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Research Article

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Genetic evaluation of BC_2F_2 and BC_2F_3 populations derived from a cross between β-carotene-rich field corn (*Zea mays* L.) and sweet corn (*Zea mays* var. saccharata) for sweetness and agro-morphological traits

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ABSTRACT

CAUM66 was found to be a superior landrace and its improved version CAUM66β$^+$ inbred line having a high productivity and beta carotene content. This landrace was reported to have a wide popularity among local farmers of Manipur and hence is a promising parent for breeding programs. DBT16 is the biofortified sweetcorn (inbred line) was found to be a superior inbred parental line during hybrid yield trial having a high productivity and sugar content. So, this study evaluated the genetic variability, heritability, and trait distribution pattern of a BC_2F_2 and BC_2F_3 population derived from a cross between β-carotene-rich field corn (CAUM66β$^+$) and biofortified (β-carotene-rich) sweet corn (DBT16). Fourteen agro-morphological traits were analysed for variability, The GCV and PCV were ranged from 3.99% to 13.49% and 5.51% to 14.75% and it revealed that the estimates of PCV was higher than GCV for all the traits studied in both the populations, revealing influence of environment. Heritability and GAM estimates ranged from 46.83% to 97.38% and 5.95 % to 26.10%, respectively, revealed that the agro-morphological traits *viz*., cob length, number of tassel-branches, tassel length, cob girth and number of kernels-per row has contributed maximum towards variability depicting the involvement of additive genetic effects and good selection potential. Skewness and kurtosis analysis revealed that number of tassel branches exhibited positive skewness and leptokurtic distribution in BC_2F_2 population, while most traits showed negative skewness and platykurtic curves, indicating polygenic control. Similarity percentage of lines in BC_2F_3 population towards recurrent parent, ranged from 79.12% to 82.88% and TSS ranged 14% to 18%. Based on these parameters best four lines from each BC_2F_3 progeny i.e., CAUM66β$^+$ × DBT16 – 7 – 25 – 5 – 15 – 14 and CAUM66β$^+$ × DBT16 – 3 – 5 – 16 – 29 – 17 was selected and these lines can be utilized in future breeding programs aimed at biofortifying sweetcorn. In the present study, successful introgression of the sweetness allele into field corn led to the development of improved lines, which exhibit strong potential for utilization in hybrid breeding programs.

KEYWORDS: Field corn, Sweet corn, Variability, Heritability, Backcross

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INTRODUCTION

Maize (*Zea mays* L.), is the genetically diverse cereal crops worldwide and is cultivated across all agro-climatic regions of India. It serves a pivotal role in industrial utility and food security, with approximately 12-13% of total global production dedicated to human consumption and the rest utilized for animal feed, industrial starch, ethanol, and other products. The crop exhibits wide morphological and functional diversity, and is classified into flint, dent, flour, popcorn, pod, waxy, and sweet corn types, based on kernel endosperm composition. Among these, flint and dent types are predominant in Indian agriculture and are used both as dry grain and as green maize for fresh consumption (Tao, 2025).

Sweet corn (*Zea mays* L. var. *saccharata*) is a distinct maize type, notable for its elevated sugar levels in the immature kernel stage, which imparts a sweet taste and a softer texture. It contains significantly higher total sugars compared to field maize (Tracy, 1996) and is also nutritionally valuable and acts as a reservoir of dietery fiber, minerals, vitamins, and antioxidants. This variety arises from mutations in genes associated with starch biosynthesis pathways, resulting in kernels with characteristics akin to both fruits and grains (Chen *et al.*, 2024). Its enhanced sensory and nutritional properties make sweet corn increasingly popular among consumers.

Despite its nutritional and consumer appeal, sweet corn often exhibits inferior agronomic performance, including reduced yield and lower stress tolerance, when compared to field corn. Hybrid breeding constitutes a fundamental approach towards the development of superior-yielding and sweet cultivars (Senthil *et al.*, 2024). However, the genetic enhancement of elite sweet corn hybrid lines is often constrained by the limited availability of diverse and superior inbred lines, especially those carrying the *sh2* (*shrunken2*) allele, which confers high kernel sugar content and prolonged sweetness retention.

To mitigate these constraints, field corn genotypes have been effectively employed in backcross breeding programs targeted towards, enhancing the yield potential and agronomic adaptability of sweet corn. Introgression of favourable alleles from field corn into sweet corn has been recognized as an effective strategy to enhance agronomic traits, which is also supported by previous research findings (Butrón *et al.*, 2008). These studies reported the use of Maize (field corn) to enhance the agronomic traits of sweet corn and further demonstrated that field maize genotypes vary in their effectiveness in improving both agronomic performance and quality. Additionally, introgression of value-added traits like β-carotene into both field and sweet corn backgrounds is gaining importance to meet nutritional security objectives (Rathinavel *et al.*, 2023).

Effective genetic enhancement relies heavily on the evaluation of genetic variability present within the breeding population, as it forms the basis for selection. Key parameters such as genetic advance, heritability, genotypic-coefficient of variation (GCV) and phenotypic-coefficient of variation (PCV), offer valuable insights into the trait inheritance and the potential effectiveness of selection. Traits exhibiting higher heritability paired with higher genetic advance are typically controlled by additive gene effects and tend to respond effectively to selection (Rao *et al.*, 2023). Therefore, estimating these parameters helps breeders prioritize traits for improvement and design efficient breeding strategies.

Beyond variability estimates, the distribution pattern of traits within segregating populations offers valuable information about gene action. Kurtosis and skewness are two key statistical metrics commonly employed in this context. Skewness reflects the asymmetry of trait distribution, with positive skewness indicating complementary gene effect, while negative skewness suggests duplicate gene action Fisher *et al.* (1932). Kurtosis measures the peakedness of the trait distribution, where leptokurtic patterns are generally associated with the influence of fewer genes, and platykurtic distributions suggest polygenic control (Robson, 1956). These descriptors can therefore indirectly inform the genetic architecture of traits and the expected response to selection.

With these objectives in mind, the present investigation sought to evaluate the backcross populations (BC_2F_2 and BC_2F_3) through comprehensive descriptive statistical analyses and assessment of frequency distribution parameters, including skewness and kurtosis, to identify elite segregants combining high yield potential with desirable agronomical traits.

MATERIALS AND METHODOLOGY

Breeding Materials

In this present investigation, CAUM66β$^+$, a superior beta-carotene enriched inbred line, used as recurrent parent. DBT16, a *sh2* mutant based sweet corn inbred line enriched with beta-carotene was used as a donor parent. The experiment took place and field trials were conducted, during Summer of 2024 at New Area Farm of Department of Millets, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore. The crop was raised by following the standard package of recommended agronomic practices.

Development of Backcross Population

A BC_2F_3 backcross population was developed from the cross CAUM66β$^+$ × DBT16 to incorporate the desirable *shrunken2* (*sh2*) allele from the donor sweet-corn parent (DBT16) into the field corn, recurrent inbred line (CAUM66β$^+$), with the goal of enhancing kernel sweetness. A single cross was made between CAUM66β$^+$ (field corn) and DBT16 (sweet corn) during Kharif 2021 to produce F_1 hybrids. These F_1 plants (ten progenies) were subjected to backcrossing with the recurrent parent CAUM66β$^+$ in Summer 2022 to obtain the BC_1F_1 generation. The BC_1F_1 plants (ten progenies) were grown in Kharif 2022 and selfing was performed to produce the BC_1F_2 generation. In Summer 2023, BC_1F_2 plants (ten progenies) were subjected to backcrossing again, with the

recurrent parent to develop the BC_2F_1 generation. The resulting BC_2F_1 progenies (ten progenies) were cultivated during Kharif 2023 and selfing was performed to produce the BC_2F_2 generation. During Summer 2024, BC_2F_2 population (ten progenies) was evaluated for genetic variability and descriptive statistical parameters and selfing was performed to produce BC_2F_3 (Figure 1). Finally, during Kharif 2024, two progenies (each consists of around 40 plants) in BC_2F_3 was evaluated for TSS, genetic variability and descriptive statistical parameters.

Observations Recorded on Agro-morphological Traits

In present study, BC_2F_2 and BC_2F_3 population were evaluated for fourteen (14) agro-morphological traits in accordance with the DUS – (Distinctiveness, Uniformity, and Stabillity), guidelines and standards prescribed by the PPV&FRA - Protection of Plant Varieties and Farmers' Rights Authority (Anon, 2007). The traits included were: - Flowering traits: DS - days to silking and DT - days to tasselling were recorded in days from sowing. Growth parameters such as, PH - plant height and, EH - Ear height (EH) were measured in centimetres at the time of maturity. Tassel-related traits, TL - tassel length in centimetres and NTB - number of tassel branches in count, were recorded to understand male inflorescence development. Leaf traits, including LL - leaf length in centimetres and LB - leaf breadth in centimetres, were recorded to estimate vegetative growth. Cob related parameters such as CL - Cob length in centimetres and CG - cob girth in centimetres were measured to determine reproductive output. Kernels arrangement parameters, such as NK/R - number of kernel-per row in count, and NKR/C - number of kernel rows per cob in count, were evaluated to determine their contribution towards yield. Additionally, 100 KW - 100 kernel weight in grams and SPY - single plant yield in grams, were recorded to evaluate yield potential.

Foreground Selection

The *crtRB1* gene has three distinguished polymorphism present- 5- TE, InDel and a 3'TE. The transposable element insertion at 3'ÚTR region of the *crtRB1* gene was used to design and construct functional marker. This marker was used to distinguish favourable and unfavourable alleles (Yan *et al.*, 2010). The marker system has 3 primers – one forward and two reverse primers given in Table 1. The F and R_1 primers were responsible for the amplification of the *crtRB1*- unfavourable allele of 296 bp. The F and R_2 primer gave rise to *crtRB1* favourable allele of 543 bp size (Yan *et al.*, 2010; Vignesh *et al.*, 2013; Muthusamy *et al.*, 2014).

To confirm the presence of the *crtRB1* allele in the two BC_2F_3 progenies, foreground selection was carried out using a gene-specific co-dominant marker targeting the *crtRB1* 3'*TE* region. PCR amplification was carried out following the protocol described by Natesan *et al.* (2020). The amplified products were separated on a 3% agarose gel and analyzed for the presence of the target allele.

The phenotypic similarity of each line within the progeny was evaluated in comparison to the recurrent parent. Total Soluble Solids (TSS) content in kernels was assessed at 24 days after pollination (DAP) using a refractometer (Baveja *et al.*, 2022).

Statistical Analysis

Data of fourteen agro-morphological traits of the individual plants in BC_2F_2 and BC_2F_3 population was recorded and the data was analysed for descriptive statistical parameters *viz.*, mean, standard deviation, range, variance, kurtosis, skewness and variability parameters *viz.*, PCV, GCV, GA, heritability, GAM using MS-EXCEL version.2019 and the frequency distribution graphs was generated by using SPSS version16.0.0.1 Phenotypic similarity was estimated by calculating the ratio of individual

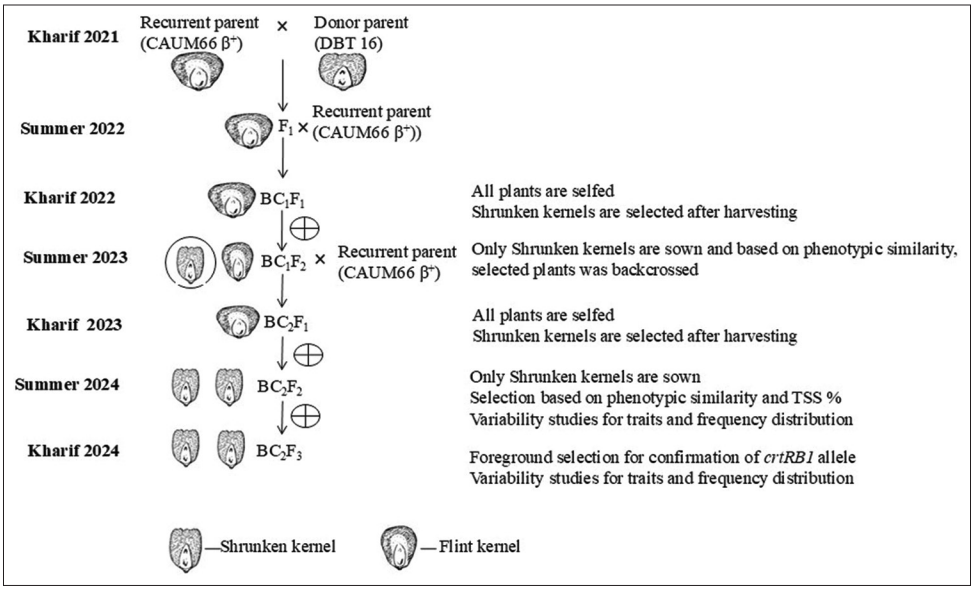

Figure 1: Scheme for the development of sweetcorn lines with improved beta carotene through marker assisted selection

Table 1: Gene Specific-Primer employed in this experiment

Marker	Sequence
*crtRB1-3′*TE F	ACACCACATGGACAAGTTCG
crtRB1 3′TE R_1	ACACTCTGGCCCATGAACAC
crtRB1 3′TE R_2	ACAGCAATACAGGGGACCAG

line means to the recurrent parent mean and expressed the result as a percentage.

Phenotypic Similarity percentage = Mean performance of Recurrent parent/Progeny Mean × 100

Estimation of Components of Variance

The environmental variance (EV) is calculated as an average variance observed in both the parents i.e., Recurrent (CAUM66β$^+$) and Donor (DBT16). Subtracting environmental variance (EV) from the phenotypic variance (PV) gives genotypic variance (GV) of each trait (Lush, 1940). GCV, PCV was calculated using the formula given by Burton (1952) classification low (<10), moderate (10 to 20) and high (>30), as described by Subramanian and Madhavamenon (1973). Heritability in broad sense is the ratio of genotypic variance to the phenotypic variance expressed in percentage. It was calculated by the formula given by Lush (1940). Heritability estimates were classified into low (<30%), medium (30-60%) and high (>60%) by following Robinson *et al.* (1949). Expected genetic advance (GA) for each character was calculated by using the formula given by Johnson *et al.* (1955). Classification of expected genetic advance as per cent of mean (GAM) low (<30%), medium (30-60%) and high (>60%), followed as described by Johnson *et al.* (1955).

RESULTS

Mean Performance

The mean plant height among the progenies was recorded high (168.20 cm), with values ranging from 139.00 to 185.00 cm, falling between the recurrent parent (182.50 cm) and donor (144.50 cm). The mean leaf breadth exhibited lesser means, varied between 6.00 cm and 9.50 cm with the average of 7.76 cm compared to 8.75 cm (recurrent) and 7.25 cm (donor). The estimates of 100 kernel weight was ranged in between 10.12 g and 13.97 g with the average of 12.40 g. which was much lower than the recurrent parent (25.77 g) and slightly higher than the donor (11.88 g). Likewise, single plant yield in the progeny averaged 47.01 g, with a range from 40.13 to 50.95 g. This was significantly lower than the recurrent parent (89.01 g), and approximately equal to the donor parent (43.96 g) (Table 2 & Figure 2). Whereas, In BC_2F_3 population, of progeny i.e., CAUM66β$^+$ × DBT16 – 7 – 25 – 5 – 15 – 14, the mean plant height among the progenies was 154.68 cm, with values ranging from 151.00 to 158.00 cm, falling between the recurrent parent (181.30 cm) and donor (145.30 cm). The mean leaf breadth exhibited lesser means, varied between 7.00 cm and 9.00 cm with the average of 7.95 cm compared to 8.85 cm (recurrent) and 7.15 cm (donor). The estimates of 100 kernel weight was ranged between 10.12 g and 13.97 g with the average of 12.40 g. which was much lower than the recurrent parent (25.77 g) and slightly higher than the donor (11.88 g). Likewise, single plant yield in the progeny averaged 47.01 g, with a range from 40.13 to 50.95 g. This was significantly lower than the recurrent parent (89.01 g), and approximately equal to the donor parent (43.96 g) (Table 3 & Figure 3). Similar trend also followed in BC_2F_3 population, of the progeny i.e., CAUM66β$^+$ × DBT16 – 3 – 5 – 16 – 29 – 17, where the mean plant height among the progenies was 158.05 cm, with values ranging from 154.00 to 162.00 cm, falling between the recurrent parent (181.30 cm) and donor (145.30 cm). The mean leaf breadth exhibited lesser means, varied between 7.00 cm and 8.50 cm with the average of 7.48 cm compared to 8.85 cm (recurrent) and 7.15 cm (donor) The estimates of 100 kernel weight was ranged in between 11.04 g and 12.99 g with the average of 11.98 g. which was much lower than the recurrent parent (26.18 g) and slightly equal to the donor (12.04 g). Likewise, single plant yield in the progeny averaged 46.25 g, with a range from 42.30 to 50.61 g. This was significantly lower than the recurrent parent (87.78 g), and approximately equal to the donor parent (42.46 g) (Table 4 & Figure 4).

Skewness and Kurtosis

In BC_2F_2 population, only NTB (number of tassels branches) exhibited positive skewness (0.53) and positive kurtosis (0.53) which shows complementary gene action. Leaf breadth displayed a nearly symmetrical mesokurtic distribution with a skewness value close to zero (-0.01). In contrast, several traits exhibited negative skewness, suggesting left-tailed distributions with values skewed toward the higher end. These included number of kernel rows-per cob (-0.27), leaf length (-0.37), single plant yield (-0.43), plant height (-0.44), 100-kernel weight (-0.45), tassel length (-0.46), cob girth (-0.50), cob length (-0.52), number of kernels per row (-0.57), days to silking (-0.59), and days to tasseling (-0.63). Regarding kurtosis, number of tassel branches (0.53) and cob girth (0.29) exhibited leptokurtic distributions, characterized by sharper peaks and heavier tails, which indicated these traits were controlled by few genes and responds well to the directional selection. On the contrary, the traits including number of kernels-per row (-0.21), days to tasseling (-0.33), leaf breadth (-0.34), ear height (-0.37), days to silking (-0.40), 100-kernel weight (-0.44), leaf length (-0.55), tassel length (-0.55), single plant yield (-0.60), cob length (-0.61), and plant height (-0.66) demonstrated platykurtic distributions (Table 2 & Figure 2)

Whereas in BC_2F_3 population, of the progeny CAUM66β$^+$ × DBT16 – 7 – 25 – 5 – 15 – 14, only LL (leaf length) exhibited positive skewness (1.31) and positive kurtosis (2.17). Other traits exhibited positive skewness are single plant yield (0.36), 100 kernel weight (0.04), number of kernel rows per cob (1.37), number of tassel branches (0.85), tassel length (0.19), ear height (0.56) and days to silking (0.23). Leaf breadth displayed a nearly symmetrical mesokurtic distribution with a skewness value close to zero (-0.01). In contrast, several traits exhibited negative skewness included plant height (-0.33), cob girth (-0.22), cob length (-0.06), number of kernels per row (-0.11) and days to tasseling (-0.10). Regarding kurtosis, leaf length (2.17) exhibited leptokurtic distributions. On the contrary, the traits including

Table 2: Descriptive statistics and variability assessment in BC_2F_2 population of CAUM66β$^+$ × DBT16 for agro-morphological traits

Traits	Recurrent Parent	Donor Parent	BC_2F_2 Population	Range		S.D	Variance	Skewness	Kurtosis	GCV	PCV	h^2	GAM
	(Mean)	(Mean)	(Mean)	Min.	Max.								
DT (days)	62.10	51.30	58.20	50.00	63.00	3.44	11.83	-0.63	-0.33	5.78	5.91	95.77	11.66
DS (days)	64.30	53.70	60.25	52.00	65.00	3.41	11.65	-0.59	-0.40	5.55	5.67	96.09	11.21
PH (cm)	182.50	144.50	168.20	139.00	185.00	11.38	129.45	-0.44	-0.66	6.68	6.76	97.38	13.57
EH (cm)	75.30	60.80	69.09	58.00	76.00	5.01	25.06	-0.70	-0.37	6.77	7.25	87.21	13.02
TL (cm)	29.80	22.90	27.31	19.00	33.00	3.92	15.37	-0.46	-0.55	13.49	14.36	88.25	26.10
NTB (No.s)	10.50	14.10	11.59	9.00	15.00	1.31	1.70	0.53	0.53	9.81	11.27	75.88	17.61
LL (cm)	71.40	59.90	67.63	58.00	74.00	4.23	17.87	-0.37	-0.55	5.77	6.25	85.29	10.98
LB (cm)	8.75	7.25	7.76	6.00	9.50	0.79	0.62	-0.01	-0.34	9.30	10.13	84.28	17.59
CL (cm)	16.45	10.10	13.58	9.00	16.00	2.00	4.01	-0.52	-0.61	11.72	14.75	63.10	19.17
CG (cm)	11.85	9.35	10.62	8.00	12.50	1.04	1.08	-0.50	0.29	8.96	9.77	84.26	16.95
NKR/C (No.s)	14.00	10.00	12.47	10.00	14.00	1.29	1.67	-0.27	-0.68	7.10	10.37	46.83	10.00
NK/R (No.s)	26.10	19.50	23.70	18.00	27.00	2.47	6.08	-0.57	-0.21	9.12	10.40	76.79	16.46
100 KW (g)	25.77	11.88	12.40	10.12	13.97	0.93	0.87	-0.45	-0.44	6.36	7.50	71.72	11.09
SPY (g)	89.01	43.96	47.01	40.13	50.95	2.59	6.71	-0.43	-0.60	3.99	5.51	52.42	5.95

S.D. - Standard deviation, GCV - Genotypic Coefficient of Variation; PCV - Phenotypic Coefficient of Variation; h^2 - Heritability; GA - Genetic Advance; GAM - Genetic Advance as per of Mean; DT - Days to tasseling; DS - Days to silking; PH - Plant height; EH - Ear height; TL - Tassel length; NTB - Number of tassel branches; LL - Leaf length; LB - Leaf breadth; CL - Cob length; CG - Cob girth; NKR/C - Number of kernel rows per cob; NK/R - Number of kernel rows; 100 KW - Kernel weight; SPY - Single plant yield

Table 3: Descriptive statistics and variability assessment in BC_2F_3 population progeny of CAUM66β$^+$ × DBT16 – 7 – 25 – 5 – 15 – 14 for agro-morphological traits

Traits	Recurrent Parent	Donor Parent	Progeny	Range		S.D	Variance	Skewness	Kurtosis	GCV	PCV	h^2	GAM
	(Mean)	(Mean)	(Mean)	Min.	Max.								
DT (days)	61.40	51.80	54.00	52.00	56.00	1.48	2.21	-0.10	-1.39	2.61	2.75	89.92	5.09
DS (days)	63.40	53.90	56.23	54.00	60.00	1.66	2.74	0.23	-0.84	2.78	2.95	89.27	5.42
PH (cm)	181.30	145.30	154.68	151.00	158.00	2.15	4.64	-0.33	-1.00	1.07	1.39	59.01	1.69
EH (cm)	74.40	60.20	64.15	60.00	71.00	2.76	7.62	0.56	-0.44	3.84	4.30	79.58	7.05
TL (cm)	30.80	23.50	24.93	23.00	27.00	1.47	2.17	0.19	-1.39	4.12	5.92	48.63	5.93
NTB (No.s)	10.60	13.80	9.60	9.00	11.00	0.78	0.61	0.85	-0.78	6.21	8.10	58.69	9.80
LL (cm)	72.70	60.60	63.88	62.00	69.00	1.60	2.57	1.31	2.17	1.77	2.51	49.71	2.57
LB (cm)	8.85	7.15	7.95	7.00	9.00	0.67	0.45	-0.01	-1.17	7.25	8.40	74.47	12.89
CL (cm)	16.90	10.15	14.53	13.00	16.00	1.34	1.79	-0.06	-1.83	8.17	9.22	78.56	14.92
CG (cm)	11.95	9.30	10.08	9.00	11.00	0.73	0.53	-0.22	-1.32	5.85	7.24	65.32	9.75
NKR/C (No.s)	14.00	10.00	12.45	12.00	14.00	0.85	0.72	1.37	-0.14	4.18	6.79	37.87	5.30
NK/R (No.s)	25.90	19.20	23.15	21.00	25.00	1.41	1.98	-0.11	-1.30	4.45	6.07	53.63	6.71
100 KW (g)	26.18	12.04	11.98	11.04	12.99	0.61	0.37	0.04	-1.31	3.46	5.07	46.39	4.85
SPY (g)	87.78	42.46	46.25	42.30	50.61	2.49	6.18	0.36	-1.11	4.68	5.37	75.89	8.40

S.D. - Standard deviation, GCV - Genotypic Coefficient of Variation; PCV - Phenotypic Coefficient of Variation; h^2 - Heritability; GA - Genetic Advance; GAM - Genetic Advance as per of Mean; DT - Days to tasseling; DS - Days to silking; PH - Plant height; EH - Ear height; TL - Tassel length; NTB - Number of tassel branches; LL - Leaf length; LB - Leaf breadth; CL - Cob length; CG - Cob girth; NKR/C - Number of kernel rows per cob; NK/R - Number of kernel rows; 100 KW - Kernel weight; SPY - Single plant yield

number of kernels-per row (-1.30), days to tasseling (-1.39), leaf breadth (-1.17), ear height (-0.44), days to silking (-0.84), 100-kernel weight (-1.31), tassel length (-1.39), single plant yield (-1.11), cob length (-1.83), plant height (-1.00), number of tassel branches (-0.78), cob girth (-1.32) and number of kernel rows per cob (-0.14) demonstrated platykurtic distributions (Table 3 & Figure 3).

In BC_2F_3 population, of the progeny CAUM66β$^+$ × DBT16 – 3 – 5 – 16 – 29 – 17, traits exhibited positive skewness are single plant yield (0.36), number of kernel rows per cob (1.20), leaf breadth (0.54), number of tassel branches (0.83) and days to silking (0.06). Tassel length displayed a nearly symmetrical mesokurtic distribution with a skewness value close to zero (-0.01). In contrast, several traits exhibited negative skewness, included plant height (-0.15), cob girth (-0.51), cob length (-0.19), number of kernels per row (-0.20), days to tasseling (-0.28) and 100 kernel eight (-0.34), leaf length (-0.22) and plant height (-0.22). Regarding kurtosis, all studied traits including number of kernels-per row (-1.49), days to tasseling (-1.38), leaf breadth (-1.13), ear height (-1.40), days to silking (-0.72), 100-kernel weight (-1.15), tassel length (-1.20), single plant yield (-0.61), cob length (-1.26), plant height (-0.96), number of tassel branches (-0.28), cob girth (-1.34), number of kernel rows per cob (-0.59) and leaf length (-1.15) demonstrated platykurtic distributions (Table 4 & Figure 4).

Variability Analysis

PCV and GCV

Substantial variability was observed among the fourteen (14) agro-morphological traits of the BC_2F_2 population, as indicated by the estimates of genetic advance as a percentage of the

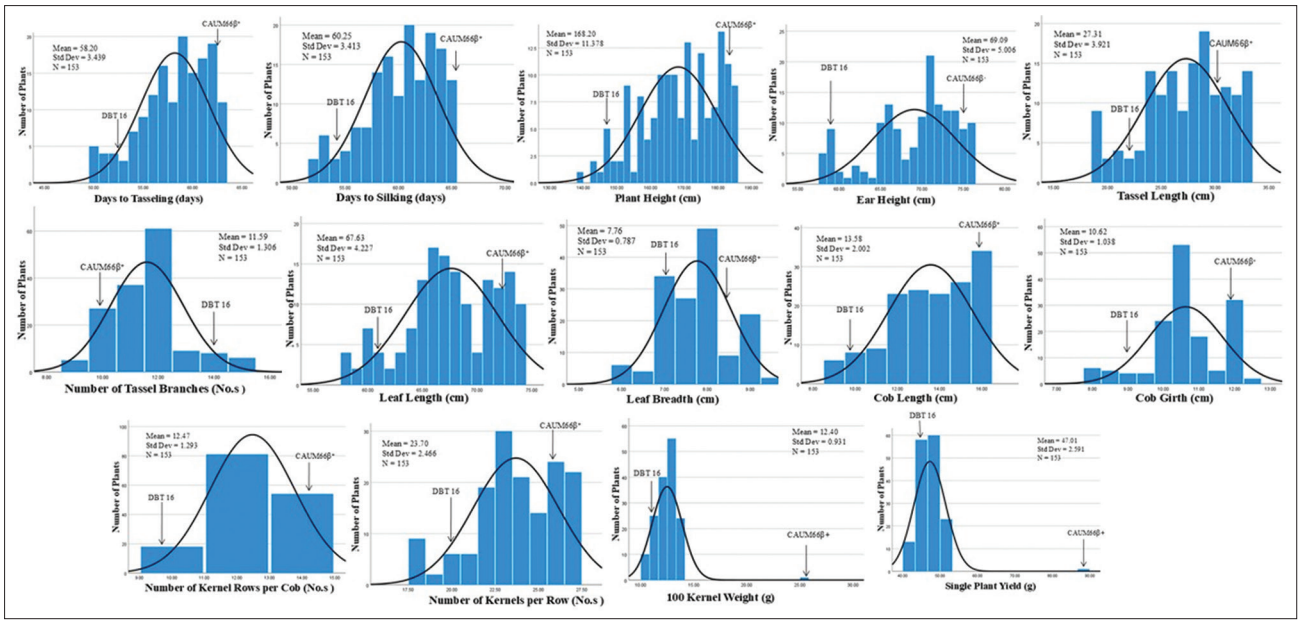

Figure 2: Frequency distribution for agro-morphological traits in BC_2F_2 population

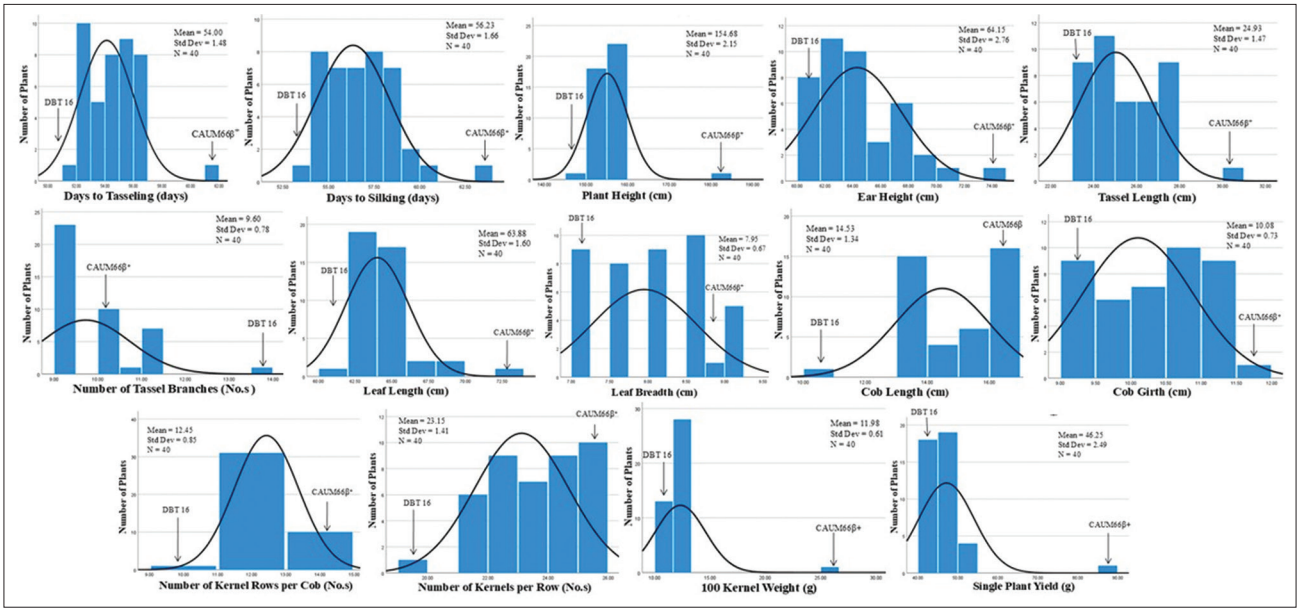

Figure 3: Frequency distribution for agro-morphological traits in BC_2F_3 population of progeny CAUM66β⁺ × DBT16 – 7 – 25 – 5 – 15 – 14

mean (GAM), heritability (h^2), phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV). In this population, GCV ranged from 3.99% to 13.49%, while PCV ranged from 5.51% to 14.75%, reflecting the presence of moderate to higher genetic variation across traits. Moderate phenotypic and genotypic coefficients of variation were recorded for traits such as cob length, number of tassel branches, and tassel length (Table 2). Reduced variability was observed in BC_2F_3 population, of progeny CAUM66β⁺ × DBT16 – 7 – 25 – 5 – 15 – 14 and GCV ranged from 1.07% to 8.17%, while PCV ranged from 1.39% to 9.22%, reflecting the presence of lesser genetic variation across traits. All the studied traits exhibited low PCV and GCV values (Table 3). Similarly, reduced variability was observed of the progeny CAUM66β⁺ × DBT16 – 3 – 5 – 16 – 29 – 17 of BC_2F_3 population and here, GCV ranged from 1.09% to 9.02%, while PCV ranged from 1.40% to 10.02% as all the studied traits exhibited low PCV and GCV values (Table 4).

Heritability

In BC_2F_2 population, broad-sense heritability estimates ranged from moderate to higher, across all traits studied, which are ranging from 46.83% in number of kernel rows-per cob to 97.38% in plant height (Table 2). Heritability estimates were found to be high for the traits, plant height (97.38%) followed by days to silking (96.09%), days to tasseling (95.77%), tassel

Table 4: Descriptive statistics and variability assessment in BC_2F_3 population progeny of CAUM66β$^+$ × DBT16 – 3 – 5 – 16 – 29 – 17 for agro-morphological traits

Traits	Recurrent Parent	Donor Parent	Progeny	Range		S.D	Variance	Skewness	Kurtosis	GCV	PCV	h^2	GAM
	(Mean)	(Mean)	(Mean)	Min.	Max.								
DT (days)	61.40	51.80	54.15	53.00	55.00	0.80	0.64	-0.28	-1.38	1.20	1.48	65.47	2.00
DS (days)	63.40	53.90	56.30	55.00	58.00	0.88	0.78	0.06	-0.72	1.24	1.57	62.23	2.01
PH (cm)	181.30	145.30	158.05	154.00	162.00	2.21	4.87	-0.22	-0.96	1.09	1.40	60.98	1.75
EH (cm)	74.40	60.20	65.93	62.00	69.00	2.37	5.61	-0.15	-1.40	3.05	3.59	72.27	5.35
TL (cm)	30.80	23.50	26.28	24.00	29.00	1.62	2.61	-0.01	-1.20	4.66	6.15	57.29	7.26
NTB (No.s)	10.60	13.80	9.53	9.00	11.00	0.64	0.41	0.83	-0.28	4.19	6.72	38.97	5.39
LL (cm)	72.70	60.60	65.25	63.00	67.00	1.35	1.83	-0.22	-1.15	1.13	2.08	29.39	1.26
LB (cm)	8.85	7.15	7.48	7.00	8.50	0.52	0.27	0.54	-1.13	5.26	6.93	57.60	8.23
CL (cm)	16.90	10.15	14.25	12.00	16.00	1.43	2.04	-0.19	-1.26	9.02	10.02	81.13	16.74
CG (cm)	11.95	9.30	10.21	9.00	11.00	0.80	0.64	-0.51	-1.34	6.60	7.83	71.12	11.47
NKR/C (No.s)	14.00	10.00	12.50	12.00	14.00	0.88	0.77	1.20	-0.59	4.56	7.02	42.22	6.10
NK/R (No.s)	25.90	19.20	22.60	21.00	24.00	1.19	1.43	-0.20	-1.49	3.16	5.28	35.70	3.89
100 KW (g)	26.18	12.04	12.03	11.05	12.88	0.57	0.32	-0.34	-1.15	2.93	4.72	38.48	3.74
SPY (g)	87.781	42.459	44.82	41.16	49.94	2.37	5.62	0.36	-0.61	4.54	5.29	73.51	8.01

S.D. - Standard deviation, GCV - Genotypic Coefficient of Variation; PCV - Phenotypic Coefficient of Variation; h^2 - Heritability; GA - Genetic Advance; GAM - Genetic Advance as per of Mean; DT - Days to tasseling; DS - Days to silking; PH - Plant height; EH - Ear height; TL - Tassel length; NTB - Number of tassel branches; LL - Leaf length; LB - Leaf breadth; CL - Cob length; CG - Cob girth; NKR/C - Number of kernel rows per cob; NK/R - Number of kernel rows; 100 KW - Kernel weight; SPY - Single plant yield

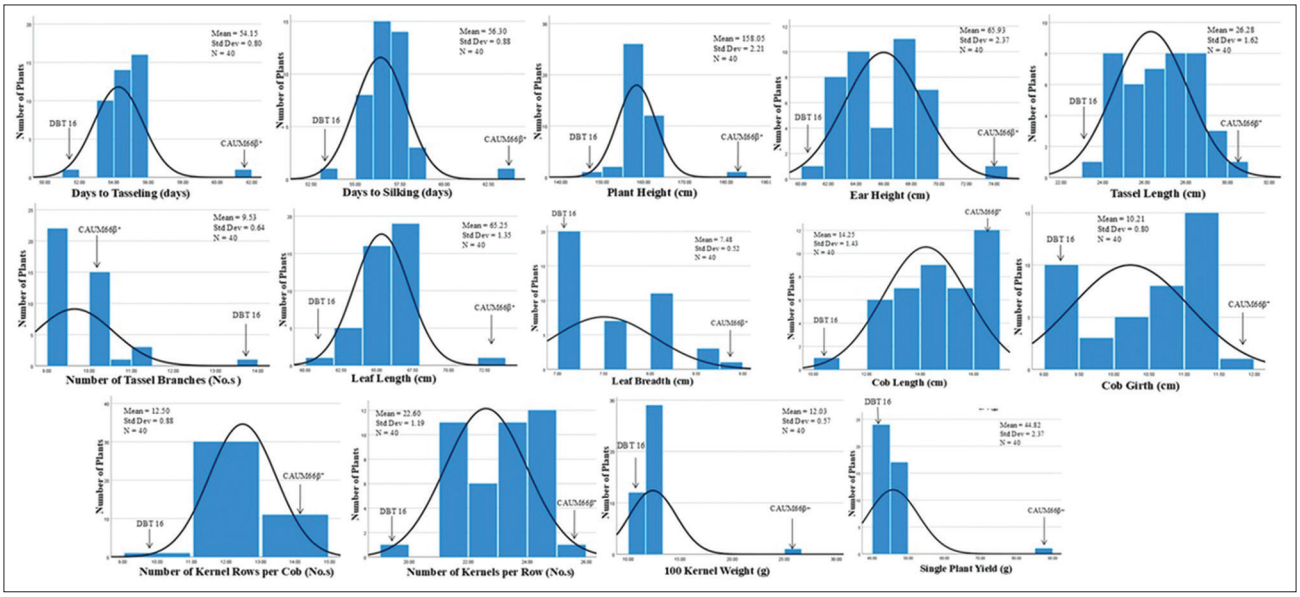

Figure 4: Frequency distribution for agro-morphological traits in BC_2F_3 population of progeny CAUM66β$^+$ × DBT16 – 3 – 5 – 16 – 29 – 17

length (88.25%), ear height (87.21%), leaf length (85.29%), leaf breadth (84.28%), cob girth (84.26%), number of kernels per-row (76.79%), number of tassel branches (75.88%), 100 kernel weight (71.72%) and cob length (63.10%). Whereas moderate heritability was observed in the traits single plant yield (52.42%) followed by the trait - number of kernel rows-per cob (46.83%).

Whereas, in BC_2F_3 population, of progeny CAUM66β$^+$ × DBT16 – 7 – 25 – 5 – 15 – 14, heritability ranging from 37.87% in number of kernel rows-per cob to 89.92% in days to tasseling (Table 3). Heritability estimates were found to be high for the traits, days to tasseling (89.92%) followed by days to silking (89.27%), ear height (79.58%), cob length (78.56%), single plant yield (75.89%), leaf breadth (74.47%) and cob girth (65.32%). Whereas moderate heritability was observed in the traits plant height (59.01%) followed by the trait – number of tassel branches, number of kernels-per row (53.63%), leaf length (49.71%), tassel length (48.63%), 100 kernel weight (46.39%) and number of kernel rows-per cob (37.87%)

In BC_2F_3 population, of progeny CAUM66β$^+$ × DBT16 – 3 – 5 – 16 – 29 – 17, broad-sense heritability estimates ranged from lower to higher, across all traits studied, which are ranging from 29.39% in leaf length to 81.13% in cob length (Table 4). Heritability estimates were found to be high for the traits, cob length (81.13%) followed by single plant yield (73.51%), ear height (72.27%), cob girth(71.12%), days to tasseling (65.7%), days to silking (62.23%) and plant height (60.98%). Whereas moderate heritability was observed in the traits leaf breadth (57.60%) followed by the trait - tassel length (57.29%),

number of kernels-per row (42.22%), number of tassel branches (38.97%), 100 kernel weight (38.48%) and number of kernels-per row (35.70%).

Genetic Advance as Percent of Mean (GAM)

In BC_2F_2 population, for all the fourteen (14) traits studied, higher to lower genetic advance as percent of mean (GAM) values was noted and ranged between 5.95% and 26.10% (Table 2). Higher genetic advance as percent of mean (GAM) values was noted in tassel length (26.10%). While the moderate estimates of genetic advance as percent of mean (GAM) values was noted in cob length (19.17%) followed by leaf breadth (17.59%), number of tassel branches (17.61%), number of kernels per row (16.46%), cob girth (16.95%), ear height (13.02%), plant height (13.57%), days to silking (11.21%), days to tasseling (11.66%), 100 kernel weight (11.09%) and number of kernel rows-per cob (10.00%) and leaf length (10.98%). Whereas in BC_2F_3 population, of progeny CAUM66β$^+$ × DBT16 – 7 – 25 – 5 – 15 – 14 moderates to lower genetic advance as percent of mean (GAM) values was noted and ranged between 1.69% and 14.92% (Table 3). Moderate estimates of genetic advance as percent of mean (GAM) values were noted in cob length (14.92%) and in leaf breadth (12.89%). Similarly, of progeny CAUM66β$^+$ × DBT16 – 3 – 5 – 16 – 29 – 17, moderate to lower genetic advance as percent of mean (GAM) values was noted and ranged between 1.26 % and 16.74% (Table 4). Moderate estimates of genetic advance as percent of mean (GAM) values were noted in cob length (16.74%) and in cob girth (11.47%).

Foreground Selection for Confirmation of β-Carotene Allele

In the BC_2F_2 population, plants showing visual resemblance to the recurrent parent were selfed. Subsequently, two progenies exhibiting the maximum phenotypic resemblance of agro-morphological traits to the recurrent parent and elevated sugar content were selected and further advanced to BC_2F_3. Further foreground screening was performed to all the lines from two selected progenies of BC_2F_3 and were confirmed for the presence of beta carotene allele using the *crtRB1* 3′TE gene-specific co-dominant marker (Figure 5 & Figure 6).

Phenotypic Similarity

In BC_2F_3 population, of progeny CAUM66β$^+$ × DBT16 – 7 – 25 – 5 – 15 – 14, phenotypic similarity percentage of lines towards recurrent parent, ranged from 79.22% to 82.43% and of progeny CAUM66β$^+$ × DBT16 – 3 – 5 – 16 – 29 – 17, phenotypic similarity percentage of lines ranged from 79.36% to 82.88% (Table 5 & Table 6).

Total Soluble Solids (TSS)

In the BC_2F_2 population, two progenies exhibiting elevated TSS (%) were selected and advanced to the BC_2F_3 generation. In BC_2F_3, the improved lines from both progenies recorded TSS values ranging from 14% to 18% (Table 5 & Table 6). Lines with higher TSS (%) and phenotypic resemblance to the recurrent parent were further advanced.

DISCUSSION

Effective selection and identification of promising genotypes and elite inbred lines for hybrid seed production is dependent on the existence of adequate genetic variability and high heritability in the base population. A comparative analysis of the BC_2F_2 and BC_2F_3 progenies obtained in this study derived from the cross CAUM66β$^+$ × DBT16, in relation to their parental lines, revealed a substantial genetic variation and exhibited intermediate performance across most agronomic traits. The presence of variability in the BC_2F_2 population could be attributed to the differential combining ability of the recurrent parent (CAUM66β$^+$) and the donor (DBT-16), which possess diverse genetic backgrounds, as also reported in the previous findings (Butrón *et al.*, 2008). Mean performance of the BC_2F_2 population and BC_2F_3 progenies were in align with results by Cox (1984).

The analysis of skewness and kurtosis revealed distinct distribution patterns among the traits. The occurrence of positive skewness indicates the presence of complementary genetic effects, whereas a negatively skewed distribution is indicative of duplicate gene interaction. In BC_2F_2, number of tassels branches exhibited positive skewness and positive kurtosis whereas in BC_2F_3, the progeny CAUM66β$^+$ × DBT16 – 7 – 25 – 5 – 15 – 14, only leaf length exhibited. Similar results are in alignment with Maqbool (2021). Both in BC_2F_2

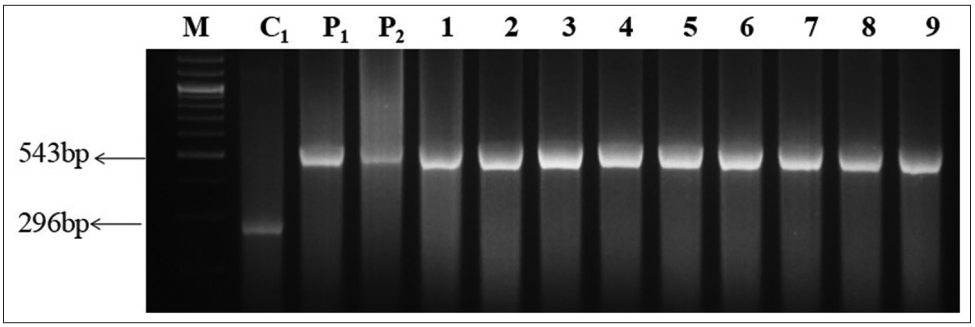

Figure 5: Foreground selection in BC_2F_3 lines of CAUM66β$^+$ × DBT16 – 7 – 25 – 5 – 15 – 14 using *crtRB1* gene specific marker. M-100bp ladder, C_1- CAUM66 (Negative control - 296bp), P_1- CAUM66β$^+$, P_2 – DBT16, 1 - 9 – Lines of the progeny

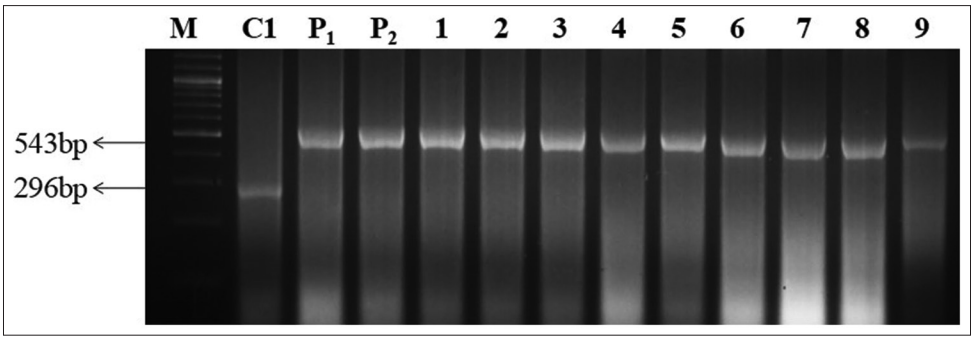

Figure 6: Foreground selection in BC_2F_3 lines of CAUM66β$^+$ × DBT16 – 3 – 5 – 16 – 29 – 17 using *crtRB1* gene specific marker. M-100bp ladder, C_1- CAUM66 (Negative control - 296bp), P_1 - CAUM66β+, P_2 – DBT16, 1 - 9 – Lines of the progeny

Table 5: Phenotypic similarity and total soluble sugars of BC_2F_3 lines of progeny CAUM66β$^+$ × DBT16 – 7 – 25 – 5 – 15 – 14

S. No.	Lines	PS (%)	TSS (%)
1	CAUM66β$^+$ × DBT16 – 7 – 25 – 5 – 15 – 14 – 3	79.90	16
2	CAUM66β$^+$ × DBT16 – 7 – 25 – 5 – 15 – 14 – 4	81.96	15
3	CAUM66β$^+$ × DBT16 – 7 – 25 – 5 – 15 – 14 – 9	80.68	17
4	CAUM66β$^+$ × DBT16 – 7 – 25 – 5 – 15 – 14 – 10	81.70	15
5	CAUM66β$^+$ × DBT16 – 7 – 25 – 5 – 15 – 14 – 11	81.71	16
6	CAUM66β$^+$ × DBT16 – 7 – 25 – 5 – 15 – 14 – 12	81.57	18
7	CAUM66β$^+$ × DBT16 – 7 – 25 – 5 – 15 – 14 – 17	79.47	17
8	CAUM66β$^+$ × DBT16 – 7 – 25 – 5 – 15 – 14 – 18	80.22	14
9	CAUM66β$^+$ × DBT16 – 7 – 25 – 5 – 15 – 14 – 19	79.12	17
10	CAUM66β$^+$ × DBT16 – 7 – 25 – 5 – 15 – 14 – 20	80.31	15
11	CAUM66β$^+$ × DBT16 – 7 – 25 – 5 – 15 – 14 – 25	79.22	14
12	CAUM66β$^+$ × DBT16 – 7 – 25 – 5 – 15 – 14 – 26	79.90	14
13	CAUM66β$^+$ × DBT16 – 7 – 25 – 5 – 15 – 14 – 27	81.43	18
14	CAUM66β$^+$ × DBT16 – 7 – 25 – 5 – 15 – 14 – 28	80.80	16
15	CAUM66β$^+$ × DBT16 – 7 – 25 – 5 – 15 – 14 – 32	80.39	17
16	CAUM66β$^+$ × DBT16 – 7 – 25 – 5 – 15 – 14 – 33	81.19	17
17	CAUM66β$^+$ × DBT16 – 7 – 25 – 5 – 15 – 14 – 34	80.72	14
18	CAUM66β$^+$ × DBT16 – 7 – 25 – 5 – 15 – 14 – 35	81.33	16
19	CAUM66β$^+$ × DBT16 – 7 – 25 – 5 – 15 – 14 – 36	80.62	17
20	CAUM66β$^+$ × DBT16 – 7 – 25 – 5 – 15 – 14 – 37	79.98	15
21	CAUM66β$^+$ × DBT16 – 7 – 25 – 5 – 15 – 14 – 38	80.02	15
22	CAUM66β$^+$ × DBT16 – 7 – 25 – 5 – 15 – 14 – 39	80.28	18
23	CAUM66β$^+$ × DBT16 – 7 – 25 – 5 – 15 – 14 – 40	79.96	15
24	CAUM66β$^+$ × DBT16 – 7 – 25 – 5 – 15 – 14 – 41	80.46	18
25	CAUM66β$^+$ × DBT16 – 7 – 25 – 5 – 15 – 14 – 42	81.63	15
26	CAUM66β$^+$ × DBT16 – 7 – 25 – 5 – 15 – 14 – 48	82.43	14
27	CAUM66β$^+$ × DBT16 – 7 – 25 – 5 – 15 – 14 – 49	80.57	16
28	CAUM66β$^+$ × DBT16 – 7 – 25 – 5 – 15 – 14 – 50	80.58	17
29	CAUM66β$^+$ × DBT16 – 7 – 25 – 5 – 15 – 14 – 51	80.29	17
30	CAUM66β$^+$ × DBT16 – 7 – 25 – 5 – 15 – 14 – 52	79.29	15
31	CAUM66β$^+$ × DBT16 – 7 – 25 – 5 – 15 – 14 – 53	80.52	15
32	CAUM66β$^+$ × DBT16 – 7 – 25 – 5 – 15 – 14 – 54	82.05	14
33	CAUM66β$^+$ × DBT16 – 7 – 25 – 5 – 15 – 14 – 55	79.99	16
34	CAUM66β$^+$ × DBT16 – 7 – 25 – 5 – 15 – 14 – 56	80.12	17
35	CAUM66β$^+$ × DBT16 – 7 – 25 – 5 – 15 – 14 – 62	81.07	17
36	CAUM66β$^+$ × DBT16 – 7 – 25 – 5 – 15 – 14 – 63	81.05	14
37	CAUM66β$^+$ × DBT16 – 7 – 25 – 5 – 15 – 14 – 64	81.80	18
38	CAUM66β$^+$ × DBT16 – 7 – 25 – 5 – 15 – 14 – 65	81.41	18
39	CAUM66β$^+$ × DBT16 – 7 – 25 – 5 – 15 – 14 – 73	80.77	18
40	CAUM66β$^+$ × DBT16 – 7 – 25 – 5 – 15 – 14 – 74	79.90	14

Table 6: Phenotypic similarity and total soluble sugars of BC_2F_3 lines of progeny CAUM66β$^+$ × DBT16 – 3 – 5 – 16 – 29 – 17

S. No.	Lines	PS (%)	TSS (%)
1	CAUM66β$^+$ × DBT16 – 3 – 5 – 16 – 29 – 17 – 2	80.63	14
2	CAUM66β$^+$ × DBT16 – 3 – 5 – 16 – 29 – 17 – 5	82.21	17
3	CAUM66β$^+$ × DBT16 – 3 – 5 – 16 – 29 – 17 – 6	82.88	15
4	CAUM66β$^+$ × DBT16 – 3 – 5 – 16 – 29 – 17 – 7	81.06	18
5	CAUM66β$^+$ × DBT16 – 3 – 5 – 16 – 29 – 17 – 10	79.36	17
6	CAUM66β$^+$ × DBT16 – 3 – 5 – 16 – 29 – 17 – 11	82.23	16
7	CAUM66β$^+$ × DBT16 – 3 – 5 – 16 – 29 – 17 – 12	81.61	17
8	CAUM66β$^+$ × DBT16 – 3 – 5 – 16 – 29 – 17 – 13	82.60	16
9	CAUM66β$^+$ × DBT16 – 3 – 5 – 16 – 29 – 17 – 14	81.26	17
10	CAUM66β$^+$ × DBT16 – 3 – 5 – 16 – 29 – 17 – 15	82.85	15
11	CAUM66β$^+$ × DBT16 – 3 – 5 – 16 – 29 – 17 – 19	81.16	15
12	CAUM66β$^+$ × DBT16 – 3 – 5 – 16 – 29 – 17 – 20	82.60	18
13	CAUM66β$^+$ × DBT16 – 3 – 5 – 16 – 29 – 17 – 21	80.33	17
14	CAUM66β$^+$ × DBT16 – 3 – 5 – 16 – 29 – 17 – 22	80.17	16
15	CAUM66β$^+$ × DBT16 – 3 – 5 – 16 – 29 – 17 – 25	81.94	17
16	CAUM66β$^+$ × DBT16 – 3 – 5 – 16 – 29 – 17 – 26	81.22	16
17	CAUM66β$^+$ × DBT16 – 3 – 5 – 16 – 29 – 17 – 27	81.82	14
18	CAUM66β$^+$ × DBT16 – 3 – 5 – 16 – 29 – 17 – 28	80.13	16
19	CAUM66β$^+$ × DBT16 – 3 – 5 – 16 – 29 – 17 – 29	81.58	15
20	CAUM66β$^+$ × DBT16 – 3 – 5 – 16 – 29 – 17 – 30	81.09	18
21	CAUM66β$^+$ × DBT16 – 3 – 5 – 16 – 29 – 17 – 34	80.81	18
22	CAUM66β$^+$ × DBT16 – 3 – 5 – 16 – 29 – 17 – 35	81.30	14
23	CAUM66β$^+$ × DBT16 – 3 – 5 – 16 – 29 – 17 – 37	81.55	15
24	CAUM66β$^+$ × DBT16 – 3 – 5 – 16 – 29 – 17 – 38	80.83	17
25	CAUM66β$^+$ × DBT16 – 3 – 5 – 16 – 29 – 17 – 39	81.80	14
26	CAUM66β$^+$ × DBT16 – 3 – 5 – 16 – 29 – 17 – 41	81.47	18
27	CAUM66β$^+$ × DBT16 – 3 – 5 – 16 – 29 – 17 – 42	81.80	14
28	CAUM66β$^+$ × DBT16 – 3 – 5 – 16 – 29 – 17 – 43	79.65	14
29	CAUM66β$^+$ × DBT16 – 3 – 5 – 16 – 29 – 17 – 45	81.20	15
30	CAUM66β$^+$ × DBT16 – 3 – 5 – 16 – 29 – 17 – 46	81.01	17
31	CAUM66β$^+$ × DBT16 – 3 – 5 – 16 – 29 – 17 – 47	82.14	14
32	CAUM66β$^+$ × DBT16 – 3 – 5 – 16 – 29 – 17 – 49	81.94	18
33	CAUM66β$^+$ × DBT16 – 3 – 5 – 16 – 29 – 17 – 51	82.74	14
34	CAUM66β$^+$ × DBT16 – 3 – 5 – 16 – 29 – 17 – 52	82.35	14
35	CAUM66β$^+$ × DBT16 – 3 – 5 – 16 – 29 – 17 – 54	81.87	17
36	CAUM66β$^+$ × DBT16 – 3 – 5 – 16 – 29 – 17 – 55	82.12	15
37	CAUM66β$^+$ × DBT16 – 3 – 5 – 16 – 29 – 17 – 56	80.88	17
38	CAUM66β$^+$ × DBT16 – 3 – 5 – 16 – 29 – 17 – 60	82.34	17
39	CAUM66β$^+$ × DBT16 – 3 – 5 – 16 – 29 – 17 – 62	81.99	15
40	CAUM66β$^+$ × DBT16 – 3 – 5 – 16 – 29 – 17 – 68	82.28	16

population and of progeny BC_2F_3 (CAUM66β$^+$ × DBT16 – 7 – 25 – 5 – 15 – 14), leaf breadth displayed a nearly symmetrical mesokurtic distribution and similarly in the another BC_2F_3 progeny (CAUM66β$^+$ × DBT16 – 3 – 5 – 16 – 29 – 17), tassel length displayed, which aligns with the previous observations reported by Saha *et al.* (2022) in tassel length and Rathinavel *et al.* (2022) in cob girth. In contrast, in both the population (BC_2F_2 and BC_2F_3), several traits exhibited negative skewness, suggesting left-tailed distributions with values skewed toward the higher end.

Regarding kurtosis, in BC_2F_2 population, number of tassel branches and cob girth, and in of progeny BC_2F_3 (CAUM66β$^+$ × DBT16 – 7 – 25 – 5 – 15 – 14), leaf length exhibited leptokurtic distributions, characterized by sharper peaks and heavier tails, which indicated these traits were controlled by few genes and responds well to the directional selection. On the contrary, all the other traits demonstrated platykurtic distributions which indicates these traits are polygenic and exhibits wide variability which is desirable for selection in segregating populations. These experimental findings are in similar agreement with the previous reports given by Monisha *et al.* (2023) and Abikkumar *et al.* (2023) in BC_2F_2 and BC_2F_3 populations respectively. In another BC_2F_3 progeny (CAUM66β$^+$ × DBT16 – 3 – 5 – 16 – 29 – 17), all studied traits demonstrated only platykurtic distributions.

In both the BC_2F_2 and BC_2F_3 populations, variability studies revealed moderate to lower GCV and PCV estimates, as presence of moderate to lesser genetic variation due to selection across traits. And estimates of PCV was higher than GCV for all the traits studied in both the populations, revealing influence of environment. Similar findings were also has been reported by Abikkumar *et al.* (2023) and Natesan *et al.* (2023). In BC_2F_2 population, single plant yield had moderate heritability and in contrast Iman (2022) and Krishnakumar (2022) reported high heritability for this trait in BC_2F_2 populations. Tassel length, cob length, leaf breadth and cob girth has found having higher to moderate GAM indicating a greater potential for improvement through selection. These outcomes are in accordance with the insights reported by Niji *et al.* (2018) and Abikkumar *et al.* (2023).

Among the 14 traits studied in BC_2F_2 and BC_2F_3, cob length exhibited high PCV and GCV estimates, along with higher genetic advance as percent of mean (GAM) and heritability (h^2), which indicates that the additive gene action was found to be predominant and a wide scope for rapid genetic gains in selection (Panse, 1957).

Foreground screening confirmed the presence of the favourable β-carotene allele in all plants, indicating meticulous execution of backcrossing and selfing procedures throughout the experiment. The selected improved lines of BC_2F_3 exhibited a higher TSS percentage, consistent with the findings of Krishnakumar (2022) and Rathinavel *et al.* (2023). However, the phenotypic similarity to the recurrent parent was comparatively low, likely due to the absence of background selection using SSR markers in the BC_1F_1 and BC_2F_1 generations. Alternatively, Jha *et al.* (2019) found a higher level of phenotypic resemblance in their investigation.

CONCLUSION

Based on the experimental findings, four lines from the progeny CAUM66β$^+$ × DBT16 – 7 – 25 – 5 – 15 – 14 *viz.*, CAUM66β$^+$ × DBT16 – 7 – 25 – 5 – 15 – 14 – 12, CAUM66β$^+$ × DBT16 – 7 – 25 – 5 – 15 – 14 – 27, CAUM66β$^+$ × DBT16 – 7 – 25 – 5 – 15 – 14 – 64 and CAUM66β$^+$ × DBT16 – 7 – 25 – 5 – 15 – 14 – 65 and along with four lines from the progeny CAUM66β$^+$ × DBT16 – 3 – 5 – 16 – 29 – 17 *viz.*, CAUM66β$^+$ × DBT16 – 3 – 5 – 16 – 29 – 17 – 20, CAUM66β$^+$ × DBT16 – 3 – 5 – 16 – 29 – 17 – 30, CAUM66β$^+$ × DBT16 – 3 – 5 – 16 – 29 – 17 – 41 and CAUM66β$^+$ × DBT16 – 3 – 5 – 16 – 29 – 17 – 49 were identified with high TSS content (18%), approximately 81% phenotypic similarity to the recurrent parent and confirmed presence of the β-carotene allele. These selected lines hold potential for use in future sweet corn biofortification programmes.

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