Original Research Article

ASSESSMENT OF GENETIC VARIATION AND CHARACTER ASSOCIATION AMONG YIELD AND YIELD ATTRIBUTING TRAITS IN SWEET CORN (*Zea mays L. saccharata*) INBRED LINES

Abstract

In this study, forty-six sweet corn inbred lines were evaluated to assess the variability and association among the yield and yield attributing traits. The traits plant height, ear height, cob length, cob girth, number of rows per ear, number of kernels per row, cob weight with husk and cob weight without husk have shown moderate to high range of PCV, GCV, heritability and genetic advance over mean displaying the importance of these traits in selecting superior sweet corn inbreds. The study revealed that cob length, cob girth, number of kernel rows per ear and cob weight without husk are the key traits to be given prime importance during selection as they exhibited significant positive direct effects with cob weight with husk.

Key words- Correlation, Genetic advance, Genetic variability, Heritability, Path coefficient analysis, Sweet corn, Total soluble sugars

INTRODUCTION

Sweet corn (*Zea mays* L. *saccharata*) (2n=20), is a speciality corn belonging to the family Poaceae. Corn types with ~~a~~ sugar content exceeding 25% during the milking stage are referred to as sweet corn (Patel *et al.*, 2023). Sweetness originates from natural recessive mutations and is characterized by the presence of at least one of the eight recessive mutant genes. The primary genes include Shrunken-2 (*sh2*) on chromosome 3, Brittle (*bt*) and Amylose Extender (*ae*) on chromosome 5, Sugary Enhancer (*se*), Sugary (*su*), and Brittle-2 (*bt2*) on chromosome 4, Waxy (*wx*) on chromosome 9 and Dull (*du*) on chromosome 10 (Tracy *et al.*, 2006). Sweet corn is consumed as both fresh and processed, while its products like sweet corn milk and soups have recently gained popularity in many nations. Green plants left over from harvest can also be fed to cattle as forage or fodder (Bian *et al.*, 2015).

Due to consumer preference, several raw and processed products sweet corn is getting the higher demand in market, as only few hybrids are available hence there is a need of development of high yielding hybrid with consumer preference sweet corn hybrids. For the development of hybrids there is a need to study variability among the inbred lines. Genetic variability not only establishes the foundation for the selection process but also offers valuable insights for identifying diverse parents suitable for hybridization. In addition to variability, heritability and genetic advance also aid in crop improvement programmes. Heritability estimates assist in determining the extent of selection intensity, while genetic advance helps in estimating genetic gains through the selection process. Thus, variability, heritability and genetic advance together help in improving the efficiency of any breeding programme.

Yield is a polygenic character that depends on various other traits, and therefore it is essential to study association among various yield attributing traits. Association studies are valuable tools for comprehending the extent and nature of relationships among various variables (Niji *et al*., 2018). Path analysis serves the purpose of dissecting the correlation coefficients related to yield, distinguishing between direct and indirect effects on yield, and ultimately quantifying the strength of the association between yield and its constituent components (Belay *et al*., 2018). These studies are limited in sweet corn and hence the current research was taken upto study variability and association among yield and yield attributing traits in sweet corn inbreds.

MATERIALS AND METHODS

A set of forty-six sweet corn genotypes collected from Maize Research Centre, Rajendranagar, Hyderabad were evaluated at the College Farm, College of Agriculture, Rajendranagar, Hyderabad located at 17.3218909^0 latitude and 78.4109061^0 longitude during *kharif*, 2022 in randomized block design with two replications.

Each genotype was taken up in two rows, with a row length of four meters. The spacing between plants was set at 20 cm, while the spacing between rows was maintained at 60 cm. Comprehensive data was collected for eleven traits associated with yield i.e., days to 50% tasseling, days to 50% silking, plant height (cm), ear height (cm), cob length (cm), cob girth (cm), number of kernel rows per ear, number of kernels per row, cob weight with husk (g), cob weight without husk (g) and the content of total soluble sugars (TSS) (%), measured using a TSS meter. For the traits days to 50% tasseling and silking data recorded on plot basis and the remaining traits randomly selected five plants and their averages are subjected for analysis.

STATISTICAL ANALYSIS

The entire data analysis was carried out in INDOSTAT software. For each trait, Analysis of Variance (ANOVA) was carried out following the approach outlined by Panse and Sukhatme (1985). Genotypic and phenotypic coefficients of variation (GCV and PCV) were computed using the methodology given by Burton (1952) and categorized into low (0–10%), moderate (10–20%) and high (>30%) was done according to Sivasubramanian and Madhavamenon (1973). According to the criteria presented by Johnson *et al*. (1955), genetic advance, expressed as a percentage of the mean, was determined and classified as low (<10%), moderate (10-20%), or high (>20%). Similarly, heritability was calculated and classified as low (<30%), moderate (30-60%), and high (>60%). The correlation coefficients were computed using the equations provided by Johnson *et al*. (1955). Path coefficient analysis, based on the methodology outlined by Wright (1921) and Dewey and Lu (1959), was employed to determine both direct and indirect effects of the yield components on genotypes.

RESULTS AND DISCUSSION

Analysis of variance (ANOVA) revealed that the mean sum of squares for eleven quantitative traits were significant indicating presence of sufficient variation for those traits among the genotypes (Table 1). The computed values for phenotypic coefficients of variation (PCV) were greater than their genotypic coefficients of variation (GCV) for all the traits due to presence of effect of environment on the genes controlling these traits. Similar results for were reported by Chavan *et al*. (2020) for days to 50% silking, ear height, cob length, cob girth, number of kernel rows per ear, number of kernels per row, cob weight with husk, cob weight without husk and the content of total soluble sugars (TSS) and Khan *et al*.(2017) for days to 50% tasseling and plant height.

High PCV and moderate GCV(Table. 2) were observed for cob weight with husk (21.51 and 19.61) and cob weight without husk (21.03 and 19.06) these results are on par with those of studied by Upadhyay *et al*. (2020) for GCV and Chavan *et al*. (2020) and Vanipraveena *et al*. (2022) for PCV. Low values of PCV and GCV were recorded for traits days to 50% tasseling (6.69 and 6.54), days to 50% silking (6.37 and 6.19), cob girth (8.45 and 6.73) and total soluble sugars (6.21 and 5.92). Similar results were reported by Niji *et al*. (2018) and Vanipraveena *et al*. (2022) for days to 50% tasseling, days to 50% silking, cob girth and TSS. Plant height (11.5 and 10.28), ear height (14.27 and 11.97), cob length (11.69 and 10.49), number of kernel rows per ear (12.11 and 10.20) and number of kernels per row (11.55 and 10.21) recorded moderate

PCV and GCV and are in accordance with results of Lal *et al*. 2014 and Barutala *et al*. (2019).

Heritability estimates for all the traits analysed in this study were high, days to 50 % silking (94 %), ear height (70 %), cob length (80 %), cob girth (63 %), number of kernel rows per ear (71 %), number of kernels per row (78 %), total soluble sugars (91 %) and cob weight with husk (83 %), plant height (79 %), cob weight without husk (82 %). It indicates that these traits were less influenced by environment making them useful for selection. The results were in consonance with findings of Chavan *et al*. (2020) for days to 50 % silking, ear height, cob length, cob girth, number of kernel rows per ear, number of kernels per row, total soluble sugars and cob weight with husk. However, both Kashiani *et al*. (2014) and Upadhyay *et al*. (2020) reported high heritability for plant height and cob weight without husk while Suhasini *et al*. (2016) reported for days to 50% tasseling.

Genetic advance as percent of mean was high for cob weight with husk (36.80), ear height (20.70) and cob weight without husk (35.61). This indicates that these specific traits are likely to be more effectively selected and utilize in future breeding programs, as the primary source of genetic variance can be attributed to additive gene action. Similar results reported by Chavan *et al*. (2020) and Upadhyay *et al*. (2020). Moderate genetic advance as percent of mean was observed for cob length (19.38), cob girth (11.05), number of kernel rows per ear (17.7), number of kernels per row (18.59) and total soluble sugars (11.64). These results are in accordance with Niji *et al*. (2018) and Vanipraveena *et al*. (2022).

The traits ear height, cob weight with husk and cob weight without husk recorded high heritability coupled with high genetic advance as percent of mean indicating that these traits are governed by additive gene action and can be selected effectively by simple selection.

ASSOCIATION STUDIES

In present study it was seen that cob weight with husk revealed significant positive association with cob length (0.4436 **), cob girth (0.6068 **), number of kernel rows per ear (0.2550 *), number of kernels per row (0.2865 **) and cob weight without husk (0.9777**), positive non-significant association with plant height (0.1476) and ear height (0.1476), negative significant correlation with days to 50 % tasseling (-0.2470 *), days to 50 % silking (-0.2286 *) and negative non-significant correlation by total soluble sugars (-0.1944). Similar results were reported by Chavan *et al*. (2020) for cob length, cob girth, TSS and cob weight without husk; Muliadi *et al.* (2021) for number of kernel rows per ear, Yuvaraja *et al.* (2017) for number of kernels per row and Vanipraveena *et al*. (2022) for days to 50% tasseling and days to 50% silking (Table. 3, Fig. 1).

The traits cob length, cob girth, number of kernel rows per ear and number of kernels per row, total soluble sugars and cob weight without husk are to given prime importance during selection and improvement as they are positively correlated with cob weight with husk whereas days to 50% tasseling and days to 50% silking are useful in developing early maturing cultivars.

As correlation alone can mislead the selection and to make effective selections, correlation study is accompanied with path analysis, that allows the breeder to split correlation coefficients into direct and indirect effects.

It was observed that the direct and indirect association through other characters by path analysis revealed that cob weight without husk (0.9962) exhibited largest direct effect on cob weight with husk followed by days to 50% tasseling (0.1267), cob girth (0.0433), number of kernel rows per ear (0.0152), cob length (0.0093) and ear height (0.0035) while the trait plant height exhibited high negative direct effect followed by days to 50% silking (-0.0848), number of kernels per row (-0.0048) and TSS (-0.0010). These results are in accordance with Mahamood *et al.* (2022) for days to 50 per cent tasseling, days to 50 per cent silking, cob length, cob girth and Chavan *et al*. (2020) for ear height, TSS, number of kernels per row and Vanipraveena *et al.* (2022) for cob weight without husk (Table. 4, Fig. 2). The residual effect of path coefficient analysis was 0.16 which is low in magnitude. This implies that the characters studied were having high percentage of variation in cob weight with husk.

Critical analysis of results obtained from correlation and path analysis revealed that selection of traits *viz.*, cob length , cob girth, number of kernel rows per ear and cob weight without husk would bring improvement in yield and yield attributing as they possess high positive significant associations and positive direct effect.

CONCLUSION

From present study on variability, correlation, and path coefficients in sweet corn inbreds it was identified that the traits cob length, cob girth, number of kernel rows per ear and cob weight without husk are the key determinants of cob weight with husk, as they possess high heritability besides moderate to high genetic advance as percent of mean and significant positive correlation. Therefore, it is pertinent to prioritize these yield attributes during the selection process for developing sweet corn varieties and hybrids with enhanced yield and quality.

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Table. 1 Analysis of Variance (ANOVA) for eleven yield attributing traits in sweet corn inbreds.

Character	Mean sum of squares		
	Replication (d.f=1)	Treatments (d.f=45)	Error (d.f=45)
Days to 50% tasseling	1.836	27.836**	0.5925
Days to 50% silking	1.0869	27.911**	0.7980
Plant height	1.9517	293.596**	34.187
Ear height	0.9401	61.984**	10.761
Cob length	0.6278	5.8126**	0.6291
Cob girth	0.3169	2.4279**	0.5427
Number of kernel rows per ear	0.1739	5.1980**	0.885
Number of kernels per row	0.391	17.130**	2.102
Total soluble sugars	0.1183	2.060**	0.0979
Cob weight without husk	509.95	1541.62**	150.50
Cob weight with husk	528.00	2782.04**	256.63

*, ** Significant at 5 % and 1 % levels, respectively

Table.2 Magnitude of variability, heritability and genetic advance as per cent of mean for different characters in sweet corn inbred lines.

Traits	**Grand mean**	**PCV (%)**	**GCV (%)**	**Heritability in broad sense (h2) (%)**	**Genetic Advance as percent of mean**
Days to 50% tasseling	56	6.69	6.54	96	13.21
Days to 50% silking	60	6.37	6.19	94	12.39
Plant height (cm)	110.98	11.55	10.28	79	18.83
Ear height (cm)	42.25	14.27	11.97	70	20.70
Cob length (cm)	15.35	11.69	10.49	80	19.38
Cob girth (cm)	14.41	8.45	6.73	63	11.05
Number of kernel rows per ear	14	12.11	10.20	71	17.7
Number of kernels per row	26.84	11.55	10.21	78	18.59
Total soluble sugars(%)	16.72	6.21	5.92	91	11.64
Cob weight without husk (g)	138.31	21.03	19.06	82	35.61
Cob weight with husk (g)	181.15	21.51	19.61	83	36.80

Table.3 Phenotypic correlation coefficients for quantitative traits in the sweet corn inbred lines.

Trait	DFT	DFS	PH	EH	CL	CG	NKRPE	NKPR	TSS	CWWOH	CWWH
DFT	1	0.9895**	-0.0381	-0.1933	-0.2604 *	-0.299 **	-0.0633	-0.3106 **	-0.0652	-0.2809 **	-0.2470 *
DFS		1	-0.0431	-0.2031	-0.2434 *	-0.289 **	-0.0579	-0.3136 **	-0.0762	-0.2616 *	-0.2286 *
PH			1	0.6325 **	0.1926	0.3277 **	0.1382	0.1329	0.0835	0.2737 **	0.1476
EH				1 **	0.3716 **	0.2526 *	-0.0699	0.3809 **	0.0967	0.2152 *	0.1312
CL					1 **	0.4436 **	0.0703	0.5353 **	0.0771	0.4571 **	0.4436 **
CG						1 **	0.3629 **	0.2515 *	-0.079	0.6169 **	0.6068 **
NKRPE							1 **	0.1504	0.0551	0.2484 *	0.2550 *
NKPR								1 **	0.2343 *	0.3050 **	0.2865 **
TSS									1 **	-0.1777	-0.1944
CWWOH										1 **	0.9777**
CWWH											1 **

DFT- Days to 50% tasseling, DFS- Days to 50% silking, PH- Plant height, EH- Ear height, CL- Cob length, CG- Cob girth, NKRPE- Number of kernel rows per ear, NKPR- Number of kernels per row, TSS- Total soluble sugars, CWWH- Cob weight with husk, CWWOH- Cob weight without husk

*, ** Significant at 5 % and 1 % levels, respectively

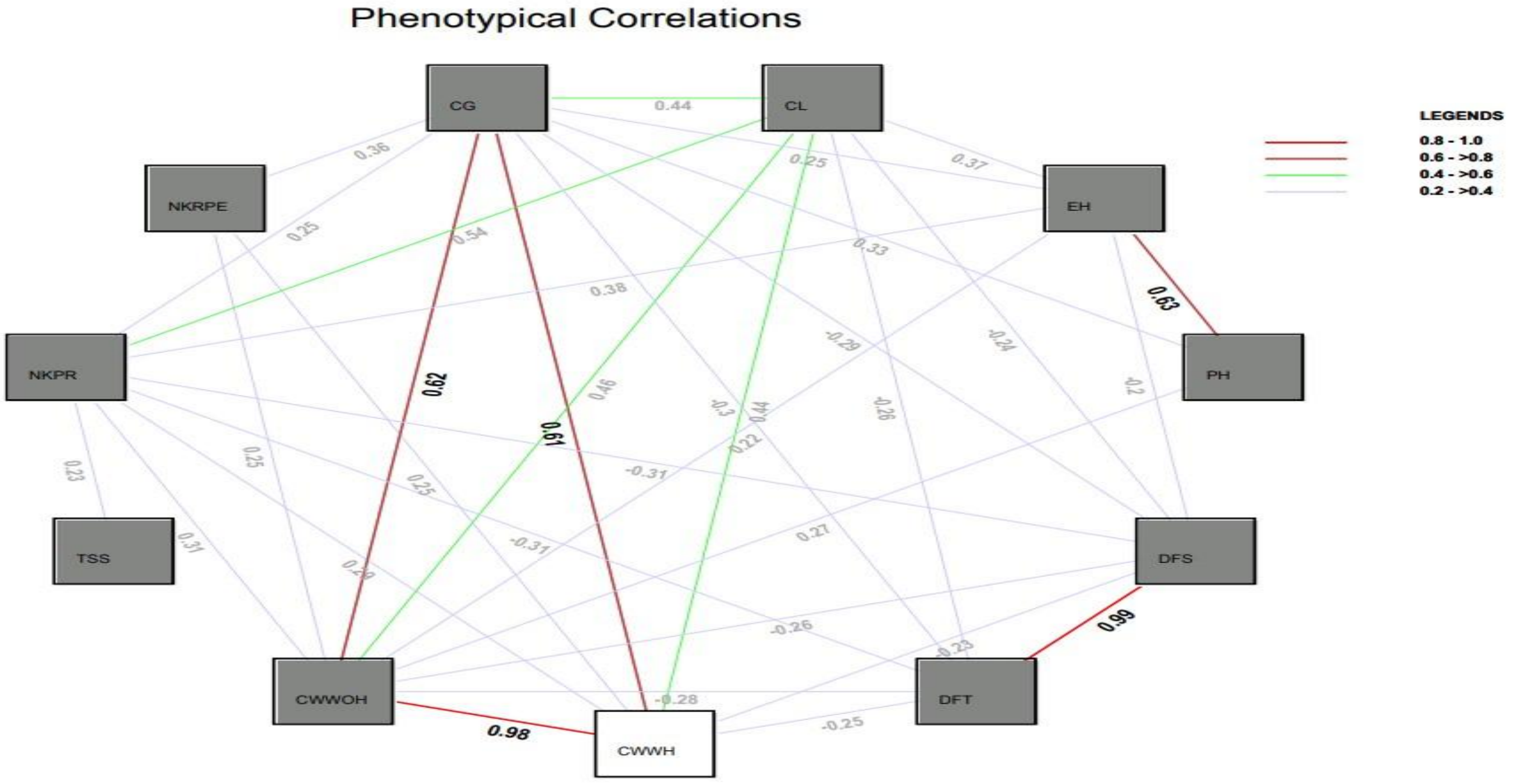
Table. 4 Path coefficients for quantitative traits in the inbred lines of sweet corn.

Character	DFT	DFS	PH	EH	CL	CG	NKRPE	NKPR	TSS	CWWOH	CWWH
DFT	**0.1267**	0.1254	-0.0048	-0.0245	-0.0330	-0.0379	-0.0080	-0.0394	-0.0083	-0.0356	-0.2470 *
DFS	-0.0839	**-0.0848**	0.0037	0.0172	0.0206	0.0245	0.0049	0.0266	0.0065	0.0222	-0.2286 *
PH	0.0055	0.0062	**-0.1434**	-0.0907	-0.0276	-0.0470	-0.0198	-0.0191	-0.0120	-0.0393	0.1476
EH	-0.0007	-0.0007	0.0022	**0.0035**	0.0013	-0.0009	-0.0002	0.0013	0.0003	0.0007	0.1312
CL	-0.0024	-0.0023	0.0018	0.0037	**0.0093**	0.0041	0.0007	0.0050	0.0007	0.0042	0.4436 **
CG	-0.0129	-0.0125	0.0142	0.0109	0.0192	**0.0433**	0.0157	0.0109	-0.0034	0.0267	0.6068 **
NKRPE	-0.0010	-0.0009	0.0021	-0.0011	0.0011	0.0055	**0.0152**	0.0023	0.0008	0.0038	0.2550 *
NKPR	0.0015	0.0015	-0.0006	-0.0018	-0.0025	-0.0012	-0.0007	**-0.0048**	-0.0011	-0.0015	0.2865 **
TSS	0.0001	0.00012	-0.0001	-0.00016	-0.0001	0.0001	-0.0001	-0.0002	**-0.0010**	0.0002	-0.1944
CWWOH	-0.2799	-0.2606	0.2727	0.2144	0.4554	0.6145	0.2474	0.3039	-0.1770	**0.9962**	0.9777**
CWWH											1 **

DFT- Days to 50% tasseling, DFS- Days to 50% silking, PH- Plant height, EH- Ear height, CL- Cob length, CG- Cob girth, NKRPE- Number of kernel rows per ear, NKPR- Number of kernels per row, TSS- Total soluble sugars, CWWH- Cob weight with husk, CWWOH- Cob weight without husk

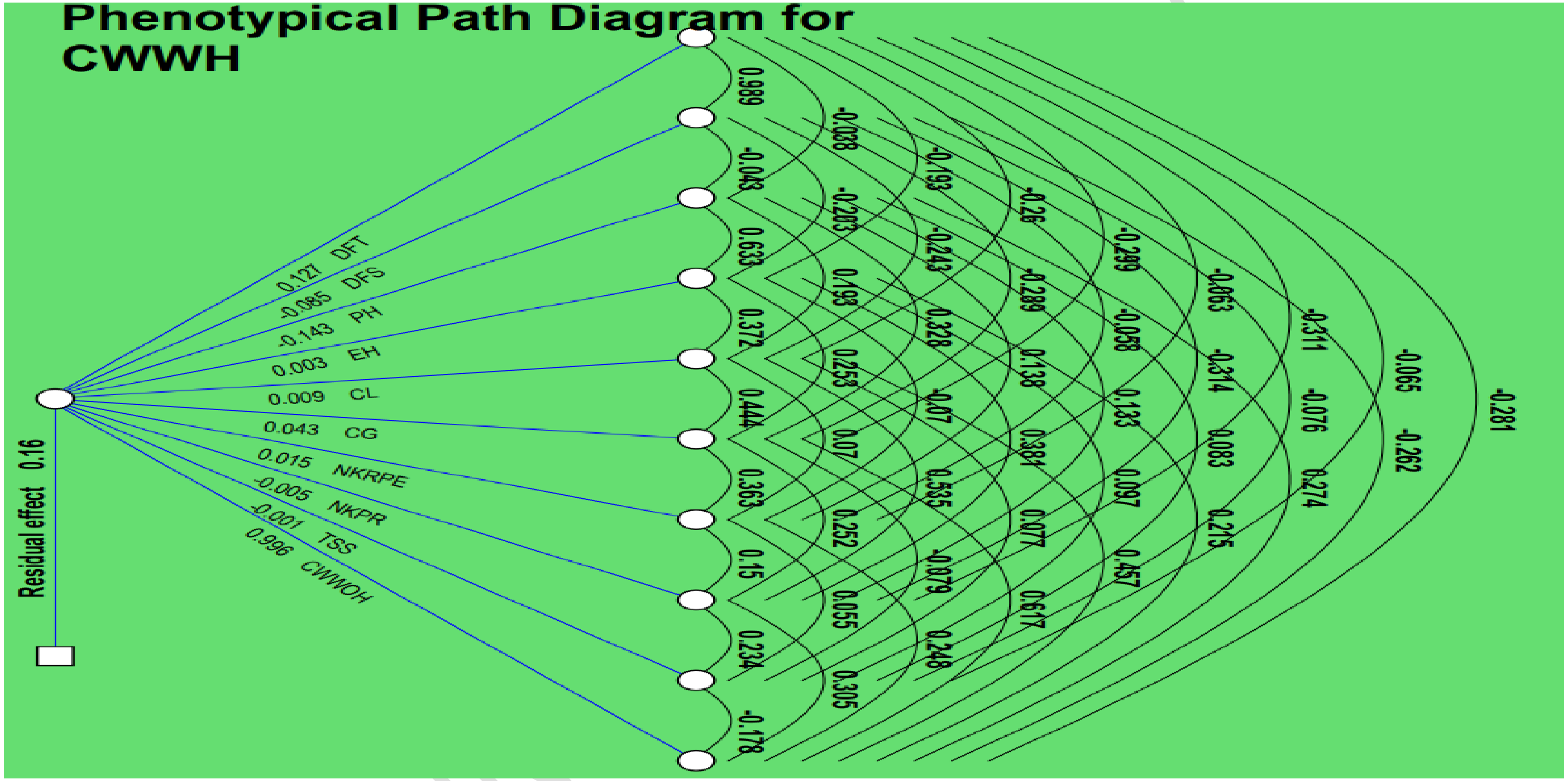
*, ** Significant at 5 % and 1 % levels, respectively and Residual effect = 0.16

Fig.1 Phenotypic correlation among various yield attributing traits in sweet corn



DFT- Days to 50% tasseling, DFS- Days to 50% silking, PH- Plant height, EH- Ear height, CL- Cob length, CG- Cob girth, NKRPE- Number of kernel rows per ear, NKPR- Number of kernels per row, TSS- Total soluble sugars, CWWH- Cob weight with husk, CWWOH- Cob weight without husk

Fig.2 Phenotypic path for various yield attributing traits in sweet corn



DFT- Days to 50% tasseling, DFS- Days to 50% silking, PH- Plant height, EH- Ear height, CL- Cob length, CG- Cob girth, NKRPE- Number of kernel rows per ear, NKPR- Number of kernels per row, TSS- Total soluble sugars, CWWH- Cob weight with husk, CWWOH- Cob weight without husk