hybrid MAI-292 × MAI-7 showed positive significant mid-parent heterosis of 34.54 per cent, whereas, MAI-292 × BGUDI-10 (-24.20 per cent showed significant negative mid-parent heterosis.

At 20 DPSE (Table 20), cross MAI-102 × MAI-7 showed significant positive heterosis of 50.00 per cent while, MAI-102 × BGUDI-13 (-66.67 %) showed significant negative heterosis followed by K -4356-1 × MAI-7 (-55.56 %) for number of cobs per plant.

For °brix content, only MAI-292 × MAI-7 (54.11 %) showed significant mid-parent heterosis. With respect to total sugar percentage in the stem, MAI-7 (54.50 %) showed significant positive mid-parent heterosis, while, K-4356-1×BGUDI-10 (-38.37 %) showed significant negative mid-parent heterosis.

With respect to reducing sugar percentage in the stem, eight crosses showed significant mid-parent heterosis, of which, MAI-292 × BGUDI -81 showed positive heterosis of 61.13 per cent, while, MAI-289 × MAI -7 showed negative heterosis of -49.97 per cent. For sucrose percentage in the stem, cross, MAI -292 × MAI-7 showed positive heterosis of 62.79 per cent while, K -4356-1 × BGUDI -10 showed significant negative heterosis of -41.31 per cent.

4.2.5.3 Mid-parent heterosis of non-sweet corn × sweet corn hybrids

At 10 DPSE (Table 21), out of nine of non-sweet × sweet corn hybrids, BGUDI-10 × MAI-289 showed significant negative mid-parent heterosis of -63.64 per cent. For °brix content, cross MAI-308 × K-4366-1 showed significant positive heterosis of 48.33 per cent.

With respect to total sugar percentage, three hybrids showed significant heterosis, of which, cross MAI-308 × K-4366-1 showed highest positive heterosis of 125.57 per cent followed by BGUDI-10 × MAI-289 (77.29 %).

For sucrose percentage in the stem, hybrid MAI-308 × K-4366-1 showed highest positive significant heterosis of 26.70 per cent followed by MAI-308 × K-4571 and BGUDI-10 × MAI-289 which showed 25.97 and 20.90 per cent of mid-parent heterosis respectively.

Table 19: Mid-parent heterosis of sweet × non-sweet corn hybrids at 10 DPSE

Sl. No.	Crosses	DTF	PH	NOL	PW	NOC	CW	SW
1	MAI-292×MAI-7	-2.75	9.78	6.38	41.75	33.33	48.78	68.2
2	MAI-284×BGUDI-80	-1.89	30.37	25.58	42.24	0	54.25	62.89
3	MAI-102×BGUDI-13	-0.93	-2.82	-4.35	9.98	-50	-17.73	7.02
4	K-4571×MAI-7	2.86	10.07	-6.67	-3.43	60.00*	-79.84	3.97
5	MAI-289×MAI-7	2.42	-18.81	-14.29	-35.95	11.11	-39.43	-35.85
6	MAI-283×BGUDI-13	2.44	-0.81	-2.13	11.83	20	-25.01	11.84
7	MAI-292×BGUDI-10	0	-3.31	2.22	-21.29	33.33	50.76	-21.21
8	MAI-14×MAI-7	1.9	-9.13	-8.33	-5.98	11.11	8.72	-5.93
9	K-4356-1×BGUDI-10	0	9.55	-1.96	16.18	33.33	-3.24	16.2
10	K-4356-1×MAI-7	-0.47	-8.04	-5.88	-24.71	-33.33	-69.26	-24.72
11	K-4571×BGUDI-81	0.48	0	13.64	47.54	14.29	52.43	47.46
12	K-4356-1×M-65	-2.86	-0.44	4.55	-21.19	33.33	-22.83	-21.11
13	MAI-289×MAI-308	0	-1.92	-12.73	-9.06	0	-36.33	-9.05
14	MAI-102×MAI-7	4.31	-7.92	-12.5	-2.95	20	120.56	-2.92
15	MAI-14×MAI-308	0.97	2.31	-4.55	24	20	119.61	24
16	MAI-292×BGUDI-81	9.9	-2.97	6.12	-28.68	14.29	-10.96	-28.61
17	MAI-325×MAI-7	12.87	-7.78	-15.38	-15.12	33.33	84.55	-15.05
CD @ 5 %		6.48	9.87	1.29	109.28	0.87	117.86	51.01
CD @ 1 %		7.52	11.44	1.5	126.74	1	136.69	59.17
Sl. No.	**Crosses**	**SG**	**JV**	**JEP**	**B**	**TS**	**RS**	**SP**
1	MAI-292×MAI-7	35.59	22.01	14.65	45.75	44.32**	54.28**	34.54**
2	MAI-284×BGUDI-80	27.49	121.82	-10.69	23.5	23.21	45.14**	13.07
3	MAI-102×BGUDI-13	-4.16	57.38	-47.31	5.88	5.73	6.13	7.87
4	K-4571×MAI-7	-9.75	35.38	-9.39	-3.8	-3.76	-20.85	0.68
5	MAI-289×MAI-7	-9.64	2.37	-38.21	-17.06	-18.15	-10.8	-16.41
6	MAI-283×BGUDI-13	0.14	60	-23.74	27.5	28.82	46.99**	16.09
7	MAI-292×BGUDI-10	0.74	-15.27	-8.59	-34.58	-34.58	-46.96**	-25.20**
8	MAI-14×MAI-7	4.88	8.31	-0.66	-29.15	-30.18	-48.40**	-19.58
9	K-4356-1×BGUDI-10	-4.55	55.95	-26.41	-18.52	-17.9	-32.21**	-13.89
10	K-4356-1×MAI-7	-8.31	-12.8	-32.91	-19.52	-19.44	-27.30**	-14.06
11	K-4571×BGUDI-81	3.49	50.97	-22.62	-6.63	-6.41	-11.98	-4.49
12	K-4356-1×M-65	1.72	33.53	-38.21	17.68	17.74	28.29**	9.28
13	MAI-289×MAI-308	19.91	8.36	-39.51	7.23	7.52	15.46	4.65
14	MAI-102×MAI-7	1.44	-17.49	-39.2	7.4	7.62	42.10**	-2.99
15	MAI-14×MAI-308	43.92	23.48	-35.72	12.11	12.56	21.66	7.85
16	MAI-292×BGUDI-81	-26.83	24.7	-20.67	-28.74	26.69	47.69**	11.98
17	MAI-325×MAI-7	8.28	-26.78	-25.47	7.84	8.02	33.70**	0.43
CD @ 5 %		2.95	13.9	26.62	1.61	0.63	0.39	0.34
CD @ 1 %		3.42	16.13	30.87	1.86	0.73	0.45	0.39

DTF: Days to 50 per cent flowering; **PH**: Plant height; **NOI**: Number of internodes; **PW**: Plant weight; **SW**: Stem weight; **SG**: Stem girth; **JV**: Juice volume; **JEP**: Juice extraction percentage; °**Bx**: °brix value; **TS**: Total sugars; **SP**: Sucrose percentage; **RS**: Reducing sugars; **CB**: Cob °brix.

Table 20: Mid-parent heterosis of sweet × non-sweet corn hybrids 20 DPSE

Sl. No.	Crosses	PH	NOI	PW	NOC	CW	SW	SG
1	MAI-292×MAI-7	8.54	13.64	70.84	33.33	223.77	-11.34	28.98
2	MAI-284×BGUDI-80	29.48	25.58	7.84	14.29	24.59	8.63	6.84
3	MAI-102×BGUDI-13	-7.37	-2.22	-28.42	-66.67**	-47.55	-21.79	-13.98
4	K-4571×MAI-7	7.18	-4.55	-15.01	33.33	34.43	-14.83	-12.51
5	MAI-289×MAI-7	-19.07	-10.64	-30.3	-9.09	-74.14	-69.79	-13.04
6	MAI-283×BGUDI-13	-1.62	6.98	20.16	-14.29	22.41	44.59	17.14
7	MAI-292×BGUDI-10	-8.46	-11.54	-10.48	-11.11	14.93	-10.89	-2.96
8	MAI-14×MAI-7	-8.52	-8.33	-7.34	0	-6.56	-5.98	2.7
9	K-4356-1×BGUDI -10	6.61	0	34.99	0	29.69	39.82	1.54
10	K-4356-1×MAI -7	-9.62	-4	-10.21	-55.56*	14.27	-8.08	-14.41
11	K-4571×BGUDI-81	-1.13	0	59.66	0	141.88	31.03	14.3
12	K-4356-1×M -65	-2.17	-8	5.71	0	-22.24	19.72	-3.97
13	MAI-289×MAI-308	-2.47	-7.69	-2.4	-45.45	-7.43	4.58	15.08
14	MAI-102×MAI-7	-10.12	-22.22	8.07	50.00*	142.6	-30.22	15.79
15	MAI-14×MAI-308	2.79	-14.29	23.34	0	180.66	2.34	35.38
16	MAI-292×BGUDI-81	-3.42	6.12	-37.2	-20	12.06	-44.17	-24.94
17	MAI-325×MAI-7	-8.59	-12	-34.1	0	26.21	-20.86	10.66
CD @ 5 %		6.09	0.61	44.33	0.76	11.87	11.17	0.78
CD @ 1 %		7.06	0.7	51.42	0.89	13.76	12.95	0.9
Sl. No.	**Crosses**	**JV**	**JEP**	**B**	**TS**	**RS**	**SP**	**CB**
1	MAI-292×MAI-7	5.52	-22.46	54.11**	54.50**	52.65**	62.79**	-2.29
2	MAI-284×BGUDI-80	14.25	33.26	-12.93	27.61	39.63**	20.93	-3.8
3	MAI-102×BGUDI-13	8.83	-30.08	28.85	26.12	41.17**	16.04	-10.05
4	K-4571×MAI-7	23.9	-20.67	-13.14	-9.16	-4.49	-9.52	1.47
5	MAI-289×MAI-7	-13.73	0.4	-25.4	-22.57	-49.97**	-6.51	4.38
6	MAI-283×BGUDI-13	77.48	18.83	4.44	6.42	1.87	9.9	4.79
7	MAI-292×BGUDI-10	0.25	8.74	-9.66	-27.2	-1.94	-47.14	-5.32
8	MAI-14×MAI-7	0.89	-26.79	-33.03	-29.95	-35.56**	-26.4	-10.11
9	K-4356-1×BGUDI-10	58.87	1.41	-23.12	-38.37**	-42.19**	-41.31**	0.52
10	K-4356-1×MAI-7	-4.04	-5.02	-17.33	-20.8	-12.03	-25.91	5.24
11	K-4571×BGUDI-81	29.41	-16.35	-27.84	-25.01	-26.85	-26.64	-4.44
12	K-4356-1×M -65	8.77	6.11	30.24	14.06	21.68	8.38	1.78
13	MAI-289×MAI -308	-6.93	12.29	-22.67	-4	28.79	-20.41	-2.5
14	MAI-102×MAI-7	-10.61	-85.35	-21.74	-20.22	-18.3	-25.71	-6.62
15	MAI-14×MAI-308	11.23	2.72	-10.19	2.6	31.31*	-14.74	-0.18
16	MAI-292×BGUDI-81	36.27	-3.84	0.57	27.85	61.13**	8.27	0
17	MAI-325×MAI -7	-22.35	-1.07	-20.48	-21.82	-18.25	-24.43	-1.59
CD @ 5 %		1.94	3.31	0.54	0.51	0.46	0.51	0.34
CD @ 1 %		2.25	3.84	0.63	0.59	0.53	0.59	0.4

PH: Plant height; **NOI**: Number of internodes; **PW**: Plant weight; **SW**: Stem weight; **SG**: Stem girth; **JV**: Juice volume; **JEP**: Juice extraction percentage; °**Bx**: °brix value; **TS**: Total sugars; **SP**: Sucrose percentage; **RS**: Reducing sugars; **CB**: Cob °brix.

Table 21: Mid-parent heterosis of non-sweet × sweet corn at 10 DPSE

Sl. No.	Crosses	DTF	PH	NOI	PW	NOC	CW	SW
1	BGUDI-13×K-4673-1	-3.14	-19.81	2.33	-42.46	-14.29	-54.68	-42.41
2	BGUDI-13×K-4366-1	1.41	-5.06	25.58	-24.47	-50	-56.95	-24.53
3	MAI-308×K-4571	-4.93	7.12	-8	-15.05	0	-38.18	-15.01
4	BGUDI-10×MAI-287	-1.82	11.06	8.7	-12.01	14.29	-31.13	-11.95
5	BGUDI-80×MAI-282	-2.3	4.91	6.38	-24.01	-55.56	-60.96	-24.13
6	MAI-308×K-4366-1	0	-3.42	-8.33	-16.33	14.29	-38.19	-16.27
7	BGUDI-81×MAI-289	3.85	-20.3	-2.13	-18.76	-33.33	-12.94	-18.81
8	BGUDI-10×MAI-289	0	-4.05	-1.89	-33.42	-63.64**	-64.4	-33.52
9	BGUDI-81×K-4366-1	2.86	5.04	10.64	23.43	20	-13.04	23.42
	CD @ 5 %	6.48	9.87	1.29	109.28	0.87	117.86	51.01
	CD @ 1 %	7.52	11.44	1.5	126.74	1	136.69	59.17
Sl. No.	**Crosses**	**SG**	**JV**	**JEP**	**B**	**TS**	**RS**	**SP**
1	BGUDI-13×K-4673-1	-34.06	-12.53	-51.81	-10.84	-10.13	-13.44	-9.02
2	BGUDI-13×K-4366-1	4.82	-22.52	76.36	-0.9	-1.38	-4.24	-0.51
3	MAI-308×K-4571	-2.17	-4.27	18.35	96.35	35.71	70.50**	25.97**
4	BGUDI-10×MAI-287	-7.59	6.72	2.04	-0.98	-0.89	5.45	-3.4
5	BGUDI-80×MAI-282	-15.63	50.26	49.48	7.81	7.49	18.81	3.04
6	MAI-308×K -4366-1	-3.51	14.62	24.65	48	48.33**	125.57**	26.70**
7	BGUDI-81×MAI-289	26.75	-48.84	38.99	-10.07	-10.75	-26.49	-6.03
8	BGUDI-10×MAI-289	-17.11	-54.69	1.16	35.66	34.69	77.29**	20.90**
9	BGUDI -81×K -4366-1	3.01	76.62	61.08	43.32	42.36	76.62	25.11
	CD @ 5 %	2.95	13.9	26.62	1.61	0.63	0.39	0.34
	CD @ 1 %	3.42	16.13	30.87	1.86	0.73	0.45	0.39

DTF: Days to 50 per cent flowering; **PH**: Plant height; **NOI**: Number of internodes; **PW**: Plant weight; **SW**: Stem weight; **SG**: Stem girth; **JV**: Juice volume; **JEP**: Juice extraction percentage; °**Bx**: °brix value; **TS**: Total sugars; **SP**: Sucrose percentage; **RS**: Reducing sugars.

At 20 DPSE (Table 22), hybrid BGUDI-81 × K-4366-1 showed significant positive heterosis of 60.00 per cent, while, BGUDI-13 × K-4366-1 (-50.00) showed significant negative mid-parent heterosis. For °brix content, three of the hybrids showed significant positive heterosis, of which, MAI-308 × K-4366-1 showed highest positive heterosis of 51.37 per cent while, BGUDI-10 × MAI-289 showed lowest positive heterosis of 34.62 per cent.

With respect to total sugar percentage in the stem, MAI-308 × K-4366-1 showed highest positive mid-parent heterosis of 38.70 per cent followed by BGUDI-10 × MAI-289 (34.26 %). For reducing sugar content also, MAI-308 × K-4366-1 showed highest positive mid-parent heterosis of 37.44 per cent followed by BGUDI-13 × K-4673-1 (26.90 %).

For sucrose percentage in the stem, BGUDI-10 × MAI-289 showed highest positive significant mid-parent heterosis of 40.05 per cent followed by MAI-308 × K-4366-1, which showed mid-parent heterosis of 38.98 per cent.

4.2.5.4 Analysis of variance for combining ability

The mean sum of squares for both lines and testers due to different sources of variation for all the chosen characters at two different reproductive phases *i.e.*, at 10 DPSE and 20 DPSE are represented in Table 23.

It was observed that there were highly significant differences ($P < 0.01$ & 0.05) at both sampling phases for soluble sugars in the stalk and contributing traits among crosses. Mean sum squares due to tester showed significant difference for plant height and plant weight at 10 DPSE, while, at 20 DPSE testers showed significant difference for plant height and stem weight. Mean sum of squares due to line × tester were significantly differed for all the characters at both the phases except plant weight at 10 DPSE.

4.2.5.5 Estimation of general combining effects of lines and testers for soluble sugar percentage in the stem and its attributing traits in corn

Estimation of GCA effects (Table 24) for soluble sugar concentration in the stem and its attributing traits at 10 DPSE revealed that for days to 50 % anthesis, it was observed that no line or tester was found to be good combiner. However, MAI-292 (0.61) found to be good general combiner while, MAI-284 (-1.14) found to have significant negative GCA effect.

Both positive and negative GCA effects were observed for plant height. Lines MAI-284 (9.79cm) and MAI-285 (13.79cm) and tester MAI-308 (12.32cm) were found to be good combiners having highly positive and significant effect for plant height whereas, lines MAI-287 (-13.71) and MAI-289 (-9.46) and tester MAI-7 (-12.32) showed highly negative and significant GCA effect.

For number of internodes no lines or testers were good combiners. However, line MAI-286 (2.04) showed highly significant positive GCA while, line MAI-14 (-0.96)

Table 22: Mid-parent heterosis of non-sweet × sweet corn at 20 DPSE

Sl. No.	Crosses	PH	NOI	PW	NOC	CW	SW	SG
1	BGUDI-13×K-4673-1	-2.42	2.33	5.01	42.86	-5.31	-11.2	-11.07
2	BGUDI-13×K-4366-1	4.02	11.63	-32.56	-50.00*	-61.03	-32.32	-22.75
3	MAI-308 × K-4571	-2.22	-12	22.86	0	22.33	32.23	8.99
4	BGUDI-10 × MAI-287	4.91	4.35	-15.22	-14.29	-56.67	-25.29	-15.66
5	BGUDI-80 × MAI-282	-3.59	-6.38	-30.06	-11.11	-28.53	-41.61	0.94
6	MAI-308 × K-4366-1	2.48	-8.33	-12.61	14.29	-23.72	-26.49	-11.7
7	BGUDI-81×MAI-289	2.9	6.38	2.69	33.33	19.55	14.91	10.59
8	BGUDI-10×MAI-289	-1.19	-13.21	-34.84	-27.27	-49.24	-16.34	-10.4
9	BGUDI-81×K-4366-1	6.3	10.64	-0.63	60.00**	-32.31	21.35	8.56
CD @ 5 %		6.09	0.61	44.33	0.76	11.87	11.17	0.78
CD @ 1 %		7.06	0.7	51.42	0.89	13.76	12.95	0.9
Sl. No.	**Crosses**	**JV**	**JEP**	**B**	**TS**	**RS**	**SP**	**CB**
1	BGUDI-13×K-4673-1	-20.89	46.07	20.83	19.29	26.90*	13.61	-1.99
2	BGUDI-13×K-4366-1	-27.15	-17.93	19.57	-3.34	-3.74	-6.2	-8.87
3	MAI-308×K-4571	-34.76	9.82	48.15**	23.62	26.02	22.91	-7.91
4	BGUDI-10×MAI-287	-10.45	-2.74	-11.37	-6.05	0.27	-13.21	-1.42
5	BGUDI-80×MAI-282	-1.55	-23.92	16.94	10.22	1.55	9.43	-13.16
6	MAI-308×K-4366-1	61.4	2.87	51.37**	38.70**	37.44**	38.98**	0.72
7	BGUDI-81×MAI-289	-5.12	12.12	-15.29	-7.92	2.99	-14.73	-4.63
8	BGUDI-10×MAI-289	-13.54	-7.24	35.66*	34.26*	21.60*	40.05**	0.7
9	BGUDI-81×K-4366-1	98.7	9.71	-4.93	29.09	30.57	27.4	-7.12
CD @5 %		1.94	3.31	0.54	0.51	0.46	0.51	0.34
CD @ 1 %		2.25	3.84	0.63	0.59	0.53	0.59	0.4

PH: Plant height; **NOI**: Number of internodes; **PW**: Plant weight; **SW**: Stem weight; **SG**: Stem girth; **JV**: Juice volume; **JEP**: Juice extraction percentage; °**Bx**: °brix value; **TS**: Total sugars; **SP**: Sucrose percentage; **RS**: Reducing sugars. **CB**: cob °brix

Table 23: Analysis of variance for combining ability for phenotypic traits recorded at two phases of harvest

Source of variance	df	DTF	Plant height		Number of internodes		Plant weight		Stem weight		Stem girth		Cob °brix
			a	b	a	b	a	b	a	b	a	b	
Crosses	13	1.86**	601.95**	764.38**	3.20**	3.67**	59156.74**	85285.30**	16743.65**	22343.74**	18.64*	42.49**	0.70**
Line	6	1.40	392.87	575.17	4.12	4.75	30205.73	85111.73	16989.7	19322.35	20.77	45.086	0.743
Tester	1	0.32	4250.89**	4942.28*	2.29	2.89	537380.10**	256723	53944.32	99796.91*	10.66	52.143	0.06
Line × tester	6	2.57**	202.89**	257.28**	2.45**	2.72**	8403.87	56885.92**	10297.49**	12456.26**	17.84*	38.29**	0.77**
Error	13	0.19	27.98	2.60	0.52	0.09	4870.17	605.20	888.29	9.64	5.42	0.062	0.019

Source of variance	df	Juice volume		Juice extraction percentage		°Brix		Total sugar percentage		Sucrose percentage		Reducing sugar percentage	
		a	b	a	b	a	b	a	b	a	b	a	b
Crosses	13	1536.26**	205.70**	238.51**	769.41**	4.97**	5.43**	5.40**	6.69**	1.16**	1.88**	1.48**	3.12**
Line	6	1896.452	159.396	286.308	893.595	3.408	7.84	3.998	8.488	1.089	2.065	0.597	4.437
Tester	1	12.893	495.938	313.56	1550.943	5.851	0.321	5.833	0.164	1.128	0.42	1.4	1.231
Line × tester	6	1429.976**	203.64**	178.215**	514.97**	6.391**	3.88**	6.74*	5.99**	1.24*	1.95**	2.39*	2.13**
Error	13	65.036	0.552	0.001	19.216	0.056	0.076	0.064	0.092	0.066	0.015	0.016	0.041

a: 10 DPSE; b: 20 DPSE

Table 24: Estimation of general combining effects of lines and testers for soluble sugar percentage in the stem and its attributing traits in corn

Traits		DTF	Plant height		Number of internodes		Plant weight		Cob weight		Stem weight		Stem girth	
Stage of harvest			a	b	a	b	a	b	a	b	a	b	a	b
Lines	MAI-14	0.36	2.54	5.25*	-0.96*	0.75*	72.07*	40.63*	48.02	65.714**	-8.71	31.273**	3.83*	-0.74*
	MAI-284	0.11	9.79*	9**	0.29	0.25	-80.93*	-149.90**	-73.23	-71.28**	-5.71	-25.46**	0.04	1.71**
	MAI-285	0.11	13.79**	19**	0.29	1.75**	87.3*	172.44**	-27.23	16.96**	133.79**	120.66**	1.54	2.51**
	MAI-286	-0.39	-4.21	-10.75**	2.04**	0.25	-88.43*	-199.36**	-80.36*	-53.78**	15.79	-68.47**	-2.46*	-2.12**
	MAI-287	-1.14**	-13.71**	-12.25**	-0.71	-1.25**	22.57	67.57**	75.52	127.71**	-20.96	-25.49**	-2.84*	-0.67*
	MAI-289	0.36	-9.46*	-11.25**	-0.46	-1.25**	-99.93*	-82.17**	-65.23	-151.54**	-68.71**	-75.12**	-0.05	-5.47**
	MAI-292	0.61*	1.29	1	-0.46	-0.5*	87.32*	150.81**	122.52*	66.21**	-45.46*	42.62**	-0.04	4.79**
Testers	MAI-7	-0.11	-12.32**	-13.29**	-0.29	-0.32*	-138.54**	-95.75**	-60.27*	-70.07**	-43.89**	-59.70**	-0.62	-1.37**
	MAI-308	0.11	12.32**	13.28**	0.29	0.32*	138.54**	95.75**	60.27*	70.07**	43.89**	59.70**	0.62	1.36**
CD @ 5 % (line)		0.51	6.58	2.834	0.79	0.44	66.14	27.695	79.3	5.939	31.61	5.532	2.01	0.431
CD @ 5 % (tester)		0.27	3.52	1.515	0.42	0.235	35.35	14.803	42.39	3.174	16.9	2.957	1.07	0.231
h^2		9.96	83.35	82.62	32.57	37.341	93.68	57.086	41.04	61.071	59.9	67.992	23.38	35.998
Genetic advance		0.25	42.38	46.304	0.91	1.135	497.38	302.748	150.78	224.427	139.82	195.375	1.64	4.056

a: 10 DPSE; b: 20 DPSE

Table 24. contd.....

Traits		Juice volume		Juice extraction		°Brix value		Total sugar		Sucrose		Reducing sugar		Cob °brix
Stage of harvest		a	b	a	b	a	b	A	b	a	b	a	b	
Lines	MAI-14	17.54**	-6.38***	-3.64*	7.201*	-0.44*	-1.49**	-0.47*	-1.12**	-0.19	-1.08**	-0.22	-0.08	-0.59**
	MAI-284	-27.46**	-1.68***	11.69**	-1.881	-0.24	1.529	-0.26	1.265	-0.14	0.31**	0.12	1.07**	0.114
	MAI-285	20.04**	-1.21**	-5.34*	27.58**	1.76**	1.27**	1.96**	2.35**	1.02**	0.74**	0.54*	1.57**	0.69**
	MAI-286	-5.21	6.79**	0.7	-15.96**	-0.64**	0.154	-0.71**	-0.57*	-0.43*	0.57**	-0.2	-1.13**	-0.39*
	MAI-287	-29.21**	-2.86**	11.14**	-0.48	-0.14	-0.42*	-0.1	-0.82**	0.15	0.14*	-0.40*	-0.99**	0.039
	MAI-289	2.04	10.59**	-10.48**	-0.061	-0.96**	-2.07**	-1.01**	-1.72**	-0.57**	-0.93**	-0.33*	-0.87**	0.31*
	MAI-292	22.29**	-5.24**	-4.08*	-16.39**	0.64**	1.03**	0.59**	0.62**	0.16	0.26**	0.49*	0.38**	-0.186
Testers	MAI-7	0.68	-4.21**	-3.35	-7.44**	0.46	-0.107	0.46**	-0.076	0.20*	0.12**	0.22*	-0.21**	-0.046
	MAI-308	-0.68	4.21**	3.35**	7.44**	-0.46**	0.107	-0.46**	0.076	-0.20*	-0.12**	-0.22*	0.21**	0.046
CD @ 5 % (line)		7.72	0.617	3.20**	3.962	0.26**	0.292	0.29	0.302	0.29	0.114	0.28	0.177	0.24
CD @ 5 % (tester)		4.13	0.33	1.71	2.118	0.14	0.156	0.15	0.162	0.15	0.061	0.15	0.094	0.128
Heritability		21.93	41.671	42.07	51.058	24.12	31.424	24.2	23.958	27.04	21.882	14.75	36.9	16.833
Genetic advance		13.67	11.342	10.75	24.125	1.02	1.09	1.05	0.98	0.52	0.504	0.36	0.988	0.236

a: 10 DPSE; b: 20 DPSE

showed negative GCA effect. With respect to plant weight, lines MAI-14 (72.07), MAI-292 (87.32) and tester MAI-308 (138.54) were found to be good general combiners. Whereas, lines MAI-284 (-80.93), MAI-286 (-88.43), MAI-289 (-82.17) and tester MAI-7 (-138.54) showed highly negative and significant GCA effect.

For cob weight, line MAI-286 (-80.36) and line MAI-292 (122.52) revealed significant negative and positive GCA effects respectively. Tester MAI-308 (60.27) found to be good combiner compare to MAI-7 (-6.27) which had negative GCA effect for cob weight (g).

Inbred line MAI-285 (133.79) and tester MAI-308 (43.89) were good general combiners while, lines MAI-289 (-68.71), MAI-292 (-45.46) and tester MAI-7 (-43.89) were poor combiners for stem weight (g). For stem girth line MAI-14 (3.83) was good general combiner. Whereas, lines MAI-286 (-2.46) and MAI-287 (-2.84) showed negative GCA effect.

With respect to juice volume (ml) line MAI-292 (22.29) found to be very good general combiner followed by MAI-285 (20.04) and MAI-14 (17.54) while, lines MAI-284 (-27.46) and MAI-287 (-29.21) showed significant negative GCA effect.

Both negative and positive GCA effects were observed for juice extraction percentage. Lines MAI-14 (-3.64), MAI-285 (-5.34), MAI-289 (-10.48), MAI-292 (-4.08) and lines MAI-284 (11.69), MAI-287 (11.14) showed significant negative and positive GAC effects respectively.

Both negative and positive GCA effects were recorded for °brix and total soluble sugars. Lines MAI-14 (-0.44, -0.47), MAI-286 (-0.64, -0.71) and MAI-289 (-0.96, -1.01) were found to have negative impact whereas, lines MAI-285 (1.76, 1.96) and MAI-292 (0.64, 0.59) were good general combiners for both °brix and total soluble sugar content in the corn stem.

With respect to sucrose and reducing sugar percentage in the corn stem, line MAI-285 (1.02, 0.54) was found to be good general combiner for both the traits, whereas, MAI-292 (0.49) was good combiner for reducing sugar percentage in the stem. Line MAI-289 (-.057, 0.33) showed significant negative GCA effect for both the traits, while, MAI-286 (-0.43) for sucrose content and MAI-287 (-0.40) for reducing sugar percentage in the corn stem.

All the lines were observed to be good combiners for all the traits at 20 d post silk emergence stage except MAI-14 for reducing sugar percentage; MAI-284 for number of internodes, juice extraction percentage, °brix, total sugar percentage in the stem and cob °brix; MAI-286 for number of internodes and °brix; MAI-287 for juice extraction percentage and cob °brix; MAI-289 for juice extraction percentage and MAI-292 for plant height and cob °brix. Both the tester showed significant GCA effect for all the traits except °brix and total sugar in the stem and for cob °brix.

4.2.5.6 Estimation of specific combining ability

The estimate of specific combining ability from 14 hybrids (Table 25) revealed both positive and negative significant effects. For days to days to 50 per cent anthesis, cross MAI-286 × MAI-7 showed good SCA effects of -1.39 days for earliness, whereas, MAI-286 × MAI-308 was the latest with SCA effect of 1.39 days.

Cross MAI-287 × MAI-308 observed as good specific combiner and had significant positive SCA effect of 11.43 for plant height, whereas, cross MAI-287 × MAI-7 was poor specific combiner with SCA effect of -11.43. For cob weight, cross MAI-285 × MAI-308 was found to be good specific combiner with the effect of 154.73 followed by MAI-289 × MAI-7 having SCA effect of 112.77 while, crosses MAI-285 × MAI-7 and MAI-289 × MAI-308 were poor combiners.

With respect to stem weight, cross MAI-284 × MAI-308 found to be good specific combiner and had significant positive SCA effect of 99.86, whereas, MAI-284 × MAI-7 was poor specific combiner. For stem girth cross MAI-289 × MAI-308 observed to be good specific combiner while, MAI-289 × MAI-7 was poor specific combiner.

For juice volume, cross MAI-286 × MAI-308 showed significant positive SCA effect of 38.57 followed by MAI-14 × MAI-308 and (MAI-284 × MAI-308, MAI-285 × MAI-308) with SCA effect of 15.18 and 14.18 respectively. Whereas, crosses MAI-286 × MAI-7, MAI-14 × MAI-7 and (MAI-284 × MAI-7, MAI-285 × MAI-7) were poor specific combiners with SCA effects of -38.57, -15.18 and -14.18 respectively.

With respect juice extraction percentage, crosses MAI-284 × MAI-308 and MAI-292 × MAI-7 were best specific combiners with significant positive effect of 10.01 and 10.81 respectively. Whereas, MAI-284 × MAI-7 and MAI-292 × MAI-308 were poor specific combiner with the SCA effect of -10.01 and -10.81 respectively.

All the crosses showed significant SCA effect for both °brix and total soluble sugar content in the stem. Among them cross MAI-14 × MAI-308 was best specific combiner and had highly significant positive effect of 1.91 and 1.99 for °brix and total soluble sugars respectively, Whereas, cross MAI-14 × MAI-7 was found to be poor specific combiner for both the traits.

For both sucrose and reducing sugar percentage in the corn stem, cross MAI-14 × MAI-308 was the best specific combiner and had highly significant positive effect of 0.71 and 1.23 respectively, whereas, cross MAI-14 × MAI-7 was found to be poor specific combiner for both the traits. For cob °brix, cross MAI-292 × MAI-308 was found to be good specific combiner followed by MAI-14 × MAI-308 and MAI-285 × MAI-7 with significant positive SCA effect of 0.63, 0.58 and 0.45 respectively, whereas, MAI-292 × MAI-7, MAI-14 × MAI-7 and MAI-285 × MAI-308 were observed to be poor specific combiners.

Table 25: Specific combining effects of hybrids for soluble sugar percentage in the stem and its attributing traits in corn

Traits	DTF	Plant height		Number of leaves		Plant weight		Cob weight		Stem weight		Stem girth	
Stages		a	b	a	b	a	b	a	b	a	b	a	b
L1×T1	0.86*	3.82	-0.96	0.54	0.82*	-9.21	-28.87	90.27	-33.43**	-19.86	31.24**	-2.25	0.99*
L2×T2	-0.86*	-3.82	0.96	-0.54	-0.82*	9.21	28.87	-90.27	33.43**	19.86	-31.24**	2.25	-0.99*
L2×T1	-0.39	9.57*	3.79	-0.21	-0.68*	-58.21	144.83**	42.27	110.57**	-99.86**	38.40**	-0.48	1.41**
L2×T2	0.39	-9.57*	-3.79	0.21	0.68**	58.21	-144.83**	-42.27	-110.57**	99.86**	-38.40**	0.48	-1.41**
L3×T1	-0.39	4.07	13.79**	-0.21	0.82*	-3.96	167.07**	-154.73*	68.32**	46.64*	82.30**	1.93	4.42**
L3×T2	0.39	-4.07	-13.79**	0.21	-0.82*	3.96	-167.07**	154.73*	-68.32**	-46.64*	-82.30**	-1.93	-4.42**
L4×T1	-1.39**	-4.43	-6.46*	-0.46	-0.68*	64.29	-150.14**	19.89	-34.43**	41.64	-24.16**	2.61	-0.50
L4×T2	1.39**	4.43	6.46*	0.46	0.68*	-64.29	150.14**	-19.89	34.43**	-41.64	24.16**	-2.61	0.50
L5×T1	0.86*	-11.43*	-5.96*	-0.71	0.32	26.79	-106.13**	-15.48	-60.93**	31.39	-27.41**	0.30	-0.56
L5×T2	-0.86*	11.43*	5.96*	0.71	-0.32	-26.79	106.13**	15.48	60.93**	-31.39	27.41**	-0.30	0.56
L6×T1	0.36	-4.68	-8.96**	-0.46	-1.18*	35.29	-40.25*	112.77*	-105.68**	9.64	-89.48**	-3.13*	-5.86**
L6×T2	-0.36	4.68	8.96**	0.46	1.18*	-35.29	40.25*	-112.77*	105.68**	-9.64	89.48**	3.13*	5.86**
L7×T1	0.11	3.07	4.79*	1.54*	0.57	-54.96	13.48	-94.98	55.57**	-9.61	-10.88*	1.03	0.11
L7×T2	-0.11	-3.07	-4.79*	-1.54*	-0.57	54.96	-13.48	94.98	-55.57**	9.61	10.88*	-1.03	-0.11
CD	0.72	9.30	4.01	1.12	0.62	93.54	39.17	112.15	8.40	44.71	7.82	2.84	0.61

a: 10 DPSE; **b**: 20 DPSE; **L1 ×T1**: MAI-14×MAI-7; **L1×T2**: MAI-14×MAI-308; **L2×T1**: MAI-284×MAI-7; **L2×T2**: MAI-284×MAI-308; **L3×T1**: MAI-285×MAI-7; **L3×T2**: MAI-285×MAI-308; **L4×T1**: MAI-286×MAI-7; **L4×T2**: MAI-286×MAI-308; **L5×T1**: MAI-287×MAI-7; **L5×T2**: MAI-287×MAI-308; **L6×T1**: MAI-289×MAI-7; **L6×T2**: MAI-289×MAI-308; **L7×T1**: MAI-292×MAI-7; **L7×T2**: MAI-292×MAI-308.

Table 25 contd.....

Traits	Juice volume (ml)		Juice extraction percentage		°Brix content		Total sugars		Sucrose per cent		Reducing sugars		Cob °brix
Stages	a	b	a	b	a	b	a	b	a	b	a	b	
L1×T1	-15.18*	-0.23	5.54*	0.73	-1.91**	-0.32	-1.99**	-1.22**	-0.71*	-0.62**	-1.23**	-0.53**	-0.58*
L2×T2	15.18*	0.23	-5.54*	-0.73	1.91**	0.32	1.99**	1.22**	0.71*	0.62**	1.23**	0.53**	0.58*
L2×T1	-14.18*	13.70**	-10.01**	-1.43	1.09**	-0.39	1.14**	-0.64*	0.40*	-0.65**	0.66*	0.02	0.02
L2×T2	14.18*	-13.70**	10.01**	1.43	-1.09**	0.39	-1.14**	0.64*	-0.40*	0.65**	-0.66*	-0.02	-0.02
L3×T1	-14.18*	1.05*	-1.39	12.80**	0.59*	-0.94**	0.53*	0.69*	-0.06**	0.04	0.80**	0.67**	0.45*
L3×T2	14.18*	-1.05*	1.39	-12.80**	-0.59*	0.94**	-0.53*	-0.69*	0.06**	-0.04	-0.80**	-0.67**	-0.45*
L4×T1	38.57**	-9.81**	-3.00	-11.78**	-0.51*	-1.02**	-0.47*	-1.02**	-0.23	-0.51**	-0.22	-0.47*	0.07
L4×T2	-38.57**	9.81**	3.00	11.78**	0.51*	1.02**	0.47*	1.02**	0.23	0.51**	0.22	0.47*	-0.07
L5×T1	4.57	-3.41**	-2.82	-8.38*	0.99**	1.56**	1.08**	1.65**	0.70*	1.32**	0.16	0.30*	0.30
L5×T2	-4.57	3.41**	2.82	8.38*	-0.99**	-1.56**	-1.08**	-1.65**	-0.70*	-1.32**	-0.16	-0.30*	-0.30
L6×T1	-1.18	-2.63**	0.85	-9.48*	-1.38**	0.01	-1.40**	-0.89**	-0.62*	0.05	-0.77*	-1.03**	0.37*
L6×T2	1.18	2.63**	-0.85	9.48*	1.38**	-0.01	1.40**	0.89**	0.62*	-0.05	0.77*	1.03**	-0.37*
L7×T1	1.57	1.32*	10.81**	17.54**	1.12**	1.11**	1.11**	1.43**	0.52*	0.36**	0.59*	1.05**	-0.63*
L7×T2	-1.57	-1.32*	-10.81**	-17.54**	-1.12**	-1.11**	-1.11**	-1.43**	-0.52*	-0.36**	-0.59*	-1.05**	0.63*
CD	10.92	0.87	4.52	5.60	0.37	0.41	0.40	0.43	0.41	0.16	0.39	0.25	0.34

a: 10 DPSE; **b**: 20 DPSE; **L1 ×T1**: MAI-14×MAI-7; **L1×T2**: MAI-14×MAI-308; **L2×T1**: MAI-284×MAI-7; **L2×T2**: MAI-284×MAI-308; **L3×T1**: MAI-285×MAI-7; **L3×T2**: MAI-285×MAI-308; **L4×T1**: MAI-286×MAI-7; **L4×T2**: MAI-286×MAI-308; **L5×T1**: MAI-287×MAI-7; **L5×T2**: MAI-287×MAI-308; **L6×T1**: MAI-289×MAI-7; **L6×T2**: MAI-289×MAI-308; **L7×T1**: MAI-292×MAI-7; **L7×T2**: MAI-292×MAI-308.

4.3 Molecular profiling of parents and hybrids using *ZmSUT1* gene specific markers

Along with the phenotypic characterization of both parents and hybrids genotypic characterization was also performed using *ZmSUT1* gene specific markers. The expected product size of the primers designed ranged from 205 bp to 744 bp and annealing temperature from 52.1 ° C to 56.2 °C. Among ten primers used in the study, four primers ZmSUT1b, ZmSUT1c, ZmSUT1f and ZmSUT1h amplified and other six primers which did not amplify were eliminated for further study. Obtained band size was compared with already reported band size in NCBI database. Out of the four amplified markers, only ZmSUT1b, ZmSUT1c and ZmSUT1f were found to be polymorphic.

The bands scored for gene specific markers are in 0, 1, 2, 3, 5 and 7 pattern (Table 26) where, 0 represents the absence of band, 1 represents the lower size band, 3 represents the higher band size and 2 represents the presence of both the bands, while, 5 and 7 represents the unusual single and heterozygous banding pattern respectively. All these banding profiles of gene specific markers are shown in Plate 8-12 and the corn genotypes were profiled into different categories based on scoring pattern of the bands.

The primer ZmSUT1h showed all the bands with expected size of 241 bp that means all the genotypes are monomorphic for this marker. Whereas, genotypes showed polymorphism for remaining markers ZmSUT1b, ZmSUT1c and ZmSUT1f which were showing different banding pattern from expected band size of 405, 362 and 490 bp respectively.

Table 26: Genotypes showing different banding profile for *ZmSUT1* specific primers

Marker	Genotypes scored as 1	Genotypes scored as 2	Genotypes scored as 3	Genotypes scored as 5	Genotypes scored as 7
ZmSUT1b	MAI-102, MAI-308, BGUDI-80, MAI-287 × MAI-7, MAI-287 × MAI-308, MAI-285 × MAI-7, MAI-308 × MAI-285, MAI-285×BGUDI-13, BGUDI-13×MAI-285, MAI-284 × M-65, MAI-7 × MAI-285, MAI-284 × MAI-7	MAI-14, K-4366-1, MAI-286 × MAI-308, M-65 × K-4366-1, MAI-283 × MAI-308, MAI-308 × MAI283	MAI-283. MAI-287, MAI-7, BGUDI-10, BGUDI-13, BGUDI-81, M-65 × MAI-284, MAI-7 × MAI-284, MAI-308 × MAI-284, K-4571 × M-65, K-4356-1 × BGUDI-10, BGUDI-10 × K-4356-1	MAI-289, MAI-292, K-4356-1, K-4571, MAI-285 × MAI-308	MAI-282, MAI-284, MAI-285, MAI-286, MAI-325, K-4673-1, M-65
ZmSUTc	MAI-282, MAI-283, MAI-284, MAI-285, MAI-292, MAI-325, K-4673-1, M-65, MAI-308, MAI-284 × M-65, M-65 × MAI-284, MAI-284 × MAI-308, MAI-308 × MAI-286, K-4356-1 × BGUDI-10, MAI-283 × MAI-308, MAI-308 × MAI283, K-4571 × BGUDI-13, MAI-284 × BGUDI-80	MAI-285 × MAI-7, MAI-7 × MAI-285, MAI-285 × MAI-308, MAI-308 × MAI-285, MAI-285 × BGUDI-13, MAI-284 × MAI-7 BGUDI-13 × MAI-285	MAI-14, MAI-102, K-4356-1, K-4366-1, K-4571, BGUDI-80, MAI-7, MAI-292 × MAI-7, MAI-102 × BGUDI-13, MAI-287 × MAI-308, MAI-308 × MAI-284	BGUDI-10, BGUDI-13, BGUDI-81, K-4366-1 × BGUDI-10, MAI-284 × MAI-7, MAI286 × MAI-308	

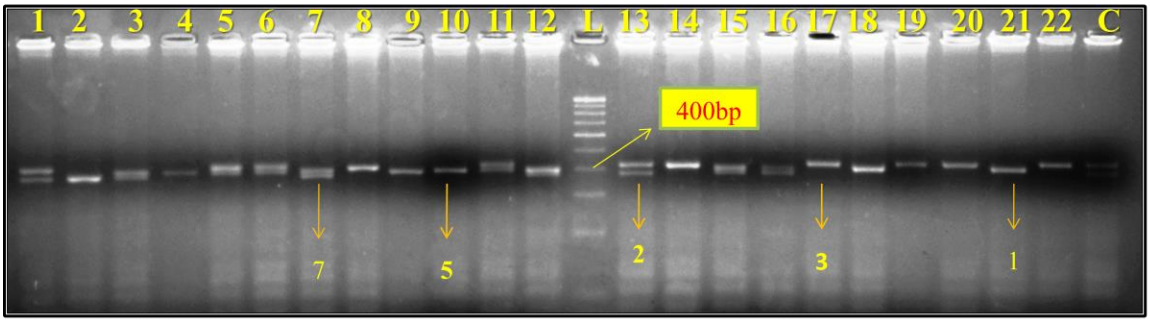


Plate 8: Agarose gel profile of ZmSUT1b for corn parents

1: MAI-14, 2: MAI-102, 3: MAI-282, 4: MAI-283, 5: MAI-284, 6: MAI-285, 7: MAI-286, 8: MAI-287, 9: MAI-289, 10: MAI-292, 11: MAI-325, 12: K-4356-1, 13: K-4366-1, 14: K-4571, 15: K-4673-1, 16: M-65, 17: MAI-7, 18: MAI-308, 19: BGUDI-10, 20: BGUDI-13, 21: BGUDI-80, 22: BGUDI-81, C: Madhuri

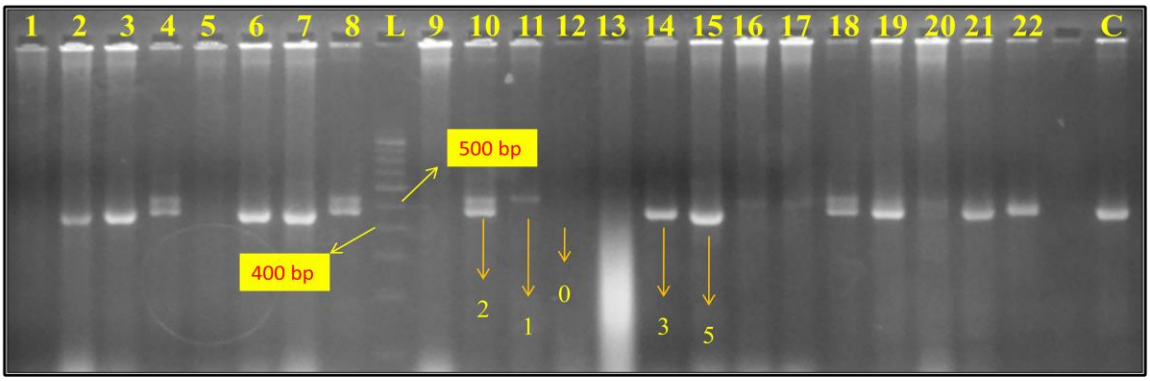


Plate 9: Agarose gel profile of ZmSUT1f of corn parents

1: MAI-14, 2: MAI-102, 3: MAI-282, 4: MAI-283, 5: MAI-284, 6: MAI-285, 7: MAI-286, 8: MAI-287, 9: MAI-289, 10: MAI-292, 11: MAI-325, 12: K-4356-1, 13: K-4366-1, 14: K-4571, 15: K-4673-1, 16: M-65, 17: MAI-7, 18: MAI-308, 19: BGUDI-10, 20: BGUDI-13, 21: BGUDI-80, 22: BGUDI-81, 23: Madhuri

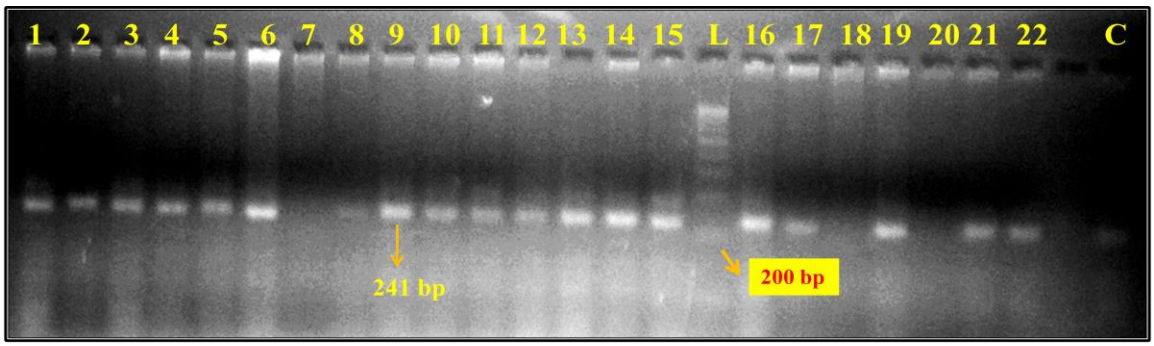


Plate 10: Agarose gel profile of ZmSUT1h for corn parents

1: MAI-14, 2: MAI-102, 3: MAI-282, 4: MAI-283, 5: MAI-284, 6: MAI-285, 7: MAI-286, 8: MAI-287, 9: MAI-289, 10: MAI-292, 11: MAI-325, 12: K-4356-1, 13: K-4366-1, 14: K-4571, 15: K-4673-1, 16: M-65, 17: MAI-7, 18: MAI-308, 19: BGUDI-10, 20: BGUDI-13, 21: BGUDI-80, 22: BGUDI-81, 23: Madhuri

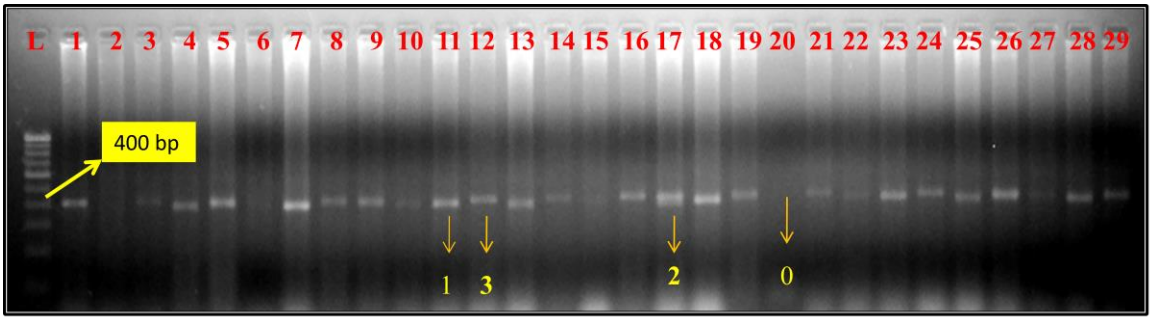


Plate 11: Agarose gel profile of ZmUT1b indicating polymorphism

1: MAI-287 × MAI-7
2: MAI-7 × MAI-287
3: MAI-287 × MAI-308
4: MAI-308 × MAI-283
5: MAI-285 × MAI-7
6: MAI-7 × MAI-285
7: MAI-285 × MAI-308
8: MAI-308 × MAI-285
9: MAI-285×BGUDI-13
10: BGUDI-13×MAI-285
11: MAI-284 × M-65
12: M-65 × MAI-284
13: MAI-284 × MAI-7
14: MAI-7 × MAI-284
15: MAI-284 × MAI-308
16: MAI-308 × MAI-284
17: MAI286 × MAI-308
18: MAI-308 × MAI-286
19: K-4571 × BGUDI-10
20: BGUDI-10 × K-4571
21: K-4571 × M-65
22: M-65 × K-4571
23: K-4356-1 × BGUDI-10
24: BGUDI-10 × K-4356-1
25: K-4366-1 × M-65
26: M-65 × K-4366-1
27: K-4366-1 × MAI-7
28: MAI-283 × MAI-308
29: MAI-308 × MAI283
L: 100 bp ladder

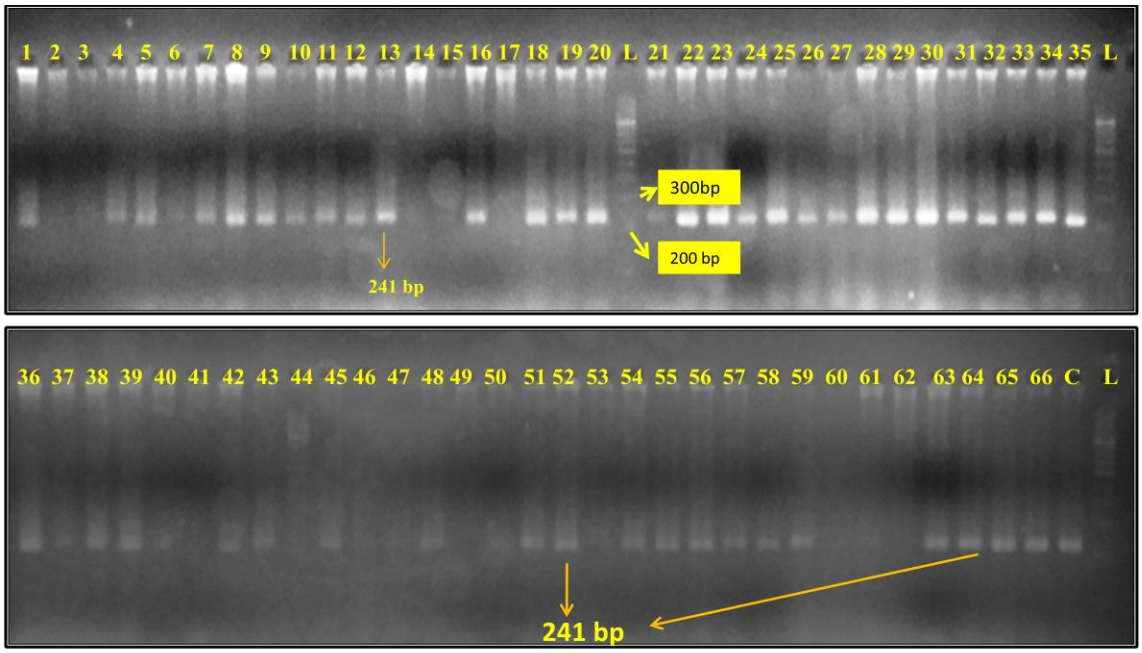


Plate 12: Agarose gel profile of ZmUT1h for all the crosses

1: MAI-287 × MAI-7
2: MAI-7 × MAI-287
3: MAI-287 × MAI-308
4: MAI-308 × MAI-283
5: MAI-285 × MAI-7
6: MAI-7 × MAI-285
7: MAI-285 × MAI-308
8: MAI-308 × MAI-285
9: MAI-285×BGUDI-13
10: BGUDI-13×MAI-285
11: MAI-284 × M-65
12: M-65 × MAI-284
13: MAI-284 × MAI-7
14: MAI-7 × MAI-284
15: MAI-284 × MAI-308
16: MAI-308 × MAI-284
17: MAI286 × MAI-308
18: MAI-308 × MAI-286
19: K-4571 × BGUDI-10
20: BGUDI-10 × K-4571
21: K-4571 × M-65
22: M-65 × K-4571
23: K-4356-1 × BGUDI-10
24: BGUDI-10 × K-4356-1
25: K-4366-1 × M-65
26: M-65 × K-4366-1
27: K-4366-1 × MAI-7
28: MAI-283 × MAI-308
29: MAI-308 × MAI283
30: K-4366-1 × BGUDI-10
31: BGUDI-10 × K-4366-1
32: MAI-292 × MAI-7
33: K-4571 ×BGUDI-13
34: MAI-284 × BGUDI-80
35: MAI-102 × BGUDI-13
36: K-4571 × MAI-7
37: MAI-284 × BGUDI-13
38: MAI-286 × MAI-7
39: MAI-289 × MAI-7
40: MAI-283 × BGUDI-13
41: MAI-292 × BGUDI-10
42:MAI-14 × MAI-7
43: K-4356-1 × BGUDI-10
44: K-4356-1 × MAI-7
45: K-4571 × BGUDI-81
46: K-4356-1 × M-65
47: MAI-289 × MAI-308
48: MAI-102 × MAI-7
49: MAI-14 × MAI-308
50: MAI-292 × BGUDI-81
51: MAI-325 × MAI-7
52: BGUDI-13 × K-4673-1
53: BGUDI-13 × 4366-1
54: MAI-308 × K-4571
55: BGUDI-10× MAI-287
56: BGUDI-80 × MAI-282
57: MAI-308 × K-4366-1
58: BGUDI-81 × MAI-289
59: BGUDI-10 × MAI-289
60: MAI-7 × MAI-286
61: BGUDI-81 × K-4366-1
62: BGUDI-13 × MAI-284
63: BGUDI-13 × K-4571
64: MAI-292 × MAI-308
65: MAI-308 × MAI-292
66: MAI-7 × K-4366-1
C: Madhuri
L: 100 bp ladder

V DISCUSSION

Corn, which belongs to C_4 plants, has known to yield more biomass per unit land area (10 t ha^{-1}). The greater energy efficiency of corn will promote the crop as a species of better choice for bioenergy feedstock. Further, based on the genetic diversity and ample germplasm availability, rapid advances can be made to improve biomass, lignocellulosic, and stalk sugar traits of this corn to meet present and the future biofuel processing and production requirements.

There has been an enormous and intensive research efforts and encouragement worldwide to utilize renewable plant resources (plant sugars) for energy purpose to reduce the extensive utilization of depleting fossil fuel resources, and the environmental pollution associated with their use (Kammen *et al*., 2010) and this advancement appears to have resulted in the pendulum swinging back towards the use of biomass as a potential energy resource.

Food crops were being used for biofuel production, which generates a direct competition between energy and food uses. Similarly, dedicated energy crops like switchgrass or giant miscanthus could also compete indirectly with food production if they are grown on agricultural land (Walsh *et al*., 2003). Hence, biofuel production using biomass residues of food crops seems an appealing alternative because it does not compete with food and does not require new inputs for cultivation.

Quantifying the genotypic variability for stalk sugar content and associated traits in various corn genotypes and investigating the accumulation of sugar within a corn stalk over time helps to determine the best selection and harvest time, upon that, higher percentage of soluble sugar in the stalk can be used to produce bio ethanol, while, the biomass that remains after extraction could be ensiled and fed to livestock.

As grain will likely remain the major product of corn, genetic improvement of corn for bioenergy uses will need to focus on enhancing biomass quantity and quality without impacting grain yield and quality. As a fact that, hybrids perform uniformly with higher productivity, they preferred over varietal populations. Hence, corn inbred lines, which were manifested with significant genetic variation for biomass yield and soluble sugar content could be select for breeding programme to develop hybrids with increase biomass yield and quality of stalk sugar.

In contrast to non-sweet corn (NS), sweet corn (S) manifested higher concentration of soluble sugar in the endosperm as well as in stalk, hence in order to find, whether the cytoplasm influence the concentration of sugar in the corn stalk and related traits. In the present study, sweet corn and non-sweet corn inbred lines were utilized as both female and male parents to perform direct as well as reciprocal crossing.

To improve soluble sugar concentration in the stem it is necessary to understand the sugar translocation from source to sink organs. Since sucrose is the predominant form of sugar transported through the phloem, study of the sucrose transporters (SUTs) is

essential. In particular sucrose transporter of the corn *ZmSUT1* which is working like a perfect thermodynamic machine of sucrose transport and capable of mediating sucrose uptake into phloem from source (mature leaves) as well as unloading (desorption) from the phloem into sink organs (stalk and reproductive parts). Hence, in order to understand the genetics of sucrose transportation, study of molecular genetics of the trait through gene specific molecular markers has been carried out in the present study.

The results of the present investigation are discussed under following headings.

5.1 Analysis of variance for traits influencing soluble sugar content in the corn stem

Analysis of variance (Table 5) revealed that there were significant differences ($P < 0.05$) for mean sum of squares of soluble sugar percentage in the stalk and all its attributing traits among genotypes at both the harvesting times *i e.*, 10 and 20 DPSE. However the interaction 10 vs 20 DPSE study exhibited significantly high differences in the genotypes for °brix, total sugar, reducing sugar and sucrose percentage in the stem, indicating that, only soluble sugar concentration in the stalk will vary with the time, while, other phenotypic traits like plant height, number of internodes, stem weight, stem girth, juice volume and juice extraction percentage had no significant difference ($P < 0.05$) between two harvesting stages.

Mean sum of squares (Table 6) of both sweet corn and non-sweet corn parents showed significant differences for all the traits except days to flowering (both S and NS parents) and for number of cobs (NS parents), further, there was a significant sweet vs non-sweet interaction for all the traits except cob weight and days to flowering, indicating that parent were not differed with respect to cob weight and days to flowering.

Among hybrids both S × NS and NS × S showed significant differences for mean sum of squares (Table 7) of all the traits. However, the interaction study of S × NS vs NS × S showed significant differences for all the traits except number of cobs, indicating that there is no cytoplasmic influence for this particular trait.

Both parents and hybrids varied themselves for soluble sugar concentration in the stalk and its related traits except days to flowering and juice extraction percentage, these results were revealed by the analysis of variance performed for mean sum of squares (Table 8-11). However, there is no significant difference between sweet corn parent and crosses involving sweet corn as female parent for the traits *viz.*, plant height, number of internodes, number of cobs and juice extraction percentage. inaddition, non- sweet corn parent showed significant differences with S × NS and NS × S for all the traits except for number of cobs, juice extraction percentage and °brix (S × NS) and for days to flowering and juice extraction percentage (NS × S).

The data from Table 5-11 showed the high degree of variability among parents and hybrids for the soluble sugar percentage in the stalk and allied traits and provides opportunity to utilize this information in genetic improvement to produce better hybrids of sweet and non-sweet corn for biofuel production.

5.2 Phenotypic performance of parents and hybrids at two phases of sampling

Mean performance of all the 22 parents and their 66 hybrids for individual trait revealed high range of values for each trait. This suggests that apart from environment genetic makeup of the individual genotypes play an important role in phenotypic performance by each individual.

There is a variation in mean performance of all the traits for parents and hybrids, for instance, juice volume ranged from 56.50 to 153.00 for sweet corn parents while, that of non-sweet corn parent ranged from 41.00 to 92.00. However it has showed even wider range of 40.50 to 170.50 for S × NS hybrids whereas, for NS × S hybrids it was from 19.00 to 129.50. These results were found to be higher than the juice yield recorded by Reid *et al*., (2015), in both corn inbred and their hybrids, this contribution might due to variation in genotypes and environmental parameters. The results of sucrose percentage of stalk in the present study were in conformity with the results of Reid *et al*., (2015). Comparison among the parents and hybrids suggested hybrids with sweet corn as female parent were better performers.

Mean performance for °brix ranged from 4.75 to 14.56 and is comparable to sweet sorghum and specialized sugar crops (Woods, 2001; Tsuchihashi and Goto, 2005). Results obtained for range of mean performance of corn genotypes for soluble sugar percentage and juice extraction percentage were in accordance with results obtained by Channappagoudar *et al*., (2007).

Mean performances of juice yield was lower at 20 DPSE compared to 10 DPSE suggesting that juice volume was decreased over time. However, soluble sugar percentage in the stem was increased in spite of decreased juice yield suggested that 20 DPSE was the right time of harvest, where corn cob was at right time for consumption. These results were confirmed by the similar study by Barros-Rios *et al*., (2015), relating to the potential of sweet corn for bioethanol production.

High heritability and genetic advance for mean along with moderate to high genetic and phenotypic co-efficient of variation was observed for soluble sugar percentage in the stem and its influencing characters suggesting that improvement and genetic progress of these traits through breeding programe lead to obtain expected results.

5.3 Test of normality

The study of distribution of quantitative traits using skewness and kurtosis provides information about nature of gene action (Fisher *et al*., 1932) and number of genes controlling the traits (Robson, 1956), respectively.

The skewed distribution of a trait in general suggests that the trait is under the control of non-additive gene action and is influenced by environmental variables. Positive skewness is associated with complementary gene interactions while, negative skewness is associated with duplicate (additive × additive) gene interactions. The genes controlling the trait with skewed distribution tend to be predominantly dominant irrespective of whether they have increasing or decreasing effect on the trait (Pooni *et al*., 1977).

Kurtosis is negative or close to zero in the absence of gene interaction and is positive in the presence of gene interactions (Choo and Reinbergs, 1982; Kotch *et al*., 1992). Platykurtic distributions are controlled by large number of genes.

Frequency distribution for different traits on corn genotypes under study revealed different patterns of distribution as shown on Fig. 2-7. From the results of frequency distribution, it was found that corn genotypes were positively skewed for juice volume (only at 10 DPSE), °brix, total sugars, reducing sugars and sucrose percentage except Juice volume and cob °brix at 20 DPSE, this right skewed distribution with values of skewness near to zero indicates that the distribution is symmetrical around the mean. Some of the possible reasons for the traits exhibiting some extent of deviation from normal distribution might be natural selection and meiotic distortion and/or due to the phenomenon of linkage drag and linkage disequilibrium.

5.4 Correlation studies for all the traits influencing sugar concentration in corn stem

Study of correlation coefficient between any two traits helps to understand whether the traits positively or negatively correlated along with degree of relationship between them. Understanding the relationship of different traits has greater importance in the indirect selection of a complex trait associated with a simple trait.

Traits which account for soluble sugar content in the stem *viz*., °brix, total sugar, reducing sugar and sucrose percentage were showed significant positive correlation with plant height, number of internodes, plant weight, stem weight, stem girth, juice volume and juice extraction percentage, whereas, significant negative correlation exist between soluble sugar in the stem and number of cobs and also cob weight.

Highest significant positive correlation found between total sugars with sucrose percentage (0.97) and reducing sugar percentage (0.97). °brix also showed highest positive correlation with total sugar percentage (0.96) followed by sucrose percentage (0.95) and reducing sugar percentage (0.92). Thus it was found out that most of the traits under study were positively correlated, where, increase in one will lead to increase in other trait. Hence increase in stem weight and stem girth is most likely to result in harvesting more juice yield per plant and selection of genotypes with high °brix will reflect in genotypes with high soluble sugar percentage which will be the favourable trait for biofuel production.

5.5 Path-coefficient analysis

Analysis of path-coefficient will helps to understand the direct and indirect effect of correlation and also explain the cause and effect relationship between traits of interest with the other allied trait.

It was found out that sucrose percentage had the highest positive direct effect and °brix had highest positive indirect effect *via.,* sucrose percentage. Further, plant height had the lowest positive direct effect on total sugar percentage in the stem, while, among direct negative effects on total sugars, cob weight and juice extraction percentage had highest and lowest direct negative effects respectively. Thus selection based on

evaluation of genotypes for °brix will be the most effective strategy recommending the genotypes for bioethanol production.

5.6 Heterosis

Heterosis over mid-parental value was estimated for sugar content in the stem and related traits in 66 hybrids, Heterotic crosses for sugar content had also been reported by Qi *et al*., (2008), Khanduri *et al*., (2010), and Sadaiah *et al*., (2013).

5.6.1 Cytoplasmic effects of sweet and non-sweet corn on mid-parent heterosis

The exploitation of heterosis is one of the most outstanding advancements in plant breeding, although its genetic basis is difficult to understand. The single most important element of a breeding program is the recognition and utilization of heterotic pattern. This recognition both simplifies and increases the efficiency of all subsequent operations (Sprague, 1984). In this regard two contrasting pool of genotypes sweet and non-sweet corn were intermated to understand the cytoplasmic effects on heterosis.

In this study, the means of reciprocal and direct crosses were used to calculate heterosis over the mid-parent, significant mid-parent heterosis was observed in only very few but imperative traits like number of cobs, °brix, total sugar percentage, reducing sugar and sucrose percentage.

Cross K-4571 × BGUDI-13 found to have highest positive significant mid-parent heterosis followed by MAI-285 × MAI-308 and K-4571 × BGUDI-10 for above mentioned traits whereas, their corresponding reciprocal crosses did not showed significant heterosis and their mid-parent values were in negative trend, indicating that cytoplasm of the sweet corn had significant effect toward these traits.

Although the significant mid-parent heterosis was not observed except for few traits among some specific crosses, both positive and negative significant difference of the heterosis of direct and corresponding reciprocal crosses were observed for all the trait in all most all the cross combinations except plant height and plant weight. These results suggest that not only sweet corn parent but also non-sweet corn parents had significant cytoplasmic effect on mid-parent heterosis in some of the crosses. However, for juice volume, °brix, total sugar and sucrose percentage the differences were positive significant indicating that not all the traits but at least significant differences for these traits were due to sweet corn cytoplasm.

5.6.2 Mid-parent heterosis of sweet × non-sweet corn hybrids

Based on the results obtained it was clear that cross MAI-292 × MA-7 was the best performer for mid-parent heterosis as it had highest positive significant heterosis for total sugar, reducing sugar and sucrose percentage at both the sampling phases. This conclusion was also supported by positive significant effect of both GCA and SCA of this particular cross.

5.6.3 Mid-parent heterosis of non-sweet × sweet corn hybrids

Among non-sweet × sweet corn crosses two hybrids MAI-308 × K-4366-1 and BGUDI-10 × MAI-289 were best as they showed highest positive significant heterosis at both the sampling stages. However these crosses had relatively low heterosis percentage compare to sweet × non-sweet corn crosses for respective traits indicating that sweet × non-sweet corn crosses were suggestible over non-sweet × sweet corn crosses for soluble sugars in the stem.

5.7 Analysis of variance for combining ability

Mean sum of squares due to fourteen crosses of seven lines and two testers were highly significant for combining ability across all the traits at both the stages of sampling.

Mean sum of squares due to lines were not significant for of any of the trait under study, whereas, highly significant differences were observed for tester with respect to plant height at both the stages of sampling and for plant weight and stem weight at 10 and 20 DPSE respectively. These results explain that the non significant difference of line mean sum of squares observed for all the traits suggest that all the lines used in the current study had comparable potential for the studies traits.

The contrast study of mean sum of squares of line vs tester for combining ability showed significant difference with respect to all the traits. This significant difference was contributed by difference in the combining ability of individual line with the corresponding tester.

5.8 General combining ability effects of lines and testers

General combining ability is the ability of the genotype to transit genes with additive effects. Hence general combining ability effects depicts the true value of a genotype and play a prominent role in deciding the parent for developing hybrids.

Inbred lines MAI-285 and MAI-292 exhibited highest GCA effects for juice volume per plant, °brix, sucrose and reducing percentage in the stem indicating that these lines were the best general combiners in the group of inbred lines studied. Whereas, from tester MAI-308 was the best general combiner as this tester had significant positive GCA effects for many traits. Thus utilizing these lines (MAI-285 and MAI-292) and tester (MAI-308) in breeding programe for improvement of the trait of interest will yield in getting good results as these lines have the potential to transfer desirable traits to progenies.

5.9 Specific combining ability effects of line × tester for soluble sugar percentage in the stem and related traits

Highly significant specific combining ability effects of crosses indicate the significant deviation from what would have been predicted based on their parental performances. Hence, those crosses with highly positive and significant estimates of SCA effect could be selected for their specific combining ability to use in corn improvement programe for traits suitable for biofuel production.

In the current study, traits like juice volume, °brix, total sugar, reducing sugar, sucrose percentage in the stem and cob °brix along with cob weight were important to recommend the crosses suitable for both grain yield and biofuel production. Crosses like MAI-286 × MAI-308, MAI-14 × MAI-308 and MAI-285 × MAI-308 were good specific combiners and found to be the best hybrids as they showed highest positive significant SCA effects.

The results of present study identified that cross combinations with desirable SCA effects for desirable traits of interest convey the possibility of developing better hybrids. Further, promising cross combinations identified in the study could be utilized for future breeding work to improve corn with traits suitable for both high grain and stalk sugar yield purpose.

5.10 Molecular profiling of parents and hybrids using *ZmSUT1* gene specific markers

All the corn genotypes were used for molecular profiling using 10 gene specific markers for sucrose transportation in corn (*ZmSUT1*). Three markers *viz*., ZmSUT1b, ZmSUT1c and ZmSUT1f were found to be polymorphic, showing different banding pattern ranging between 362 and 490 bp respectively. This varied banding pattern was scored as 1, 2, 3, 5 and 7 based on the profile. It indicates the presence of genotypic variation among them for the specific trait of interest. In conclusion, all the genotypes having highly diverse genotypic composition showing capacity to improve the genetic background for beneficial traits through screening followed by selection process.

VI SUMMARY

In the present study, fifteen sweet corn and seven non-sweet corn inbred lines were selected for crossing programe in order to study the phenotypic variation for soluble sugar content in the stem and its attributing traits. Both direct and reciprocal crosses were planned to study the cytoplasmic influence on stem sugar content. Crossing programme was done in *Kharif* 2014 at Department of Plant Biotechnology, UAS, GKVK, Bengaluru, India. A total of 20 both direct and reciprocal crosses, 17 sweet corn × non-sweet corn and nine non-sweet corn × sweet corn crosses were obtained. All the hybrids along with parents and check (Madhuri) were evaluated for soluble sugars in the stem and for related traits in Summer 2015.

Analysis of variance revealed that there was significant variation present for all the characters studied among genotypes at both phases of sampling that is at 10 and 20 DPSE.

Traits which account for soluble sugar content in the stem *viz*., °brix, total sugar, reducing sugar and sucrose percentage showed significant positive correlation with plant height, number of internodes, plant weight, stem weight, stem girth, juice volume and juice extraction percentage. High to moderate GCV and PCV combined with high heritability and genetic advance as per cent mean were recorded for soluble sugars and attributing traits suggesting that improvement and genetic progress of these traits through breeding programe lead to obtain expected results.

Sweet corn parents such as K-4356-1, MAI-285, MAI-292, MAI-282 and K-4671-1 were found to be best performers with respect juice volume and soluble sugars in the stem. Cross K-4571 × BGUDI-13 found to have highest positive significant mid-parent heterosis followed by MAI-285 × MAI-308 and K-4571 × BGUDI-10 for traits mentioned above. Whereas, their corresponding reciprocal crosses did not show significant heterosis and their mid-parent values had negative trend, indicating that cytoplasm of the sweet corn had significant effect on these traits.

The sweet corn inbred lines MAI-285, MAI-286 and MAI-292 and non-sweet corn line MAI-308 showed highest positive significant general combining ability effects suggesting that utilization of these lines in breeding programe for improving the trait of interest will lead to better genotypes as these lines have the potential to transfer desirable traits to progenies. As expected MAI-286 × MAI-308, MAI-14 × MAI-308 and MAI-285 × MAI-308 were good specific combiners and found to be the best hybrids as they showed highest positive significant SCA effects.

ZmSUT1, a gene responsible for sucrose transport in corn was explored in the present study by designing a total of 10 primers specific to the gene using NCBI database. Out of them, ZmSUT1b, ZmSUT1c and ZmSUT1f were found to be polymorphic on 2.5 per cent agarose gel, indicating the presence of genotypic variation among them for the specific trait of interest.

Combined results obtained from both phenotypic and genotypic studies suggest the possibility to improve the corn genotypes for increased juice volume and soluble sugars in the stem using the available wide genetic diversity for these traits. As present study also revealed that cytoplasmic effect of sweet corn towards the traits suitable for bioethanol production, it is suggestible that sweet corn genotypes along with hybrids developed using sweet corn as female parent will be suitable resources as biofuel feed stock without compromising the grain yield. This kind of dual purpose of corn cultivation will definitely beneficial to both farming and industrial community.

Future line of work

- Improving the sugar accumulation along with increase in juice content and other attributing traits can be possible using plant breeding.
- Along with *ZmSUT1* many other genes associated with sucrose synthesis and translocation to be explored and the bioinformatics resources could be utilized to a greater extent to improve efficiency.
- Genetic variability in the Chloroplast and Mitochondrial DNA could be used to identify the actual differences among the reciprocal crosses.

VII REFERENCES

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APPENDIX

10DPSE	DTF	PH	NOL	PW	NOC	CW	SW	SG	JV	JEP	B	RS	SP	TS
	Sweet corn check-hybrid													
Madhuri	52.50	241.50	14.50	983.50	1.50	143.50	573.50	30.82	133.00	63.64	12.45	4.69	7.69	13.05
	Sweet corn parents													
MAI-14	53.50	215.00	11.50	885.50	1.00	169.50	549.50	29.59	92.50	59.61	11.40	4.17	7.65	11.88
MAI-102	52.50	236.00	13.00	836.50	2.00	249.00	447.00	23.80	94.50	82.76	10.25	3.84	6.78	10.68
MAI-282	51.00	232.50	12.00	965.50	1.50	55.50	635.00	25.60	116.50	72.92	12.55	4.76	7.85	13.25
MAI-283	50.50	230.00	12.00	944.00	2.00	453.00	479.00	30.88	95.50	62.16	11.35	3.43	8.28	11.84
MAI-284	52.00	218.00	12.50	883.00	1.50	167.50	601.50	29.20	93.00	68.63	10.10	3.63	6.79	10.54
MAI-285	52.00	205.50	11.00	954.50	3.50	154.00	635.50	29.71	141.50	75.83	8.70	2.79	6.20	9.05
MAI-286	55.50	209.00	11.50	810.00	3.00	154.00	519.50	22.30	97.00	74.21	10.50	3.33	7.48	10.93
MAI-287	50.50	205.00	11.00	734.00	2.00	328.00	411.00	20.38	82.50	68.12	8.05	2.80	5.77	8.36
MAI-289	49.50	205.00	11.50	538.00	1.50	146.50	335.50	19.80	76.00	40.36	8.25	2.45	6.06	8.56
MAI-292	50.50	215.50	11.50	846.00	2.00	137.00	648.00	27.83	132.00	80.74	8.50	2.56	6.21	8.84
MAI-325	53.00	212.50	13.00	794.00	1.50	129.00	577.50	26.99	56.50	53.28	9.35	3.31	6.37	9.73
K-4356-1	54.00	226.50	12.00	1228.50	2.00	84.00	704.00	30.70	153.00	72.37	9.25	3.25	6.33	9.62
K-4366-1	53.00	208.50	13.00	743.50	1.50	66.50	482.50	20.52	67.50	72.81	8.45	2.60	6.16	8.78
K-4571	52.50	218.50	11.50	927.00	1.50	141.00	662.00	27.50	131.00	68.00	9.25	3.31	6.32	9.63
K-4673-1	29.50	203.50	10.50	616.00	2.00	253.00	390.50	23.44	122.00	72.08	12.50	4.68	7.83	13.03
Non-sweet corn parents														
M-65	55.00	199.50	11.50	384.50	1.50	125.50	235.00	26.25	65.50	40.57	8.00	2.45	5.69	8.30
MAI-7	56.00	180.50	9.50	372.00	1.00	51.00	229.50	21.75	87.00	40.38	8.10	2.77	5.74	8.40
MAI-308	55.00	173.50	10.50	526.00	1.50	233.50	282.00	22.55	57.00	62.23	7.50	2.20	5.49	7.77
BGUDI-10	55.50	178.50	11.50	600.00	1.50	107.00	258.00	21.65	87.50	42.77	7.75	2.29	5.62	8.04
BGUDI-13	54.00	188.00	11.50	662.50	1.50	166.50	238.50	22.23	49.00	38.89	9.75	3.57	6.50	10.14
BGUDI-80	56.50	187.50	11.00	609.00	2.00	216.00	327.00	23.10	41.00	69.58	10.50	3.86	6.69	10.93
BGUDI-81	53.50	189.50	12.00	505.50	1.50	242.50	209.00	21.19	92.00	45.92	7.55	3.05	5.07	7.82

10DPSE	DTF	PH	NOL	PW	NOC	CW	SW	SG	JV	JEP	B	RS	SP	TS
Sweet corn * Non-sweet corn hybrids														
MAI -287 × MAI -7	52.00	172.50	10.00	800.50	2.50	292.50	401.50	25.51	61.00	52.44	10.25	2.80	7.36	10.73
MAI 287 × MAI-308	50.50	220.00	12.00	1024.00	2.00	444.00	513.00	26.15	50.50	64.76	7.35	2.03	5.56	7.66
MAI -283 × MAI-308	51.50	217.50	10.50	764.00	1.00	992.50	382.50	27.46	70.50	79.45	8.25	2.40	6.01	8.56
MAI-285 ×MAI -7	52.00	215.50	11.50	834.50	1.50	50.50	418.00	31.52	91.50	37.39	11.75	4.37	7.48	12.24
MAI -285× MAI -308	53.00	232.00	12.50	1119.50	2.50	480.50	561.00	28.90	118.50	46.85	9.65	2.33	7.19	10.26
MAI -285× BGUDI -13	51.00	212.00	13.00	994.00	1.50	186.25	497.75	27.67	97.00	47.17	11.75	4.33	7.56	12.05
MAI-284×M65	53.00	237.50	11.00	1239.00	1.50	326.25	620.25	29.19	170.50	56.57	12.40	4.60	7.82	12.81
MAI -284× MAI -7	52.00	217.00	11.50	612.00	2.00	201.50	307.00	27.61	44.00	45.79	10.25	3.82	6.78	10.63
MAI-284×MAI -308	53.00	222.50	12.50	1005.50	1.50	237.50	503.50	29.81	71.00	72.50	7.15	2.05	5.58	7.44
MAI-286×MAI308	53.50	222.50	14.50	875.50	1.50	252.75	438.50	24.21	40.50	54.50	8.35	2.61	5.91	8.59
K -4571× BGUDI-10	51.50	221.00	10.50	899.50	1.50	179.00	450.50	31.54	111.00	68.01	7.10	1.93	5.38	7.35
K -4571×M -65	52.00	229.50	9.50	1021.00	1.50	172.00	511.25	24.48	97.50	77.18	9.25	3.24	6.34	9.58
K -4356-1× BGUDI -10	51.50	221.00	13.00	1088.50	1.50	297.00	545.00	29.77	121.00	75.99	8.25	2.64	5.87	8.57
K -4366-1×M -65	53.00	227.50	13.50	1235.50	1.00	159.00	618.25	25.15	112.00	63.32	8.45	1.84	6.83	8.73
K -4366-1×MAI -7	51.00	202.50	12.50	768.50	1.00	111.00	384.75	24.66	92.00	52.33	8.50	2.67	5.99	8.80
K -4366-1×BGUDI -10	49.50	216.00	11.50	1016.00	2.00	218.50	509.00	30.54	87.50	50.39	9.15	3.01	6.38	9.50
K -4571×BGUDI -13	48.00	222.50	12.50	1106.50	2.00	216.50	554.25	31.41	127.00	39.76	6.85	1.79	5.24	7.12
MAI-286×MAI -7	50.50	189.00	13.00	727.00	1.50	172.00	364.25	28.20	119.00	41.82	8.25	2.62	5.87	8.56
MAI-284×BGUDI -13	53.00	220.50	10.00	1170.50	2.00	570.50	586.25	28.22	105.00	35.91	8.00	2.49	5.76	8.31
MAI -292×MAI-7	53.00	202.00	12.50	783.50	2.00	260.00	392.75	29.04	109.50	50.84	11.15	4.11	7.19	11.45
MAI-284×BGUDI -80	52.00	235.00	13.50	1040.50	2.00	354.00	521.25	30.43	122.00	40.78	12.35	4.62	7.84	12.86
MAI-102×BGUDI -13	53.00	198.00	11.00	898.00	1.00	271.50	449.50	23.60	72.00	35.39	9.45	3.12	6.61	9.83
K -4571×MAI -7	54.00	224.00	10.50	613.00	2.00	124.50	307.50	21.95	110.00	56.80	7.60	2.16	5.58	7.88
MAI-289×MAI -7	53.00	231.50	13.50	865.50	1.00	140.00	433.25	32.05	112.50	43.31	11.70	4.38	7.44	12.18
MAI-283×BGUDI -13	53.00	183.50	10.50	686.50	2.50	280.00	344.50	24.87	86.50	34.48	7.05	1.94	5.33	7.33
MAI-292×BGUDI -10	52.50	213.00	11.50	983.00	1.50	442.00	492.25	27.60	134.00	48.28	12.75	4.94	7.87	13.27
MAI-14×MAI -7	52.50	219.00	11.50	816.00	2.00	284.00	409.00	30.58	111.00	42.94	7.90	2.38	5.72	8.19

10DPSE	DTF	PH	NOL	PW	NOC	CW	SW	SG	JV	JEP	B	RS	SP	TS
K -4356-1×BGUDI -10	53.50	204.00	11.00	814.00	2.50	370.75	408.25	29.63	88.00	46.02	7.05	1.59	5.62	7.29
K -4356-1×MAI -7	52.00	238.00	12.50	1161.50	2.00	205.00	581.75	27.43	131.00	44.03	7.70	2.16	5.66	8.00
K -4571×BGUDI -81	53.00	211.50	12.00	796.00	1.00	89.00	398.50	24.48	92.00	37.26	8.35	2.62	5.90	8.62
K -4356-1×M -65	52.00	219.00	12.50	1115.00	2.00	290.00	558.50	30.61	117.00	44.03	8.10	2.53	5.81	8.41
MAI-289×MAI -308	51.00	225.00	11.50	798.50	2.00	158.00	400.25	27.61	112.50	46.24	9.65	3.39	6.51	10.02
MAI-102×MAI -7	52.50	217.50	12.00	893.00	1.50	175.00	447.25	32.37	87.50	39.47	8.90	3.03	6.17	9.23
MAI-14×MAI -308	54.50	206.50	10.50	1036.00	1.50	372.75	518.75	28.75	92.00	39.93	8.35	2.68	5.92	8.65
MAI-292×BGUDI -81	52.00	221.00	10.50	1109.50	1.50	310.75	555.50	35.36	117.00	41.62	9.95	3.60	6.65	10.35
MAI-325×MAI -7	55.50	212.00	13.00	750.50	2.00	229.50	376.25	22.07	130.00	50.13	6.20	4.17	6.86	11.45
MAI-292 ×MAI-308	57.00	207.50	11.00	994.00	2.00	346.50	498.00	30.62	87.50	38.42	8.25	2.42	6.06	8.56
	Non-sweet corn * sweet corn hybrids													
MAI -7 × MAI -287	54.50	164.50	11.00	470.00	2.50	288.50	236.25	25.37	34.00	43.21	6.70	1.71	5.16	6.95
MAI -308 × MAI -287	56.00	216.50	12.00	957.50	2.00	437.00	479.75	25.86	34.00	55.09	4.75	0.51	4.27	4.90
MAI -308 × MAI -283	53.00	199.50	12.00	530.00	1.50	273.50	265.75	24.04	46.50	51.43	7.10	1.90	5.36	7.37
MAI -7 × MAI 285	54.00	212.00	12.50	652.50	2.00	234.00	327.25	24.43	62.50	37.72	6.75	1.83	5.20	7.08
MAI -308× MAI -285	52.00	207.00	12.00	769.50	1.50	276.50	385.50	29.57	51.50	40.08	7.75	2.35	5.66	8.05
BGUDI -13×MAI -285	51.00	197.00	11.50	845.00	3.00	460.50	424.00	23.25	61.00	34.56	6.80	1.81	5.21	7.07
M65 ×MAI -284	56.00	208.00	14.00	959.00	3.50	305.38	481.25	27.62	129.50	36.01	6.15	1.39	4.90	6.35
MAI-7× MAI284	53.00	190.00	11.50	479.00	1.00	172.00	240.00	23.60	25.50	38.81	7.60	2.27	5.56	7.89
MAI-308×MAI -284	54.00	192.00	13.50	824.50	1.00	210.00	412.75	23.99	36.50	48.57	8.65	2.80	6.05	8.98
MAI-308× MAI286	52.00	195.50	10.00	740.00	2.00	371.00	371.00	24.18	19.00	45.82	9.05	3.14	6.22	9.41
BGUDI -10× K -4571	51.00	197.00	12.50	469.00	2.00	145.50	235.50	24.83	72.50	49.99	5.75	1.15	4.74	5.96
M -65× K -4571	55.00	200.50	13.00	747.50	1.50	172.25	374.50	23.22	83.50	13.24	7.75	2.33	5.63	8.04
BGUDI -10× K -4356-1	57.00	210.50	13.00	802.50	3.00	379.50	402.75	23.07	67.00	43.01	6.30	1.48	4.98	6.54
M-65×K -4366-1	53.00	208.50	12.50	878.00	2.00	154.50	440.00	29.20	76.50	55.42	6.65	1.57	5.15	6.75
MAI -7×K -4366-1	56.00	199.00	12.50	528.50	2.00	232.00	265.25	26.19	37.00	41.23	8.25	2.60	5.83	8.59
BGUDI -10×K -4366-1	54.50	204.00	13.00	890.00	2.00	236.00	446.00	27.58	69.00	60.20	7.25	2.16	5.37	7.63
BGUDI -13×K -4571	54.00	176.50	13.50	593.00	1.50	131.50	297.25	25.01	62.50	42.35	7.25	1.99	5.37	7.51

10DPSE	DTF	PH	NOL	PW	NOC	CW	SW	SG	JV	JEP	B	RS	SP	TS
MAI -7×MAI -286	53.00	217.50	13.50	825.50	2.00	174.50	413.75	28.81	61.50	47.41	7.00	2.09	5.25	7.36
BGUDI -13×MAI -284	52.50	205.50	10.50	894.50	2.00	414.00	448.25	26.92	79.50	52.87	8.25	2.54	5.88	8.53
MAI-308 × MAI-292	54.00	166.00	11.00	584.00	1.50	163.00	292.75	19.58	78.50	18.88	7.40	2.21	5.45	7.73
BGUDI -13×K -4673-1	54.00	183.00	13.50	596.50	1.00	129.00	298.75	31.83	58.50	74.80	8.25	2.54	5.87	8.53
BGUDI -13×K -4366-1	53.00	229.50	11.50	725.50	2.00	206.00	363.75	23.44	78.50	62.26	10.75	3.98	7.01	11.09
MAI -308×K -4571	54.00	226.00	12.50	670.50	2.00	213.50	336.25	25.26	71.50	45.84	7.60	2.28	5.51	7.89
BGUDI -10×MAI -287	53.00	197.50	12.50	426.50	1.00	102.00	213.75	21.01	72.50	60.49	7.25	2.10	5.34	7.54
BGUDI -80×MAI -282	54.00	204.50	11.00	722.50	2.00	220.50	362.25	26.74	49.00	59.31	9.25	3.22	6.29	9.60
MAI-308×K -4366-1	54.00	158.00	11.50	558.50	1.50	319.50	280.00	29.97	27.50	59.76	6.25	1.36	4.96	6.44
BGUDI -81×MAI -289	55.00	201.50	13.00	536.50	1.00	96.00	268.75	21.57	43.50	37.30	8.75	2.85	6.11	9.04
BGUDI -10×MAI -289	54.00	208.50	13.00	770.50	1.50	195.00	386.00	27.39	68.00	63.54	11.00	4.08	7.02	11.34
BGUDI -81×K -4366-1	53.00	179.00	12.50	712.00	1.50	119.75	356.75	25.38	72.50	58.24	9.00	3.01	6.16	9.31
Sem±	2.62	4.00	0.52	44.25	0.35	47.73	20.66	1.19	5.63	10.78	0.65	0.25	0.14	0.16
CD @ P=0.05	7.38	11.23	1.47	124.39	0.98	134.16	58.07	3.36	15.83	30.30	1.83	0.72	0.38	0.44
CV%	7.04	2.72	6.23	7.76	28.04	28.39	7.25	6.38	9.40	30.61	10.79	3.98	3.13	7.98

20 DPSE	PH	NOI	PW	NOC	CW	SW	SG	JV	JEP	B	TS	RS	SP	CB
Sweet corn check-hybrid														
Madhuri	244.00	14.00	1551.00	2.00	536.50	592.55	29.58	111.80	61.27	12.40	13.80	8.80	4.78	14.93
Sweet corn parents														
MAI-14	214.00	12.00	1147.00	2.00	463.00	378.28	28.29	48.85	96.30	11.40	13.13	4.82	8.05	14.25
MAI-102	214.00	11.00	740.50	1.50	112.50	412.88	25.29	88.85	55.56	10.25	11.95	4.28	7.53	15.40
MAI-282	242.00	13.50	1139.00	2.00	368.50	507.26	28.96	116.00	43.71	12.55	13.99	5.38	8.34	14.95
MAI-283	243.00	14.00	857.00	2.00	250.50	391.12	25.37	96.00	58.91	8.55	13.44	4.33	8.48	13.95
MAI-284	237.50	11.00	1285.00	1.50	160.50	254.12	25.51	86.50	31.22	10.10	11.27	3.99	7.21	14.70
MAI-285	226.00	12.50	816.50	1.50	200.00	341.13	32.16	93.50	51.51	8.70	9.49	3.25	6.09	14.15
MAI-286	205.50	9.50	617.00	2.00	283.50	505.50	23.67	98.50	54.94	10.50	12.02	4.61	7.31	15.12
MAI-287	217.00	13.00	1016.50	2.00	256.50	464.80	28.57	104.50	52.46	8.05	9.81	4.18	5.28	13.70

20 DPSE	PH	NOI	PW	NOC	CW	SW	SG	JV	JEP	B	TS	RS	SP	CB
MAI-289	212.00	14.00	498.00	1.00	74.00	275.64	21.75	99.50	45.82	8.25	9.42	4.10	4.92	14.60
MAI-292	214.50	11.50	891.50	2.00	235.50	398.54	26.54	87.50	49.50	8.50	9.74	3.95	5.20	14.75
MAI-325	219.00	13.00	1162.00	2.50	547.00	391.75	30.03	107.00	48.97	9.65	10.38	4.22	5.52	14.85
K-4356-1	224.00	13.00	1242.50	3.00	500.50	466.98	30.27	114.50	66.38	9.50	10.56	4.57	5.66	14.60
K-4366-1	231.00	14.00	1114.50	2.00	303.50	503.13	29.45	120.50	46.20	8.45	11.62	4.92	6.93	15.35
K-4571	241.50	12.00	1186.00	2.50	411.50	496.18	28.12	102.50	38.66	9.55	10.33	4.10	5.91	15.15
K-4673-1	228.00	12.00	1160.00	2.50	466.00	458.14	32.15	82.50	46.05	12.50	14.56	5.09	9.16	14.90
Non-sweet corn parents														
M-65	214.00	12.00	829.50	1.00	51.50	526.11	28.70	89.50	64.01	7.80	8.46	3.58	5.18	14.70
MAI-7	204.00	11.50	368.50	1.00	101.00	138.36	18.96	21.50	39.26	8.10	9.13	4.13	4.97	14.35
MAI-308	185.50	10.50	707.50	2.00	246.50	280.41	24.68	44.50	51.27	7.50	8.64	3.73	4.59	14.15
BGUDI-10	181.50	9.50	571.00	1.50	148.50	278.68	22.12	39.50	59.07	7.75	8.43	3.55	4.69	13.25
BGUDI-13	180.50	11.00	633.00	1.50	89.00	347.08	21.62	53.00	38.54	8.70	10.16	4.47	5.68	13.70
BGUDI-80	206.50	12.00	996.50	2.50	477.50	317.41	25.37	35.50	48.90	10.50	11.27	5.02	6.18	13.90
BGUDI-81	199.00	12.50	851.00	1.50	186.00	461.15	27.17	103.00	56.30	6.85	8.06	3.43	4.21	12.95
Sweet corn * Non-sweet corn hybrids														
MAI -287 × MAI -7	182.50	10.50	1011.86	2.00	486.50	243.34	25.65	75.19	43.68	10.25	11.52	3.21	8.09	13.95
MAI 287 × MAI-308	221.00	10.50	1415.62	3.50	748.50	417.56	29.50	96.82	58.43	7.35	8.37	3.02	5.20	13.45
MAI -283 × MAI-308	219.00	9.50	1070.80	1.50	299.00	310.25	23.02	74.56	52.87	10.65	11.55	4.37	7.03	14.25
MAI-285 ×MAI -7	233.50	14.00	1389.93	2.50	505.00	499.21	33.82	114.43	48.22	9.45	13.74	6.13	7.41	14.75
MAI -285× MAI -308	232.50	13.00	1247.29	2.00	508.50	454.00	27.70	103.72	54.13	11.55	12.50	5.22	7.08	13.95
MAI -285× BGUDI -13	214.00	12.00	1012.73	2.00	464.00	319.47	24.11	76.44	47.41	7.35	12.91	5.55	7.17	14.95
MAI-284×M65	245.00	12.00	1220.98	2.00	339.00	456.89	29.20	107.02	50.86	9.70	12.85	5.70	7.01	14.40
MAI -284× MAI -7	213.50	11.00	1045.34	3.00	459.00	309.17	30.00	70.73	58.20	10.25	11.31	4.98	6.29	13.75
MAI-284×MAI -308	232.50	13.00	947.18	2.00	378.00	351.78	29.92	88.47	41.58	11.25	12.75	5.37	7.34	13.80
MAI-286×MAI308	223.00	13.00	1192.70	2.50	540.50	371.33	28.00	84.74	73.27	10.50	11.30	3.66	7.45	13.25
K -4571× BGUDI-10	229.50	14.00	827.80	1.00	95.00	481.05	23.55	110.09	65.91	12.20	13.08	4.74	8.31	14.40
K -4571×M -65	227.50	12.00	1305.61	2.00	469.50	516.40	27.58	118.38	52.07	9.25	11.64	4.88	6.69	14.30
K -4356-1× BGUDI -10	223.00	13.00	1266.36	3.00	570.00	451.05	28.25	103.30	50.06	8.25	9.56	3.40	6.12	14.75

20 DPSE	PH	NOI	PW	NOC	CW	SW	SG	JV	JEP	B	TS	RS	SP	CB
K -4366-1×M -65	230.00	13.00	994.32	1.00	243.00	417.82	26.11	95.74	52.01	9.65	10.74	4.91	5.77	15.05
K -4366-1×MAI -7	202.50	12.50	820.97	1.00	0.11	295.92	24.66	92.00	46.50	8.90	9.69	2.39	7.19	13.15
K -4366-1×BGUDI -10	216.00	11.50	1223.56	2.00	0.22	536.43	30.54	87.50	51.53	9.15	9.96	3.66	6.22	14.55
K -4571×BGUDI -13	224.00	12.00	1462.53	3.00	613.50	565.52	29.23	129.62	54.29	11.10	12.64	4.60	7.90	13.20
MAI-286×MAI -7	183.50	11.00	700.91	2.00	331.50	203.61	24.27	46.30	43.89	8.25	9.11	2.30	6.69	13.30
MAI-284×BGUDI -13	223.50	11.00	1379.26	3.00	570.50	469.14	34.30	55.00	50.23	9.25	10.03	3.65	6.28	14.15
MAI-292 ×MAI-308	206.50	12.50	1214.71	2.00	541.50	327.97	31.78	75.19	44.73	11.25	12.74	5.32	7.24	12.80
MAI -292×MAI-7	235.00	13.50	886.92	2.00	358.50	320.70	25.25	73.23	54.78	8.25	13.83	5.36	8.32	13.30
MAI-284×BGUDI -80	198.00	11.00	863.28	1.00	321.50	287.42	23.60	72.00	37.53	11.50	12.39	5.68	6.60	12.30
MAI-102×BGUDI -13	224.00	10.50	816.70	2.00	326.00	328.49	21.95	110.00	43.30	7.60	8.91	3.72	5.09	13.80
K -4571×MAI -7	231.50	13.50	1287.94	1.00	384.50	507.64	32.05	112.50	44.15	12.55	13.56	5.41	8.12	13.30
MAI-289×MAI -7	183.50	10.50	928.00	2.50	162.50	131.64	24.87	86.50	56.51	7.05	8.08	2.06	5.74	14.30
MAI-283×BGUDI -13	213.00	11.50	1251.75	1.50	467.00	455.27	27.60	134.00	59.58	9.40	13.01	5.05	7.80	15.30
MAI-292×BGUDI -10	219.00	11.50	1168.67	2.00	485.00	425.98	30.58	111.00	53.87	8.65	9.68	5.80	3.81	13.80
MAI-14×MAI -7	204.00	11.00	1062.18	2.50	452.00	358.75	29.63	88.00	41.12	7.30	8.34	3.29	4.92	12.45
K -4356-1×BGUDI -10	238.00	12.50	1322.86	2.00	546.00	469.27	27.43	131.00	45.12	7.15	7.91	3.16	4.26	14.45
K -4356-1×MAI -7	211.50	12.00	1083.61	1.00	502.50	380.67	24.48	92.00	58.95	8.35	9.56	4.12	5.36	14.55
K -4571×BGUDI -81	219.00	12.50	1495.33	2.00	670.00	517.73	30.61	117.00	51.91	8.10	9.15	3.56	5.36	13.45
K -4356-1×M -65	225.00	11.50	1190.73	2.00	329.50	519.71	27.61	112.50	49.68	13.35	13.91	6.23	7.60	14.30
MAI-289×MAI -308	217.50	12.00	1200.00	1.50	514.00	430.00	32.37	87.50	69.24	7.25	10.01	4.54	5.40	13.65
MAI-102×MAI -7	206.50	10.50	984.55	1.50	410.00	313.64	28.75	92.00	8.64	8.55	9.50	3.94	5.23	13.75
MAI-14×MAI -308	221.00	10.50	1311.42	1.50	659.00	415.68	35.36	117.00	50.62	8.15	10.94	4.77	5.92	13.70
MAI-292×BGUDI -81	212.00	13.00	781.82	2.00	319.50	275.64	22.07	130.00	48.84	8.75	12.48	5.68	6.68	14.65
MAI-325×MAI -7	207.50	11.00	809.50	2.00	540.50	389.09	30.62	87.50	52.58	8.25	9.14	3.89	5.17	13.90
Non-sweet corn * sweet corn hybrids														
MAI -7 × MAI -287	164.50	11.00	537.82	2.50	249.50	304.20	25.37	34.00	61.78	5.65	7.47	3.13	4.32	15.60
MAI -308 × MAI -287	216.50	12.00	1250.36	2.00	598.50	410.19	25.86	34.00	50.13	4.75	6.05	2.62	3.30	13.80
MAI -308 × MAI -283	199.50	12.00	796.00	1.50	546.50	321.93	24.04	46.50	48.35	8.90	8.97	3.62	5.29	14.30
MAI -7 × MAI 285	212.00	12.50	1358.59	2.00	674.00	413.14	24.43	62.50	47.96	6.75	7.41	3.34	3.95	14.80

20 DPSE	PH	NOI	PW	NOC	CW	SW	SG	JV	JEP	B	TS	RS	SP	CB
MAI -308× MAI -285	207.00	12.00	1017.42	1.50	487.00	414.71	29.57	51.50	45.86	8.00	8.75	3.95	4.74	13.80
BGUDI -13×MAI -285	197.00	11.50	1079.46	3.00	556.00	335.28	23.25	61.00	51.90	6.80	7.25	2.91	4.12	13.80
M65 ×MAI -284	208.00	14.00	1094.91	3.50	380.00	453.82	27.62	129.50	47.22	6.15	7.41	3.43	3.89	13.80
MAI-7× MAI284	190.00	11.50	901.59	1.00	421.50	287.36	23.60	25.50	40.04	9.25	9.82	4.15	5.49	14.30
MAI-308×MAI -284	192.00	13.50	888.67	1.00	351.00	395.96	23.99	36.50	42.17	8.65	9.96	4.24	5.50	14.30
MAI-308× MAI286	195.50	10.00	851.72	2.00	392.00	255.72	24.18	19.00	51.31	8.70	10.02	4.32	5.65	13.30
BGUDI -10× K -4571	197.00	12.50	1094.81	2.00	469.50	406.08	24.83	72.50	47.48	5.75	6.90	3.09	3.71	13.80
M -65× K -4571	200.50	13.00	1096.51	1.50	405.50	334.47	23.22	83.50	48.12	7.75	9.00	4.02	4.86	13.80
BGUDI -10× K -4356-1	210.50	13.00	854.96	3.00	331.50	308.83	23.07	67.00	24.14	6.30	7.66	3.44	4.00	15.30
M-65×K -4366-1	208.50	12.50	950.54	2.00	299.50	402.12	29.20	76.50	49.27	6.70	7.51	3.35	4.08	14.80
MAI -7×K -4366-1	199.00	12.50	746.70	2.00	295.50	282.09	26.19	37.00	40.60	8.25	9.12	4.03	4.94	14.80
BGUDI -10×K -4366-1	204.00	13.00	1449.07	2.00	538.00	533.45	27.58	69.00	50.46	7.25	7.41	3.40	3.97	14.35
BGUDI -13×K -4571	176.50	13.50	873.54	1.50	433.50	247.04	25.01	62.50	44.33	7.25	8.72	4.04	4.80	13.50
MAI -7×MAI -286	217.50	13.50	926.46	2.00	252.00	425.41	28.81	61.50	44.21	7.00	8.10	3.56	4.36	13.45
BGUDI -13×MAI -284	205.50	10.50	1227.10	2.00	552.00	368.13	26.92	79.50	36.16	9.50	9.68	4.42	5.11	12.45
MAI-308 × MAI-292	202.00	11.00	942.00	2.50	450.00	312.00	26.40	71.00	44.71	10.15	11.12	4.97	5.91	13.55
BGUDI -13×K -4673-1	200.50	12.00	623.56	1.00	177.00	243.61	23.46	55.00	46.12	8.25	8.90	3.80	4.80	13.35
BGUDI -13×K -4366-1	209.50	11.00	1248.39	2.00	561.50	453.44	26.12	53.50	54.35	10.00	11.45	5.23	6.13	13.10
MAI -308×K -4571	213.50	12.00	680.59	1.50	235.50	265.62	23.05	60.00	49.08	7.60	8.51	3.76	4.54	13.90
BGUDI -10×MAI -287	181.50	11.00	663.17	2.00	330.00	209.42	25.13	47.50	41.75	7.25	8.20	3.28	4.53	13.20
BGUDI -80×MAI -282	217.00	11.00	990.87	2.00	414.00	303.21	24.47	69.00	49.37	9.65	10.26	4.52	5.58	13.90
MAI-308×K -4366-1	204.00	12.50	963.00	3.00	659.00	377.59	26.15	51.00	56.20	6.65	7.47	3.36	4.01	13.40
BGUDI -81×MAI -289	207.50	11.50	799.37	2.00	267.50	362.63	23.32	83.00	44.14	8.75	9.95	4.11	5.49	14.40
BGUDI -10×MAI -289	211.00	13.00	953.48	2.00	307.50	425.98	28.86	76.50	47.12	8.20	11.98	5.29	6.51	13.05
BGUDI -81×K -4366-1	171.50	10.00	865.48	1.50	347.50	268.22	24.33	60.50	48.92	9.00	10.09	4.56	5.38	14.95
Sem±	2.46	0.25	17.95	4.81	4.81	4.52	0.31	1.34	0.78	0.22	0.21	0.19	0.21	0.25
CD @ P=0.05	6.93	0.69	50.47	13.51	13.51	12.71	0.88	3.77	2.20	0.61	0.58	0.52	0.58	0.59
CV%	1.64	2.93	2.52	1.75	1.75	1.69	1.66	2.24	2.26	3.51	2.87	4.47	6.94	3.61