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Genotypic correlation and path coefficient analysis of yield and associated traits in sweet corn genotypes

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Abstract

The present study was conducted to assess the association among yield and quality traits and identify suitable selection criteria for cob yield improvement in sweet corn. Twenty genotypes were evaluated in a randomized block design with three replications during *Kharif* 2025 at Kolhapur, Maharashtra. Genotypic correlation and path coefficient analyses were performed for 17 traits. Cob yield per plant showed strong positive correlations with number of kernels per row (0.870), kernel rows per cob (0.704), number of cobs per plot (0.700) and 100-kernel weight (0.609). Path analysis revealed the highest positive direct effects for number of kernels per row (0.663), number of cobs per plot (0.400) and kernel rows per cob (0.319). Sugar traits showed weak or negligible associations with cob yield. Thus, number of kernels per row, number of cobs per plot and kernel rows per cob may serve as effective selection criteria for improving cob yield in sweet corn.

Keywords: Sweet corn, genotypic correlation, path coefficient analysis, cob yield, yield components and sugar traits

Introduction

Sweet corn (*Zea mays* L. var. *saccharata*) is an important specialty maize type valued for its tender kernels, sweetness, palatability and nutritional quality. Its characteristic sweetness is mainly associated with soluble sugars accumulated during the milk stage, with sucrose, glucose and fructose being the major sugars (Hale *et al.*, 2005) [6]. Improvement of cob yield along with desirable quality traits is therefore an important objective in sweet corn breeding. Cob yield is a complex quantitative trait influenced by several interrelated morphological, phenological and yield-component characters. Understanding their association with cob yield is essential for identifying suitable selection criteria and improving breeding efficiency. Significant associations among yield components have been reported in sweet corn and maize (Kashiani and Saleh, 2010; Suhaisini *et al.*, 2016; Vani Praveena *et al.*, 2022) [8, 22, 24]. Correlation analysis helps determine the direction and magnitude of association among traits; however, it cannot distinguish between direct and indirect effects, particularly when yield components are interrelated. Path coefficient analysis overcomes this limitation by partitioning correlations into direct and indirect effects, thereby helping to identify traits with greater direct association with yield (Dewey and Lu, 1959) [4]. Previous studies have successfully used path analysis to identify important yield-contributing traits in maize and sweet corn (Raghu *et al.*, 2011; Khazaei *et al.*, 2010; Vani Praveena *et al.*, 2022) [9, 16, 24]. Therefore, the present study was undertaken to estimate genotypic correlations and path coefficients among cob yield and associated quantitative and quality traits in sweet corn genotypes and to identify important traits useful as selection criteria for improving cob yield under the conditions of the present study.

Materials and methods

The experiment was carried out in a Randomized Block Design (RBD) with three replications at the R.K. Nagar Farm of the All India Coordinated Research Project on Maize, Shenda Park farm, Kolhapur during *Kharif* 2025. The experimental material consisted of 20 sweet corn genotypes (including 17 genotypes and 3 check varieties) obtained from the AICRP on Maize.

Each entry was sown in plot of 4.00 m length, adopting a spacing of 60 cm between rows and 20 cm between plants. The recommended fertilizer dose of 60 kg N, 60 P₂O₅ and 40 kg K₂O ha⁻¹ was applied as basal, and the remaining 60 kg N ha⁻¹ was top-dressed at 45 days after sowing. Standard agronomic practices and plant protection measures were uniformly followed during the entire crop growth period.

In each replication, five plants were selected at random and tagged at 35 days after sowing for recording observations on quantitative traits, viz., 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, along with biochemical traits, viz., total soluble solids (TSS; °Brix), reducing sugar (%) and sucrose (%). TSS was measured using a hand refractometer, while reducing sugar was estimated by Fehling's reagent method.

The genotypic correlation coefficient worked out as described by Singh and Chaudhary (1985) [20]. The Path coefficient analysis done as per the method suggested by Dewey and Lu (1959) [4].

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)

Result and Discussion

Corelation

The genotypic correlation analysis revealed critical interrelationships among morpho-agronomic traits, yield components and sugar parameters as studied in Table 2. Primary yield drivers demonstrated strong positive correlations with cob yield per plant with husk, led by the number of kernels per row (0.869), followed closely by kernel rows per cob (0.704), total cobs per plot (0.700), and 100-kernel weight (0.608). Regarding plant architecture, plant count at harvest (0.623) and cob height (0.612) correlated positively with total yield, with plant count at harvest showing the strongest association with overall cobs per plot (0.929). Plant height (0.529) displayed positive associations with 100-kernel weight (0.681), cob height (0.564) and total yield. Ear dimensions further reflected strong internal consistency: mean cob length with husk correlated almost perfectly with dehusked length (0.960) and both maintained moderate positive correlations with total cob yield (0.486) and (0.514) respectively. Similarly, husked cob girth correlated strongly with dehusked girth (0.891), showing comparable positive associations with yield (0.403) and (0.412) respectively. Among phenological traits, days to 50% tasseling correlated near-perfectly with days to 50% silking (0.979) while exhibiting positive associations with plant height (0.375) and kernels per row

(0.263). Days to 50% silking mirrored these trends with plant height (0.344) and kernels per row (0.281). Quality parameters indicated that brix percentage correlated strongly with reducing sugar percentage (0.726) and sucrose percentage (0.629), while exhibiting negligible negative correlations with total yield (-0.008 to -0.081). Reducing sugar percentage correlated strongly with sucrose (0.826) and weakly with yield (0.174), whereas sucrose percentage showed a near-zero correlation with cob yield (-0.016). The strong positive genotypic correlations between cob yield traits namely kernels per row, kernel rows per cob and 100-kernel weight demonstrate that sweet corn productivity is primarily governed by ear dimensions and seed-filling capacity. Structural attributes such as plant height and cob height provide the essential vegetative frame and canopy biomass. These findings align with earlier observations by Kumar and Kumar (2000) [10]. Direct selection for maximum length and girth cobs bearing higher kernel counts efficiently boosts overall yield, consistent with reports by Wannows *et al.*, (2010) [25] and Barua *et al.*, (2017) [2]. The primary influence of ear dimensions and kernel weight in driving final yield is further corroborated by Ram Reddy *et al.*, (2012) [18] and Vani Praveena *et al.*, (2022) [24]. Furthermore, the linear relationships established between husked and dehusked ear traits parallel the phenotypic patterns detailed by Rajasekar *et al.*, (2024) [17]. The robust association between harvest plant count and total cobs per plot underscores the necessity of maintaining optimal plant populations to maximize unit yield, agreeing with Khazaei *et al.*, (2010) [9]. Positive interrelationships between flowering parameters and vegetative height accord with findings by Raghu *et al.*, (2011) and Vani Praveena *et al.*, (2022) [16, 24], though environmental variation can occasionally weaken silking-yield relationships, as observed by Natraj *et al.*, (2014). Regarding quality traits, the high positive correlations among brix, reducing sugars and sucrose validate brix as a dependable indirect selection metric for endosperm sweetness, supporting conclusions by Kumari *et al.*, (2007) [11] and St. Subaedah *et al.*, (2021). Simultaneous accumulation of reducing sugars and sucrose during the milk stage reflects standard physiological sink behavior, as noted by Geeta *et al.*, (2017) and Hemavathy *et al.*, (2008) [5, 7]. Crucially, the absence of significant negative correlations between sugar parameters and total cob yield indicates that selecting for high endosperm sugar concentration does not incur a yield. This confirms the feasibility of concurrently breeding high-yielding and high-sugar sweet corn hybrids, as previously demonstrated by Suhaisini *et al.*, (2016) and A. Thanga Hemavathy (2020) [1, 7, 22].

Path Analysis

From Table No. 3, path coefficient analysis, executed as per the methodology of Dewey and Lu (1959) [4], was applied to partition the phenotypic correlation coefficients into direct and indirect effects, offering a clearer understanding of the primary yield-contributing traits in sweet corn. The evaluation revealed that the strongest positive direct effects on cob yield per plant with husk were exerted by the number of kernels per row (0.6626), number of cobs per plot at harvest (0.3998) and number of kernel rows per cob (0.3187). Additionally, mean cob girth with husk (0.2358), reducing sugar percentage (0.1102), Brix percentage (0.0918) and days to 50 per cent silking (0.0540)

demonstrated positive direct contributions to yield. These results underline the critical role of kernel parameters and ear characteristics as primary criteria for direct selection in yield improvement programs, aligning with prior studies by Bello *et al.*, (2010)^[3], Raghu *et al.*, (2011)^[16] and Reddy *et al.*, (2022)^[19]. Conversely, direct negative effects were recorded for plant count at harvest (-0.2571), mean cob girth without husk (-0.2151), sucrose percentage (-0.1612), cob length with husk (-0.0628) and cob length without husk (-0.0401), corroborating the observations of Matin *et al.*, (2017)^[14].

Assessment of indirect pathways indicated that key structural traits such as cob length, cob girth, plant height, and cob height exerted significant positive indirect contributions to cob yield through the number of kernels per

row and number of cobs per plot. Flowering attributes, including days to 50 per cent tasseling and silking, indirectly supported yield by lengthening the reproductive phase and enhancing sink capacity, consistent with findings by Singh *et al.*, (1999)^[21] and Kumar *et al.*, (2006)^[11]. Furthermore, biochemical traits such as brix, reducing sugars and sucrose exhibited favorable positive mutual indirect pathways without compromising kernel development, supporting reports by Lertrat and Pulam (2007)^[13] and St. Subaedah *et al.*, (2021). Overall, path analysis demonstrates that simultaneous selection for number of kernels per row, number of cobs per plot and kernel rows per cob provides the most effective selection strategy for maximizing cob yield in sweet corn.

Table 2: Genotypic correlation of 17 characters of 20 genotypes of Sweet corn.

	DFT	DFS	PCH	NCH	MCL WH	MCL WOH	MCG WH	MCG WOH	NKR	NKPR	PH	CH	HKW	BRIX	RS	SC	CYPP
DFT	1.000	0.979**	0.247	0.240	0.225	0.213	0.167	0.209	0.226	0.263*	0.375*	0.152	0.249	0.021	0.118	0.144	0.250
DFS		1.000	0.244	0.247	0.224	0.208	0.181	0.209	0.188	0.281*	0.344*	0.121	0.237	0.042	0.139	0.146	0.264
PCH			1.000	0.929**	0.507**	0.530**	0.463**	0.445**	0.575**	0.622**	0.514**	0.727**	0.687**	0.069	0.072	0.078	0.623**
NCH				1.000	0.612**	0.614**	0.557**	0.569**	0.622**	0.654**	0.558**	0.768**	0.723**	0.101	0.134	0.065	0.700**
MCL WH					1.000	0.960**	0.605**	0.595**	0.583**	0.425**	0.459**	0.545**	0.537**	0.098	0.160	-0.091	0.486**
MCL WOH						1.000	0.585**	0.586**	0.593**	0.479**	0.426**	0.592**	0.592**	0.099	0.165	-0.076	0.514**
MCG WH							1.000	0.891**	0.508**	0.314*	0.376*	0.512**	0.582**	-0.182	-0.052	-0.049	0.403**
MCG WOH								1.000	0.584**	0.354**	0.441**	0.522**	0.660**	-0.112	-0.071	0.020	0.412**
NKR									1.000	0.588	0.614**	0.636**	0.710**	-0.011	0.176	0.041	0.704**
NKPR										1.000	0.496**	0.576**	0.610**	-0.092	0.106	-0.012	0.869**
PH											1.000	0.564**	0.681**	0.020	0.124	0.015	0.529
CH												1.000	0.685**	0.115	0.097	0.018	0.612
HKW													1.000	-0.052	0.060	0.071	0.608**
BRIX														1.000	0.726	0.629	-0.081
RS															1.000	0.826	0.174
SC																1.000	-0.016
CYPP																	1.000

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, NKPR= 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.

Table 3: Direct (diagonal) and Indirect (above and below diagonal) path effects of different characters towards cob yield with husk at genotypic level in sweet corn.

	DFT	DFS	PCH	NCH	MCL WH	MCL WOH	MCG WH	MCG WOH	NKR	NKPR	PH	CH	HKW	BRIX	RS	SC
DFT	-0.0272	-0.0267	-0.0067	-0.0065	-0.0061	-0.0058	-0.0046	-0.0057	-0.0062	-0.0072	-0.0102	-0.0041	-0.0068	-0.0006	-0.0032	-0.0039
DFS	0.0529	0.0540	0.0132	0.0134	0.0121	0.0113	0.0098	0.0113	0.0102	0.0152	0.0186	0.0066	0.0128	0.0023	0.0075	0.0079
PCH	-0.0635	-0.0630	-0.2571	-0.2390	-0.1304	-0.1362	-0.1192	-0.1145	-0.1480	-0.1600	-0.1324	-0.1869	-0.1767	-0.0178	-0.0185	-0.0202
NCH	0.0960	0.0990	0.3718	0.3998	0.2449	0.2456	0.2230	0.2277	0.2488	0.2617	0.2233	0.3073	0.2893	0.0405	0.0538	0.0261
MCL WH	-0.0141	-0.0141	-0.0318	-0.0384	-0.0628	-0.0603	-0.0380	-0.0374	-0.0366	-0.0267	-0.0288	-0.0342	-0.0338	-0.0062	-0.0101	0.0006
MCL WOH	-0.0086	-0.0084	-0.0213	-0.0247	-0.0386	-0.0401	-0.0235	-0.0235	-0.0238	-0.0192	-0.0171	-0.0238	-0.0238	-0.0040	-0.0066	0.0003
MCG WH	0.0396	0.0427	0.1094	0.1315	0.1429	0.1380	0.2358	0.2101	0.1199	0.0742	0.0888	0.1209	0.1373	-0.0431	-0.0123	-0.0115
MCG WOH	-0.0450	-0.0451	-0.0958	-0.1225	-0.1281	-0.1261	-0.1917	-0.2151	-0.1256	-0.0762	-0.0950	-0.1123	-0.1420	0.0242	0.0001	-0.0044
NKR	0.0722	0.0600	0.1835	0.1983	0.1821	0.1890	0.1620	0.1861	0.3187	0.1876	0.1958	0.2029	0.2265	-0.0037	0.0563	0.0132
NKPR	0.1749	0.1867	0.4123	0.4337	0.2820	0.3178	0.2085	0.2347	0.3900	0.6626	0.3289	0.3818	0.4046	-0.0615	0.0706	-0.0085
PH	-0.0035	-0.0032	-0.0048	-0.0052	-0.0043	-0.0040	-0.0035	-0.0041	-0.0057	-0.0046	-0.0093	-0.0053	-0.0064	-0.0002	-0.0012	-0.0001

CH	-0.0045	-0.0036	-0.0217	-0.0229	-0.0163	-0.0177	-0.0153	-0.0156	-0.0190	-0.0172	-0.0168	-0.0298	-0.0205	-0.0034	-0.0029	-0.0006
HKW	-0.0106	-0.0101	-0.0292	-0.0308	-0.0229	-0.0252	-0.0248	-0.0281	-0.0302	-0.0260	-0.0290	-0.0291	-0.0425	0.0022	-0.0026	-0.0030
BRIX	0.0020	0.0039	0.0064	0.0093	0.0090	0.0091	-0.0168	-0.0103	-0.0011	-0.0085	0.0018	0.0106	-0.0048	0.0918	0.0667	0.0578
RS	0.0131	0.0153	0.0079	0.0148	0.0177	0.0182	-0.0058	-0.0001	0.0195	0.0117	0.0137	0.0108	0.0067	0.0801	0.1102	0.0911
SC	-0.0233	-0.0236	-0.0127	-0.0105	0.0015	0.0012	0.0079	-0.0033	-0.0067	0.0021	-0.0025	-0.0030	-0.0115	-0.1015	-0.1333	-0.1612
CYPP	0.2502	0.2640	0.6235	0.7002	0.4867	0.5147	0.4037	0.4123	0.7041	0.8695	0.5298	0.6121	0.6086	-0.0008	0.1746	-0.0165

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

The study revealed that number of kernels per row, number of cobs per plot and number of kernel rows per cob were the most important traits contributing to cob yield in sweet corn, as evidenced by their strong positive genotypic correlations and high positive direct effects. These traits can therefore be considered effective selection criteria for improving cob yield. Sugar traits showed weak or negligible association with yield, indicating the possibility of simultaneous improvement of yield and sweetness in sweet corn.

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