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Genetic variability and heritability of yield-related traits in sweet corn genotypes

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Abstract

The present study was conducted to assess genetic variability, heritability and genetic advance for yield and quality traits in 20 sweet corn genotypes comprising 17 test entries and three checks. The experiment was conducted during *Kharif* 2025 at Kolhapur in a randomized block design with three replications. Significant differences among genotypes were observed for all 17 traits studied, indicating substantial genetic variability. The genotypic coefficient of variation was lower than the phenotypic coefficient of variation for all traits, suggesting environmental influence on trait expression. High broad-sense heritability was observed for reducing sugar (87.36%), sucrose (79.72%), cob height (70.61%) and 100-kernel weight (60.85%), with reducing sugar showing the highest genetic advance as percentage of mean (38.22%). The findings indicate good potential for selection based on traits exhibiting high heritability coupled with higher genetic advance. Among the genotypes, 60009 recorded the highest cob yield per plant (323.00 g), while PTKSC 25406 exhibited desirable quality attributes with the highest Brix (17.03%), reducing sugar (3.27%) and sucrose (24.69%). These genotypes may serve as promising materials for further evaluation and sweet corn breeding programmes.

Keywords: Sweet corn, genetic variability, GCV, PCV, heritability, genetic advance, Brix, reducing sugar and sucrose

Introduction

Sweet corn (*Zea mays* L. var. *saccharata*) is an important vegetable and specialty type of maize valued for its tender kernels, sweetness, palatability and nutritional quality. Its kernels contain higher levels of sugars during the milk to early dough stage, with sucrose being the predominant sugar (Oktem and Oktem., 2005; Hale *et al.*, 2005) [4, 8]. Thus, both yield and kernel quality are important targets in sweet corn improvement. The success of a breeding programme depends largely on the magnitude and nature of genetic variability available in the breeding material. Genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance as a percentage of mean (GAM) are useful parameters for assessing variability and predicting the potential response to selection (Burton, 1953; Johnson *et al.*, 1955) [3, 10]. Evaluation of these parameters for yield components and quality traits can help identify characters with greater selection potential. Although genetic variability and heritability for yield and quality traits have been reported in sweet corn, information on the simultaneous selection potential of yield components and sweetness-related traits in specific germplasm under local growing conditions remains limited (Dagla *et al.*, 2015; Niji *et al.*, 2018; Rajasekar *et al.*, 2024) [4, 13, 15]. Identification of genotypes combining high cob yield with desirable quality attributes is therefore important for sweet corn improvement.

Hence, the present study was undertaken to assess genetic variability, heritability and expected genetic advance for yield and quality traits among sweet corn genotypes and to identify promising genotypes and traits for selection in future breeding programmes.

Materials and Methods

The field experiment was conducted during the *Kharif* season of 2025 at the R.K. Nagar Farm of the All India Coordinated Research Project (AICRP) on Maize, located at Kolhapur

(Shenda Park farm). The experimental location features red-coloured soil characterized by effective drainage and high moisture retention capacity suitable for sweet corn cultivation.

The experimental material comprised 20 coded sweet corn genotypes (including 17 test genotypes and three checks) obtained from the AICRP on Maize Improvement Project at Kasba Bawada, Kolhapur which are given in Table No. 1. The trial was laid out in a Randomized Block Design (RBD) with three replications. Each entry in each replication was sown with the plot size of 4.00 x 1.20 m with a spacing of 60 cm between rows and 20 cm between plants. A standard fertilizer dose of 120:60:40 kg/ha of N, P₂O₅ and K₂O was adopted, applying a basal dose of 60:60:40 kg/ha alongside a split application of the remaining 60 kg N at 45 days after sowing.

Observations were recorded from five randomly selected plants tagged at 35 days after sowing within each treatment and replication and average values per plant were computed. Important quantitative traits were evaluated: days to 50% tasseling, days to 50% silking, plant count at harvest, number of cobs per plot at harvest, mean cob length with husk (cm), mean cob length without husk (cm), mean cob girth with husk (cm), mean cob girth without husk (cm), number of kernel rows per cob, number of kernels per row, plant height (cm), cob height (cm), 100-kernel weight (g) and cob yield per plant with husk (g). In addition, three biochemical characteristics were analyzed: Reducing sugar (%) using the Fehling's reagent titration method with methylene blue indicator, Sucrose content (%) derived by subtracting reducing sugars from total sugars estimated and Brix (%) measured via a refractometer at milk stage.

Statistical analysis of the mean values was carried out by subjecting the data to Analysis of Variance (ANOVA) as per Gomez and Gomez (1984). Genotypic, phenotypic and environmental variances were calculated as per Lush (1940), while genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were computed following Burton and Devane (1953) [3]. Broad-sense heritability (h^2 b.s.) was assessed as per Hanson *et al.*, (1956) and classified into low (<30%), moderate (30-60%) and high (>60%) categories as outlined by Johnson *et al.* (1955) [10]. Expected genetic advance (GA) and genetic

advance as a percentage of mean (GAM) were calculated using the formulas of Burton (1953) [3] and Johnson *et al.*, (1955) [10] with GAM categorized as low (<10%), moderate (10-20%) and high (>20%). Genotypic and phenotypic correlation coefficients were computed following Singh and Chaudhary (1985).

Table 1: List of sweet corn genotypes used

Sr. No.	Genotypes	Sr. No.	Genotypes
1.	60001	11.	PTKSC 25401
2.	60002	12.	PTKSC 25402
3.	60003	13.	PTKSC 25403
4.	60004	14.	PTKSC 25405
5.	60005	15.	PTKSC 25406
6.	60006	16.	PTKSC 25408
7.	60007	17.	PTKSC 25409
8.	60008	18.	PTKSC 25404 (Check)
9.	60009	19.	PTKSC 25407 (Check)
10.	60010	20.	PTKSC 25410 (Check)

Results and Discussion

Analysis of Variance

The analysis of variance for different quantitative characters, as shown in Table 2, revealed that the mean sum of squares due to genotypic differences was highly significant for all characters studied. This indicates a substantial level of variability among the 17 genotypes and 3 check varieties. Specifically, significant variations were observed in developmental and growth parameters, such as days to 50 per cent tasseling (13.02), days to 50 per cent silking (14.67), plant height (211.11 cm) and cob height (150.29 cm). Population and ear physical traits also demonstrated significant differences, including plant count at harvest (76.78), number of cobs per plot (76.52), mean cob length with husk (13.77 cm) and without husk (12.25 cm), mean cob girth with husk (7.14 cm) and without husk (4.95 cm), as well as kernel characteristics like the number of kernel rows per cob (6.68), number of kernels per row (11.86) and 100 kernel weight (23.39 gm). Furthermore, highly significant variation was present in overall productivity and quality profiles, notably cob yield per plant with husk (1101.62 gm), brix percentage (2.31%), reducing sugar percentage (0.59%) and sucrose percentage (12.45%).

Table 2: Analysis of variance for different characters in sweet corn

Sr. No.	Characters	Mean sum of square		
		Replication	Treatment	Error
		df = 2	df = 19	df = 38
1	Days to 50 per cent tasseling	5.01	13.02**	4.13
2	Days to 50 per cent silking	7.40	14.67**	3.71
3	Plant count at harvest	79.40	76.78**	27.94
4	No. of cobs per plot at harvest	54.45	76.52**	15.60
5	Mean cob length with husk (cm)	6.07	13.77**	4.18
6	Mean cob length without husk (cm)	3.34	12.25**	3.25
7	Mean cob girth with husk (cm)	1.26	7.14**	2.07
8	Mean cob girth without husk (cm)	0.34	4.95**	1.85
9	No. of kernel rows per cob	0.20	6.68**	1.74
10	No. of kernels per row	16.58	11.86**	5.12
11	Plant height (cm)	339.06	211.11**	106.20
12	Cob height (cm)	20.21	150.29**	18.31
13	100 kernel weight (gm)	1.60	23.39**	4.13
14	Cob yield per plant with husk (gm)	2.40	1101.62**	356.03
15	Brix%	5.99	2.31**	0.46
16	Reducing Sugar%	0.007	0.59**	0.02
17	Sucrose%	0.39	12.45**	0.97

*, ** significant at 5% and 1% respectively.

Genetic Variability

The range of variability, estimates for the genotypic and phenotypic coefficients of variation (GCV and PCV), heritability in the broad sense (%), genetic advance and genetic advance as a percentage of the mean are given in Table 3.

Assessment of variability forms the basis of a successful breeding programme focused on improving yield and quality traits. Hence, estimation of genotypic and phenotypic coefficients of variation is important to understand the nature and magnitude of variation. Genetic variability together with heritability estimates, provides a better understanding of the potential genetic gains from selection (Burton, 1953)^[3].

Range and Mean

Based on mean values which are mentioned in Table 3 and Table 4, The analysis revealed significant variability across the 17 sweet corn characters evaluated in the 20 genotypes. The range for days to 50 per cent tasseling varied from 47.67 to 58.33 days with a mean of 54.23 days while days to 50 per cent silking ranged from 50.00 to 61.33 days with an average of 56.95 days. Plant count at harvest ranged from 63.67 to 80.67 with a mean of 72.20. Number of cobs per

plot at harvest varied between 56.00 and 73.67 with an average of 65.05. Mean cob length with husk ranged from 19.23 cm to 26.93 cm with a mean of 23.31 cm whereas mean cob length without husk varied from 16.83 cm to 23.73 cm with an average of 20.22 cm. Mean cob girth with husk ranged from 15.00 cm to 23.17 cm with a mean of 18.75 cm while mean cob girth without husk varied from 13.16 cm to 17.93 cm with an average of 15.98 cm. The number of kernel rows per cob ranged from 12.67 to 17.33 with an average of 15.20 and the number of kernels per row ranged from 31.32 to 39.18 with an average of 36.05. Plant height ranged from 133.00 cm to 166.20 cm with a mean of 152.85 cm while cob height varied between 52.47 cm and 77.93 cm with an average of 61.21 cm. 100 kernel weight ranged from 23.25 gm to 28.12 gm with an average of 23.25 gm. Cob yield per plant with husk ranged from 247.00 gm to 323.00 gm with a mean of 291.95 gm. Quality parameters also showed noticeable variation; Brix percentage ranged from 13.40 per cent to 17.03 per cent with a mean of 14.96 per cent, reducing sugar percentage ranged from 1.67 per cent to 3.27 per cent with an average of 2.19 per cent and sucrose percentage ranged from 17.66 per cent to 24.69 per cent with a mean of 20.86 per cent.

Table 3: Estimates of genetic variability parameters for 17 characters evaluated across 20 sweet corn genotypes

Sr. No.	Characters	Mean	Range		Coefficient of variation%		Heritability % (b.s.)	Genetic advance	G.A. as per cent of mean
			Min.	Max.	GCV%	PCV%			
1	Days to 50 per cent tasseling	54.23	47.67	58.33	3.17	4.91	41.70	2.28	4.22
2	Days to 50 per cent silking	56.95	50.00	61.33	3.35	4.76	49.58	2.77	4.86
3	Plant count at harvest	72.20	63.67	80.67	5.58	9.21	36.81	5.04	6.98
4	No. of cobs per plot at harvest	65.05	56.00	73.67	6.93	9.22	56.54	6.98	10.73
5	Mean cob length with husk (cm)	23.31	19.23	26.93	7.66	11.65	43.32	2.42	10.39
6	Mean cob length without husk (cm)	20.22	16.83	23.73	8.56	12.36	48.01	2.47	12.23
7	Mean cob girth with husk (cm)	18.75	15.00	23.17	6.93	10.34	44.95	1.79	9.57
8	Mean cob girth without husk (cm)	15.98	13.16	17.93	6.35	10.63	35.72	1.25	7.82
9	No. of kernel rows per cob	15.20	12.67	17.33	8.44	12.11	48.55	1.84	12.11
10	No. of kernels per row	36.05	31.32	39.18	4.15	7.53	30.46	1.70	4.72
11	Plant height (cm)	152.85	133.00	166.20	3.86	7.77	24.77	6.06	3.96
12	Cob height (cm)	61.21	52.47	77.93	10.83	12.89	70.61	11.48	18.75
13	100 kernel weight (gm)	23.25	23.25	28.12	10.89	13.97	60.85	4.07	17.51
14	Cob yield per plant with husk (gm)	291.95	247.00	323.00	5.40	8.42	41.11	20.82	7.13
15	Brix%	14.96	13.40	17.03	5.25	6.94	57.19	1.22	8.18
16	Reducing Sugar%	2.19	1.67	3.27	19.85	21.24	87.36	0.83	38.22
17	Sucrose%	20.86	17.66	24.69	9.37	10.50	79.72	3.59	17.24

Coefficients of Variation

The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) serve as critical metrics for quantifying population variability. Together with heritability estimates, PCV and GCV enable breeders to project selection efficiency and anticipate potential genetic gains for specific traits.

High PCV values were recorded for reducing sugar percentage (21.24%). Moderate PCV values were observed for 100 kernel weight (13.97%), cob height (12.89%), mean cob length without husk (12.36%), number of kernel rows per cob (12.11%), mean cob length with husk (11.65%), mean cob girth without husk (10.63%), sucrose percentage (10.50%) and mean cob girth with husk (10.34%). Low PCV values were recorded for plant count at harvest (9.21%), number of cobs per plot at harvest (9.22%), cob yield per plant with husk (8.42%), plant height (7.77%), number of kernels per row (7.53%), Brix percentage

(6.94%), days to 50 per cent tasseling (4.91%) and days to 50 per cent silking (4.76%).

In contrast, high GCV values were not observed, but reducing sugar percentage (19.85%) recorded a high-moderate estimate near the threshold. Moderate GCV values were recorded for 100 kernel weight (10.89%) and cob height (10.83%). Low GCV values were recorded for sucrose percentage (9.37%), mean cob length without husk (8.56%), number of kernel rows per cob (8.44%), mean cob length with husk (7.66%), mean cob girth with husk (6.93%), number of cobs per plot at harvest (6.93%), mean cob girth without husk (6.35%), plant count at harvest (5.58%), cob yield per plant with husk (5.40%), brix percentage (5.25%), number of kernels per row (4.15%), plant height (3.86%), days to 50 per cent silking (3.35%) and days to 50 per cent tasseling (3.17%).

The GCV was consistently lower than the PCV for all characters indicating that environmental factors played a role in the expression of these characters, similar result were

reported by Dagla *et al.*, (2015) ^[4], Niji *et al.*, (2018) ^[13], Rajasekar *et al.*, (2024) ^[15] and Mittal *et al.*, (2026) ^[12] in sweet corn.

Heritability

In this study, heritability in the broad sense varied across the characters indicating varying degrees of genetic influence. High heritability estimates were recorded for reducing sugar percentage (87.36%), sucrose percentage (79.72%), cob height (70.61%) and 100 kernel weight (60.85%). Moderate heritability values were observed for brix percentage (57.19%), number of cobs per plot at harvest (56.54%), number of kernel rows per cob (48.55%), mean cob length without husk (48.01%), mean cob girth with husk (44.95%), mean cob length with husk (43.32%), days to 50 per cent tasseling (41.70%), cob yield per plant with husk (41.11%), plant count at harvest (36.81%), mean cob girth without husk (35.72%) and number of kernels per row (30.46%).

Low heritability estimates recorded for plant height (24.77%) while days to 50 per cent silking (49.58%) exhibited moderate heritability. These findings are similar with research by Gazal *et al.*, (2018) ^[5] and Ahmed *et al.*, (2020) ^[1] which reported high heritability for characters such as reducing sugar, sucrose, cob height and 100 kernel weight suggesting that these characters are strongly influenced by genetic factors. High heritability values indicate that selection for traits such as reducing sugar, sucrose, cob height and 100 kernel weight would likely yield progress due to strong genetic control.

Genetic advance

GA varied substantially across the characters. The highest genetic advance value were observed for cob yield per plant with husk (20.82). Moderate GA value recorded for cob height (11.48).

Lower GA values were recorded for number of cobs per plot at harvest (6.98), plant height (6.06), plant count at harvest (5.04), 100 kernel weight (4.07), sucrose percentage (3.59),

days to 50 per cent silking (2.77), mean cob length without husk (2.47), mean cob length with husk (2.42), days to 50 per cent tasseling (2.28), number of kernel rows per cob (1.84), mean cob girth with husk (1.79), number of kernels per row (1.70), mean cob girth without husk (1.25), brix percentage (1.22) and reducing sugar percentage (0.83). According to Ghosh *et al.*, (2014) ^[6] assessing genetic advance is critical for understanding the sort of gene activity that influences polygenic features. High genetic advance values indicate the presence of additive gene action, while lower values indicate the involvement of non - additive gene action.

Genetic Advance as Percent of Mean

The highest GA as a percentage of the mean was observed for reducing sugar percentage (38.22%). Moderate genetic advance as a percentage of the mean was recorded for cob height (18.75%), 100 kernel weight (17.51%), sucrose per cent (17.24%), mean cob length without husk (12.23%), number of kernel rows per cob (12.11%), number of cobs per plot at harvest (10.73%) and mean cob length with husk (10.39%).

Low genetic advance as a percentage of the mean was recorded for mean cob girth with husk (9.57%), brix percentage (8.18%), mean cob girth without husk (7.82%), cob yield per plant with husk (7.13%), plant count at harvest (6.98%), days to 50 per cent silking (4.86%), number of kernels per row (4.72%), days to 50 per cent tasseling (4.22%) and plant height (3.96%).

In the present study, high heritability was coupled with high to moderate genetic advance as a percentage of the mean for characters such as reducing sugar per cent, sucrose per cent, cob height and 100 kernel weight, indicating that selection for these characters would be effective for genetic improvement. High heritability combined with high GAM strongly predicts additive gene action, ensuring selection efficiency (Bello *et al.*, 2010) ^[2].

Table 4: Mean performance of 20 genotypes for 17 characters of sweet corn

Sr. No	Genotypes	DFT	DFS	PCH	NCH	MCL WH (cm)	MCL WOH (cm)	MCG WH (cm)	MCG WOH (cm)	NKR	NKPR	PH (cm)	CH (cm)	HKW (gm)	CYPP (gm)	Brix %	RS %	SC %
1	60001	52.00	54.67	63.67	56.00	19.23	16.83	15.00	13.16	12.67	31.32	133.00	52.47	18.98	247.00	14.83	1.95	19.90
2	60002	55.00	57.67	72.33	66.00	22.27	19.20	18.67	16.17	15.33	36.03	153.07	60.47	22.38	291.67	14.08	1.74	18.00
3	60003	54.67	57.67	67.67	61.67	21.70	18.37	18.33	15.24	14.67	35.48	152.73	59.80	21.33	284.67	15.52	2.72	22.98
4	60004	52.67	55.00	70.33	63.33	21.87	18.83	18.50	16.03	15.33	36.01	150.53	55.63	21.85	289.67	14.12	1.77	18.18
5	60005	55.33	58.33	75.67	67.67	25.70	22.23	19.17	16.82	16.67	37.17	157.60	63.17	24.73	302.33	15.64	2.81	23.36
6	60006	56.00	58.33	72.33	65.67	24.57	21.20	18.67	16.33	15.33	36.29	152.80	60.40	23.42	293.00	15.13	2.51	22.49
7	60007	53.33	56.00	73.00	67.00	24.40	20.60	18.67	16.67	15.33	37.08	157.20	62.53	23.68	294.00	14.29	1.78	18.61
8	60008	54.00	56.33	79.33	71.67	25.87	22.90	20.50	17.93	17.33	37.92	166.20	77.93	27.34	311.00	14.58	1.82	19.38
9	60009	54.67	57.00	80.67	73.67	25.50	22.53	20.33	17.12	17.33	39.18	162.53	74.07	28.12	323.00	15.37	2.67	22.67
10	60010	47.67	50.00	64.33	56.67	20.87	18.27	17.67	13.98	12.67	31.67	134.40	52.87	19.24	251.00	14.91	2.07	21.07
11	PTKSC 25401	56.00	58.00	68.00	60.33	21.70	18.33	18.00	15.24	14.00	35.38	151.33	57.63	21.07	286.33	14.93	2.27	22.15
12	PTKSC 25402	55.00	58.00	74.33	66.33	24.57	21.27	19.00	16.67	15.33	37.09	157.20	62.30	24.46	302.00	14.57	1.80	19.28
13	PTKSC 25403	55.00	58.00	79.33	70.67	26.93	23.73	23.17	17.93	17.33	38.33	160.90	68.53	27.86	314.33	13.40	1.67	17.66
14	PTKSC 25405	58.33	61.33	67.33	59.67	21.27	18.80	17.67	14.44	13.33	35.02	148.67	54.07	20.81	281.33	14.80	1.90	19.41
15	PTKSC 25406	55.67	58.67	76.67	69.67	25.93	23.00	19.17	16.97	16.67	37.36	160.67	68.53	25.25	305.00	17.03	3.27	24.69
16	PTKSC 25408	54.33	57.67	66.00	59.33	21.33	18.00	17.67	14.43	13.33	33.93	143.93	52.90	19.76	271.33	14.97	2.29	22.26
17	PTKSC 25409	53.33	56.33	71.67	65.00	21.90	19.10	18.33	15.70	14.67	35.82	150.13	54.33	22.12	291.33	15.46	2.71	22.88
18	PTKSC 25404 (C)	54.00	57.00	77.67	70.33	24.93	21.37	19.67	16.95	16.67	37.91	158.33	66.20	26.55	310.33	14.91	2.11	21.63
19	PTKSC 25407 (C)	54.67	57.67	70.00	63.00	21.93	18.53	18.17	15.37	14.67	35.69	151.87	58.53	21.85	288.33	14.84	2.00	20.00
20	PTKSC 25410 (C)	53.00	55.33	73.67	67.33	23.83	21.30	18.67	16.53	15.33	36.30	153.93	61.73	24.20	301.33	14.89	2.04	20.69

Mean	54.23	56.95	72.20	65.05	23.31	20.22	18.75	15.98	15.20	36.05	152.85	61.21	23.25	291.95	14.96	2.19	20.86
Range	47.67	50.00	63.67	56.00	19.23	16.83	15.00	13.16	12.67	31.32	133.00	52.47	18.98	247.00	13.40	1.67	17.66
	58.33	61.33	80.67	73.67	26.93	To 23.73	To 23.17	To 17.93	17.33	39.18	166.20	77.93	28.12	323.00	17.03	3.27	24.69
C.V. (%)	3.75	3.38	7.32	6.07	8.77	8.91	7.67	8.52	8.68	6.28	6.74	6.99	8.74	6.46	4.54	7.55	4.73
S. E.	1.17	1.11	3.05	2.28	1.18	1.04	0.83	0.78	0.76	1.3	5.94	2.47	1.17	10.89	0.39	0.09	0.56
C.D. (5%)	3.36	3.18	8.73	6.53	3.38	2.98	2.37	2.25	2.18	3.74	17.03	7.07	3.35	31.18	1.12	0.27	1.63

DFT= Days to 50 per cent tasseling, DFS= Days to 50 per cent silking, PCH= Plant count at harvest, NCH= No. of cobs per plot at harvest, MCLWH= Mean cob length with husk, MCLWOH= Mean cob length without husk, MCGWH= Mean cob girth with husk, MCGWOH= Mean cob girth without husk, NKR= No. of kernel rows per cob, NKPR= No. of kernels per row, PH= Plant height, CH= Cob height, HKW= 100 kernel weight, CYPP= Cob yield per plant with husk, RS= Reducing Sugar, SC = Sucrose.

Conclusion

Significant genetic variability was observed among the 20 sweet corn genotypes for all 17 traits. High heritability with moderate to high genetic advance indicated good selection potential for reducing sugar, sucrose, cob height and 100-kernel weight. Genotype 60009 showed the highest cob yield, while PTKSC 25406 showed superior quality traits. These genotypes may be useful for further evaluation and sweet corn breeding.

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