SELECTION OF CHARACTERS THROUGH ESTIMATION OF GENETIC PARAMETERS, ASSOCIATION AND PATH ANALYSIS IN SWEET CORN (*Zea mays* L. saccharata)

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ABSTRACT
Present study was aimed to detection of green cob yield and yield attributing traits for identification of high yielding sweet corn genotypes. Green cob yield (0.62,54.74), TSS (0.67,24.81), days to 50% pollen shedding (0.93, 26.82) and silking (0.89, 25.06) had recorded high heritability together with high genetic advance % of mean which suggests that these traits are mainly under the control of additive gene action and selection may be effective. At genotypic and phenotypic level green cob yield registered positively significant correlation with plant height (0.6565, 0.8609), cobs/plot (0.6346, 0.7853) and days to 50% silking (0.0518, 0.1308) and negatively with TSS (-1.1637, -0.2102). Path analysis studies reveled that all the characters recorded low magnitude of direct effects on the green cob yield.

INTRODUCTION

Among the various specialty corns, sweet corn has a very huge market potentiality not only in national market but also in global market as well. Sweet corn is the type of corn with a thin pericarp layer, translucent, horny appearance of kernels when matured and wrinkled when it dries, and consumed at immature grain stages of endosperm at twenty days after fertilization. Total sugar content in sweet corn at milky stage ranges 25 to 30% as compared to 2 to 5% of normal corn. Fresh and new sweet corn ears are consumed after cooking as well as in roasted form and increasingly in high demand in the hotels for the preparations of delicious sweet corn soup. Mature kernels are crushed to produce the confection pinhole as a fermentable source for the production of an alcoholic beverage, chichi. It is also served as a raw material for various industrial products such as starch syrup, dextrose and dextrin *etc.* Thus sweet corn with varied use has a great potential in export as well as domestic market. Sweet corn matures early and green ears can be harvested in 75-80 days after planting. The left over stalk can serve as useful fodder for the livestock. Thus, it can fit easily in multiple or inter cropping systems.

To increase the farmers' income throughout year cultivation of sweet corn is an attractive option for the farmer, but the available public cultivars are low yielding. Some private hybrids are very popular like Sugar 75 and Misthi where seed is very costly. Hence, there is necessitated to develop high yielding hybrids with sugar content is need of the hour. Conventional sweet corn breeding methods have been used

to develop commercial hybrids by breeders for more than century. This method involves the development of homozygous inbred lines by selfing and selection of desired phenotypes using pedigree selection from broad based breeding populations, the crossing of these inbred lines and the evaluation of the hybrids from the crosses to determine which have yield potential (Kamol and Taweesak, 2007). For the selection of desirable inbred line knowledge on heritability establishes appropriate selection methods coupled with the prediction of any grains from selection while also helping to establish the magnitude of the genetic effects. Burton (1952) had suggested that the genetic components of variation together with heritability estimates would give the best picture of amount of genetic advance to be expected from the selection. Response to selection depends on various factors such as the interrelationship of the characters. Plant breeder's work with some yield components related to yield in the selection programs and it is very important to decide relative importance of such characters contributing to yield directly or indirectly. Correlation and path coefficient analyses can assist to determine certain characters to be used in the improvement of the complex character such as yield (Joshi, 2005). Many workers reported importance of genetic parameters, correlation and path analysis in sweet corn and highlighted the important traits for selection of high yielding genotypes. Manal henfy, 2011(cob weight per plant, ear length, days to 50% silking and ear diameter), Guripendar Singh *et al.*, 2017 (ear length, days to maturity, kernel rows per ear and grains per ear), Gonclalves *et al.*, 2018 (ear

diameter and ear length), Atom Atanasio Ladu Stansluos et al. 2019 (ear diameter) and Abe and Adelegan, 2019 (husked and dehusked ear weight) reported priority could be given while selecting the character for yield improvement sweet corn. However, green cob yield was negatively correlated with total soluble sugar (Atom Atanasio Ladu stansluos *et al.*,2019). Information on association characters in sweet corn has been still very limited. Therefore, keeping in view the significance of these parameters, present investigation was undertaken in sweet corn to recognize important traits for selection of high yielding sweet corn genotypes from the segregating material.

MATERIALS AND METHODS

A total of 138 hybrids were evaluated with two rows 4m length in randomized complete block with two replications during kharif, 2018 at Maize Research Centre, Agricultural Research Institute, Rajendranagar, Hyderabad (Altitude of 542.6 m and around 79°23'E longitude and 17°19'N latitude). Recommended agronomic package of practices followed for raising the good crop. Observations were collected on seven quantitative characters on individual plant and plot basis at appropriate growth stages. The observations were recorded on the characters like total soluble solids(TSS), plant height(cm), ear height(cm), cobs/plot, days to 50% pollen shed, days to 50% silking and green cob yield (kg/ha). Sugar content present in each grain in percentage (TSS) at milky stage was recorded by using brix meter.

Data analyzed for each trait by using WINDOW STAT 9.2 version as standard procedures were given by Panse and Sukhatme 1985(analysis variance), Hanson *et al.*, 1956 (heritability in broad sense), Johnson *et al.*,1955 (genetic advance and genetic advance as per cent of the mean), Burton 1952 (phenotypic and genotypic coefficient of variation) and Dewey and Lu 1959 (phenotypic and genotypic correlations and path coefficient analyses) as detailed below

i)Phenotypic coefficient of variation (PCV) =

$$PCV = \frac{\sqrt{\sigma^2 P}}{x} X100$$

where

$\sigma^2 p$ = phenotypic variance;
X = mean of that trait

ii)Genotypic coefficient of variation (GCV)

$$GCV = \frac{\sqrt{\sigma^2 g}}{x} X100$$

where
$\sigma^2 p$ = genotypic variance;
X = mean of that trait
iii)Broad sense heritability

$$h^2B = \frac{\sigma^2 g}{\sigma^2 p}$$

$\sigma^2 p$ = genotypic variance;

$\sigma^2 p$ = phenotypic variance

iv)Expected genetic advance

$$GA = Kx\sqrt{\sigma^2 p} \ x \ h^2B$$

where

K = constant that represents the selection intensity (when k is 5% the value is 2.06);

$\sqrt{\sigma^2 p}$ = standard deviation of phenotypic variance;

h^2B = heritability in a broad sense

RESULTS AND DISCUSSION

The mean sum of squares due to genotypes was found to be highly significant for all the traits (table 1), revealed that there is a considerable variation present among the genotypes selected. Mean, range, heritability and genetic advance as % of mean are presented in table 2. The genotypes evaluated in this study exhibited wide range of mean values ranging from 9.55-20.70 for TSS (%), 125.50-195.00 for plant height(cm), 26.50-72.50 for ear height(cm), 2.50-41.50 for cobs/plot. Genotypes recorded mean values ranging from 59.00-81.50 for days to 50% pollen shed and 61.00-83.50 for days to 50% silking. Signifying the presence of considerable variability among the genotypes, which is desirable for selection of superior genotypes.

Phenotypic coefficient of variation (PCV) greater than the genotypic coefficient of variation (GCV) for all traits indicating that almost all the characters are more influenced by the environment. Asghar and Mehdi (1999), Saleh et al. (2002) and Alan *et al.*(2013) also reported influence of environment in sweet corn. High GCV and PCV values observed for green cob yield (26.28, 33.90) and cobs/plot (20.55, 32.25). Moderate values were recorded for ear height (15.92, 22.38), TSS (11.41, 13.85), days to 50% pollen shedding (10.54, 10.94), days to 50% silking (10.05, 10.64) and plant height (6.74, 10.15). Hence, selection on the basis of phenotype can be effective for improvement of these traits.

The efficacy of selection not only depends on the amount of variability present in a trait but also the extent of heritability of the desirable character. Estimates of broad sense heritability ranged between 40.6% (cobs/plot) to 92.9% (days to 50% pollen shed) and it was found to be highest for days to 50% pollen shedding (92.9%) followed by days to 50% silking (89.2%), TSS (67.9%), green cob yield (62.3%), ear height (50.6%), plant height (41.7%) and cobs/plot (40.6%). Alan *et al.* (2013), Niji *et al.* (2018) and Abe and Adelegan (2019) also highlighted for most of the traits. In a selection of genotypes, heritability values as well as genetic advance were more valuable than heritability alone (Johnson *et al.*(1955)). Green

Table 1: Analysis of variance for cob yield and its component traits in sweet corn

Source of variation	d.f.	TSS	Plant height	Ear height	Cobs / plot	Days to 50% pollen shed	Days to 50% silking	Cob wt. + husk1 (kg/ha)
Replication	1	1.03	0.028	12.78	688.75**	15.3	39.94	2572691
Genotypes	137	6.88**	373.70**	147.60**	74.50**	107.61**	105.88**	14694236.35**
Error	137	1.31	153.83	48.38	31.45	3.95	6.01	3417242

Table 2: Estimates of mean, range, heritability and genetic advance in sweet corn

Characters	Mean	Range	GCV	PCV	h² (Broad Sense)	Genetic Advance ment 1%	Gen.Adv as % of Mean 1%
TSS (%)	14.62	9.55-20.70	11.405	13.845	0.679	3.628	24.803
Plant height (cm)	155.47	125.50-195.00	6.744	10.447	0.417	17.87	11.494
Ear height (cm)	44.24	26.50-72.50	15.922	22.379	0.506	13.229	29.907
Cobs/plot	22.58	2.50-41.50	20.555	32.246	0.406	7.808	34.589
Days to 50% pollen shed	68.3	59.00-81.50	10.541	10.935	0.929	18.321	26.825
Days to 50% silking	70.31	61.00-83.50	10.051	10.639	0.892	17.623	25.066
Green cob yield (Kg/ha)	9035.56	2229.50-15520.50	26.28	33.305	0.623	4946.583	54.746

Table 3: Phenotypic and genotypic correlations between cob yield and yield component traits in sweet corn

Characters		TSS (%)	Plant height (cm)	Ear height (cm)	Cobs /plot	Days 50% pollen shed	Days 50% silking	Green cob yield (Kg/ha)
TSS (%)	P	1.0000	-0.1049	-0.0822	0.006	-0.3955 ***	-0.3829 ***	-0.1637**
	G	1.0000	-0.1082	-0.0309	0.0653	-0.5165	-0.4898	-0.2102**
Plant height (cm)	P		1 .0000	0.8265 **	0.3400 **	0.1264 *	0.1285 *	0.6565**
	G		1 .0000	0.9212	0.3586	0.2681	0.2789	0.8609**
Ear height (Cm)	P			1.0000	0.3024 **	0.1406 *	0.1495 *	0.5862**
	G			1.0000	0.2911	0.3067	0.3099	0.06825
Cobs /plot	P				1 .0000	-0.2088 **	-0.1996 ***	0.6346**
	G				1 .0000	-0.2477	-0.2493	0.7853**
Days 50% pollen shed	P					1 .0000	0.9658 ***	0.0518
	G					1 .0000	0.9996	0.1308*
Days 50% silking	P						1 .0000	0.0624**
	G						1 .0000	0.1486*
Green cob yield (Kg/ha)	P							1.0000
	G							1.0000

*, ** significant at 5% and 1% levels

Table 4: Direct (diagonal) and indirect effects of yield contributing characters in sweet corn

Characters		TSS (Cubic Feet)	Plant height (cm)	Ear height (cm)	Cobs /plot	days 50% pollen shed	days 50% silk	Cob Wt+ husk1 (Kg/ha)
TSS (Cubic Feet)	P	0 .0001	0.00001	0.0001	0.0001	0.0001	0.0001	-0.1637**
	G	0.0002	0.0001	0.0001	0.0001	-0.0001	-0.0001	-0.2102**
Plant height (cm)	P	0.0001	0.0001	0.0001	0.0001	0.0001	0 .0001	0.6565**
	G	-0.0002	0.0015	0.0014	0.0005	0.0004	0.0004	0.8609**
Ear height (cm)	P	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.5862**
	G	0.0001	-0.0009	-0.001	-0.0003	-0.0003	-0.0003	0.06825
Cobs /plot	P	0.0001	0.0001	0 .0001	0 .0001	0.0001	0.0001	0.6346**
	G	0.0001	0.0002	0.0001	0.0005	-0.0001	-0.0001	0.7853**
days 50% pollen shed	P	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0518
	G	-0.0032	0.0017	0.0019	-0.0015	0.0062	0.0062	0.1308*
days 50% silking	P	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0624**
	G	0.0029	-0.0017	-0.0019	0.0015	-0.006	-0.006	0.1486*

cob yield followed by cobs/plot, ear height, days to 50% pollen shed, days to 50% silking, TSS and plant height registered high values of genetic advance and genetic advance as percentage of mean.

High heritability coupled with high genetic advance were recorded for TSS, days to 50% pollen shed, days to 50% silking and green cob yield which suggests that these traits are predominantly under the control of additive gene action and selection may be effective. Suhasini et al.(2016), Niji et al. (2018) and Chinthiya et al. (2019) reported for above traits.

Correlation coefficients generally show interaction among independent variables and the degree of linear relation between these characteristics. Genotypic correlations were more than phenotypic correlations (table 3). Sharma, 1988

reported in most cases, the genotypic correlation was higher than that of phenotypic correlation reveals that association may be largely due to genetic reason (strong coupling linkage). Green cob yield registered positively significant with plant height, cobs/plot and days to 50% silking and negatively with TSS at genotypic and phenotypic level (table 3). Ear height was positively significant at phenotypic level and days to 50% pollen shedding at genotypic level with green cob yield. Similar agreements were made by Oktem (2008), Ilker (2011), Begum *et al.* (2016) and Chozin *et al.* (2017) for plant height. However, Asbish Khanduri *et al.* (2010), Sadaiah *et al.*(2013), Suhaisini *et al.* (2016) and Niji *et al.* (2018) reported TSS was non significant association with yield in sweet corn. This indicates that the difficulty of simultaneous improvement of sweet corn for both yield ability and kernel quality (Saleh *et al.*, 2002). Hence, consider the other traits *viz.*, cobs/plot, plant height and days to 50% silking while selecting the genotypes having high sugar content can be considered for improvement of yield as well as sweetness.

The inter relationships between green ear cob yield components like days to 50% pollen shedding and silking showed significant positive correlations with plant and ear height and negative correlations with TSS and cobs/plot. Days to 50% pollen shedding and silking showed significant positive correlations with plant and ear height also reported by Nataraj *et al.* (2014) and Begum *et al* (2016). Esiyok *et al.*,2011 highlighted the importance of genotypic correlation for examining degree of relationships among traits due to phenotypic correlation obtains from genotype and environment interaction.

Correlations coefficients along with path effects together provide more reliable information which can be effectively used in crop improvement programme. Path analysis studies reveled that all the characters recorded low magnitude of direct effects on the green ear cob yield (table 4). Albayrak *et al.* (2003) illustrated that if the correlation between causal factor and direct effect is more or less of equal magnitude, it explains the true and perfect relationship between the traits and direct selection through these traits will be rewarding. Hence, plant height, cobs/plot and days to 50% silking traits considered for selection of genotypes as recorded significant positive correlations with green cob yield and low agnitude of direct effects. Oktem (2008), Ilker (2011), Begum *et al.* (2016) and Chozin *et al.* (2017) also reported for the most of the traits.

From the above study, it can be concluded that for improvement of green cob yield in sweet corn traits like cobs /plot, days to 50% silking and plant height are the important as they show high heritability coupled with high genetic advance, positive significant correlations and low direct effects on green cob yield.

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