

## Trait associations and path coefficient analyses of agronomic and fresh ear yield traits in *shrunk-2* super-sweet corn (*Zea mays* L. var *saccharata*)

Ayodeji Abe

Department of Crop and Horticultural Sciences, Faculty of Agriculture, University of Ibadan, Ibadan, Nigeria

Correspondence to the author: E-mail: [ayodabe@yahoo.com](mailto:ayodabe@yahoo.com); Tel: +2348065019295

### Abstract

Fresh ear yield (FEY) in sweet corn (*Zea mays* L. var *saccharata*) is a complex trait subject to influence and interaction of many other traits usually affected by genetic and environmental factors. Development of selection criteria for FEY improvement requires knowledge of its inter-relationships with associated traits. Correlation and path coefficient analyses were used to investigate the nature of association and relative importance of 12 agronomic [(days to anthesis, days to silking (DS), anthesis-silking interval, plant height, ear height, husk cover score, ear length (EL), ear diameter (ED), number of kernel rows (NKR)] and FEY [number of ears (NE), ear yield (EY), number of marketable ears (NME), marketable ear yield (MEY)] traits to FEY in *shrunk-2* super-sweet corn genotypes. Genotypic and phenotypic correlations among the traits were estimated. Path coefficient analyses were carried out with MEY as dependent variable. Estimates of genotypic correlation were in most cases higher in magnitude than their corresponding phenotypic correlations. Marketable ear yield was positively and significantly, correlated with NME, EY, EL and ED at the genotypic and phenotypic levels. Path coefficient analysis, based on genotypic correlations, indicated EY, NKR, DS, and NME had positive direct effects on MEY. Phenotypically, EY, ED and NME exhibited positive, direct effects on MEY. No one trait was exclusively important for fresh ear yield in super-sweet corn. Selection criteria based on multiple traits, which should include EY, NME, EL, ED, NKR, and DS would be effective in breeding for high fresh ear yield in *shrunk-2* super-sweet corn.

**Keywords:** Genotypic correlation coefficient, marketable ear yield, phenotypic correlation coefficient, *Shrunk-2* super sweet corn

### Introduction

Sweet corn (*Zea mays* L. var *saccharata*), is a natural mutant of field maize grown primarily as a vegetable for fresh human consumption (Lizaso et al., 2007; Anonymous, 2017; Mousavi et al., 2024) because of its high total sugars, fiber, minerals, vitamins and antioxidant content (Tracy, 1997; Dewanto, Wu and Liu, 2002; Lertrat and Pulam, 2007; Sheng et al., 2018; Mousavi et al., 2024). Sweet corn is harvested 21 to 23 days after silking when ears are immature and kernels milky, and consumed fresh, canned or frozen (Tracy, 2001; Khanduri et al., 2011; Mehta et al., 2017). Elevated sugar content of sweet corns can be traced to the spontaneous mutation in the *su* ("sugary") gene of field maize, which controls synthesis of starch from sugar in the endosperm (Singh et al., 2014; Revilla et al., 2021). Of the 8 mutant monogenic and recessive genes preventing conversion of sugars to starch (Santos et al., 2014), the *shrunk-2* (*sh-2*) super-sweet corn type has the greatest commercial value (Yousef and Juvik, 2002) and higher protein content than other sweet corn types of similar background (Goldman and Tracy, 1994).

Due to widening food preferences and the increasing globalization and popularity of sweet consumption (Abe et al., 2019; Revilla et al., 2021) there has been an increased level of imports of packaged and canned sweet corn into Nigeria. In Nigeria, local sweet corn production is virtually non-existent, except for a very few individuals who rely on highly expensive seeds imported from countries like Brazil. Currently, production statistics for sweet corn is not available in Nigeria. With the vast agricultural land in Nigeria, coupled with her population and therefore market, it is expedient to develop sweet corn genotypes suitable for cultivation under the tropical conditions of the country.

In the development of improved genotypes, information on the extent and direction of associations among traits are required for efficient simultaneous selection of traits of interest. The complex trait, yield, is subject to influence and interaction of many traits, which are usually dependent on genotype, environment, and the interaction between genotype and environment. Selection decisions based on direct improvement of yield alone may not be effective because it does not consider inter-relationships among all contributing traits (Kang, 2015). Information on inter-relationships among yield and yield components allows for simultaneous selection for more traits. Genotypic and phenotypic correlations are important in determining the extent of association between yield contributing traits. Correlation analysis in combination with path coefficient analysis provides a better understanding of the nature of association of different traits with yield. Path coefficient analysis provides a means of assessing the magnitude of relationships between yield and associated traits, and to identify traits which could be used as indirect selection criteria for yield (Mohammadi et al., 2003; Kang, 2015).

Previous studies (Öktem, 2008; Kashiani and Saleh, 2010; Ilker, 2011; Alan et al., 2013; Kashiani et al., 2014; Niji et al., 2018; Gonçalves et al., 2018) have reported on association and contribution of different traits to fresh ear yield in sweet corn. Results from these studies have not been consistent due partly to differences in genetic materials, environmental conditions and traits included in the analysis. There appears to be no such information on sweet corns developed and grown under the tropical environmental conditions in Nigeria. This study was conducted to assess associations and levels of contribution of agronomic and fresh ear yield traits towards marketable ear yield in super-sweet corn.

### Materials and methods

The study was conducted under rain-fed conditions at the experimental field of the Department of Crop and Horticultural Sciences, Faculty of Agriculture, University of Ibadan (7°26' N, 3°54' E), Ibadan, Nigeria during the 2016 and 2017 growing seasons. In 2016, planting was carried out on 22 May, while in 2017, it was done on 17 May. Experimental materials comprised of 12 *sh-2* super-sweet corn populations, 11 of which were derived from crosses between a *sh-2* population and tropical field corn genotypes, while the remaining one was a composite population adapted to the condition in Nigeria after four cycles of mass selection (Adetimirin, 2008). The soil at the experimental site is sandy loam with pH (1:1 H<sub>2</sub>O) 6.0. The site was cleared, plowed and harrowed. The experiment was laid in a randomized complete block design replicated three times. Plots consisted of four rows 5.0 m long. Plant and row spacing were 0.50 and 0.75 m, respectively. Planting was done on the flat. Five seeds were sown per hole and later thinned to two plants per stand at 2 weeks after planting (WAP). This was done to ensure good plant stand, since germination failure is a common feature in super-sweet corn with the *sh-2* gene. Fertilizer using NPK 15:15:15 was applied at the rate of 300 kg ha<sup>-1</sup> at 2 WAP, which provided 45 kg N ha<sup>-1</sup>, 20 kg P ha<sup>-1</sup> and 36 kg K ha<sup>-1</sup>. This was top-dressed at 4 WAP using urea at the rate of 25 kg N ha<sup>-1</sup>. Infestation by fall armyworms was controlled by the use of Ampligo (100 g L<sup>-1</sup> chlorantraniliprole + 50 g L<sup>-1</sup> lambda-cyhalothrin) following manufacturer's instructions. Plots were kept weed free by hand weeding.

Data were collected on days to anthesis (DA): number of days from planting to when 50% of plants in a plot shed pollen, and days to silking (DS): number of days from planting to when 50% of plants in a plot had emerged silk. Anthesis-silking interval (ASI) was calculated as the difference between DS and DA. Plant height (PH) and ear height (EH) were measured two weeks after silking on all plants in the two middle rows of a plot, as the average distance from the soil level to the collar of the uppermost leaf and collar of the leaf bearing the uppermost ear, respectively. Husk cover (HC) was scored as per Badu-Apraku et al. (2010) using a scale of 1 to 9 (1 = husk tightly covers ear tip and extends beyond it; 9 = poor husk cover with ear tip clearly exposed). Harvesting for yield was carried out between stages R3 and R4 (Kling, 1996) when ears were immature and milky at 21 days after silking using plants in the two middle rows of a plot. Yield data included: (i) number of ears (NE) as total number of ears (fresh ears with husk removed) harvested per plot; (ii) ear yield (EY) as total weight of ears (fresh ears with husk removed) harvested per plot; (iii) number of marketable ears (NME) as number of ears at least 10 cm long with approximately 250 filled edible kernels per cob (Solomon et al. 2012); (iv) marketable ear yield (MEY) as total weight of marketable ears per plot; (v) number of kernel rows (NKR) as average number of kernel rows of 10 best ears; (vi) ear length (EL) as the average length of the cob of 10 best ears; (vii) ear diameter (ED) measured with an electronic 6 in. digital caliper (model 47257, Harbor Freight Tools, Camarillo, CA) as average diameter, taken at the middle portion of the 10 best ears.

Estimates of genotypic- and phenotypic-correlation coefficients, and their standard errors, computed as described by Holland (2006). Correlation coefficients were considered significant at 5 and 1% levels when coefficients were more than twice or three times their standard errors, respectively. Marketable ear yield was the dependent trait, other traits were considered independent. To understand the association of independent and dependent traits, genotypic and phenotypic correlation coefficients were subjected to path coefficient analysis (Li, 1975; Williams, Demment and Jones, 1990) using the SASPath programme (Kang, 2015) in SAS (ver. 9.1.3. SAS/STAT user's guide, SAS Institute Inc., Cary, NC). Path coefficients are direct effects expressed as standardized partial regression coefficients which can assume values >1. Total correlation between any independent trait and the dependent trait was determined by summing direct effect of the trait on the dependent trait with indirect effects of all other independent traits on the dependent trait.

### Results

Estimates of genotypic- and phenotypic-correlation coefficients among measured traits varied (Table 1). Estimates of genotypic correlation were, in most cases, higher in magnitude than their corresponding phenotypic correlations, and in the same direction. The MEY was positively, and significantly, correlated with NME, EY, EL and ED at genotypic and phenotypic levels. The MEY was significantly, but negatively, correlated with EH at the genotypic level and ASI at the phenotypic level. At both the genotypic and phenotypic levels, NME was significantly, and positively, correlated with EY and NE, but negatively associated with NKR. The EY was significantly, and positively, associated EL and ED at genotypic and phenotypic levels. At both levels, the

association of EY with ASI was significant, but negative. At both levels, the relationship between NE and NKR was significant, but negative, while its associations with flowering dates were positive, and significant. At genotypic and phenotypic levels, HC and NKR were significantly, and positively, associated. The relationships between PH and EH, as well as between DA and DS at genotypic and phenotypic levels were positive, and significant.

Results of path coefficient analyses based on genotypic- and phenotypic-correlations that estimate the strength of association between MEY and other measured traits varied (Table 2, 3). Path coefficient analyses at genotypic and phenotypic levels indicated the traits accounted for 98.4 and 91.7%, respectively, of total variation in MEY. Path coefficient analysis based on genotypic correlation coefficients indicated EY had the highest positive direct effect on MEY followed by NKR, DS and NME. Although ED was significantly and positively correlated genotypically with MEY, it had the highest negative direct effect on MEY followed by NE. The significant, positive, genotypic correlation coefficients of EL and ED with MEY were primarily a consequence of high indirect effect of EY. Direct contributions of other measured traits to MEY were negligible. In the path analysis, based on phenotypic correlation coefficients, EY manifested the highest positive direct effect on MEY, followed by EL and NME. The magnitude of contribution of EY to final correlations of all other traits included in the path coefficient analyses with MEY at genotypic and phenotypic levels was substanti

**Table 1. Genotypic (above the diagonal) and phenotypic (below the diagonal) correlation coefficients among traits assessed in 12 *shrunk-2* super-sweet corn populations grown for two years in Ibadan, Nigeria<sup>a</sup>**

	MEY <sup>b</sup> (t ha <sup>-1</sup> )	NME	EY (t ha <sup>-1</sup> )	NE	NKR	EL (cm)	ED (mm)	HC	PH (cm)	EH (cm)	DA	DS	ASI
MEY (t ha <sup>-1</sup> )		0.599*	0.992**	0.258	-0.397	0.554*	0.623*	-0.121	-0.636	-0.576*	0.402	0.069	-1.000
NME	0.691**		0.563*	0.657*	-0.629*	-0.042	-0.003	-0.426	-0.587	-0.405	0.454	0.368	-0.499
EY (t ha <sup>-1</sup> )	0.882**	0.591**		0.279	-0.481	0.617*	0.575*	-0.312	-0.468	-0.458	0.506*	0.187	-1.000*
NE	0.230	0.505**	0.281		-0.885**	0.160	-0.503	-0.253	-0.495	-0.403	0.834**	0.982**	-0.099
NKR	-0.222	-0.469*	-0.286	-0.608**		-0.019	0.435	0.598*	0.448	0.310	-0.599*	-0.740	-0.020
EL (cm)	0.672**	0.250	0.563**	0.111	-0.043		0.684*	0.186	-0.379	-0.074	0.515	0.438	-0.509
ED (mm)	0.476*	0.121	0.495**	-0.301	0.413*	0.329		0.278	0.499	0.079	0.089	-0.445	-1.000
HC	-0.147	-0.362	-0.289	-0.187	0.405*	0.075	0.025		-0.150	-0.286	-0.098	0.075	0.519
PH (cm)	-0.160	-0.259	-0.130	-0.230	0.157	0.082	0.028	0.002		0.755**	-0.121	0.257	1.000
EH (cm)	-0.205	-0.246	-0.197	-0.336	0.243	0.092	0.081	-0.139	0.643**		-0.282	-0.134	0.562
DA	0.188	0.202	0.344	0.569**	-0.451*	0.269	0.081	-0.110	-0.033	-0.169		0.963**	-0.693
DS	-0.051	0.087	0.003	0.605**	-0.378	0.046	-0.035	0.012	-0.181	-0.166	0.732**		-0.472
ASI	-0.328*	-0.160	-0.469**	0.036	0.109	-0.309	-0.160	0.168	-0.200	0.008	-0.386*	0.346	

\*, \*\*= significant at 0.05 and 0.01 levels of probability, respectively.

<sup>a</sup> = correlation coefficient were significant when values were at least 2 or 3 times the standard error

<sup>b</sup>MEY = Marketable ear yield; NME = Number of marketable ears; EY = ear yield; NE = Number of ears; NKR = Number of kernel rows; EL = Ear length; ED = Ear diameter; HC = Husk cover; PH = Plant height; EH = Ear height; DA = Days to anthesis; DS = Days to silking; ASI = Anthesis-silking interval

**Table 2. Genotypic correlation-based path coefficient analysis indicating direct (bold and underlined on the diagonal) and indirect (off the diagonal) effects of selected agronomic and yield traits on marketable ear yield of 12 *shrunk-2* super-sweet corn populations grown for two years in Ibadan, Nigeria (Residual effect= 0.128; Coefficient of determination = 0.984)**

Traits	Indirect effects										Genotypic correlation with MEY
	(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)	(10)	
(1) NME	<b>0.380</b>	0.833	-0.434	-0.369	-0.002	0.002	0.002	0.030	0.016	0.141	0.599
(2) EY (t ha <sup>-1</sup> )	0.214	<b>1.480</b>	-0.184	-0.282	0.022	-0.382	0.002	0.034	0.018	0.071	0.992
(3) NE	0.250	0.413	<b>-0.660</b>	-0.519	0.006	0.334	0.002	0.030	0.029	0.375	0.258
(4) NKR	-0.239	-0.712	0.584	<b>0.586</b>	-0.001	-0.289	-0.002	-0.023	-0.021	-0.283	-0.397
(5) EL (cm)	-0.016	0.913	-0.106	-0.011	<b>0.036</b>	-0.454	0.002	0.005	0.018	0.167	0.554
(6) ED (mm)	-0.001	0.851	0.332	0.255	0.024	<b>-0.664</b>	-0.002	-0.006	0.003	-0.170	0.623
(7) PH (cm)	-0.223	-0.692	0.327	0.263	-0.014	-0.331	<b>-0.004</b>	-0.055	-0.004	0.098	-0.636
(8) EH (cm)	-0.154	-0.678	0.266	0.182	-0.003	-0.052	-0.003	<b>-0.073</b>	-0.010	-0.051	-0.576
(9) DA	0.172	0.749	-0.551	-0.351	0.018	-0.059	0.000	0.021	0.035	0.368	0.402
(10) DS	0.140	0.277	-0.648	-0.434	0.016	0.295	-0.001	0.010	0.033	0.382	0.069

MEY: Marketable ear yield; NME: Number of marketable ears; EY: Ear yield; NE: Number of ears; NKR: Number of kernel rows; EL: Ear length; ED: Ear diameter; HC: Husk cover score; PH: Plant height; EH: Ear height; DA: Days to anthesis; DS: Days to silking; ASI: Anthesis-silking interval

**Table 3. Phenotypic correlation-based path coefficient analysis indicating direct (bold and underlined on the diagonal) and indirect (off the diagonal) effects of selected agronomic and yield traits on marketable ear yield of 12 *shrunk-2* super-sweet corn populations grown for two years in Ibadan, Nigeria (Residual effect = 0.288; Coefficient of determination = 0.917)**

Traits	Indirect effects										Phenotypic correlation with MEY
	(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)	(10)	
(1) NME	0.330	0.308	-0.037	0.008	0.083	0.010	-0.009	0.030	-0.038	0.006	0.691
(2) EY (t ha <sup>-1</sup> )	0.195	0.520	-0.020	0.005	0.188	0.040	-0.004	0.024	-0.065	0.000	0.882
(3) NE	0.167	0.146	-0.073	0.010	0.037	-0.024	-0.008	0.041	-0.108	0.042	0.230
(4) NKR	-0.155	-0.149	0.044	-0.017	-0.014	0.033	0.005	-0.029	0.086	-0.026	-0.222
(5) EL (cm)	0.083	0.293	-0.008	0.001	0.334	0.026	0.003	-0.011	-0.051	0.003	0.672
(6) ED (mm)	0.040	0.258	0.022	-0.007	0.110	0.080	0.001	-0.010	-0.015	-0.002	0.476
(7) PH (cm)	-0.086	-0.068	0.017	-0.003	0.027	0.002	0.034	-0.078	0.006	-0.012	-0.160
(8) EH (cm)	-0.081	-0.103	0.024	-0.004	0.031	0.007	0.022	-0.121	0.032	-0.011	-0.205
(9) DA	0.067	0.179	-0.041	0.008	0.090	0.007	-0.001	0.020	-0.190	0.050	0.188
(10) DS	0.029	0.002	-0.044	0.006	0.015	-0.003	-0.006	0.020	-0.139	0.069	-0.051

MEY: Marketable ear yield; NME: Number of marketable ears; EY: ear yield; NE: Number of ears; NKR: Number of kernel rows; EL: Ear length; ED: Ear diameter; HC: Husk cover score; PH: Plant height; EH: Ear height; DA: Days to anthesis; DS: Days to silking; ASI: Anthesis-silking interval

## Discussion

Sweet corn is an annual perishable vegetable crop, grown primarily for fresh consumption. Fresh ear yield in sweet corn is a quantitative trait influenced by action, and interaction, of other traits which vary with genotype and environment. Higher genotypic than phenotypic correlation coefficients, obtained for most traits, indicated the relationships of traits with marketable ear yield were due more to genetic than environmental causes. The positive, significant, associations of marketable ear yield, and ear yield, with number of marketable ears, ear length and ear diameter at genotypic and phenotypic levels, were consistent with findings of Kashiani and Saleh (2010), Alan et al. (2013), Kashiani et al. (2014), Gonçalves et al. (2018) and Niji et al. (2018). In addition, they reported positive, significant, genetic relationship between fresh ear yield and number of kernel rows. In this study it was determined there was no significant correlation for marketable ear yield and ear yield with number of kernel rows. Neither marketable ear yield nor ear yield, was associated with plant height. This indicates that selection for plant height in the populations might not have serious implications on fresh ear yield. The results agree with Öktem (2008) and Alan et al. (2013). Contrary to these findings, studies by Kashiani and Saleh, (2010), Kashiani et al., (2014), and Niji et al., (2018) reported significant positive genetic association between plant height and fresh ear yield in sweet corn. A significant negative association between ear yield and plant height, at genetic and phenotypic levels, has also been reported (Gonçalves et al., 2018). Genetically and phenotypically, marketable ear yield was not affected by flowering date, an indication that time of flowering could have no genetic effect on marketable ear yield. A similar result was reported by Kashiani et al. (2014). These results contradict reports of significant negative genetic correlations of fresh ear yield with tasseling and silking traits in sweet corn (Kashiani and Saleh, 2010; Gonçalves et al., 2018; Niji et al., 2018). These conflicting findings could be attributed to differences in conditions under which the studies were conducted and genetic materials used; which highlights the need to design breeding strategies for specific growing environments.

In this study, some traits could be considered adequate for sweet corn breeding. At the genotypic level, ear yield, number of kernel rows, days to silking and number of marketable ears were the most important traits to marketable ear yield, while ear yield, ear length and number of marketable ears were most important at the phenotypic level. These traits could be used as selection criteria in breeding for high marketable ear yield in sweet corn. These results agree with Öktem (2008) and Ilker (2011) who recommended ear length and fresh ear weight as important yield components that should be used as selection criteria in sweet corn. In breeding for high green ear yield in tropical field maize, Abe (2017) recommended use of yield of husked ears, yield of unhusked ears and number of marketable ears as selection criteria. On the contrary, ear diameter and ear length were the most important traits in breeding for ear yield in super-sweet corn (Gonçalves et al., 2018). The results of the present study indicated that no one trait was exclusively important for fresh ear yield in sweet corn. Multiple traits which should include ear yield, number of marketable ears, ear length, number of kernel rows and days to silking should be considered as selection criteria in sweet corn breeding for high fresh ear yield in super-sweet corn in Nigeria.

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## Conflict of interest

The author declares no conflict of interest.

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