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Research Article

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Variability studies of yield related traits and its correlation in advance segregating populations of sweet corn

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ABSTRACT

The present study was aimed at examining 14 biometric traits in the BC_2F_2 and BC_2F_3 generations of sweet corn from the cross SCM-Se-O-1 × DBT 17 with a view to determining high-yielding genotypes through variability and correlation studies. Statistical parameters such as mean values, genotypic and phenotypic coefficients of variation (GCV and PCV), heritability, and genetic advance as a percentage of the mean (GAM) were estimated. In both generations, the PCV was greater than the GCV for most of the traits, reflecting high environmental influence. The BC_2F_2 generation had a greater level of variability, while the BC_2F_3 generation reflected signs of stabilization of traits as well as positive skewness. High heritability with high GAM for cob weight and single plant yield reflects that these are controlled by additive gene effects and are amenable to efficient selection for improvement. Correlation analysis revealed single plant yield to be highly and significantly correlated with cob weight, cob length, number of kernels per row, and number of kernel rows per cob, particularly in the BC_2F_3 generation. Cob weight also reflected significant positive correlations with important yield components. The findings reflect the possibility of yield improvement of sweet corn through selection based on traits with high heritability and positive correlations.

KEYWORDS: Sweet corn, Yield related traits, Correlation, Heritability, Descriptive statistics

INTRODUCTION

Zea mays var. *saccharata*, sweet corn, sugar corn, or pole corn, is a cereal plant with high sugar content (Mehta *et al.*, 2017). The crop is used mainly in the fresh state as a vegetable, while dried kernels are used as grain. Sweet corn is a nutritious crop and a major source of dietary fiber with valuable nutrients like vitamin B, folate, potassium, and magnesium (Upasana *et al.*, 2021). In addition, it is also found to contain antioxidants like lutein and zeaxanthin, which are linked with many health benefits. Sweet corn is harvested at the milky stage and is eaten fresh, tinned, or frozen, in contrast to field corn. Its sweetness and palatability are mostly influenced by certain recessive genes that restrict the kernels' ability to convert sugar into starch, leading to increased sugar accumulation. Six recessive mutant genes—brittle1 (*bt1*), brittle2 (*bt2*), shrunken1 (*sh1*), shrunken2 (*sh2*), sugary1 (*su1*), and sugary enhancer1 (*se1*)—are active in the endosperm and control the sweetness of sweet maize kernels (Tracy *et al.*, 1984).

The aim of this study was to analyze descriptive statistics and frequency distribution trends in the BC_2F_2 and BC_2F_3 populations to enable the selection of promising lines having improved agronomic performance. Estimation of variability through parameters such as phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (h^2), and genetic advance (GA) is critical for effective selection in plant breeding programs (Kishore *et al.*, 2015). Proper knowledge of these genetic parameters enhances the efficacy and precision of selection procedures in crop improvement (Khan *et al.*, 2018). Skewness, an indicator of the symmetry of the distribution of the traits, decipher us about the nature of gene action involved (Fisher *et al.*, 1932). In the same way, kurtosis shows about the number of genes controlling a trait and whether the distribution is narrow or broad-tailed (Robson, 1956). Skewness and kurtosis are generally affected by the genotype, with non-additive gene action giving rise to large deviations. Complementary gene action is indicated by positive skewness, and duplicate gene action by negative skewness. Traits can be leptokurtic (positive), platykurtic (negative), or mesokurtic (neutral) on the basis of kurtosis (Kapur, 1981). Correlation analysis is a valuable statistical tool in plant breeding to determine the strength and direction of association among yield and yield-contributing traits. It helps breeders select multiple positively correlated traits simultaneously to enhance genetic gain in sweet corn (Reddy *et al.*, 2022). Thus, the objective of the present study was to evaluate and identify high-performing individuals using statistical analysis of yield and yield traits in the SCM-Se-O-1 × DBT 17 crosses in BC_2F_3 and BC_2F_3 generations.

MATERIALS AND METHODS

The breeding program was conducted in Field No. 2G of the new area situated within the Department of Millets, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University (TNAU), Coimbatore, Tamil Nadu, India. The test site is located at an altitude of 411.98 meters above average sea level, positioned at 11°N latitude and 77 °E longitude. The experimental field is mainly composed of black soil, and the area experiences an average yearly rainfall of around 730 mm.

The experimental materials included a sweet corn recurrent parent SCM-Se-O-1 and a beta-carotene donor parent DBT 17, both developed at the Centre for Plant Molecular Biology and Biotechnology, TNAU, India, with the aim to introgress *crtRB1* gene in the recurrent parent. A new cross was started between SCM-Se-O-1 and DBT 17 to generate F_1 seeds. The F_1 plants were verified for heterozygosity and then backcrossed with the recurrent parent (SCM-Se-O-1) to produce BC_1F_1. Additionally, BC_1F_1 plants were crossed back once more to the recurrent parent to create the BC_2F_1 generation. Chosen BC_2F_1 plants were selfed to produce BC_2F_2, and ultimately progressed to BC_2F_3 generation via selfing. The BC_2F_3 generation was cultivated in Summer 2022, while BC_2F_3 was grown in Kharif 2022. Typical agronomic techniques and plant safeguarding measures were implemented during the entire crop season to promote robust crop development.

Fourteen biometric traits were documented from randomly chosen plants in both BC_2F_2 and BC_2F_3 populations. The characteristics consist of: Days to 50% tasselling (DT), Days to 50% silking (DS), Plant height (PH) in cm, Ear height (EH) in cm, Tassel length (TL) in cm, Leaf length (LL) in cm, Leaf width (LW) in cm, Cob length (CL) in cm, Cob girth (CG) in cm, Number of kernel rows per cob (NKRC), Number of kernels per row (NKR), 100-kernel weight (GW) in g, Cob weight (CW) in g, Single plant yield (SPY) in g. Trait assessment and nomenclature adhered to the Maize Descriptors as specified by the International Board for Plant Genetic Resources (IBPGR) and the methodology detailed by Sarankumar *et al.* (2019).

Descriptive statistics, including mean, standard deviation, variance, skewness, and kurtosis, were calculated utilizing SPSS software version 16.0 to evaluate the distribution pattern and gene action related to different traits. The broad-sense heritability (H^2) and genetic advance as a percentage of the mean (GAM) were determined following the method suggested by Johnson *et al.* (1955). Heritability was classified as: Low (<30%), Moderate (30–60%), High (>60%). GAM was classified as: Low (<10%), Moderate (10–20%), High (>20%). Pearson's correlation coefficients for yield and yield-contributing traits were calculated using the 'metan' package in R software (version 4.3.1) to examine the strength and direction of relationships between traits in both BC_2F_2 and BC_2F_3 populations. R software was used to create graphical representations of correlation matrices and distribution patterns to enhance the visualization of interrelationships and trait performance.

RESULTS

Phenotypic and Genetic Variability in BC_2F_2 and BC_2F_3 Generations of SCM-Se-O-1 × DBT 17

The populations BC_2F_2 and BC_2F_3 are developed from the SCM-Se-O-1 × DBT 17 cross, were studied for fourteen biometric traits, such as growth, phenological, and yield-related characteristics. These characteristics were examined regarding range, mean, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability in broad sense (h^2), and genetic advance as a percentage of the mean (GAM) (Tables 1 & 2).

In the BC_2F_2 generation, the height of the plants (PH) varied between 123.5 cm and 147.8 cm, averaging at 138.30 cm. It demonstrated moderate variability (GCV: 4.51%, PCV: 4.31%) and high heritability (91.31%), indicating that selection might be successful. Ear height (EH) exhibited a comparable trend, averaging 74.54 cm with a high heritability of 95.51%. Tassel length (TL) displayed moderate variability (GCV: 6.71%) and extremely high heritability (98.93%). Leaf length (LL) showed greater variability (GCV: 15.43%) with an average of 47.34 cm and high heritability (98.31%), indicating robust additive genetic regulation. Leaf width (LW) exhibited slight variation (GCV: 8.26%) and had moderate heritability (86.33%).

Among the yield components, cob weight (CW) exhibited the greatest GCV (30.06%) and PCV (29.76%), along with an exceptionally high heritability (99.90%) and GAM (23.20%), underscoring the opportunity for yield enhancement via direct selection. Likewise, single plant yield (SPY) demonstrated a high GCV of 25.02% and heritability of 99.39%, along with a GAM of 15.56%, suggesting the dominance of additive genetic influences. Cob girth (CG) and cob length (CL) demonstrated moderate to high heritability levels (85.68%

Table 1: Estimation of variability in BC_2F_2 of SCM-Se-0-1×DBT 17

S. No.	Traits	Mean	Range		GCV (%)	PCV (%)	h_2 (%)	GAM (%)
			Min.	Max.				
1	DT	56.55	54	58	2.04	1.96	41.75	0.99
2	DS	59.30	57	62	1.99	1.92	69.89	1.70
3	PH (cm)	138.30	123.5	147.8	4.51	4.31	91.31	11.74
4	EH (cm)	74.54	69.4	82	4.74	4.60	95.51	6.95
5	TL (cm)	24.90	21.5	28.4	6.71	6.57	98.93	3.41
6	LL (cm)	47.34	31	57.5	15.43	15.29	98.31	14.79
7	LW (cm)	5.67	4.8	6.5	8.26	8.07	86.33	0.83
8	CL (cm)	15.52	11.2	19.4	12.84	12.72	77.38	3.17
9	CG (cm)	16.28	13	19	8.12	7.64	85.68	2.33
10	NKRC	29.27	20	33	9.91	9.86	99.43	5.94
11	NKR	17.87	14	22	10.46	8.84	82.84	3.19
12	CW (g)	37.49	12.41	58.2	30.06	29.76	99.90	23.20
13	GW (g)	13.34	9	16.97	15.62	14.92	99.30	4.26
14	SPY (g)	30.37	14.42	46.53	25.02	24.86	99.39	15.56

GCV - Genotypic Coefficient of Variation, PCV - Phenotypic Coefficient of Variation, h^2 – Heritability, GAM - Genetic Advance as per of Mean, DT - Days to 50% tasseling, DS - Days to 50% silking, PH - Plant height, EH - Ear height, TL - Tassel length, CW - Cob Weight, LL - Leaf length, LB - Leaf breadth, CL - Cob length, CG - Cob girth, NKRC - Number of kernels per row per cob, NKR - Number of kernels per row, GW - 100 kernel weight, SPY- Single plant yield

Table 2: Estimation of variability in BC_2F_3 of SCM-Se-0-1×DBT 17

S. No.	Traits	Mean	Range		GCV (%)	PCV (%)	h^2 (%)	GAM (%)
			Min.	Max.				
1	DT	56.55	54.00	58.00	1.53	2.04	56.42	2.37
2	DS	59.30	57.00	62.00	1.78	1.99	79.93	3.28
3	PH (cm)	140.27	125.40	149.40	4.47	4.66	92.07	8.84
4	EH (cm)	75.61	70.40	84.00	4.29	4.40	94.94	8.61
5	TL (cm)	25.78	22.50	29.70	5.51	6.09	81.75	10.26
6	LL (cm)	48.62	32.00	58.00	14.29	15.54	84.49	27.06
7	LW (cm)	5.83	4.90	6.80	7.65	8.08	89.61	14.91
8	CL (cm)	13.17	11.20	16.20	10.24	10.46	95.89	20.66
9	CG (cm)	17.06	15.50	18.80	4.68	4.74	97.10	9.49
10	NKRC	27.68	24.00	33.00	7.47	7.52	98.88	15.31
11	NKR	17.45	14.00	22.00	11.68	12.51	87.20	22.48
12	CW (g)	49.70	46.00	55.80	4.75	4.80	97.82	9.68
13	GW (g)	11.90	10.20	13.80	7.35	7.78	89.48	14.33
14	SPY (g)	42.05	37.50	48.50	5.99	6.03	98.69	12.25

GCV - Genotypic Coefficient of Variation, PCV - Phenotypic Coefficient of Variation, h^2 – Heritability, GAM - Genetic Advance as per of Mean, DT - Days to 50% tasseling, DS - Days to 50% silking, PH - Plant height, EH - Ear height, TL - Tassel length, CW - Cob Weight, LL - Leaf length, LB - Leaf breadth, CL - Cob length, CG - Cob girth, NKRC - Number of kernels per row per cob, NKR - Number of kernels per row, GW - 100 kernel weight, SPY- Single plant yield

and 77.38%, respectively), while the number of kernels per row per cob (NKRC) and 100-kernel weight (GW) exhibited both high heritability (99.43% and 99.30%) and significant genetic progress.

In the BC_2F_3 generation, many traits exhibited a slight decrease in variability compared to BC_2F_2, likely because of genetic stabilization over selection cycle. Plant height varied from 125.40 to 149.40 cm, averaging 140.27 cm, showing moderate genetic coefficient of variability (4.47%) and high heritability (92.07%). Ear height demonstrated a comparable trend with somewhat reduced variation yet still exhibited high heritability (94.94%). Tassel length exhibited moderate variability and heritability (GCV: 5.51%, h^2: 81.75%). Leaf characteristics continued to exhibit significant variation. Leaf length showed high GCV (14.29%) and GAM (27.06%) along with a heritability of 84.49%, whereas leaf width revealed moderate GCV (7.65%) and high heritability (89.61%).

Yield components remained indicative of robust genetic regulation in BC_2F_3. The length and girth of the cob exhibited significant heritability (95.89% and 97.10%) with GAMs of 20.66% and 9.49%, respectively. The kernel rows per cob (NKRC) and the kernels per row (NKR) showed high heritability levels, at 98.88% and 87.20%, respectively. Cob weight exhibited high genetic efficiency, showing a heritability of 97.82% and a GAM of 9.68%. The yield per single plant (SPY) showed a moderate GCV of 5.99%, alongside a very high heritability of 98.69% and a GAM of 12.25%. Significantly, days to 50% tasselling (DT) and days to 50% silking (DS) in both generations showed minimal genetic variability (GCV < 2%) and moderate heritability, suggesting restricted selection response for these phenological characteristics.

The characteristics such as cob weight, yield per single plant, row count of kernels, and leaf length consistently exhibited high heritability and moderate to high GAM in both generations, highlighting the dominance of additive gene effects and potential for efficient selection within early segregating populations.

Skewness and Kurtosis Analysis

Positive skewness was noted for traits such as leaf width (LW), tassel length (TL), number of kernels per row (NKR), cob weight (CW), cob length (CL), hundred kernel weight (GW), and single plant yield (SPY) in BC_2F_3, reflecting a predominance of plants with lower trait values and implying a potential concentration of advantageous alleles in a limited number of individuals depicted in Table 3. The skewness varied from 0.03 (LW) to 0.972 (GW). In contrast, characteristics like plant height (PH), leaf length (LL), ear height (EH), days to 50% tasselling (DT), days to 50% silking (DS), number of kernel rows per cob (NKRC), and cob girth (CG) showed negative skewness in BC_2F_2 and/or BC_2F_3 populations, with values going from -0.09 (CG) to -1.43 (NKRC). Negative skewness indicates that individuals with higher trait values are more common and points to selection pressure or genetic constraints against lower trait values.

The majority of traits displayed platykurtic distributions (negative kurtosis), suggesting a flatter distribution compared to normal, frequently linked to duplicate gene activity. Characteristics like DT, DS, PH, LL, LW, CG, GW, and SPY consistently exhibited negative kurtosis in both generations. Nonetheless, tassel length (TL) and cob length (CL) showed leptokurtic distributions (positive kurtosis) in BC_2F_3, with values of 0.45 and 0.51, respectively, indicating a peaked distribution characteristic of traits governed by dominant or major genes. Moreover, the number of kernel rows per cob (NKRC) showed significant leptokurtosis (2.56) in BC_2F_3, emphasizing the influence of several key genes in its expression. These trends underscore the intricacy of inheritance and indicates that although many traits are probably controlled by polygenic and duplicated gene effects, certain traits that contribute to yield may be affected by significant or dominant genes, necessitating varied selection approaches (Figures 1 and 2).

Table 3: Frequency distribution for BC_2F_2 and BC_2F_3 generations of SCM-Se-O-1×DBT 17

S. No.	Traits	SCM-Se-O-1×DBT 17			
		BC_2F_2		BC_2F_3	
		Skewness	Kurtosis	Skewness	Kurtosis
1	DT	-0.28	-0.98	-0.28	-0.98
2	DS	0.26	-0.70	0.26	-0.70
3	PH	-0.24	-0.75	-0.19	-0.90
4	EH	0.60	-0.40	0.68	0.03
5	TL	0.31	-0.46	0.36	0.45
6	LL	-1.06	-0.02	-1.07	-0.21
7	LW	-0.12	-0.90	-0.03	-0.84
8	CL	-0.19	-0.77	0.53	-0.58
9	CG	-0.09	-0.21	0.31	-0.68
10	NKRC	-1.43	2.56	0.08	0.26
11	NKR	0.11	-0.17	0.27	-0.52
12	CW	-0.46	-0.08	0.84	0.51
13	GW	-0.20	-0.78	0.27	-0.71
14	SPY	0.00	-0.68	0.26	0.46

PH - Plant height; LL - Leaf length; LW - Leaf Width; EH - Ear height; TL - Tassel length; DT - Days to 50% tasselling; DS - Days to 50% Silking; NKR - Number of kernels per row; NKRC - Number of kernel rows per cob; CW - Cob Weight; CG - Cob girth; CL - Cob length; GW - 100 Kernel weight; SPY - Single plant yield

Correlation Analysis

According to Pearson's correlation coefficient in the BC_2F_2 generation, the yield of single plants showed a strong and highly significant positive correlation with 100 grain weight (0.57; $p<0.001$) and cob weight (0.54; $p<0.001$). Cob weight demonstrated a robust relationship with 100 grain weight (0.80; $p<0.001$), and also exhibited positive and significant correlations with the number of kernels per row (0.45) and cob length (0.66). Furthermore, cob length showed a positive relationship with the number of kernels per row (0.43; $p<0.05$), 100 grain weight (0.49; $p<0.05$), and cob weight (0.68; $p<0.001$).

Within the vegetative characteristics, plant height displayed a notable positive correlation with ear height (0.56; $p<0.001$), while days to 50% tasselling revealed a robust and highly significant positive relationship with days to 50% silking (0.82; $p<0.001$). Conversely, traits like tassel length, leaf length, and leaf width exhibited a negative and non-significant correlation with single plant yield, suggesting their minimal direct impact on grain yield (Figures 3 and 4).

In the BC_2F_3 generation, there was a strong and highly significant positive correlation between single plant yield and cob weight (0.56; $p<0.001$). In addition, cob weight showed notable positive correlations with the number of kernels per row (0.59; $p<0.001$), the number of kernel rows per cob (0.64; $p<0.001$), and the weight of 100 kernels (0.48; $p<0.01$). The count of kernels per row demonstrated a very strong positive correlation with the count of kernel rows per cob (0.87; $p<0.001$), emphasizing their joint impact on cob productivity.

Moreover, ear height showed a noteworthy positive correlation with plant height (0.59; $p<0.001$), suggesting a stable vertical plant structure. The trait of cob girth exhibited positive and significant correlations with cob weight (0.39; $p<0.05$), the number of kernels per row (0.32), and the number of kernels per cob (0.41). Conversely, tassel length and the duration to 50% silking showed both positive and negative correlations with the other traits, primarily remaining non-significant. Yield traits like individual plant yield, weight of 100 kernels, and cob weight showed a negative correlation with leaf length, although these relationships lacked statistical significance.

DISCUSSION

In this study, the assessment of sweet corn crosses developed from the cross SCM-Se-O-1 × DBT 17 across the BC_2F_2 and BC_2F_3 generations revealed significant variability and important trait correlations, suggesting opportunities for

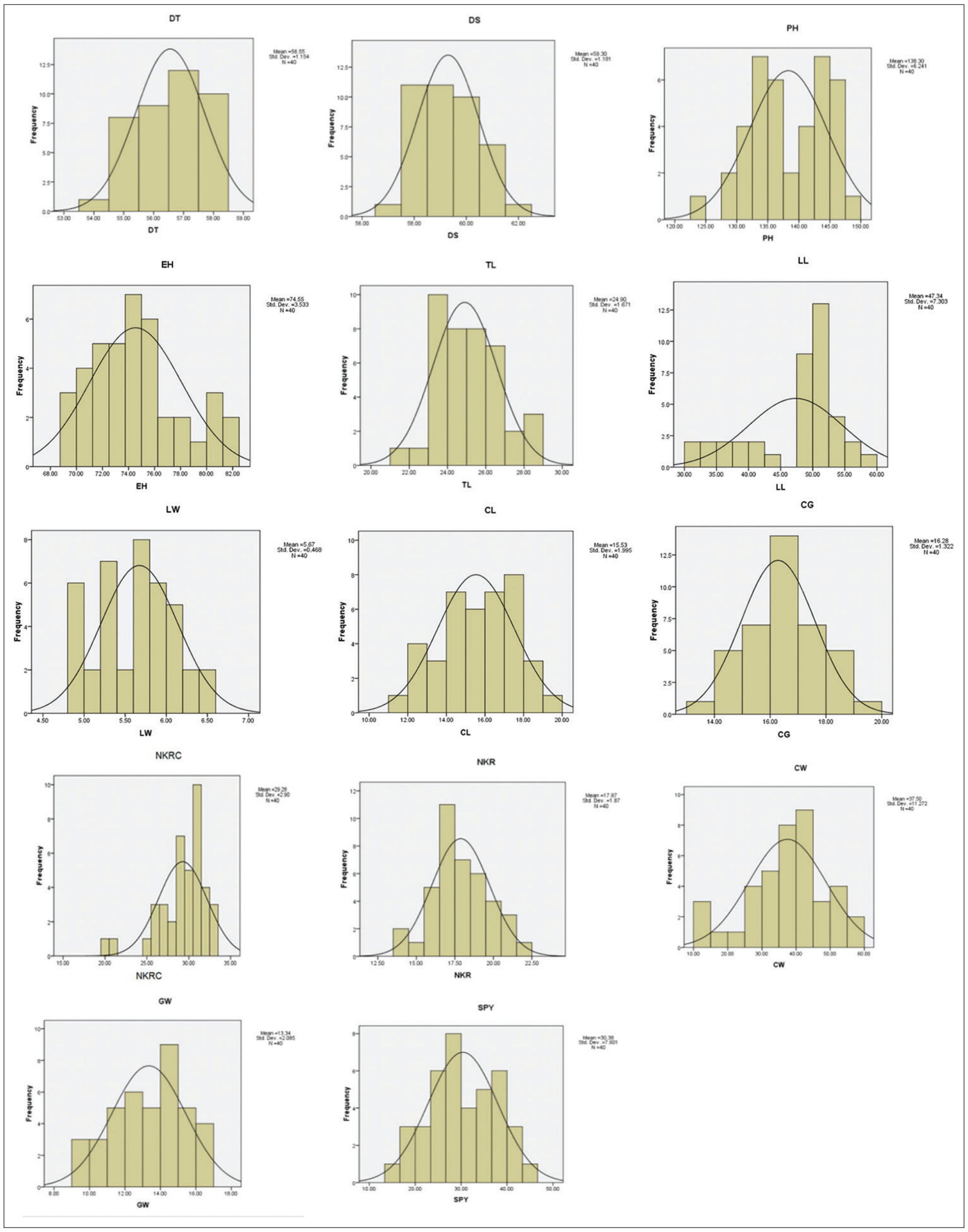

Figure 1: Frequency distribution for biometrical traits SCM-Se-O-1 x DBT17 of BC_2F_2 generation. DT - Days to 50% tasseling, DS - Days to 50% silking, PH - Plant height, EH - Ear height, TL - Tassel length, CW - Cob Weight, LL - Leaf length, LB - Leaf breadth, CL - Cob length, CG - Cob girth, NKRC - Number of kernel rows per cob, NKR - Number of kernel rows, GW - 100 kernel weight, SPY- Single plant yield

genetic enhancement. The averages of the agronomic parameters such as plant height, cob length, cob weight, and single plant yield were significantly high in both generations. Comprehensive genetic metrics like heritability, genotypic coefficient of variation (GCV), and phenotypic coefficient of variation (PCV) are crucial for effective selection of the lines, especially with regard to polygenic traits involving, and depending solely on mean performance may lead to poor decisions (Izzam *et al.*, 2017).

Notable genotypic and phenotypic variation was detected in all the characteristics. The PCV values were typically greater than the GCV, which could be due to the impact of environmental elements on phenotypic expression. Abe and Adelegan (2019) also observed similar results, whereas Sadimantara et al. (2021) reported contrasting findings of higher GCV compared to PCV. Among the characteristics, cob weight and single plant yield exhibited elevated GCV and PCV values, along with significant heritability and genetic advance as a percentage of mean (GAM), indicating the dominance of additive gene action and the possibilities for successful phenotypic selection. These results are similar with of Nagalakshmi (2018) and Saha *et al.* (2022). Similarly, 100 kernel weight and cob length demonstrated high heritability

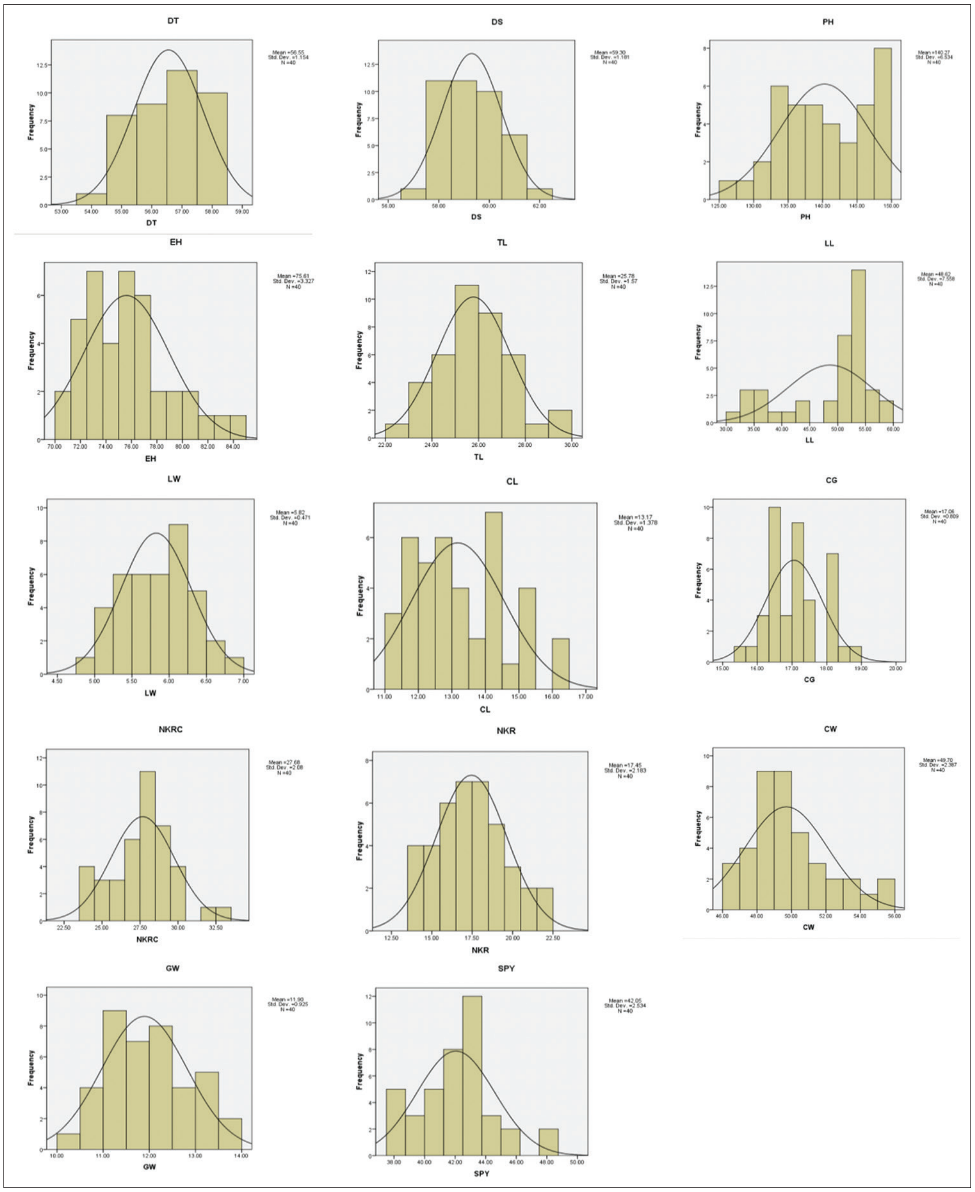

Figure 2: Frequency distribution for biometrical traits SCM-Se-O-1 x DBT17 of BC_2F_3 generation. DT - Days to 50% tasseling, DS - Days to 50% silking, PH - Plant height, EH - Ear height, TL - Tassel length, CW - Cob Weight, LL - Leaf length, LB - Leaf breadth, CL - Cob length, CG - Cob girth, NKRC - Number of kernel rows per cob, NKR - Number of kernel rows, GW - 100 kernel weight, SPY- Single plant yield

and moderate genetic variation, thus serving as further dependable traits for selection.

The examination of skewness and kurtosis gave additional understanding of the characteristics of gene action. In the BC_2F_2 generation, characteristics like ear height, tassel length, days to 50% silking, number of kernels per row, and individual plant yield showed positive skewness, suggesting complementary gene action. In contrast, the BC_2F_3 generation exhibited negative skewness for traits such as plant height, leaf length, ear height, days to 50% tasselling, days to 50% silking, number of kernel rows per cob, and cob girth, indicating potential duplicate gene action. The leptokurtic distributions for the number of kernels per row (BC_2F_2) and cob length (BC_2F_3) suggest oligogenic control, whereas the platykurtic distributions seen in most other traits reflect polygenic inheritance along with environmental interactions. These findings align with those reported by Sarankumar *et al.* (2019), Neelima *et al.* (2020), and Rathinavel *et al.* (2022).

The analysis of the correlation coefficient uncovered important relationships between yield components, facilitating indirect selection methods. In the BC_2F_2 generation, yield per single

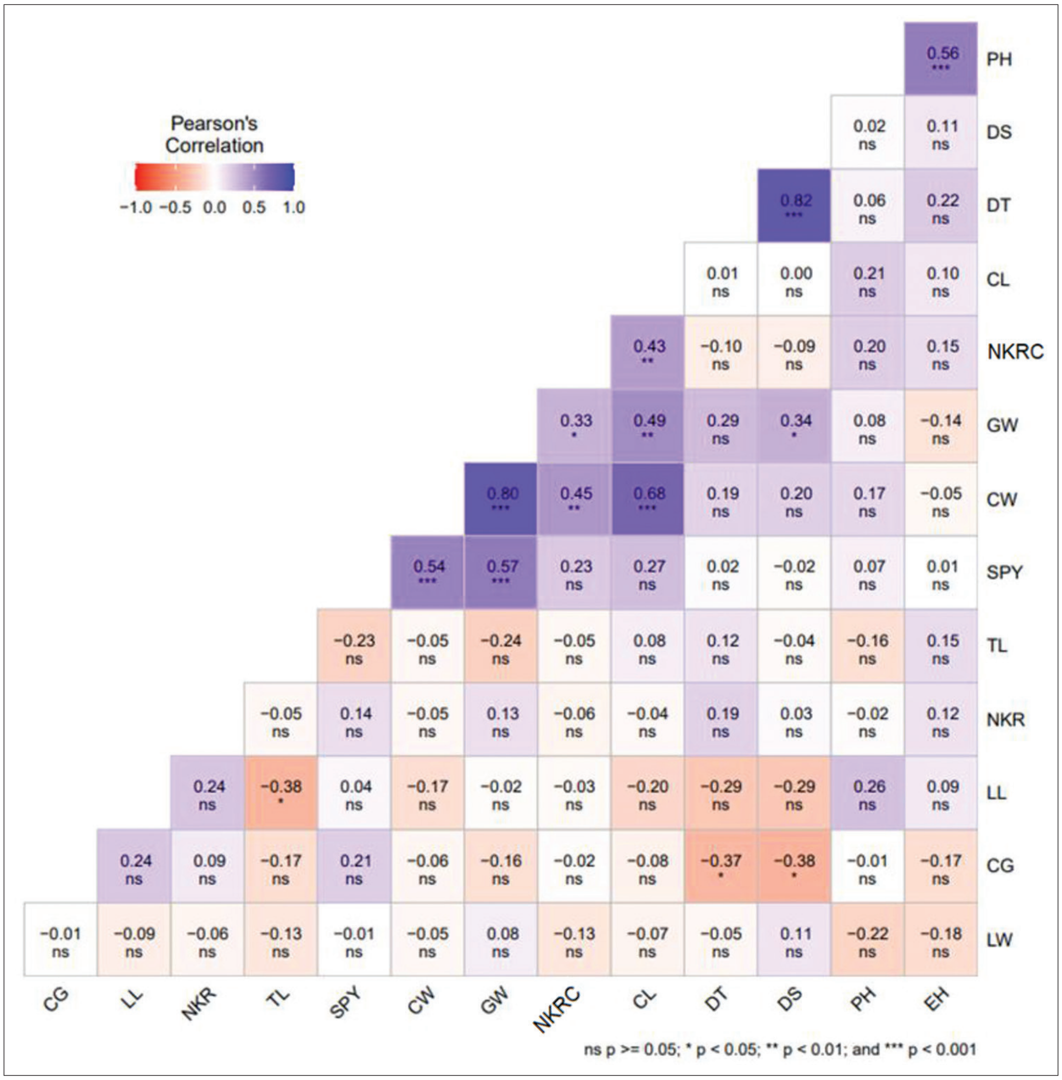

Figure 3: Correlation plot representing the morphological and yield related traits for the sweet corn inbred SCM-Se-O-1 x DBT17 of BC_2F_2 generation. DT - Days to 50% tasseling, DS - Days to 50% silking, PH - Plant height, EH - Ear height, TL - Tassel length, CW - Cob Weight, LL - Leaf length, LB - Leaf breadth, CL - Cob length, CG - Cob girth, NKRC - Number of kernel rows per cob, NKR - Number of kernel rows, GW - 100 kernel weight, SPY- Single plant yield

plant displayed a robust positive correlation with cob weight (0.54; $p<0.001$) and weight of 100 kernels (0.57; $p<0.001$), whereas cob weight significantly correlated with cob length (0.66), weight of 100 grains (0.80; $p<0.001$), and the count of kernels per row (0.45). There was a significant correlation between plant height and ear height (0.56; $p<0.001$), as well as a significant relationship between days to 50% tasselling and days to 50% silking (0.82; $p<0.001$). Some other characteristics like tassel length, leaf length, and leaf width exhibited a negative and non-significant correlation with individual plant yield and restricting their involvement in direct selection for yield.

The yield in individuals of BC_2F_3 plants showed a strong and highly significant relationship with cob weight (0.56; $p<0.001$). Cob weight showed a notable correlation with the number of kernels per row (0.59; $p<0.001$), the number of kernel rows per cob (0.64; $p<0.001$), and the weight of 100 kernels (0.48; $p<0.01$). Also, a strong correlation was noted between the number of kernels per row and the number of kernel rows per cob (0.87; $p<0.001$), indicating their combined effect on yield. There was a significant correlation between ear height and plant height (0.59; $p<0.001$). Cob circumference showed a positive correlation with cob weight (0.39), the count of kernels per row (0.32), and the total number of kernels per cob (0.41) at $p<0.05$. These connections aid in choosing traits that boost yield to increase productivity, aligning with findings by Chandana (2018) and Chinthiya *et al.* (2019).

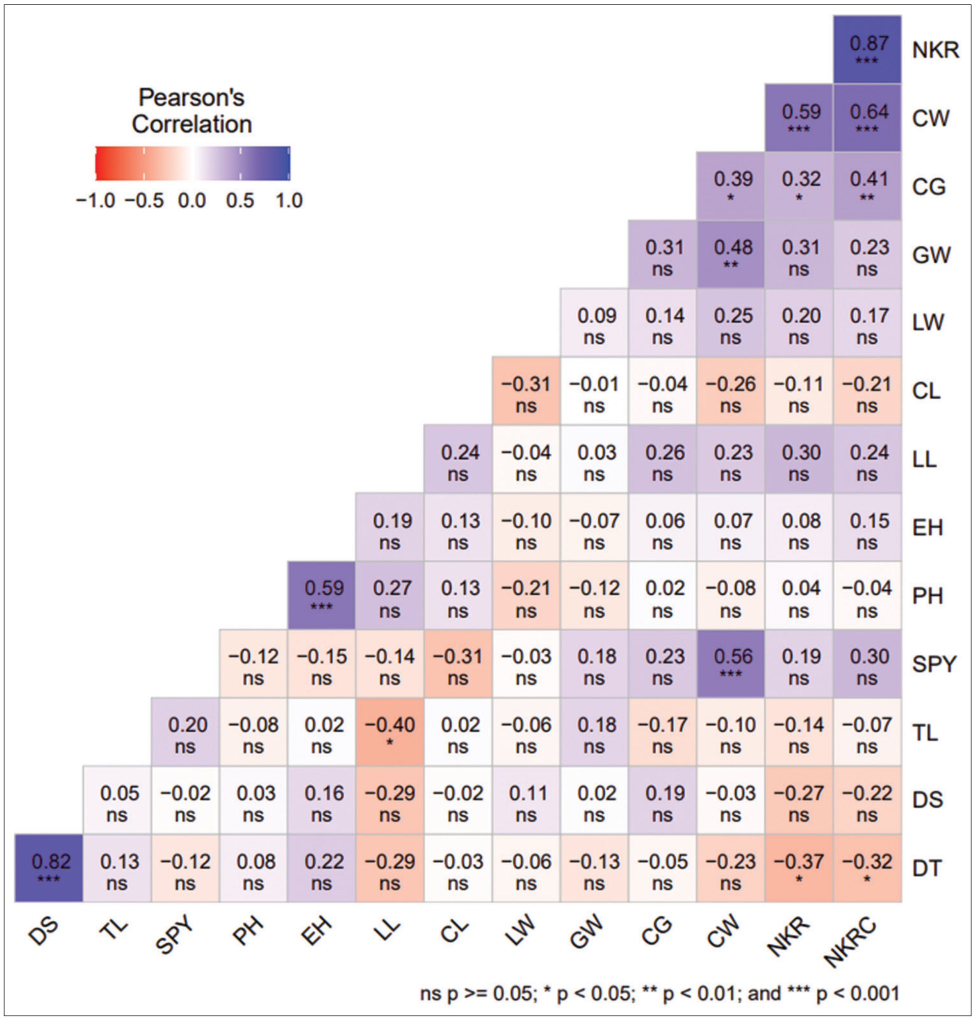

Figure 4: Correlation plot representing the morphological and yield related traits for the sweet corn inbred SCM-Se-O-1 x DBT17 of BC_2F_3 generation. DT - Days to 50% tasseling, DS - Days to 50% silking, PH - Plant height, EH - Ear height, TL - Tassel length, CW - Cob Weight, LL - Leaf length, LB - Leaf breadth, CL - Cob length, CG - Cob girth, NKRC - Number of kernel rows per cob, NKR - Number of kernel rows, GW - 100 kernel weight, SPY- Single plant yield

CONCLUSION

The current study concentrated on assessing two generations (BC_2F_2 and BC_2F_3) obtained from the backcross population of sweet corn utilizing the cross SCM-Se-O-1 × DBT 17. The BC_2F_2 generation exhibited considerable variation in biometric and yield-associated traits, offering a broad range for selection. Conversely, the BC_2F_3 generation exhibited partial stabilization of these traits, showing decreased phenotypic variability along with significant enhancement in specific crucial agronomic features. Although BC_2F_2 displayed a mix of skewness (both positive and negative), involving both complementary and duplicate gene interactions under environmental effects, the BC_2F_3 generation mainly showed positive skewness, possibly a genetic shift towards more favorable phenotypes. Correlation studies in BC_2F_3 generation, showed positive correlations with cob weight, kernels per row, and cob length. These trait associations strengthen the possibility of using indirect selection methods for enhancing yield. The genetic advancement from BC_2F_2 to BC_2F_3 shows consistent enhancement and emphasizes the possibility of creating high-yield, nutritionally enhanced sweet corn varieties. These results provide important guidance for upcoming breeding initiatives focused on improving yield and nutritional value in sweet corn to tackle food and nutritional security.

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REFERENCES

Abe, A., & Adelegan, C. A. (2019). Genetic variability, heritability and genetic advance in shrunken-2 super-sweet corn (*Zea mays* L. *saccharata*).

Journal of Plant Breeding and Crop Science, 11(4), 100-105. https://doi.org/10.5897/JPBCS2018.0799

Chandana, A. S. (2018). Genetic variability and correlation studies of yield and phytic acid in F2 populations of maize (*Zea mays* L.). *Electronic Journal of Plant Breeding, 9*(4), 1469-1475. https://doi.org/10.5958/0975- 928X.2018.00182.5

Chinthiya, A., Ganesan, K. N., Ravikesavan, R., & Senthil, N. (2019). Combining ability and association studies on different yield contributing traits for enhanced green cob yield in sweet corn (*Zea mays* con Var *saccharata*). *Electronic Journal of Plant Breeding, 10*(2), 500-511. https://doi.org/10.5958/0975-928X.2019.00063.2

Fisher, R. A., Immer, F. R., & Tedin, O. (1932). The genetical interpretation of statistics of the third degree in the study of quantitative inheritance. *Genetics, 17*(2), 107-124. https://doi.org/10.1093/genetics/17.2.107

Izzam, A., Sohail, H. R. A., Shahzad Ali, M., & Hussain, Q. (2017). Genetic variability and correlation studies for morphological and yield traits in maize (*Zea mays* L.). *Pure and Applied Biology, 6*(4), 1234-1243. https://doi.org/10.19045/bspab.2017.600131

Johnson, H. W., Robinson, H. F., & Comstock, R. E. (1955). Estimates of genetic and environmental variability in soybeans. *Agronomy Journal, 47*(7), 314-318. https://doi.org/10.2134/agronj1955.00021 962004700070009x

Kapur, S. K. (1981). Elements of practical statistics. (2nd ed.). New Delhi, India: Oxford and IBH Publishing Co.

Khan, A. S., Ullah, H., Shahwar, D., Fahad, S., Khan, N., Yasir, M., Fazli, W., Muhammad, A., & Noor, M. (2018). Heritability and correlation analysis of morphological and yield traits in Maize. *Journal of Plant Biology and Crop Research, 2*, 1008. https://doi.org/10.33582/2637-7721/1008

Kishore, N. S., Srinivas, T., Nagabhushanam, U., Pallavi, M., & Sameera, S. K. (2015). Genetic variability, correlation and path analysis for yield and yield components in promising rice (*Oryza sativa* L.) genotypes. *SAARC Journal of Agriculture, 13*(1), 99-108. https://doi. org/10.3329/sja.v13i1.24184

Mehta, B., Hossain, F., Muthusamy, V., Baveja, A., Zunjare, R., Jha, S. K., & Gupta, H. S. (2017). Microsatellite-based genetic diversity analyses of sugary1-, shrunken2-and double mutant-sweet corn inbreds for their utilization in breeding programme. *Physiology and Molecular Biology of Plants, 23*, 411-420. https://doi.org/10.1007/s12298-017-0431-1

Nagalakshmi, R. M. (2018). Genetic variability, heritability and genetic advance studies in backcross populations of maize (*Zea mays* L.). *Electronic Journal of Plant Breeding, 9*(3), 1137-1145. https://doi.org/10.5958/0975-928X.2018.00142.4

Neelima, C., Sarankumar, C., Sudha, M., Ganesan, K. N., Ravikesavan, R., & Senthil, N. (2020). Estimation of variability, heritability, genetic advance and assessment of frequency distribution for morphological traits in intercross population of maize. *Electronic Journal of Plant Breeding, 11*(2), 574-580.

Rathinavel, K., Chandran, S., Manoharan, B., Doraiswamy, U., Rajasekaran, R., Zachariah, J. K., & Natesan, S. (2022). Determining genetic variability of traits in backcross populations of sweet corn (*Zea mays* L. var. *Saccharata*). *Journal of Phytology, 14*, 132-135. https://doi.org/10.25081/jp.2022.v14.8099

Reddy, S. G. M., Lal, G. M., Krishna, T. V., Reddy, Y. V. S. and Sandeep, N. (2022) Correlation and Path Coefficient Analysis for Grain Yield Components in Maize (*Zea mays* L.). *International Journal of Plant & Soil Science, 34*(23), 24-36. https://doi.org/10.9734/ijpss/2022/v34i2331558

Robson, D. S. (1956). Applications of the k4 statistic to genetic variance component analyses. *Biometrics, 12*(4), 433-444. https://doi.org/10.2307/3001682

Sadimantara, G. R., Yusuf, D. N., Febrianti, E., Leomo, S., & Muhidin, M. (2021). The performance of agronomic traits, genetic variability, and correlation studies for yield and its components in some red rice (*Oryza sativa*) promising lines. *Biodiversitas Journal of Biological Diversity, 22*(9), 3994-4001. https://doi.org/10.13057/biodiv/d220947

Saha, I., Krishnakumar, R., Bharani, M., Adhimoolam, K., Vellaikumar, S., Ravikesavan, R., Muthurajan, R., & Natesan, S. (2022). Genetic variation of morphological and yield-related traits in backcrossed and selfed population of maize. *Journal of Phytology, 14*, 95-99. https://doi.org/10.25081/jp.2022.v14.7935

Sarankumar, C., Karthikeyan, A., Vanniarajan, C., Kokiladevi, E., Ravikesavan, R., & Senthil, N. (2019). Frequency distribution of yield related traits in BC1F1, BC2F1 and BC2F2 backcross population of maize. *Electronic Journal of Plant Breeding, 10*(2), 592-600. https://doi.org/10.5958/0975-928X.2019.00075.9

Tracy, W. F., Shuler, S. L., & Dodson-Swenson, H. (2019). The Use of Endosperm Genes for Sweet Corn Improvement: A Review of Developments in Endosperm Genes in Sweet Corn since the Seminal Publication in Plant Breeding Reviews, Volume 1, by Charles Boyer and Jack Shannon (1984). In I. Goldman (Ed.), *Plant Breeding Reviews* (Vol. 43, pp. 215-241) New Jersey, US: John Wiley & Sons, Inc. https://doi.org/10.1002/9781119616801.ch6

Upasana, J. P., Deshmukh, S. P., Khadadiya, M. B., & Desai, N. B. (2021). Effect of different levels, split and foliar application of nitrogen on growth and yield of sweet corn (*Zea mays* var. *saccharata*). *International Journal of Chemical Studies, 9*(1), 918-922. https://doi.org/10.22271/chemi.2021.v9.i1m.11344