Original Research Article

Studies on Genetic Parameters, Correlation and Path Analysis for Yield and Yield Attributing Traits in Sweet Corn (*Zea mays* L. *saccharata*)

Sonal Chavan[1*], D. Bhadru[2], V. Swarnalatha[3] and B. Mallaiah[2]

[1]*Department of Genetics and Plant breeding, College of Agriculture, Rajendranagar, Professor Jayashankar Telangana State Agricultural University, Hyderabad-500030*
[2]*Maize Research Centre, Rajendranagar, Hyderabad, India*
Seed Research and Technology Centre, Rajendranagar, Hyderabad, India

*Corresponding author

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The present investigation was carried out in 25 sweet corn inbred lines during *Rabi* 2019-20. Significant differences among genotypes for most of the traits were noticed, indicating the presence of substantial genetic variability. Phenotypic coefficients of variation (PCV) were higher than genotypic coefficients of variation (GCV), indicating the role of experimental variance to the total variance. Moderate to high range of GCV, PCV, heritability and genetic advance over mean were recorded for ear height, ear length, number of rows per ear, number of kernels per row, cob weight with husk and without husk and PFSR disease score, which indicates the importance of these traits in selection of sweet corn inbred lines. Ear height, ear length, number of rows per ear, number of kernels per row, cob weight without husk were very important for selection of sweet corn genotypes as they recorded positive significant correlations and direct effects were also recorded by some of these traits on cob weight with husk i.e. green cob yield.

Introduction

Among the various specialty corns, sweet corn is gaining popularity in India and other Asian countries. It also has a very huge market potential not only in national market but in global market as well. Fresh and raw sweet corn ears are consumed after cooking as

well as in roasted form and are increasingly in high demand in the hotels for the preparations of delicious sweet corn soup. Sweet corns are eaten green as highly valued fresh products like baby corn; immature kernels are parboiled and/or dried to produce candy, mature kernels are crushed to produce the confection pinnole as a fermentable source for

the production of an alcoholic beverage, chichi and also used as material for deriving large number of industrial products such as starch syrup, dextrose and dextrin etc. In India, composites like Madhuri and Priya (ANGRAU), HSC-1, win orange and Punjab Sweet Corn 1 from the public sector and only few hybrids (Sugar 75 and Misti) have been developed by the private sector. No sweet corn hybrid has been released so far by the public sector. The available public cultivars are low yielding, so the farmers have to depend on private sector hybrids which are sold to farmers at high cost. So development of high yielding sweet corn hybrids is need of the hour.

For the development of productive and adapted cultivars to supply the market demand, understanding of genetic variability present in a given crop species for the traits under improvement is imperative for the success of any plant breeding program (Sankar *et al.,* 2006). Genotypic and phenotypic coefficients of variation (GCV and PCV) are useful in detecting the amount of variability present in a given characteristic. The efficiency with which genotypic variability can be exploited by selection depends upon heritability and genetic advance (GA) of individual trait (Bilgin *et al.,* 2010). Heritability is a measure of the phenotypic variance attributable to genetic causes and it predicts the extent to which a particular character can be transmitted to successive generations. Whereas genetic advance shows the degree of gain obtained for the characters under a particular selection pressure (Niji *et al.,* 2018). Heritability estimates along with genetic advance are normally more helpful in predicting gain under selection than heritability estimates alone as it is not sufficiently informative about the existence of gene action (additive/non-additive) and involvement of other factors in the expression of traits (Johnson *et al.,* 1955).

As yield is a dependent character and it is based on number of quantitative characters, it is important to study the association between pairs of these attributes for faster assessment of high yielding genotypes in selection programme. Correlation studies reflect the extent of association between two characters and helps in determining the yield contributing characters. Genotypic correlations reveal the real association between traits, as it does not include the environmental effects as such in case of phenotypic correlations and thereby is more important compared to phenotypic correlation. Correlation coefficients generally show relationships among independent variables and the degree of linear relation between these characteristics but it does not sufficiently predict the success of selection. However, path-coefficient analysis that is originally developed by Wright (1929) is the most valuable tool to establish the exact correlation in terms of cause and effect. It allows one to identify the direct, indirect and total (direct + indirect) causal effect, as well as to remove any spurious effect that may be present (Hefny, 2011).

Keeping in view the significance of these parameters, present investigation was undertaken in sweet corn on genetic parameters, correlation and path coefficient analysis.

Materials and Methods

The present investigation was carried out in *Rabi,* 2019-20 at Maize Research Centre, Rajendranagar, Hyderabad, which is located at an altitude of 542.6 m and at 79º23'E longitude and 17º19'N latitude. Twenty five sweet corn inbred lines were evaluated in randomized block design with two replications with spacing of 60 x 10 cm. The observations were collected on thirteen yield and yield contributing traits viz., days to 50%

tasseling, days to 50% silking, plant height (cm), ear height (cm), ear length (cm), ear diameter (cm), number of kernel rows per ear, number of kernels per row, cob weight with husk (kg/ha), cob weight without husk (kg/ha), total soluble sugars (%) by using brix meter, green fodder yield (kg/ha) and post flowering stock rot (PFSR) disease score *(Macrophomina phaseolina)* by tooth pick method.

Statistical analysis

The data collected was subjected to statistical analysis using INDOSTAT software version 9.2 and the methods adopted by the software for the analysis of variance (ANOVA) was as described by Panse and Sukhatme (1985), mean, standard error and range were calculated as per Singh and Chaudhary (1985). Phenotypic and genotypic coefficients of variation (PCV and GCV) were as per Burton (1952) and were categorized as low (0-10%), moderate (10-20%) and high (>30%) as indicated by Sivasubramanian and Madhavamenon (1973). Heritability in broad sense was estimated as the ratio of genotypic variance to the phenotypic variance as suggested by Hanson *et al.,* (1956) and it was as categorized as low (0-30%), moderate (30-60%) and high (>60%) as indicated by Johnson *et al.,* (1955).

Genetic advance (GA) and genetic advance as per cent of the mean (GAM) were calculated by using the formulae given by Johnson *et al.,* (1955). The GA as percent of the mean was categorized as low (0-10%), moderate (10-20%) and high (>20%) according to Johnson *et al.,* (1955). Correlation coefficients were calculated by using the formulae given by Johnson *et al.,* (1955). The direct and indirect effects for genotypes were estimated by using path coefficient analysis suggested by Wright (1921) and Dewey and Lu (1959).

Results and Discussion

The analysis of variance revealed significant difference among genotypes for all traits except for the traits like days to 50% tasseling, plant height and green fodder yield (Table 1) indicating the presence of considerable significant variation among the genotypes selected, which is pre-requisite for the breeder to take up any breeding programme.

In the present study, estimates of PCV were found to be slightly higher than their corresponding GCV for most of the traits (Table 2), which indicates that the expressions of these traits were influenced by environment to a limited extent and there is possibility of improvement of these traits by using phenotypic selection. Similar findings of higher PCV than GCV were reported by Alan *et al.,* (2013), Niji *et al.,* (2018) and Ayodeji Abe and Adelegan (2019) in sweet corn. The difference between PCV and GCV estimates were found to be more for the traits days to 50% tasseling, plant height and green fodder yield, indicating that for these traits the phenotypic selection may be misleading. Bello *et al.,* (2012), Nzuve *et al.,* (2014) and Sesay *et al.,* (2016) have also reported high difference between PCV and GCV estimates for plant height. Low to medium PCV and GCV estimates were recorded for most of the traits. The trait PFSR disease score, cob weight without husk, cob weight with husk and ear height registered more than 20 percent of GCV and PCV and these traits were considered for selection of sweet corn inbred lines. Hefny (2011) for yield per plant, Reddy *et al.,* (2012) and Meena *et al.,* (2016) for ear height and Niji *et al.,* (2018) for green cob yield reported high estimates of PCV and GCV.

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 (Burton, 1952). Traits days to 50% silking, ear height, ear length, ear diameter, no. of kernel rows per ear, ear length, no. of kernels per row, cob weight with husk, total soluble sugars and PFSR disease score registered high estimates of broad sense heritability. However, selection for improvement of such characters may not be useful, because broad sense heritability is based on total genetic variance which includes additive, dominant and epistatic variances. Thus, heritability estimates coupled with high genetic advance would be more reliable and useful on correlating selection criteria (Reddy *et al.,* 2012). The traits ear height, ear length, no. of kernel rows per ear, no. of kernels per row, cob weight with husk, cob weight without husk and PFSR disease score exhibited high estimates of genetic advance as per cent of mean.

High heritability accompanied with high genetic advance as per cent of mean were recorded for ear height, ear length, no. of kernel rows per ear, no. of kernels per row, cob weight with husk and PFSR disease score, indicating that the heritability is due to additive gene effects. Moderate heritability with high genetic advance as per cent of mean was recorded for cob weight without husk, indicating the role of additive gene effects, the moderate heritability may be due to environmental effects and selection would be rewarding for this trait. Thus the traits are fixable and selection would be effective for these traits. Similar findings were reported by Reddy *et al.,* (2012) for ear height, ear length and no. of kernels per row, Begum *et al.,* (2016) for ear height, Sesay *et al.,* (2016) for yield and Niji *et al.,* (2018) for green cob weight.

While selecting the sweet corn genotype, priority should be given for characters like ear height, ear length, number of kernels rows per ear, number of kernels per row, cob weight with husk and without husk and PFSR disease score as showed moderate to high range of GCV, PCV, heritability and genetic advance over mean.

Plant height, ear height, ear length, ear diameter, number of kernels per row and cob weight without husk were observed to exhibit significant positive correlations with cob weight with husk at phenotypic and genotypic level (Table 3). Whereas, number of rows per ear and PFSR disease score recorded non-significant positive correlation with cob weight with husk at both levels. Days to 50% tasseling recorded non-significant negative at phenotypic and significant negative correlation at genotypic level with cob weight with husk. Days to 50% silking and total soluble sugars recorded non-significant negative correlations and green fodder yield recorded significant positive at phenotypic and significant negative correlation at genotypic level with cob weight with husk. The results were in agreement with the findings of Raghu *et al.,* (2011), Reddy *et al.,* (2013), Suhasini *et al.,* (2016) and Niji *et al.,* (2018) for the traits plant height, ear height, ear length, ear girth and no. of kernel rows per ear, Raghu *et al.,* (2011) and Suhasini *et al.,* (2016) for the trait no. of kernels per row, Kumara *et al.,* (2011) and Chinthiya *et al.,* (2019) for traits plant height, cob length, cob diameter and no. of kernels per row. Hence simultaneous selection can be done in these positively correlated traits through further breeding programmes.

Inter correlations among yield components revealed that days to 50% silking recorded significant positive correlation with days to 50% tasseling. Similarly, ear height with plant height, trait ear length with plant height, trait ear diameter with plant height, ear height and ear length, trait number of kernel rows per ear

with ear height and ear diameter, trait number of kernels per row with ear length and ear diameter, trait cob weight without husk with plant height, ear height, ear length, ear diameter and no. of kernels per row recorded significant positive correlations.

Table.1 Analysis of variance for yield and yield attributing traits in 45 sweet corn inbred lines

Source of variation	Mean sum of squares of		
	Replications	Genotypes	Error
d.f	1	24	24
Days to 50% tasseling	0.02	13.6	8.1
Days to 50% silking	2	14.4**	2.54
Plant height (cm)	1.3	565.8	293.8
Ear height (cm)	0.7	177.8**	0.7
Ear length (cm)	2.2*	10.3**	0.3
Ear diameter (cm)	2	3.0**	0.5
No. of kernel rows per ear	0	5.9**	0.6
No. of kernels per row	5.1	44.0**	1.4
Cob weight with husk (kg/ha)	492523.3	27460145.0**	972427.9
Cob weight without husk (kg/ha)	3843	24726071.6**	6214186.9
Total soluble sugars (%)	0.7	3.5**	0.2
Green fodder yield (kg/ha)	1201647	12327470	23217966
PFSR disease score	0	4.0**	0.3

*, ** Significant at 5% &1% level respectively.

Table.2 Genetic parameters for yield and yield attributing traits in sweet corn

Character	Mean	Range		PCV (%)	GCV (%)	Heritability (%) in broad sense	GA	GAM (%)
		Minimum	Maximum					
Days to 50% tasseling	74	70	79	4.43	2.23	25	1.72	2.32
Days to 50% silking	77	73	82	3.79	3.18	70	4.21	5.48
Plant height (cm)	143	119	175	14.49	8.15	31	13.51	9.44
Ear height (cm)	47	32	67	20.29	20.21	99	19.3	41.45
Ear length (cm)	15	10	20	15.1	14.56	93	4.43	28.94
Ear diameter (cm)	12	10	15	10.96	9.07	68	1.9	15.47
No. of kernel rows per ear	14	12	20	12.32	11.01	79	2.98	20.25
No. of kernels per row	27	18	37	17.74	17.15	93	9.18	34.15
Cob weight with husk (kg/ha)	17329	10429	25408	21.75	21	93	7235.83	41.75
Cob weight without husk (kg/ha)	13267	6581	20211	29.64	22.93	59	4847.75	36.53
Total soluble sugars (%)	14.1	11.7	17.2	9.76	9.14	87	2.49	17.62
Green fodder yield (kg/ha)	30771	24220	35072	13.7	7.58	-30	-2660.77	-8.64
PFSR disease score	4.8	3	7.5	30.34	27.94	84	2.58	53.01

Table.3 Phenotypic (P) and genotypic (G) correlations for yield and yield attributing traits in sweet corn

Character		Days to 50% tasseling	Days to 50% silking	Plant height (cm)	Ear height (cm)	Ear length (cm)	Ear diameter (cm)	Number of rows per ear	Number of kernels per row	Cob weight without husk (kg/ha)	Total soluble sugars (%)	Green fodder yield (kg/ha)	PFSR disease score	Cob weight with husk (kg/ha)
Days to 50% tasseling	P	1	0.9484**	0.1542	-0.1192	-0.2099	-0.0839	0.1067	-0.266	0.163	0.2458	0.5327**	0.0579	-0.0234
	G	1	1.1808**	-1.9185**	-0.1833	-0.5130**	-1.1882**	0.0513	-0.5684**	-0.9559**	0.5463**	1.5505**	0.3268*	-0.4538**
Days to 50% silking	P		1	-0.0254	-0.1395	-0.2349	-0.2222	0.0935	-0.2831*	0.0498	0.2746	0.3478*	0.0677	-0.0649
	G		1	-0.9187**	-0.148	-0.3191*	-0.6691**	0.0303	-0.3508*	-0.4042**	0.3550*	0.4637**	0.1753	-0.2259
Plant height (cm)	P			1	0.6733**	0.3693**	0.6601**	0.1437	0.2677	0.6576**	-0.0142	0.6113**	0.0212	0.5503**
	G			1	1.2497**	0.6258**	0.5740**	0.2002	0.4749**	0.3229*	0.0002	1.0573**	0.2232	0.6752**
Ear height (cm)	P				1	0.2785	0.5410**	0.3383*	0.1306	0.3478*	0.1979	0.1812	0.2193	0.4062**
	G				1	0.2870*	0.6674**	0.3936**	0.1258	0.4776**	0.1977	-0.3959**	0.2311	0.4260**
Ear length (cm)	P					1	0.3847**	-0.2119	0.8368**	0.6613**	-0.06	0.3270*	0.2914*	0.7153**
	G					1	0.4122**	-0.2663	0.8590**	0.8369**	-0.0802	-0.5394**	0.3553*	0.7287**
Ear diameter (cm)	P						1	0.4637**	0.4084**	0.6601**	-0.0281	0.5241**	0.2971*	0.6395**
	G						1	0.5450**	0.4573**	0.5457**	-0.0311	0.0454	0.4874**	0.6387**
Number of rows per ear	P							1	-0.1966	0.0298	0.0204	0.0367	0.2505	0.0393
	G							1	-0.2389	-0.0458	0.0383	0.0551	0.3046*	0.0111
Number of kernels per row	P								1	0.6495**	-0.2412	0.2964*	0.107	0.6999**
	G								1	0.8511**	-0.2958*	-0.5438**	0.1401	0.7290**
Cob weight without husk (kg/ha)	P									1	-0.155	0.6748**	0.1636	0.9487**
	G									1	-0.2003	0.0924	0.3309*	1.0719**
Total soluble sugars (%)	P										1	-0.0365	0.3826**	-0.175
	G										1	0.0129	0.3578*	-0.1945
Green fodder yield (kg/ha)	P											1	0.0364	0.4760**
	G											1	-0.3332*	-0.4152**
PFSR disease score	P												1	0.1882
	G												1	0.2569

Table.4 Phenotypic (P) and genotypic (G) path coefficients for yield and yield attributing traits in sweet corn

Character		Days to 50% tasseling	Days to 50% silking	Plant height (cm)	Ear height (cm)	Ear length (cm)	Ear diameter (cm)	Number of rows per ear	Number of kernels per row	Cob weight without husk (kg/ha)	Total soluble sugars (%)	Green fodder yield (kg/ha)	PFSR disease score	Cob weight with husk (kg/ha)
Days to 50% tasseling	P	**-0.4783**	-0.4536	-0.0738	0.0570	0.1004	0.0401	-0.0510	0.1272	-0.0779	-0.1175	-0.2548	-0.0277	-0.0234
	G	**-0.7218**	-0.8524	1.3848	0.1323	0.3703	0.8577	-0.0371	0.4103	0.6900	-0.3944	-1.1192	-0.2359	-0.4538**
Days to 50% silking	P	0.4355	**0.4592**	-0.0117	-0.0640	-0.1079	-0.1020	0.0429	-0.1300	0.0229	0.1261	0.1597	0.0311	-0.0649
	G	1.1549	**0.9780**	-0.8985	-0.1447	-0.3121	-0.6544	0.0296	-0.3431	-0.3954	0.3472	0.4535	0.1714	-0.2259
Plant height (cm)	P	-0.0193	0.0032	**-0.1252**	-0.0843	-0.0462	-0.0826	-0.0180	-0.0335	-0.0823	0.0018	-0.0765	-0.0027	0.5503**
	G	-0.1649	-0.0790	**0.0860**	0.1074	0.0538	0.0493	0.0172	0.0408	0.0278	0.0000	0.0909	0.0192	0.6752**
Ear height (cm)	P	-0.0112	-0.0131	0.0632	**0.0938**	0.0261	0.0508	0.0317	0.0123	0.0326	0.0186	0.0170	0.0206	0.4062**
	G	0.0174	0.0140	-0.1183	**-0.0947**	-0.0272	-0.0632	-0.0373	-0.0119	-0.0452	-0.0187	0.0375	-0.0219	0.4260**
Ear length (cm)	P	-0.0232	-0.0260	0.0409	0.0308	**0.1107**	0.0426	-0.0235	0.0927	0.0732	-0.0066	0.0362	0.0323	0.7153**
	G	0.0027	0.0017	-0.0033	-0.0015	**-0.0053**	-0.0022	0.0014	-0.0046	-0.0045	0.0004	0.0029	-0.0019	0.7287**
Ear diameter (cm)	P	-0.0122	-0.0324	0.0961	0.0788	0.0560	**0.1456**	0.0675	0.0595	0.0961	-0.0041	0.0763	0.0433	0.6395**
	G	0.0667	0.0376	-0.0322	-0.0375	-0.0231	**-0.0561**	-0.0306	-0.0257	-0.0306	0.0017	-0.0025	-0.0274	0.6387**
Number of rows per ear	P	-0.0040	-0.0035	-0.0054	-0.0126	0.0079	-0.0173	**-0.0373**	0.0073	-0.0011	-0.0008	-0.0014	-0.0093	0.0393
	G	0.0037	0.0022	0.0146	0.0287	-0.0194	0.0397	**0.0729**	-0.0174	-0.0033	0.0028	0.0040	0.0222	0.0111
Number of kernels per row	P	0.0178	0.0189	-0.0179	-0.0087	-0.0559	-0.0273	0.0131	**-0.0668**	-0.0434	0.0161	-0.0198	-0.0072	0.6999**
	G	0.0597	0.0368	-0.0498	-0.0132	-0.0902	-0.0480	0.0251	**-0.1050**	-0.0893	0.0310	0.0571	-0.0147	0.7290**
Cob weight without husk (kg/ha)	P	0.1693	0.0517	0.6832	0.3613	0.6870	0.6858	0.0310	0.6747	**1.0389**	-0.1611	0.7011	0.1700	0.9487**
	G	-0.8710	-0.3683	0.2942	0.4352	0.7626	0.4972	-0.0418	0.7755	**0.9112**	-0.1825	0.0842	0.3015	1.0719**
Total soluble sugars (%)	P	-0.0092	-0.0102	0.0005	-0.0074	0.0022	0.0010	-0.0008	0.0090	0.0058	**-0.0372**	0.0014	-0.0142	-0.175
	G	0.0021	0.0014	0.0000	0.0008	-0.0003	-0.0001	0.0001	-0.0012	-0.0008	**0.0039**	0.0001	0.0014	-0.1945
Green fodder yield (kg/ha)	P	-0.0861	-0.0562	-0.0989	-0.0293	-0.0529	-0.0848	-0.0059	-0.0479	-0.1091	0.0059	**-0.1617**	-0.0059	0.4760**
	G	-0.0161	-0.0048	-0.0110	0.0041	0.0056	-0.0005	-0.0006	0.0056	-0.0010	-0.0001	**-0.0104**	0.0035	-0.4152**
PFSR disease score	P	-0.0024	-0.0028	-0.0009	-0.0092	-0.0122	-0.0125	-0.0105	-0.0045	-0.0069	-0.0161	-0.0015	**-0.0420**	0.1882
	G	0.0129	0.0069	0.0088	0.0091	0.0140	0.0192	0.0120	0.0055	0.0130	0.0141	-0.0131	**0.0394**	0.2569

Phenotypic and genotypic residual effects 0.1340 and 0.0264 respectively.

Green fodder yield recorded significant positive correlation with days to 50% tasseling, days to 50% silking and plant height; PFSR disease score recorded significant positive correlation with total soluble sugars, ear length and ear diameter. Whereas, total soluble sugars recorded significant positive genotypic correlation with days to 50% tasseling and days to 50% silking. These traits can be improved through simultaneous selection of other traits.

High correlation coefficients may not be always giving the true picture or could mislead the decision because the correlation between two variables may be due to a third factor. Therefore, it is necessary to analyze the cause and effect relationship between dependent and independent variables to reveal the nature of relationship between the variables.

Path coefficient analysis revealed that the trait days to 50% silking recorded highest direct effect (0.9780) followed by cob weight without husk (0.9112), plant height (0.0860), no. of kernel rows per ear (0.0729), PFSR disease score (0.0394) and total soluble sugars (0.0039) (Table 4) at genotypic level and these characters are significantly associated with cob weight with husk. Similar results were obtained in findings of Raghu *et al.,* (2011), Reddy *et al.,* (2013) and Begum *et al.,* (2016) for plant height and no. of kernel rows per ear, Ilker (2011) for ear weight and no. of kernels rows per ear, Sadaiah *et al.,* (2014) for sugar content and Pavlov *et al.,* (2015) for plant height. Thus direct selection for these traits would be effective i.e., with slight increase in one of the above traits may directly contribute to increase in cob weight with husk.

On the other hand, days to 50% tasseling, ear height, ear length, ear diameter, no. of kernels per row and green fodder yield exhibited negative direct effect on cob weight with husk. These findings were in harmony with the findings of Raghu *et al.,* (2011) for days to 50% tasseling, ear length and ear height, Begum *et al.,* (2016) for days to 50% tasseling and ear height Dan Singh Jakhar *et al.,* (2017) for ear height. Most of the traits exhibited indirect influence on cob weight with husk through days to 50% tasseling, days to 50% silking, plant height, ear height, ear length, ear diameter, no. of kernel rows per ear, no. of kernels per row and total soluble sugars. The results thus emphasize that selection could be more effective by indirect selection of these traits.

Phenotypic and genotypic residual effects were 0.1340 and 0.0264 respectively, indicating that some characters which had due weightage in selection for yield improvement are to be included.

From the findings of the present investigation, it may be concluded that characters ear height, ear length, number of kernel rows per ear, number of kernels per row, cob weight without husk and PFSR disease score were important for selection of sweet corn genotypes as these traits recorded moderate to high range of GCV, PCV, heritability, genetic advance over mean and exhibited positive significant correlations and some of these traits also had direct effects on cob weight with husk i.e. green cob yield.

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