

RESEARCH ARTICLE

Evaluation of beta-carotene-enriched sweet corn inbreds for yield, quality and nutritional traits across diverse environmental conditions

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ABSTRACT

Sweet corn (*Zea mays* var. *saccharata* L.) is an important vegetable crop valued for its sweetness, tenderness, and nutritional quality. Biofortification with beta-carotene offers an effective strategy to alleviate vitamin A deficiency while maintaining desirable agronomic performance. The present investigation was undertaken to evaluate the performance of eight beta-carotene-rich sweet corn inbred lines across three locations, namely Coimbatore, Vagarai, and Bhavanisagar, during the Rabi 2023 and Summer 2024 seasons. The experiment was conducted in a randomized complete block design with three replications, and observations were recorded on days to tasselling, days to silking, plant height, cob length, cob width, number of kernel rows per cob, number of kernels per row per cob, green cob yield, total soluble solids, and beta-carotene content. Combined analysis of variance revealed significant ($P < 0.01$) differences among genotypes and genotype $\times$ environment interactions for all the studied traits, indicating the existence of substantial genetic variability and differential environmental response. Across seasons and locations, DBT 26 $\beta+$ recorded the highest green cob yield (169.00 – 191.00 g) and consistently maintained high total soluble solids indicating its superior yield potential and eating quality. The genotypes DBT 18 $\beta+$ (10.50-11.80 $\mu\text{g g}^{-1}$) as well as DBT 25 $\beta+$ (10.00 -10.80 $\mu\text{g g}^{-1}$) exhibited higher beta-carotene content. The substantial variability observed among the evaluated genotypes for yield, quality, and nutritional traits demonstrates considerable scope for genetic improvement through selection. DBT 18 $\beta+$ DBT 25 $\beta+$ and DBT 26 $\beta+$ emerged as promising genetic resources for the development of high-yielding, beta-carotene-rich sweet corn cultivars with broad adaptation across diverse environments.

Keywords: Sweet corn; beta-carotene biofortification; mean performance; locations

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1. INTRODUCTION

Sweet corn (*Zea mays* var. *saccharata* L.) is an economically important vegetable crop valued for its tender kernels, pleasant sweetness and nutritional quality. Unlike field maize, sweet corn is harvested at the milk stage, when kernels contain high concentrations of sugars and moisture, making it highly preferred for fresh consumption and processing industries. The increasing demand for healthy foods and functional crops has led to a rapid expansion of sweet corn cultivation worldwide. In India, sweet corn has emerged as a profitable crop owing to its short duration, high market value, and growing consumer preference for nutritious vegetables (Tracy, 2001; Lertrat and Pulam, 2007). Sweetcorn also holds an important place in the export potential among the agricultural products. Micronutrient malnutrition commonly referred to as “hidden hunger,” affects more than two billion people worldwide especially in low- and middle-income countries where cereal-based diets predominate. Vitamin A deficiency remains one of the important form of micronutrient deficiency leads to impaired vision, weakened immunity, increased susceptibility to infections, and childhood mortality. However, these deficiencies can be eliminated through properly channeled biofortification programmes. In this case, maize and sweetcorn biofortification with vitamin A, has emerged as a sustainable and cost-effective strategy for addressing micronutrient deficiencies through the development of nutrient-dense crop varieties using conventional breeding, agronomic approaches, and modern biotechnology (Bouis and Saltzman, 2017; Li *et al.*, 2024).

Among the provitamin-A carotenoids, beta-carotene is the most important because it serves as a direct precursor of vitamin A in humans. Maize kernels naturally accumulate carotenoids, including beta-carotene, lutein, zeaxanthin, and β -cryptoxanthin. Considerable genetic variability for carotenoid concentration and composition has been reported in diverse maize germplasm, facilitating the development of provitamin-A-rich cultivars through biofortification programmes (Harjes *et al.*, 2008; Yan *et al.*, 2010). Furthermore, advances in molecular breeding, genomic prediction and marker-assisted selection have accelerated the enhancement of beta-carotene content in maize, making it an important crop for addressing vitamin A deficiency in developing countries (Menkir *et al.*, 2025). In comparison of maize and

sweetcorn biofortification, the maize which undergoes a number of processing and cooking after harvest leads to the losses in the beta-carotene due to degradation, contrasting with the sweetcorn which is consumed fresh and therefore higher beta-carotene retention.

The development of beta-carotene-enriched sweet corn varieties can therefore contribute significantly to improving nutritional security while maintaining consumer-preferred quality. Carotenoid accumulation in maize kernels is regulated by several genes involved in the carotenoid biosynthetic pathway. Among these, lycopene epsilon cyclase (*lcyE*) and beta-carotene hydroxylase 1 (*crtRB1*) are key genes controlling the partitioning and accumulation of provitamin-A carotenoids in maize endosperm. Favorable alleles of *lcyE* redirect metabolic flux toward the beta-carotene branch of the pathway, while favorable alleles of *crtRB1* reduce beta-carotene hydroxylation, resulting in increased beta-carotene accumulation. These genes have been extensively utilized in marker-assisted breeding and biofortification programmes for developing provitamin-A-rich maize cultivars. Furthermore, studies on biofortified sweet corn have demonstrated that reduced expression of *crtRB1* is associated with significantly higher beta-carotene and total provitamin-A concentrations during kernel development, confirming its importance in nutritional enhancement strategies (Babu *et al.*, 2013).

The effectiveness of crop improvement programme depends largely on the availability and utilization of genetic variability. Evaluation of germplasm for flowering traits, plant architecture, cob characteristics, yield components and quality parameters is essential for identifying superior genotypes and potential donor parents. Traits such as days to tasselling, days to silking, plant height, cob length, cob width, kernel row number, kernels per row, green cob yield, total soluble solids, and beta-carotene content directly influence productivity, marketability, and nutritional quality in sweet corn (Rajasekar *et al.*, 2024; Khomphet, 2025). Genotype performance is often influenced by environmental factors, resulting in genotype $\times$ environment (G $\times$ E) interactions. Consequently, the evaluation of breeding materials across diverse environments is necessary to identify stable and widely adapted genotypes. Multi-location testing provides valuable information on adaptability, performance stability, and suitability of genotypes for commercial

cultivation under varying agro-climatic conditions. Multi-environment trials (METs) enable breeders to quantify G×E interactions and identify genotypes with either broad or specific adaptation, thereby improving selection efficiency and cultivar recommendation (Yan and Tinker, 2006; Pour-Aboughadareh et al., 2022).

In the present study, eight beta-carotene-enriched sweet corn inbreds were evaluated across three locations during Rabi 2023 and Summer 2024 seasons to assess their performance for morphological, yield, and quality traits. The study aimed to identify superior genotypes combining high green cob yield, enhanced sweetness, and elevated beta-carotene content for use in sweet corn improvement programmes and nutritional biofortification initiatives.

2. MATERIALS AND METHODS

2.1 Plant materials

Eight beta-carotene-enriched sweet corn (*Zea mays* L. var. *saccharata*) inbred lines, namely DBT 15 β+, DBT 16 β+, DBT 17 β+, DBT 18 β+, DBT 23 β+, DBT 24 β+, DBT 25 β+, and DBT 26 β+, developed in Centre for Plant Molecular Biology and Biotechnology, Tamil Nadu Agricultural University, Coimbatore were used in the present study. The inbred lines were selected based on their genetic diversity for agronomic performance and provitamin-A content and represented advanced breeding materials targeted for sweet corn biofortification (Figure 1). The parentage and pedigree of the inbred lines are give below

Inbred line	Parentage	Pedigree of line
DBT15 β+	USC1-2-3-1 × UMI1230β+	DBT15-1-15-3-12-11
DBT16 β+	SC1107 × UMI1230β+	DBT16-1-11-22-7-9
DBT17 β+	SC11-2 × UMI1230β+	DBT17-1-1-1-35-1
DBT18 β+	SC 12039-1 × UMI1230β+	DBT18-1-18-5-4-7
DBT23 β+	SCM-se-O-1 × DBT17	DBT23-7-3-2-5-8
DBT24 β+	SCM-se-Y-1 × UMI1230β+	DBT24-1-7-15-12-28
DBT25 β+	SCM-sh-Y-2 × DBT17	DBT25-4-7-34-4-22
DBT26 β+	DBT16 × CAUM66β+	DBT26-1-2-1-42-7

2.2 Experimental sites

The multi-environment evaluation was conducted

during the Rabi 2023 and Summer seasons of 2024 at three experimental locations representing contrasting agro-ecological conditions of Tamil Nadu, India: Coimbatore, Vagarai, and Bhavanisagar.

2.3 Experimental design and crop management

Field experiments at each location were established using a randomized complete block design (RCBD) with three replications. Each genotype was grown in a single-row plot following the recommended spacing of 60 cm between rows and 20 cm between plants. Standard agronomic practices recommended by Tamil Nadu Agricultural University for sweet corn cultivation were uniformly adopted across all experimental sites. Fertilizer application, irrigation scheduling, weed management and plant protection measures were implemented following the regional package of practices to ensure optimal crop growth throughout the growing period.

2.4 Phenotypic evaluation

Phenotypic observations were recorded from five randomly selected competitive plants within each experimental plot. The following agronomic and quality traits were evaluated. Days to tasselling (DT) and days to silking (DS) were recorded as the number of days from sowing until 50% of plants in a plot exhibited tassel emergence and silk emergence, respectively. Plant height (PH; cm) was measured from the soil surface to the tip of the tassel at physiological maturity. Cob length (CL; cm) was measured on dehusked cobs from the base to the apex, while cob width (CW; cm) was determined at the midpoint using a digital Vernier caliper. Kernel rows per cob (NKR) were counted manually, and kernels per row per cob (NKRC) were determined from the central row of each representative cob. Green cob yield (GCY; g cob⁻¹) was recorded as the fresh weight of marketable cobs harvested at the milk stage.

2.5 Beta-carotene estimation

The beta-carotene estimation protocol of Galicia et al. (2009) improved Kurilich and Juvik (1999) beta-carotene estimation was used. Samples were collected at 24 days to pollination (DAP), which is the consumption stage of sweetcorn. Freshly harvested sweet corn kernels cannot be processed like maize kernels due to its higher moisture and therefore, before powdering, a light-sealed vacuum desiccator was used to dry kernels for 48 hours. Extract of 600



Figure. 1. Representative ears of eight beta-carotene-enriched sweet inbred lines (DBT 15 β^+ , DBT 16 β^+ , DBT 17 β^+ , DBT 18 β^+ , DBT 23 β^+ , DBT 24 β^+ , DBT 25 β^+ , and DBT 26 β^+).

mg powder and 6 mL 0.1% butylated hydroxytoluene in mixed in ethanol. The tubes are vortexed and added with 120 μ L 80% KOH at 85 °C. Each stage of hexane extraction was centrifuged at 3,000 rpm for 10 mins and supernatants were collected and pooled. For HPLC analysis, the combined hexane fractions were dried under nitrogen and resuspended in 45:20:35 acetonitrile, methanol, and methylene chloride. An 80:10:10 mobile phase comprising acetonitrile, methanol, and ethyl acetate eluted samples at 1 mL/min on a C18G 120A column. The standard curve for beta-carotene (0.1-100 μ g/g) was established by detecting samples at 450 nm.

2.6. Statistical analysis

Trait data from all environments were subjected to individual and combined analyses of variance using R statistical software (R Core Team, 2024). In the combined analysis, genotype (G), environment (E), and genotype $\times$ environment interaction (G $\times$ E) were considered fixed effects, whereas replication was nested within environments. Mean separation was performed using the appropriate post hoc test at the 5% probability level where treatment effects were significant. Trait means are presented as mean $\pm$ standard deviation. Heat maps were generated using standardized trait values

(Z-scores) to facilitate comparative visualization of genotype performance across traits. Data visualization was performed using the Complex Heatmap and ggplot2 packages in R.

3. RESULTS AND DISCUSSION

3.1. Analysis of variance

The analysis of variance (ANOVA) for morphological, yield and quality traits of beta-carotene-enriched sweet corn genotypes evaluated across three locations during the Rabi 2023 and Summer 2024 seasons is presented in Tables 1 and 2. The ANOVA revealed highly significant differences among genotypes for all the traits studied, namely days to tasselling, days to silking, plant height, cob length, cob width, number of kernel rows per cob, number of kernels per row per cob, green cob yield, total soluble solids and beta-carotene. The significant genotypic variation observed for these traits indicates the existence of substantial genetic variability among the evaluated sweet corn genotypes, thereby providing ample scope for selection and genetic improvement.

The environmental effects were comparatively lower than genotypic effects for most traits, indicating that the expression of these traits was predominantly governed by genetic factors. For instance, the mean squares for genotypes were substantially larger than those for environments for traits like PH (23977.98 vs. 761.58), NKR (790.10 vs. 8.73), and GCY (58342.24 vs. 658.69) during both seasons. This suggests that while the environment does influence these traits, the genetic makeup of the genotypes plays a more dominant role in their trait expression. A similar trend was observed for quality traits like TSS and beta-carotene, where genotypic mean squares (123.38 and 14.809, respectively) were considerably higher than environmental mean squares (7.492 and 0.232), reinforcing the strong genetic control over these nutritional parameters. The genotype $\times$ environment ($G \times E$) interaction was highly significant for all the studied traits during both seasons. The significant interaction indicates that the relative performance of genotypes varied across locations, suggesting differential adaptability and stability of genotypes under varying environmental conditions. Such interactions are commonly observed in sweet corn and other maize types due to their sensitivity to environmental fluctuations. The presence of significant $G \times E$ interaction highlights the importance of multi-location evaluation for identifying stable and widely

adapted genotypes. The significant $G \times E$ mean squares for GCY (272.23) and beta-carotene (1.208) indicate that the ranking of genotypes for these economically important traits would likely change depending on the growing location, necessitating careful selection.

Therefore, selection of superior genotypes should be based on performance across multiple environments to identify stable, high-yielding, and nutritionally enriched sweet corn cultivars suitable for commercial cultivation. Similar observations of significant genetic variability for agronomic and quality traits in maize have been reported by Hallauer *et al.* (2010) and Beyene *et al.* (2016).

3.2. Mean performance beta-carotene rich sweet corn inbreds during Rabi 2023 and Summer 2024 in different locations

The mean performance of eight beta-carotene-enriched sweet corn genotypes evaluated across three locations during Rabi 2023 and summer 2024 revealed substantial variability for flowering, morphological, yield, and quality traits (Table 3 and 4; Figure 2).

3.2.1. Flowering traits

Days to Tasselling (DT) and Days to Silking (DS)

During the Rabi 2023 season, significant variation was observed among the evaluated sweet corn genotypes for flowering traits. The earliest flowering was recorded in DBT 15 β +, which exhibited the lowest days to tasselling (47.50 days) and days to silking (49.50 days) at Vagarai, whereas DBT 16 β + flowered significantly later, recording the highest days to tasselling (58.70 days) and days to silking (62.00 days) at Bhavanisagar. A similar trend was observed during the Summer 2024 season, where DBT 15 β + remained the earliest flowering genotype, recording the minimum days to tasselling (49.5 days) and days to silking (51.4 days) at Vagarai, whereas DBT 16 β + exhibited the latest flowering, with 63.9 days to tasselling and 65.9 days to silking at Bhavanisagar. The anthesis-silking interval (ASI) across genotypes ranged from 2.0 to 5.0 days during Rabi and 2.0 to 4.0 days during Summer, with DBT 15 β + consistently showing the shortest ASI (2.0 days at all locations), indicating better synchrony between male and female flowering. Earliness is an important breeding objective in sweet corn because it facilitates crop intensification and enables plants to escape terminal moisture stress. The considerable variation

Table 1. Analysis of variance for morphological, yield and quality traits of beta-carotene-enriched sweet corn genotypes evaluated across three locations during Rabi 2023

Source of variation	DF	DT	DS	PH	CL	CW	NKR	NKRC	GCY	TSS	BC
Replication	2	0.129	9.148	4.989	0.674	0.116	0.267	0.076	12.894	0.27	0.105
Genotypes	7	355.50**	531.169**	23977.98**	167.069**	56.679**	790.100**	425.88**	58342.240**	123.38**	14.809**
Environment	2	76.997	94.552	761.582	6.632	6.070	8.732	10.87	658.69	7.492	0.232
Genotype × Environment	14	30.502**	40.868**	104.097**	3.687**	6.070**	5.027**	1.47**	272.23**	0.948**	1.208**
Error	46	94.047	77.295	764.466	7.927	5.035	11.334	13.289	1149.253	8.062	3.47

Table 2. Analysis of variance for morphological, yield and quality traits of beta-carotene-enriched sweet corn genotypes evaluated across three locations during summer 2024

Source of Variation	DF	DT	DS	PH	CL	CW	NKR	NKRC	GCY	TSS	BC
Replications	2	0.129	9.148	4.989	0.674	0.116	0.267	0.076	12.894	0.27	0.105
Genotypes	7	355.500**	531.169**	23977.980**	167.069**	56.679**	790.100**	425.88**	58342.24**	123.38**	14.809**
Environment	2	76.997	94.552	761.582	6.632	6.07	8.732	10.87	658.69	7.492	0.232
Genotype × Environment	14	30.502**	40.868**	104.097**	3.687**	6.07**	5.027**	1.47**	272.23**	0.948**	1.208**
Error	48	94.047	77.295	764.466	7.927	5.035	11.334	13.289	1149.253	8.062	3.47

DT – Days to tasselling

DS – Days to silking

PH – plant height (cm)

CL – cob length (cm)

CW – cob width (cm)

NKR – Number of kernel rows per cob

NKRC – Number of kernel per row per cob

GCY – Green Cob Yield (g)

TSS - Total soluble solids (° Brix)

BC – Beta-carotene Content (µg g⁻¹)

* significance @ 5 % level of significance

** significance @ 1 % level of significance

observed for flowering traits, with a difference of approximately 11 days between the earliest and latest genotypes for tasselling, indicates the existence of diverse maturity groups among the evaluated genotypes. The consistent expression of flowering differences across seasons demonstrates the stability of maturity characteristics among the tested genotypes. Similar variability in flowering behaviour and maturity among sweet corn genotypes has been reported by Peixoto *et al.* (2024), Yang *et al.* (2024) and Nguyen *et al.* (2024).

3.2.2. Morphological trait

Plant height

Plant height exhibited considerable variation among the beta-carotene-enriched maize genotypes across seasons and locations. During Rabi 2023, plant height ranged from 110.70 cm in DBT 16 β+ at Vagarai to 181.60 cm in DBT 17 β+ at Bhavanisagar, whereas in Summer 2024, it ranged from 107.7 cm in DBT 16 β+ at Vagarai to 177.2 cm in DBT 17 β+ at Bhavanisagar.

Across both seasons, DBT 17 β+ consistently exhibited the tallest plants, with a mean height of 176.30 cm (Coimbatore, Rabi) and 172.00 cm (Coimbatore, Summer), while DBT 16 β+ remained the shortest, recording 114.10 cm and 111.00 cm at the same location, indicating distinct genetic differences in vegetative growth. The greater plant height observed in DBT 17 β+ may be attributed to enhanced vegetative vigour and biomass accumulation, whereas the shorter stature of DBT 16 β+ reflects comparatively lower vegetative growth potential. The reduction in plant height from Rabi to Summer for most genotypes (e.g., DBT 17 β+ at Coimbatore: 176.30 cm to 172.00 cm; DBT 15 β+: 143.20 cm to 140.50 cm; DBT 26 β+: 172.00 cm to 160.20 cm) suggests a marginal environmental influence, with summer temperatures potentially limiting vegetative extension. The substantial variation in plant height among the evaluated genotypes suggests the combined influence of genetic diversity and environmental adaptation. Similar variability in plant height among maize and sweet corn genotypes has been reported by Revilla *et al.* (2002),

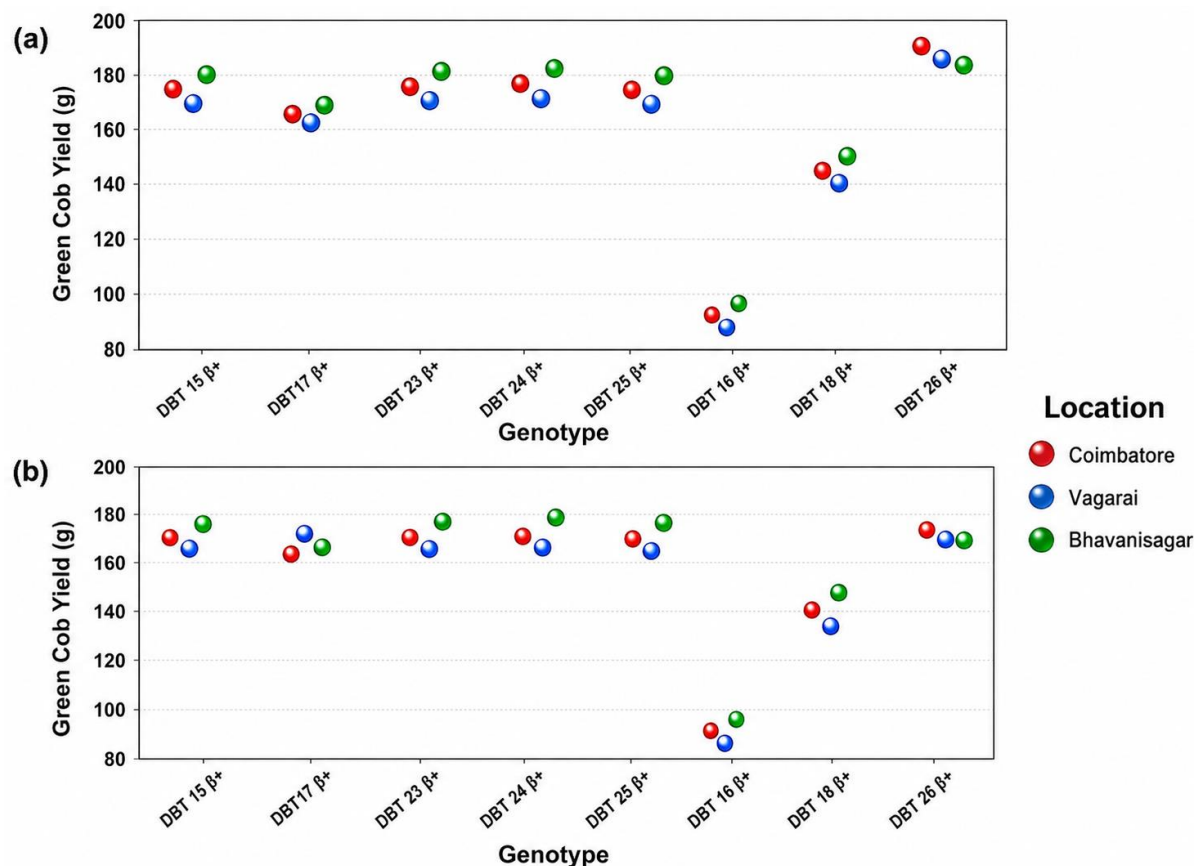


Figure 2. Green cob yield of beta-carotene-enriched sweet corn genotypes in a) Rabi 2023 and b) Summer 2024.

Table 3. Mean performance of morphological and quality traits in sweet corn genotypes during Rabi 2023 season in three locations

S.No	Genotypes	Location	DT	DS	PH	CL	CW	NKR	NKRC	GCY	TSS	BC
1	DBT 15 β+	Coimbatore	49.00 ± 0.32	51.00 ± 0.22	143.20 ± 2.63	19.70 ± 0.07	13.90 ± 0.28	12.20 ± 0.50	15.00 ± 0.61	175.00 ± 6.36	15.20 ± 0.04	10.50 ± 0.09
		Vagarai	47.50 ± 1.33	49.50 ± 0.22	138.90 ± 6.01	19.10 ± 0.57	13.50 ± 0.15	11.80 ± 0.35	14.60 ± 0.09	169.80 ± 2.60	14.70 ± 0.12	10.20 ± 0.45
		Bhavanisagar	50.50 ± 1.87	52.50 ± 0.80	147.50 ± 0.27	20.30 ± 0.05	14.30 ± 0.18	12.60 ± 0.40	15.50 ± 0.13	180.30 ± 4.88	15.70 ± 0.23	10.50 ± 0.18
2	DBT17 β+	Coimbatore	54.00 ± 0.05	56.00 ± 0.50	176.30 ± 6.36	15.80 ± 0.36	11.80 ± 0.16	12.20 ± 0.15	14.50 ± 0.50	166.00 ± 5.84	13.20 ± 0.54	10.20 ± 0.41
		Vagarai	52.40 ± 2.22	54.30 ± 0.34	171.00 ± 0.92	15.50 ± 0.38	13.50 ± 0.10	12.80 ± 0.37	14.10 ± 0.56	163.40 ± 6.33	12.80 ± 0.57	10.40 ± 0.34
		Bhavanisagar	55.60 ± 1.10	57.70 ± 0.68	181.60 ± 5.07	15.10 ± 0.48	13.40 ± 0.06	12.50 ± 0.30	14.90 ± 0.43	168.60 ± 1.22	13.60 ± 0.32	10.50 ± 0.37
3	DBT 23 β+	Coimbatore	54.00 ± 0.05	59.00 ± 2.34	161.30 ± 0.58	17.40 ± 0.33	15.40 ± 0.68	11.30 ± 0.59	18.20 ± 0.46	176.00 ± 5.87	15.00 ± 0.32	10.40 ± 0.08
		Vagarai	52.40 ± 1.37	57.20 ± 2.27	156.50 ± 5.08	16.90 ± 0.47	14.90 ± 0.09	11.80 ± 0.58	17.70 ± 0.41	170.70 ± 6.00	14.60 ± 0.12	10.40 ± 0.18
		Bhavanisagar	55.60 ± 1.05	60.80 ± 2.69	166.10 ± 0.45	17.90 ± 0.79	15.90 ± 0.20	11.80 ± 0.35	18.80 ± 0.83	181.30 ± 7.68	15.50 ± 0.63	10.60 ± 0.19
4	DBT 24 β+	Coimbatore	52.00 ± 2.20	55.00 ± 0.20	142.90 ± 1.16	18.30 ± 0.18	14.00 ± 0.14	12.30 ± 0.24	17.80 ± 0.53	177.00 ± 6.22	14.80 ± 0.15	10.00 ± 0.44
		Vagarai	50.40 ± 1.09	53.40 ± 0.58	138.60 ± 2.25	17.80 ± 0.14	13.60 ± 0.49	11.80 ± 0.21	17.30 ± 0.06	171.70 ± 2.63	14.40 ± 0.36	9.80 ± 0.25
		Bhavanisagar	53.60 ± 0.48	56.70 ± 0.20	147.20 ± 0.66	18.90 ± 0.32	14.40 ± 0.39	12.80 ± 0.35	18.30 ± 0.56	182.30 ± 0.99	15.20 ± 0.42	10.20 ± 0.07
5	DBT 25 β+	Coimbatore	53.00 ± 1.39	55.00 ± 0.30	158.20 ± 5.70	15.70 ± 0.57	13.60 ± 0.21	12.00 ± 0.23	16.00 ± 0.55	175.00 ± 0.95	14.50 ± 0.60	10.80 ± 0.18
		Vagarai	51.40 ± 1.39	53.40 ± 2.07	153.50 ± 3.32	15.20 ± 0.11	13.20 ± 0.12	12.60 ± 0.55	15.50 ± 0.45	169.80 ± 5.36	14.10 ± 0.28	10.70 ± 0.04
		Bhavanisagar	54.60 ± 0.98	56.70 ± 0.41	163.00 ± 5.14	16.20 ± 0.00	14.00 ± 0.08	12.40 ± 0.09	16.50 ± 0.09	180.30 ± 7.31	14.90 ± 0.44	10.40 ± 0.17
6	DBT 16 β+	Coimbatore	57.00 ± 0.98	62.00 ± 1.23	114.10 ± 0.51	14.80 ± 0.52	12.80 ± 0.12	11.70 ± 0.80	20.50 ± 0.65	93.00 ± 0.34	14.80 ± 0.52	10.40 ± 0.12
		Vagarai	55.30 ± 2.09	57.10 ± 2.47	110.70 ± 1.10	14.40 ± 0.22	12.40 ± 0.32	11.10 ± 0.83	19.90 ± 0.70	90.20 ± 0.16	14.40 ± 0.36	10.60 ± 0.22
		Bhavanisagar	58.70 ± 1.32	60.90 ± 1.48	117.50 ± 1.59	15.20 ± 0.33	13.20 ± 0.52	12.30 ± 0.04	21.10 ± 0.86	95.80 ± 4.06	15.20 ± 0.36	10.70 ± 0.46
7	DBT 18 β+	Coimbatore	51.00 ± 1.10	53.00 ± 2.15	151.50 ± 1.78	16.90 ± 0.56	14.00 ± 0.01	12.50 ± 0.57	22.00 ± 0.63	145.00 ± 5.88	15.50 ± 0.18	11.70 ± 0.42
		Vagarai	50.50 ± 0.41	52.40 ± 0.38	147.00 ± 5.70	16.40 ± 0.43	13.60 ± 0.49	11.50 ± 0.79	21.30 ± 0.04	140.70 ± 5.33	15.00 ± 0.01	11.40 ± 0.01
		Bhavanisagar	52.50 ± 2.22	54.60 ± 0.84	156.10 ± 4.36	17.40 ± 0.64	14.40 ± 0.58	13.50 ± 0.47	22.70 ± 0.61	149.40 ± 4.71	16.00 ± 0.63	11.80 ± 0.37
8	DBT 26 β+	Coimbatore	55.60 ± 1.95	57.70 ± 1.72	172.00 ± 7.60	17.80 ± 0.74	15.00 ± 0.19	13.40 ± 0.72	16.80 ± 0.61	191.00 ± 4.99	17.90 ± 0.74	10.40 ± 0.07
		Vagarai	54.20 ± 1.61	56.50 ± 0.25	169.70 ± 7.34	17.50 ± 0.30	15.20 ± 0.42	13.30 ± 0.73	17.00 ± 0.49	187.30 ± 6.92	18.20 ± 0.38	10.20 ± 0.05
		Bhavanisagar	53.20 ± 1.29	55.90 ± 0.76	170.60 ± 1.08	17.70 ± 0.22	15.50 ± 0.48	12.60 ± 0.27	17.20 ± 0.57	184.60 ± 0.83	18.40 ± 0.50	10.10 ± 0.35

DT – Days to tasselling

DS – Days to silking

PH – plant height (cm)

CL – cob length (cm)

CW – cob width (cm)

NKR – Number of kernel rows per cob

NKRC – Number of kernel per row per cob

GCY – Green Cob Yield (g)

TSS - Total soluble solids °Brix

BC – beta-carotene Content (µg g⁻¹)

Table 4. Mean performance of morphological and quality traits in sweet corn genotypes during summer 2024 in three locations

Entry	Genotypes	Location	DT	DS	PH	CL	CW	NKR	NKRC	GCY	TSS	BC
1	DBT 15 β+	Coimbatore	51.0 ± 2.12	53.0 ± 1.17	140.5 ± 1.89	19.1 ± 0.66	13.5 ± 0.43	11.8 ± 0.02	14.2 ± 0.54	169.0 ± 4.27	14.4 ± 0.33	10.3 ± 0.41
		Vagarai	49.5 ± 0.8	51.4 ± 1.07	136.3 ± 4.42	18.5 ± 0.17	13.1 ± 0.44	11.5 ± 0.12	13.8 ± 0.6	163.9 ± 5.32	14.0 ± 0.57	10.2 ± 0.17
		Bhavanisagar	52.5 ± 2.27	54.6 ± 1.28	144.7 ± 0.91	19.7 ± 0.53	13.9 ± 0.38	12.2 ± 0.44	14.6 ± 0.34	174.1 ± 5.81	14.8 ± 0.19	10.3 ± 0.18
2	DBT17 β+	Coimbatore	56.0 ± 1.87	58.0 ± 0.78	172.0 ± 1.4	15.4 ± 0.42	12.5 ± 0.21	10.8 ± 0.57	14.0 ± 0.06	162.0 ± 5.84	14.9 ± 0.17	10.1 ± 0.05
		Vagarai	54.3 ± 0.2	56.3 ± 0.51	166.8 ± 5.11	15.1 ± 0.63	13.3 ± 0.25	10.5 ± 0.5	14.6 ± 0.59	169.5 ± 5.35	13.5 ± 0.02	10.4 ± 0.41
		Bhavanisagar	57.7 ± 2.55	59.7 ± 2.58	177.2 ± 7.19	15.7 ± 0.04	12.8 ± 0.03	10.1 ± 0.12	14.4 ± 0.6	164.5 ± 5.78	14.3 ± 0.05	10.2 ± 0.16
3	DBT 25 β+	Coimbatore	55.0 ± 1.04	57.0 ± 0.98	155.0 ± 6.29	15.3 ± 0.34	13.3 ± 0.37	11.5 ± 0.37	15.2 ± 0.18	168.0 ± 5.0	13.8 ± 0.39	10.2 ± 0.45
		Vagarai	53.4 ± 0.91	55.3 ± 0.95	150.4 ± 3.39	14.8 ± 0.36	12.9 ± 0.28	11.1 ± 0.18	14.7 ± 0.34	163.0 ± 5.73	13.4 ± 0.57	10.0 ± 0.3
		Bhavanisagar	56.7 ± 0.92	58.7 ± 1.85	159.7 ± 6.05	15.8 ± 0.16	13.7 ± 0.11	11.9 ± 0.45	15.7 ± 0.58	173.0 ± 0.16	14.2 ± 0.2	10.1 ± 0.36
4	DBT 23 β+	Coimbatore	59.0 ± 2.02	61.0 ± 1.65	158.0 ± 0.43	16.9 ± 0.02	15.0 ± 0.03	12.8 ± 0.3	17.5 ± 0.17	170.0 ± 6.59	14.2 ± 0.09	9.8 ± 0.32
		Vagarai	57.2 ± 1.5	59.2 ± 2.35	153.3 ± 1.38	16.4 ± 0.3	14.6 ± 0.39	12.3 ± 0.15	17.0 ± 0.28	164.9 ± 3.27	13.8 ± 0.52	9.8 ± 0.36
		Bhavanisagar	60.8 ± 0.71	62.8 ± 0.85	162.7 ± 0.0	17.4 ± 0.09	15.5 ± 0.2	12.3 ± 0.4	18.0 ± 0.49	175.1 ± 4.89	14.6 ± 0.45	9.9 ± 0.09
5	DBT 24 β+	Coimbatore	55.0 ± 1.74	57.0 ± 1.54	139.5 ± 2.77	17.8 ± 0.05	13.6 ± 0.07	12.7 ± 0.2	17.0 ± 0.6	169.0 ± 0.91	14.0 ± 0.47	9.8 ± 0.15
		Vagarai	53.4 ± 1.49	55.3 ± 0.55	135.3 ± 2.44	17.3 ± 0.31	13.2 ± 0.02	13.2 ± 0.33	16.5 ± 0.51	163.9 ± 5.32	13.6 ± 0.42	9.5 ± 0.17
		Bhavanisagar	56.7 ± 0.46	58.7 ± 0.16	143.7 ± 4.02	18.3 ± 0.16	14.0 ± 0.5	13.2 ± 0.44	17.5 ± 0.03	174.1 ± 4.08	14.4 ± 0.51	9.9 ± 0.26
6	DBT 16 β+	Coimbatore	62.0 ± 0.0	64.0 ± 0.98	111.0 ± 4.1	14.2 ± 0.54	12.4 ± 0.47	11.0 ± 0.29	19.8 ± 0.41	89.0 ± 2.17	14.0 ± 0.18	10.2 ± 0.05
		Vagarai	60.1 ± 2.49	62.1 ± 1.96	107.7 ± 0.68	13.8 ± 0.61	12.0 ± 0.14	11.4 ± 0.58	19.2 ± 0.73	86.3 ± 3.58	13.6 ± 0.48	10.1 ± 0.36
		Bhavanisagar	63.9 ± 1.9	65.9 ± 0.24	114.3 ± 0.41	14.6 ± 0.57	12.8 ± 0.4	11.6 ± 0.51	20.4 ± 0.13	91.7 ± 0.41	14.4 ± 0.19	10.2 ± 0.31
7	DBT 18 β+	Coimbatore	53.0 ± 1.19	55.0 ± 1.44	148.0 ± 6.4	16.3 ± 0.71	13.6 ± 0.05	12.2 ± 0.21	21.0 ± 0.11	139.0 ± 0.88	14.7 ± 0.21	10.5 ± 0.46
		Vagarai	51.4 ± 1.16	53.4 ± 1.68	143.6 ± 4.53	15.8 ± 0.3	13.2 ± 0.51	11.3 ± 0.31	20.4 ± 0.66	134.8 ± 3.28	14.3 ± 0.19	10.2 ± 0.37
		Bhavanisagar	54.6 ± 0.59	56.7 ± 0.46	152.4 ± 3.02	16.8 ± 0.51	14.0 ± 0.42	12.1 ± 0.7	21.6 ± 0.74	143.2 ± 2.19	15.1 ± 0.04	10.8 ± 0.23
8	DBT 26 β+	Coimbatore	56.0 ± 0.45	58.0 ± 0.42	160.2 ± 4.33	17.3 ± 0.42	14.3 ± 0.52	10.5 ± 0.16	19.2 ± 0.57	172.0 ± 0.62	14.8 ± 0.53	10.9 ± 0.06
		Vagarai	54.0 ± 1.27	56.0 ± 1.77	157.7 ± 3.41	17.9 ± 0.44	14.5 ± 0.26	10.8 ± 0.4	19.9 ± 0.09	169.0 ± 3.05	14.6 ± 0.42	10.6 ± 0.11
		Bhavanisagar	57.0 ± 0.77	55.0 ± 0.69	156.5 ± 0.85	17.4 ± 0.36	14.7 ± 0.6	10.9 ± 0.58	19.6 ± 0.6	170.0 ± 2.15	14.5 ± 0.55	10.7 ± 0.11

DT – Days to tasselling

DS – Days to silking

PH – plant height (cm)

CL – cob length (cm)

CW – cob width (cm)

NKR – Number of kernel rows per cob

NKRC – Number of kernel per row per cob

GCY – Green Cob Yield (g)

TSS - Total soluble solids °Brix

BC – beta-carotene Content (µg g⁻¹)

Hallauer *et al.* (2010), Muthusamy *et al.* (2015) and Prasanna *et al.* (2020), who demonstrated that plant height is strongly influenced by both genotype and growing environment. Furthermore, Beyene *et al.* (2016) reported considerable genetic variability for plant height among tropical maize germplasm, while Badu-Apraku *et al.* (2020) observed significant differences in plant architecture across multiple environments, emphasizing the importance of multi-location evaluation for identifying stable and high-performing genotypes.

Cob length and Cob width

Cob length and cob width exhibited considerable variation among the beta-carotene-enriched maize genotypes across seasons and locations. During Rabi 2023, cob length ranged from 14.40 cm in DBT 16 $\beta+$ at Vagarai to 20.30 cm in DBT 15 $\beta+$ at Bhavanisagar, while cob width varied from 11.80 cm in DBT 17 $\beta+$ at Coimbatore to 15.90 cm in DBT 23 $\beta+$ at Bhavanisagar. In summer 2024, cob length ranged from 13.8 cm in DBT 16 $\beta+$ at Vagarai to 19.7 cm in DBT 15 $\beta+$ at Bhavanisagar, whereas cob width ranged from 12.0 cm in DBT 16 $\beta+$ at Vagarai to 15.5 cm in DBT 23 $\beta+$ at Bhavanisagar. Among the evaluated genotypes, DBT 15 $\beta+$ consistently produced longer cobs, with mean values of 19.70 cm (Coimbatore, Rabi), 19.10 cm (Vagarai, Rabi), and 20.30 cm (Bhavanisagar, Rabi), while DBT 23 $\beta+$ recorded the greatest cob width across locations, with values ranging from 15.40 cm to 15.90 cm during Rabi and 15.00 cm to 15.50 cm during Summer. The consistency of DBT 23 $\beta+$ for cob width (15.90 cm at Bhavanisagar in Rabi; 15.50 cm at Bhavanisagar in Summer) and DBT 15 $\beta+$ for cob length (20.30 cm at Bhavanisagar in Rabi; 19.70 cm at Bhavanisagar in Summer) across locations suggests that these traits are under strong genetic control, as also indicated by the ANOVA (Table 1 and 2) where genotypic mean squares for CL (167.069) and CW (56.679) were substantially higher than environmental effects. The larger cob dimensions exhibited by these genotypes indicate greater kernel-bearing capacity and consequently higher green cob yield potential. Considerable variation for cob length and cob width among maize genotypes has been widely reported and is attributed to both genetic diversity and environmental influence. Hallauer *et al.* (2010) reported substantial variability for ear traits in maize and emphasized their importance in yield improvement. Similar differences in cob length and cob width among maize and sweet corn genotypes have been reported by Revilla *et al.*,

Muthusamy *et al.* (2015) and Prasanna *et al.* (2020) observed that these traits are strongly influenced by both genotype and growing environment. Furthermore, Badu-Apraku *et al.* (2020) reported that ear length and ear diameter are major yield contributing traits and significantly influence grain yield across diverse environments.

During Rabi 2023, the number of kernel rows per cob ranged from 11.10 in DBT16 $\beta+$ at Vagarai to 13.40 in DBT26 $\beta+$ at Coimbatore. During Summer 2024, the number of kernel rows per cob varied from 10.10 in DBT17 $\beta+$ at Bhavanisagar to 13.20 in DBT24 $\beta+$ at Vagarai and Bhavanisagar. Among the evaluated genotypes, DBT18 $\beta+$ recorded 12.50, 11.50, and 13.50 kernel rows per cob at Coimbatore, Vagarai, and Bhavanisagar, respectively, during Rabi 2023, while the corresponding values during Summer 2024 were 12.20, 11.30, and 12.10. Minor seasonal variation in kernel row number was observed across the evaluated genotypes, indicating the influence of environmental conditions on trait expression. Overall, the observed variation in kernel row number among the genotypes reflects the existing genetic diversity for this yield-contributing trait. Kernel number per row is one of the principal yield components in sweet corn and directly contributes to green cob yield by increasing sink capacity. The substantial genotypic variation observed in the present study indicates considerable potential for improving productivity through selection for superior ear architecture. Similar findings were reported by Hallauer *et al.* (2010), who emphasized kernel number per ear as a major determinant of maize yield. Likewise, Badu-Apraku *et al.* (2020) reported that kernel number is the most influential yield component determining maize productivity across diverse environmental conditions. Significant variation in kernel number per row among maize genotypes has also been documented by Sharma *et al.* (2022) and Bhattarai *et al.* (2026), who observed that superior-performing hybrids consistently exhibited higher kernel numbers per row and greater yield potential across environments. Furthermore, Chen *et al.* (2021) demonstrated that kernel number per row is strongly associated with grain yield and is governed by several stable genomic regions, highlighting its importance as a key target in maize improvement programmes.

Green Cob Yield

Under Rabi 2023 conditions, green cob yield ranged from 90.20 g in DBT 16

$\beta+$ at Vagarai to 191.00 g in DBT 26 $\beta+$ at Coimbatore. Across the summer 2024 season, green cob yield varied from 86.30 g in DBT 16 $\beta+$ at Vagarai to 175.10 g in DBT 23 $\beta+$ at Bhavanisagar. Among the evaluated genotypes, DBT 23 $\beta+$ and DBT 26 $\beta+$ consistently recorded superior green cob yield across locations, with DBT 26 $\beta+$ showing 191.00 g (Coimbatore, Rabi), 187.30 g (Vagarai, Rabi), and 184.60 g (Bhavanisagar, Rabi), whereas DBT 16 $\beta+$ exhibited the lowest yield in both seasons, with values ranging from 86.30 g to 95.80 g. The enhanced yield performance of DBT 26 $\beta+$ can be attributed to its favourable combination of moderate cob length (17.80 cm), wide cob (15.00 cm), and tall stature (172.00 cm), while DBT 23 $\beta+$ combined good cob length (17.90 cm), the widest cob (15.90 cm), to achieve high yields of 181.30 g at Bhavanisagar. The marked yield reduction observed for DBT 26 $\beta+$ from Rabi to Summer (191.00 g to 172.00 g at Coimbatore; 187.30 g to 169.00 g at Vagarai) and for DBT 23 $\beta+$ (181.30 g to 175.10 g at Bhavanisagar) indicates that summer conditions, possibly higher temperatures, negatively impacted yield potential, confirming the significant G×E interaction observed in the ANOVA (Tables 1 and 2). Green cob yield is a complex quantitative trait governed by the cumulative effects of several yield-contributing characters, and improvements in ear architecture and kernel traits are often reflected in enhanced productivity. Similar findings were reported by Hallauer *et al.* (2010), who demonstrated the importance of ear and kernel traits in determining maize yield. Likewise, Badu-Apraku *et al.* (2020) reported that ear-related traits and kernel characteristics contribute significantly to yield performance across contrasting environments and emphasized that improvements in grain and cob yield are largely achieved through the simultaneous enhancement of yield-contributing traits and the selection of superior genotypes with stable performance. Furthermore, Naji *et al.* (2021) observed a positive association of cob length, cob diameter, and kernel number with fresh cob yield in sweet corn genotypes. Prasanna *et al.* (2020) highlighted that exploiting genetic variability for yield-related traits is fundamental to the development of high-yielding maize hybrids adapted to diverse agro-climatic conditions. More recently, Cairns *et al.* (2023) emphasized that integrating superior yield components with broad environmental adaptation is essential for achieving sustained genetic gains in maize breeding programmes.

3.2.4. Quality traits

Total Soluble Solids

During the Rabi 2023 season, total soluble solids (TSS) ranged from 12.80 °Brix in DBT 17 $\beta+$ at Vagarai to 18.40 °Brix in DBT 26 $\beta+$ at Bhavanisagar. In the summer 2024 evaluation, TSS values varied from 13.40 °Brix in DBT 25 $\beta+$ at Vagarai to 15.10 °Brix in DBT 18 $\beta+$ at Bhavanisagar. Among the evaluated genotypes, DBT 26 $\beta+$ and DBT 18 $\beta+$ consistently recorded higher TSS values across locations, with DBT 26 $\beta+$ showing 17.90 °Brix (Coimbatore, Rabi), 18.20 °Brix (Vagarai, Rabi), and 18.40 °Brix (Bhavanisagar, Rabi), and DBT 18 $\beta+$ recording 15.50 °Brix (Coimbatore, Rabi), 15.00 °Brix (Vagarai, Rabi), and 16.00 °Brix (Bhavanisagar, Rabi), indicating superior sweetness and eating quality. The substantial decline in TSS from Rabi to Summer for most genotypes is noteworthy, with DBT 26 $\beta+$ dropping from 18.40 °Brix to 14.50 °Brix at Bhavanisagar and from 18.20 °Brix to 14.60 °Brix at Vagarai, and DBT 18 $\beta+$ declining from 16.00 °Brix to 15.10 °Brix at the same location. This marked seasonal reduction, averaging 3.0 to 4.0 °Brix across genotypes, suggests that higher summer temperatures may accelerate sugar metabolism or respiration, leading to lower sugar accumulation. Despite this, DBT 26 $\beta+$ maintained the highest TSS across both seasons, demonstrating genetic superiority for sweetness. Total soluble solids are widely recognized as one of the principal quality attributes determining sweetness, consumer preference, and market acceptance in sweet corn. Similar variability in TSS among sweet corn genotypes was reported by Azanza *et al.* (1996), who demonstrated the potential for enhancing sweetness through breeding. Likewise, Duvick (2005) emphasized that kernel composition traits, particularly sugar content, are key selection targets in maize improvement programmes aimed at enhancing fresh-market quality. Furthermore, Lertrat and Pulam (2007) reported significant genotypic differences in sweetness and eating quality among sweet corn cultivars and identified TSS as a reliable criterion for selecting superior genotypes. More recently, Muthusamy *et al.* (2023) highlighted that improving kernel sugar content and associated quality traits remains a primary objective in sweet corn breeding programmes, with TSS serving as an important selection criterion for developing consumer-preferred hybrids.

Beta-carotene Content

During the Rabi 2023 season, beta-carotene content ranged from $9.80 \mu\text{g g}^{-1}$ in DBT 24 $\beta+$ at Vagarai to $11.80 \mu\text{g g}^{-1}$ in DBT 18 $\beta+$ at Bhavanisagar. In the summer 2024 evaluation, beta-carotene content varied from $9.50 \mu\text{g g}^{-1}$ in DBT 24 $\beta+$ at Vagarai to $10.90 \mu\text{g g}^{-1}$ in DBT 26 $\beta+$ at Coimbatore. Among the evaluated genotypes, DBT 18 $\beta+$ and DBT 26 $\beta+$ consistently recorded higher beta-carotene content across locations, with DBT 18 $\beta+$ showing $11.70 \mu\text{g g}^{-1}$ (Coimbatore, Rabi), $11.40 \mu\text{g g}^{-1}$ (Vagarai, Rabi), and $11.80 \mu\text{g g}^{-1}$ (Bhavanisagar, Rabi), while DBT 25 $\beta+$ also exhibited comparatively higher provitamin A levels, with values of $10.80 \mu\text{g g}^{-1}$ (Coimbatore, Rabi) and $10.70 \mu\text{g g}^{-1}$ (Vagarai, Rabi), highlighting their potential as valuable donor parents in provitamin A biofortification programmes. The seasonal stability of beta-carotene content is particularly notable, with DBT 18 $\beta+$ maintaining values of $11.80 \mu\text{g g}^{-1}$ (Rabi) and $10.80 \mu\text{g g}^{-1}$ (Summer) at Bhavanisagar, and DBT 26 $\beta+$ recording $10.40 \mu\text{g g}^{-1}$ and $10.90 \mu\text{g g}^{-1}$ at the same location, indicating that beta-carotene accumulation is less sensitive to seasonal variation compared to traits like TSS and GCY. This stability is consistent with the relatively lower G $\times$ E mean squares for beta-carotene (1.208) compared to GCY (272.23) as shown in the ANOVA (Tables 1 and 2). The observed variation, with a range of approximately $2.0 \mu\text{g g}^{-1}$ between the highest and lowest genotypes, is of considerable nutritional significance because beta-carotene is the principal provitamin A carotenoid in maize and plays a vital role in alleviating vitamin A deficiency. Similar genetic variability for provitamin A carotenoids among maize germplasm was reported by Muthusamy *et al.* (2015), indicating ample opportunity for the selection of nutritionally superior genotypes. Likewise, Pixley *et al.* (2013) demonstrated substantial variation in provitamin A concentrations among tropical maize germplasm and emphasized the effectiveness of conventional breeding for enhancing carotenoid content. Furthermore, Wurtzel *et al.* (2012) and Giuliano (2017) recognized maize as an ideal target crop for provitamin A biofortification because of its inherent capacity for carotenoid biosynthesis and accumulation in the endosperm. Bouis and Saltzman (2017) further highlighted biofortification as a sustainable strategy for improving micronutrient density in staple crops, with provitamin A maize. More recently, Nyoni *et al.* (2024) demonstrated that both genotype and crop management practices significantly

influence carotenoid accumulation, underscoring the importance of evaluating genotypes across diverse environments to identify stable, nutrient-rich cultivars.

Heat map-based assessment of genotypic performance across seasons in sweet corn

The heat map (Figure. 3 and 4) depicting standardized Z-score performance of beta-carotene-enriched sweet corn genotypes across Rabi 2023 and Summer 2024 revealed substantial genetic variability for flowering, morphological, yield, quality, and nutritional traits. The use of Z-score normalization enabled comparison of traits across different measurement scales and clearly highlighted genotype $\times$ environment interactions. Marked variation was observed for flowering traits across both seasons. DBT 15 $\beta+$ consistently exhibited earliness with strongly negative Z-scores for days to tasselling (DT: -1.48 in Rabi 2023; -2.11 in Summer) and days to silking (DS: -1.31 in Rabi 2023; -1.93 in Summer), indicating its suitability for short-duration and stress-escaping cultivation systems. In contrast, DBT 16 $\beta+$ recorded the highest positive Z-scores for flowering duration (DT: $+1.69$ in Rabi 2023; $+1.45$ in Summer and DS: $+1.72$ in Rabi 2023; $+1.72$ in Summer), indicating consistent late maturity across environments. Considerable differences were observed for plant height and yield components. DBT 26 $\beta+$ showed consistently high positive Z-scores for plant height (PH: $+0.80$ in Rabi 2023; $+0.65$ in Summer), cob length (CL: $+0.72$ in Rabi 2023; $+0.49$ in Summer), cob width (CW: $+0.81$ in Rabi 2023; $+0.88$ in Summer), and green cob yield (GCY: $+1.64$ in Rabi 2023; $+0.74$ in Summer). This indicates its superior vegetative vigour and yield stability across environments. Similarly, DBT 23 $\beta+$ exhibited stable positive Z-scores for GCY ($+0.16$ in Rabi 2023; $+0.63$ in Summer) and cob traits, indicating good adaptability and yield stability. In contrast, DBT 16 $\beta+$ recorded strong negative values for plant height (-1.86 in Rabi 2023; -2.12 in Summer) and green cob yield (-2.10 in Rabi 2023; -2.21 in Summer), reflecting poor agronomic performance across seasons. Pronounced variability was observed for kernel traits. DBT 18 $\beta+$ exhibited the highest Z-scores for kernel rows per cob (NKR: $+1.88$ in Rabi 2023; $+1.64$ in Summer) and kernels per row per cob (NKRC: $+1.96$ in Rabi 2023; $+1.53$ in Summer), indicating superior ear sink capacity and reproductive efficiency. These traits directly contribute to higher yield potential in sweet

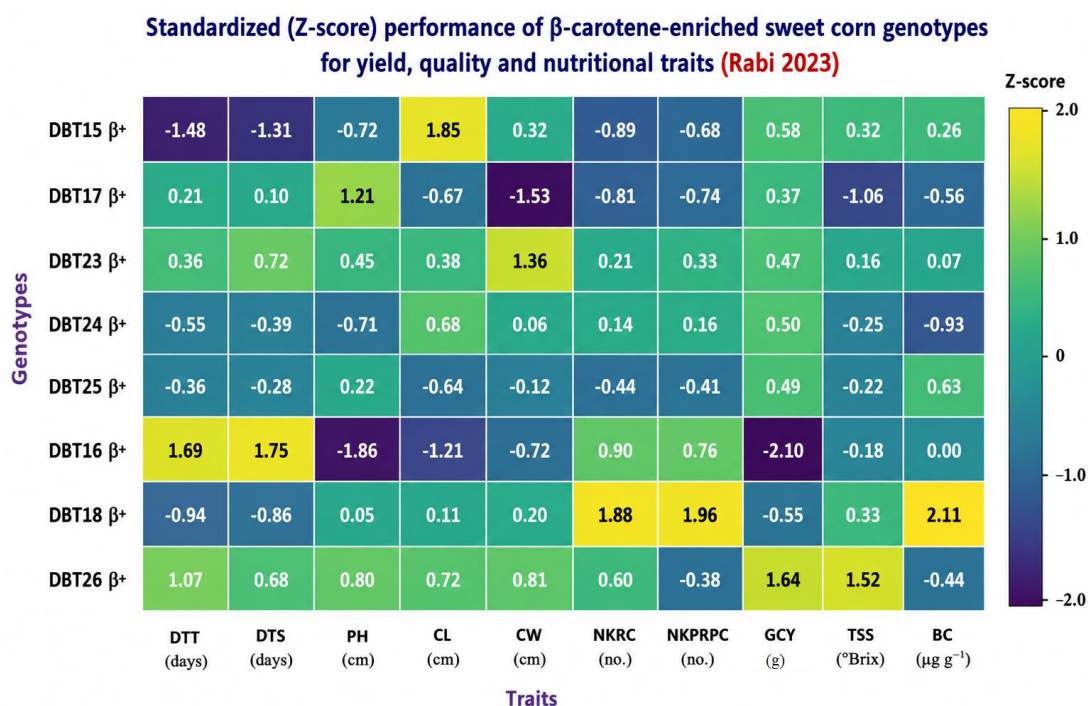


Figure 3. Heat map depicting the relative performance (Z-scores) of beta-carotene-enriched sweet corn genotypes evaluated during Rabi 2023

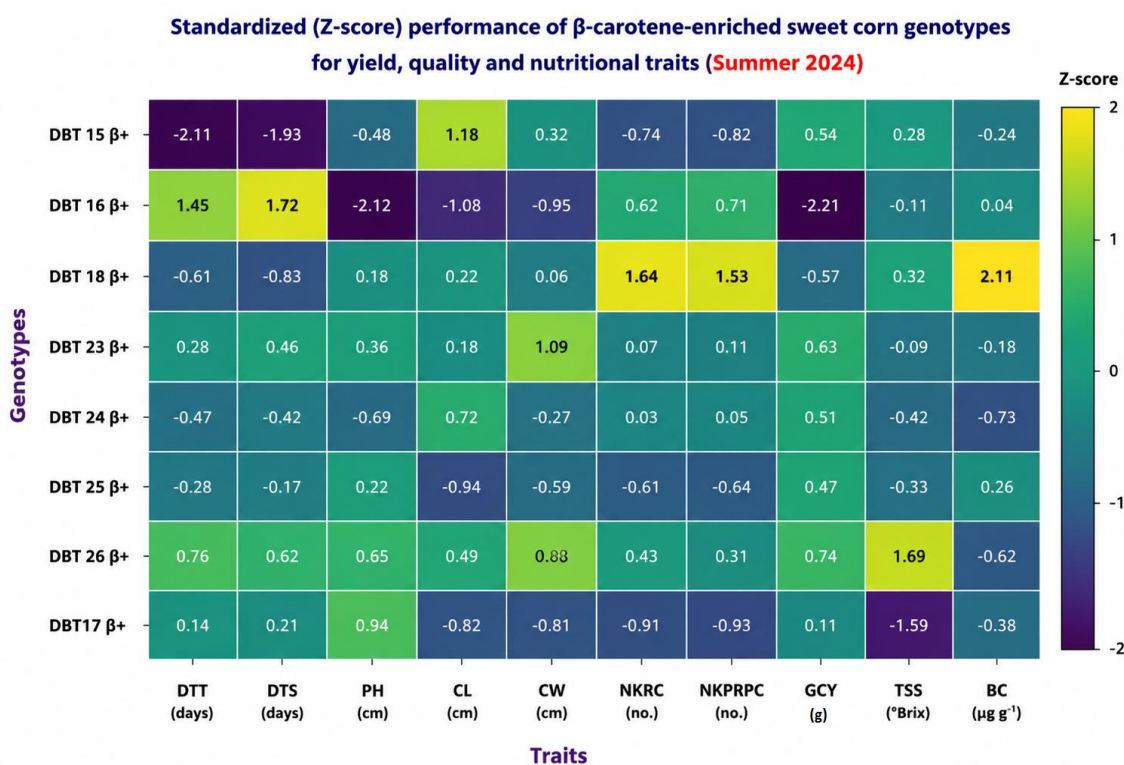


Figure 4. Heat map depicting the relative performance (Z-scores) of beta-carotene-enriched sweet corn genotypes evaluated during Summer 2024

corn. For total soluble solids (TSS), DBT 26 β + recorded consistently high positive Z-scores (TSS: +1.52 in Rabi 2023; +1.69 in Summer), confirming its superior sweetness and consumer acceptability. In terms of nutritional quality, DBT 18 β + showed the highest beta-carotene Z-scores (BC: +2.11 in Rabi 2023; +2.11 in Summer), indicating strong stability for provitamin-A accumulation across environments. DBT 25 β + also recorded moderate positive beta-carotene values (BC: +0.63 in Rabi 2023; +0.26 in Summer), suggesting its potential as a secondary donor parent for biofortification. Across both seasons, distinct functional grouping of genotypes was evident. DBT 26 β + emerged as the best performer for yield and sweetness stability, DBT 18 β + and DBT 25 β + as superior donors for beta-carotene content. DBT 23 β + showed moderate but stable performance across environments, indicating adaptability. The consistency of Z-score patterns across Rabi 2023 and Summer seasons highlights the reliability of these genotypes for multi-environment selection. The superior sweet corn genotypes identified could be used as effective donors in hybridization programme for both productivity and nutritional enhancement.

4. CONCLUSION

The evaluation of eight beta-carotene-enriched sweet corn inbred lines across three locations during the Rabi 2023 and summer 2024 seasons revealed significant genetic variability and genotype $\times$ environment interactions for all morphological, yield and quality traits studied. The results demonstrated considerable scope for the improvement of sweet corn through the selection of superior genotypes combining high yield, enhanced sweetness and increased beta-carotene content. Among the evaluated inbreds, DBT 26 β + emerged as the best-performing genotype for green cob yield, sweetness, and nutritional quality. DBT 18 β + consistently recorded superior kernel traits and high beta-carotene content, while DBT 25 β + was identified as an elite donor for provitamin A biofortification. DBT 23 β + showed excellent yield potential, whereas DBT 15 β + was identified as an early-maturing genotype with desirable cob characteristics. The marked seasonal differences observed for quality and yield traits highlight the influence of environmental conditions on trait expression, supporting the significant G $\times$ E interaction observed in the ANOVA. These inbreds represent valuable genetic resources for sweet corn improvement and may serve as promising parental lines for the development of

high-yielding and nutritionally enriched sweet corn cultivars. Further multi-environment evaluation using stability analyses would facilitate the identification of broadly adapted genotypes suitable for commercial cultivation. Similar observations of significant genetic variability for agronomic and quality traits in maize have been reported by Hallauer et al. (2010), Beyene et al. (2016), Yan and Tinker (2006) and Beyene et al. (2016).

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The manuscript is an original work.

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Author Contributions:

Shivakumar Ravichandran: Conceptualization, Data curation, Formal analysis, Investigation, Methodology, Writing – original draft, Writing – review

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REFERENCES

- Azanza, F., Bar-Zur, A., & Juvik, J. A. (1996). Variation in sweet corn kernel characteristics associated with quality. *Journal of Food Quality*, 19, 247-256. <https://doi.org/10.1007/BF00022959>
- Babu, R., Rojas, N. P., Gao, S., Yan, J., & Pixley, K. V. (2013). Validation of the effects of molecular marker polymorphisms in *lcyE* and *crtRB1* on provitamin A concentrations for marker-assisted selection in maize. *Theoretical and Applied Genetics*, 126, 389-399. <https://doi.org/10.1007/s00122-012-1987-3>
- Beyene, Y., Semagn, K., Mugo, S., Tarekegne, A., Babu, R., Meisel, B., Sehabiaque, P., Crossa, J., & Prasanna, B. M. 2016. Genetic gains in grain yield through genomic selection in eight bi-parental maize populations under drought stress. *Crop Science*, 56(1): 154-163. <https://doi.org/10.2135/cropsci2014.07.0460>
- Bhattarai, B., *et al.* (2026). Assessment of combining ability for grain yield and its attributing traits in maize (*Zea mays* L.). *Discover Agriculture*. <https://doi.org/10.1007/s44279-026-00571-x>
- Bouis, H. E., & Saltzman, A. (2017). Improving nutrition through biofortification: A review of evidence from HarvestPlus, 2003 through 2016. *Global Food Security*, 12, 49-58. <https://doi.org/10.1016/j.gfs.2017.01.009>
- Brown, P. J., Upadyayula, N., Mahone, G. S., Tian, F., Bradbury, P. J., Myles, S., Holland, J. B., Flint-Garcia, S., McMullen, M. D., Buckler, E. S. and Rocheford, T. R. 2011. Distinct genetic architectures for male and female inflorescence traits of maize. *PLoS Genetics*, 7(11): e1002383. <https://doi.org/10.1371/journal.pgen.1002383>
- Cairns, J. E., Sonder, K., Zaidi, P. H., Verhulst, N., Mahuku, G., Babu, R., Nair, S. K., Das, B., Govaerts, B., & Prasanna, B. M. (2023). Maize production in a changing climate: Impacts, adaptation, and breeding strategies. *Plant Breeding Reviews*, 47, 1-48. <https://doi.org/10.1016/B978-0-12-394275-3.00006-7>
- Chen, L., *et al.* (2021). Genetic architecture of maize yield traits dissected by QTL mapping and genome-wide association study in maize. *The Crop Journal*. <https://doi.org/10.1016/j.cj.2021.09.004>
- Duvick, D. N. 2005. The contribution of breeding to yield advances in maize (*Zea mays* L.). *Advances in Agronomy*, 86: 83-145. [https://doi.org/10.1016/S0065-2113\(05\)86002-X](https://doi.org/10.1016/S0065-2113(05)86002-X). [https://doi.org/10.1016/S0065-2113\(05\)86002-X](https://doi.org/10.1016/S0065-2113(05)86002-X)
- Galicia, L., Nurit, E., Rosales, A., and Palacios-Rojas, N. 2009. *Laboratory Protocols 2009: Maize Nutrition Quality and Plant Tissue Analysis Laboratory*. Mexico, D.F.: International Maize and Wheat Improvement Center (CIMMYT). ISBN: 978-970-648-169-6. Giuliano, G. 2017. Provitamin A biofortification of crops: A strategy for combating vitamin A deficiency. *Trends in Plant Science*, 22(7): 497-504. <https://doi.org/10.1016/j.tplants.2017.04.004>
- Hallauer, A. R., Carena, M. J., & Miranda Filho, J. B. (2010). *Quantitative genetics in maize breeding* (3rd ed.). Springer. <https://doi.org/10.1007/978-1-4419-0766-0>
- Harjes, C. E., Rocheford, T. R., Bai, L., Brutnell, T. P., Kandianis, C. B., Sowinski, S. G., Stapleton, A. E., Vallabhaneni, R., Williams, M., Wurtzel, E. T., Yan, J., & Buckler, E. S. (2008). Natural genetic variation in lycopene epsilon cyclase tapped for maize biofortification. *Science*, 319(5861), 330-333. <https://doi.org/10.1126/science.1150255>
- Khomphet, T. (2025). Genetic variability, correlation and path analysis of agronomic traits and yield components of Thai sweet corn. *Indian Journal of Agricultural Research*, 59(2), 198–205. <https://doi.org/10.18805/IJARE.AF-886>
- Kurilich, A. C. & Juvik, J. A. 1999. Quantification of carotenoid and tocopherol antioxidants in *Zea mays*. *J Agric Food Chem*, 47, 1948-55. <https://doi.org/10.1021/jf981029d>
- Lertrat, K., & Pulam, T. (2007). Breeding for increased sweetness in sweet corn. *International Journal of Plant Breeding*, 1, 27-30. Li, J., Martin, C. & Fernie, A.R. (2024). Biofortification's contribution to mitigating micronutrient deficiencies. *Nature Food*, 5, 19-27. <https://doi.org/10.1038/s43016-023-00905-8>
- Menkir, A., Dieng, I., Meseka, S., Maziya-Dixon, B., Bossey, B., Muhyideen, O., Ewool, M., Coulibaly, M. and

- Mengesha, W., 2025. Concurrent enhancement of provitamin A and yield in tropical maize hybrids. *Frontiers in Plant Science*, 16, 1611495. <https://doi.org/10.3389/fpls.2025.1611495>
- Muthusamy, V., Hossain, F., Nepolean, T., Saha, S., Agrawal, P. K., Guleria, S. K., & Gupta, H. S. (2015). Genetic variability and interrelationship of kernel carotenoids among indigenous and exotic maize inbreds. *Cereal Research Communications*, 43, 567-578. <https://doi.org/10.1556/0806.43.2015.012>
- Naji, A. M., Al-Jubouri, H. A. and Al-Saadi, A. H. 2021. Evaluation of yield and yield components of sweet corn (*Zea mays* var. *saccharata* L.) genotypes under different environmental conditions. *IOP Conference Series: Earth and Environmental Science*, 761: 012058. <https://doi.org/10.1088/1755-1315/761/1/012058>
- Nguyen, T. H., Nguyen, V. T., Tran, T. T., *et al.* (2024). Phenotypic diversity and selection of superior tropical sweetcorn inbred lines by multivariate method and combining ability analysis. *Environmental and Experimental Botany*, 30, 100215. <https://doi.org/10.1016/j.egg.2023.100215>
- Njeri, S.G., Makumbi, D., Beyene, Y., *et al.* (2023). Genotype × environment interaction and stability analysis of provitamin A maize hybrids under diverse environments in eastern and southern Africa. *Frontiers in Plant Science*, 14, 1186405.
- Nyoni, K., Derera, J., Mashingaidze, K., *et al.* (2024). Multi-environment evaluation of provitamin A maize hybrids for agronomic performance and stability under contrasting production conditions. *Plants*, 13, 1005.
- Peixoto, M. A., Leach, K. A., Jarquin, D., Flannery, P., Zystro, J., Tracy, W. F., Bhering, L., & Resende, M. F. R. (2024). Utilizing genomic prediction to boost hybrid performance in a sweet corn breeding program. *Frontiers in Plant Science*, 15. <https://doi.org/10.3389/fpls.2024.1293307>
- Pixley, K. V., Palacios-Rojas, N., Babu, R., Mutale, R., Surles, R., & Simpungwe, E. (2013). Biofortification of maize with provitamin A carotenoids. In *Carotenoids and Human Health* (pp. 271-292). Humana Press. https://doi.org/10.1007/978-1-62703-203-2_17
- Pour-Aboughadareh, A., Khalili, M., Poczai, P., & Olivoto, T. (2022). Stability and adaptation analyses of genotype × environment interactions in crops: A review. *Agronomy*, 12, 1136. <https://doi.org/10.3390/agronomy12051136>
- Prasanna, B. M., Palacios-Rojas, N., Hossain, F., Muthusamy, V., Menkir, A., Dhlwayo, T., Ndhlela, T., San Vicente, F., Nair, S. K., Vivek, B. S., Zhang, X., Olsen, M., & Fan, X. (2020). Molecular breeding for nutritionally enriched maize: Status and prospects. *Frontiers in Genetics*, 10, 1392. <https://doi.org/10.3389/fgene.2019.01392>
- Rajasekar, Ajay Kumar, Akilan, M., & Nirmalaruban, R. (2024). Morphological characterization and genetic diversity analyses of yield and yield attributing traits in sweet corn (*Zea mays* var. *saccharata*). *Journal of Scientific Research and Reports*, 30(7), 635–646. <https://doi.org/10.9734/jsrr/2024/v30i72177>
- Revilla, P., Butrón, A., Malvar, R. A., & Ordás, B. (2018). Sweet corn: From field to table. In: *Corn: Chemistry and Technology* (3rd ed.). AACC International Press, St. Paul, Minnesota, USA. ISBN: 978-0-12-811971-6.
- Revilla, P., Malvar, R.A., Butrón, A., Tracy, W.F., Abedon, B.G. and Ordás, A., 2002. Response to selection for the timing of vegetative phase transition in a maize population. *Crop science*, 42(5), 1471-1474. <https://doi.org/10.2135/cropsci2002.1471>
- Sharma, P., Kamboj, M. C., Singh, N., Kumar, R., & Kumar, N. (2022). Generation mean analysis in maize (*Zea mays*) for yields and yield attributing traits. *The Indian Journal of Agricultural Sciences*, 92(1), 110-117. <https://doi.org/10.56093/ijas.v92i1.120854>
- Tollenaar, M. and Lee, E. A. 2011. Strategies for enhancing grain yield in maize. *Plant Breeding Reviews*, 34: 37-82. <https://doi.org/10.1002/9780470880579.ch2>
- Tracy, W. F. (2001). Sweet corn. In A. R. Hallauer (Ed.), *Specialty corns* (2nd ed., pp. 155-197). CRC Press. <https://doi.org/10.1201/9781420038569.ch6>
- Wurtzel, E. T., Cuttriss, A., & Vallabhaneni, R. (2012). Maize provitamin A carotenoids, current resources, and future metabolic engineering challenges. *Frontiers in Plant Science*, 3, 29. <https://doi.org/10.3389/fpls.2012.00029>
- Yan, J., Kandianis, C. B., Harjes, C. E., Bai, L., Kim, E. H., Yang, X., Skinner, D. J., Fu, Z., Mitchell, S., Li, Q., Salas Fernandez, M. G., Zaharieva, M., Babu, R., Fu, Y., Palacios, N., Li, J., Dellapenna, D., Brutnell, T., Buckler, E. S., Warburton, M. L., & Rocheford, T. R. (2010). Rare genetic variation at *Zea mays* crtRB1 increases β-carotene in maize grain. *Nature Genetics*, 42(4), 322-327. <https://doi.org/10.1038/ng.551>

- Yan, W. and Tinker, N. A. 2006. Biplot analysis of multi-environment trial data: Principles and applications. *Canadian Journal of Plant Science*, 86: 623-645. <https://doi.org/10.4141/P05-169>
- Yang, J., Zhao, Y., Chen, X., Wang, B. and Wang, H. 2024. Regulation mechanism and breeding application of flowering time in maize. *Chinese Bulletin of Botany*, 59(6): 912-931. <https://doi.org/10.11983/CBB24127>