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Genetic analysis of sweet corn inbred lines and hybrids

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Abstract

In the present investigation, analysis of variance revealed highly significant differences among treatments in respect of all the characters studied indicating that the genotypes under study were genetically diverse. Genotypic and phenotypic coefficients of variability were high for grain yield per plant and ear height. High heritability estimates coupled with high genetic advance as per cent of mean. The genotypic correlation coefficients were higher than the phenotypic correlation coefficients for almost all the characters under study. Character association revealed significant positive association of Plant height (cm), rows per cob, cob diameter (cm), weight of cob with husk (g) weight of cob without husk(g), seed index (100 grain weight in g), shoot length (cm), root length (cm), seeding fresh weight (g) and seedling dry weight (g) both at phenotypic and genotypic levels. Germination percent recorded positive but nonsignificant association with the grain yield at both the levels. Path analysis was carried out for grain yield in order to obtain a clear picture of inter relationship between yield and its component characters. Estimates of direct and indirect effects of component characters on grain yield at genotypic level revealed that ear girth contributed for maximum direct effect on 100 seed grain followed by cob diameter, weight of cob without husk, germination percentage, plant height, number of kernels per row, shoot length, seedling dry weight.

Keywords: Hybrids, *Zea mays*, Asian and African countries

Introduction

Maize (*Zea mays* L., $2n=20$), is considered as queen of the cereals, is one of the most important cereal crop in the world next to rice and wheat. In the United States of America, the major producer of maize (with nearly half of the total maize production) it is cultivated mainly for livestock feed and industrial purposes. But it is a staple food crop of tropical Asian and African countries.

Indian maize is mainly grown for grain purpose and is consumed either as food or as feed. Utilization of maize for specialized purpose is rare and the main reasons behind this are unavailability of high-yielding varieties, lesser attention to appropriate production technologies and lack of awareness among the farmers, traders and industrialists about multidimensional uses. Out of the various specialty corns, consumptions of green cobs by rural areas has got popularity among metro and urban areas also as aristocratic food. Thus, big market potential especially if the storage and packing for large-scale production are taken care of. This has potentiality not only in domestic market but in international market as well. Sweet corn is the type of corn with a thin pericarp layer and it is consumed at immature grain stages of endosperm after 20-25 days of fertilization as roasted form dried sweet corn cobs are consumed after short period of cooking in boiling water. Sweet corn cobs before pollination can also be used as baby corn for preparation of various recipes and other value-added products. Discovery of 'su' genes as mutant in corn stock initiated the utilization pattern of maize as sweet corn as sugary genes slower down the conversion of sugars into starch resulting shrunken of kernels after drying and sweeter than normal corn as green cob stage. Several more genes are also identified which enhance the synthesis of more sugars and conversion in starch get reduced.

In India, the most widely cultivated type of maize belongs to flint or semi-flint type and considering the high productivity and untapped potentiality of maize crop, the need for diversifying its utility is felt. Due to non-availability of high yielding suitable sweet-grained types, the green ears of flint-grained local varieties which are relatively sweeter and taste better are normally consumed as roasted ears. However, low productivity of these local maize lines has some limitations. Therefore, enhancement of kernel sugar content, in addition to higher productivity will be a desirable attribute in facilitating diversified utilization through human consumption of fresh kernel and as well as processed food.

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This necessitates evaluation, analysis and identification of suitable maize cultivars, which meet these specific requirements.

Early maturity is also an important trait to fit sweet corn into specific cropping sequence as well as inter cropping. Single cross hybrids are in general, found to exhibit heterosis for early flowering and maturity and this can be taken advantage of. Selections among the prospective parental lines for early maturity may also be fruitful to some extent. This is especially attractive, due to the availability of a large number of maize inbred lines, thanks to the higher focus towards the development of single cross hybrids in India, since a decade. Some of the elite maize inbred lines can be crossed with the standard sweet corn lines and subsequently handled in specific ways, depending on the interests and objectives to be fulfilled. These include enhancement of productivity or incorporating earliness in the sweet corn genotypes or enhancing the kernel sugar content in the field corn (normal) lines. The green plants after harvest of sweet green cobs provides nutritious forage for working animals which is an additional plus point of sweet corn. Seed viability and higher germination in field is a major problems associated with sweet corn genotypes due to lower starch content in kernels which provides nutrition to the germinating embryos during the process of field exposure.

However more comprehensive efforts are warranted in both the approaches of genetic analysis among the sweet corn inbred lines as well as wider and better choice of field corns in analyzing the combinations with sweet corn lines.

The present study was undertaken with the objectives to characterize high sugary maize stocks derived from different source populations and evaluation for their adoptability and productive potentiality and to analyze the genetic components of variation determining economically important traits associated with germination of healthy seedlings.

Material and Methods

The experimental material comprising of 15 morphologically diverse genotypes of sweet corn (*Zea mays* L. var. *Sacharata*) was conducted in a randomized block design with three replications during Rabi 2017-2018 in the Department, of Genetics and Plant Breeding, C.S. Azad University of Agriculture and Technology, Kanpur. Each strain was sown 5-meter-long three rows. The spacing between rows and plants was kept 60cm and 20cm respectively. All the recommended cultural practices were adopted, to raise healthy crop. Five randomly selected plants were taken in each plot and individual plant observation was recorded on the metric traits namely plant height (cm), cob weight with husk (gm), cob weight without husk (gm), number of row per cob, number of kernels per cob, base diameter of cob (cm), seed index, germination % of the seed, root length of germinate seed (cm), shoot length of germinate seeds (cm), seedling fresh weight (gm) and seedling dry weight (gm).

Analysis of variances were worked out to test the significance of the differences between treatment means followed by F tests. It was carried out as suggested by Panse and Sukhatme (1985) [5]. Heritability estimates with regards to each character was calculated by the formula as proposed by Burton Devane (1953) [3]. Correlation coefficient as measures the degree of mutual association between two variables without employing any cause and effect relationship. This was calculated based on genotypic and phenotypic variances and covariances as suggested by Hanson *et al.* (1956) [6]. Similarly, path coefficient as per standardized partial regression coefficient

and measures the direct influence of one variable upon another (Dewey and Lu, 1959) [4].

Result and Discussion

The Analysis of Variance for the experiment involving a set of fifteen genotypes of maize for 12 yield and seed characters namely Plant height (cm), rows per cob, cob diameter (cm), weight of cob with husk (g) weight of cob without husk(g), seed index (100 grain weight in g), germination %, shoot length (cm), root length (cm), seeding fresh weight (g) and seedling dry weight (g) revealed highly significant mean sum of squares for all the characters indicating greater diversity among the genotypes. The variability present for various characters can be attributed to the differential breeding procedures and also to the geo-ecological differences from which they were originated. The analysis of variance indicated the existence of sufficient variation in the material selected for studied.

Most of the characters exhibited wide range of values of means for the characters Plant height (cm), rows per cob, cob diameter (cm), weight of cob with husk (g) weight of cob without husk(g), seed index (100 grain weight in g), germination %, shoot length (cm), root length (cm), seeding fresh weight (g) and seedling dry weight (g). This indicated ample scope for exploitation of the above characters through the process of selection.

This could be seen from the highest magnitude of both PCV (38.41%) and GCV (38.22%) for shoot length per plant followed by number of kernel (29.04% - 28.96%) respectively showed higher magnitudes of both PCV and GCV, suggesting that these characters were under the influence of genetic control (Table 1). So the characters can be subjected for simple selection for further improvement. Higher the differences between PCV and GCV for 100 seed weight, rows per cob and germination % indicated that these characters are more influenced by environment. Lower the differences between these two showed stabilities of the characters and it indicated that the selections based on these traits can more helpful for genetic improvement.

The characters root length (cm) (24.29%-24.16%), seedling fresh weight (24.38%-24.03%), weight of cob with husk (18.16%-17.99%) and weight of cob without husk (16.48%-16.37%) were recorded for moderate magnitudes of both PCV and GCV, respectively. However, rows per cob (17.07%-12.30%), cob diameter (14.00%-13.63%) and 100 seed weight (19.19%-17.39%) had moderate magnitude of PCV and low magnitude of GCV, respectively. The traits germination % (0.99%-0.23%) and plant height (7.16% - 6.94%) showed lower magnitudes of both PCV and GCV, respectively.

The difference between the estimates of PCV and GCV were low Plant height (cm), cob diameter (cm), weight of cob with husk (g) weight of cob without husk(g), seed index (100 grain weight in g), germination %, shoot length (cm), root length (cm), seeding fresh weight (g) and seedling dry weight (g) showing thereby lesser role played by the environment in the expression of these characters and the difference between the estimates of PCV and GCV was high for shelling percentage indicating the significant role played by the environment in the expression of this character.

Heritability (h^2 bs)

Heritability estimates revealed the heritable portion of variability for different characters. The knowledge of heritability enables the plant breeder to decide the choice of

selection procedure to be followed under a given situation (Li and Yang, 1985).

In present study all the characters showed high estimates of heritability (Table 2) except germination percentage (16.1 %). Broad sense heritability estimates ranged from 16.1 percent (germination percentage) to 99.5 percent (root length). The characters like root length (99.5%), weight of cob without husk (99.4%), number of kernel (99.3%), shoot length (99.3%), seedling dry weight (99.2%), weight of cob with husk (98.2%), seedling fresh weight (97.1%), cob diameter (95.5), plant height (94.2%) and seed index (82.1%) were exhibited high heritability. Moderate estimates of heritability were noticed for shelling percentage (32.9%).

Genetic advance over mean

The genetic advance expressed as mean (Table 2) values ranged from 1.24 (germination percentage) to 78.44 (shoot length). The character, shoot length (78.44) recorded for highest magnitude of genetic advance as percent over mean followed by no. of kernel (59.44), root length (49.51), seedling fresh weight (48.78), weight of cob with husk (36.69), weight of cob without husk (33.48), seedling dry weight (33.33), 100 seed weight (32.47) and cob diameter (27.40). The trait germination percentage (1.24) recorded the lowest magnitude of genetic advance over mean followed by plant height (13.88) and rows per cob (18.24). Maximum amount of genetic advance was found for weight of number of kernels (177.48), followed by cob with husk (107.89) and weight of cob without husk (91.52).

High heritability was observed for most of the characters, indicating that they were least influenced by the environmental effects. However, the 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 values coupled with genetic advance would be more reliable and useful on correlating selection criteria.

High heritability with moderate genetic advance was recorded for number of kernel rows per ear, ear girth and days to 50% tasseling. These traits appear to be under the control of both additive and non-additive gene actions. High heritability with low genetic advance was recorded for days 50% silking and days to maturity. Whereas shelling percentage exhibited moderate heritability with low genetic advance, indicating that these characters were more influenced by the environment and could not be exploited through simple selection scheme and need some modifications.

In the present study, high heritability coupled with high genetic advance was observed for plant height, number of kernels per row, 100 seed weight and shoot length. Thus, these traits are predominantly under the control of additive gene action and these characters can be improved by pedigree method of selection.

Correlation studies

Grain yield, being a complex character, is the cumulative and interactive effect of a number of component traits. Direct selection for yield *per se* generally results in low genetic gain because of its low heritability in general dictating plant breeders to realize the importance of component traits. However, inclusion of all the component traits in selection scheme is impractical because of obvious reasons and here the knowledge of association of various characters comes to the rescue in formulating an effective and efficient selection scheme. Therefore, a sound knowledge of character association forms an integral part of a programme for making improvements in complex characters like yield.

Genotypic correlations reveal the existence of real associations, whereas the phenotypic correlations may occur by chance. Significant phenotypic correlations without genotypic associations are of no value. If the genotypic correlation is significant but phenotypic correlation is not significant, it means that existing real association is masked by environmental effect. This indicates the importance of genotypic correlations compared to phenotypic correlations. Phenotypic correlation indicates the extent of the observation having relation between two characters while genotypic correlation provides an estimate of inherent association between the genes controlling any two characters.

In general, genotypic correlation coefficients at genotypic level were higher than their counterparts at phenotypic level for all the traits which indicates a strong inherent association between the characters (Table 3).

Path analysis

Correlation between different characters is important in planning selection programmes. But the correlation coefficients only denoted the total association existing between a pair of characters which themselves are the result of the interaction between features of the plant. Thus a dependent character is an interaction production of many mutually associated component characters and change in any one component will alter the whole system of cause and effect. The analysis takes into account the cause and effect relationship between the variable and is unique in partitioning the association into direct and indirect effects through other independent variables.

The path coefficient analysis also measures the relative importance of causal factors involved. In order to obtain a clear picture of the inter-relationship between different characters, the direct and indirect effects of the important quantitative characters on the grain yield were worked separately, using path coefficient analysis both at genotypic and phenotypic levels (Table 4a and 4b). Direct or indirect effects are categorized as follows, negligible when values are between 0.00 and 0.09, low when values range from 0.10 to 0.19, moderate for values between 0.20 to 0.29, high for values 0.30 to 0.99 and the values more than 1.00 are categorized as very high.

Critical analysis of the results obtained from character association and path analysis revealed that selection of the traits viz., rows per cob, cob diameter, length, number of kernels per row and 100 seed weight would bring improvement in yield and yield attributes as they possessed high positive significant associations and positive direct effects.

Table 1: Genotypic and Phenotypic coefficient of variation for yield and seed traits in sweet corn

S. N.	Character	GCV	PCV
1.	Plant height(cm)	6.94	7.16
2.	Row per cob	12.30	17.07
3.	Cob diameter(cm)	13.63	14.00
4.	No. of kernels	28.96	29.04
5.	Weight of cob with husk(g)	17.99	18.16
6.	Weight of cob without husk(g)	16.37	16.48
7.	Seed index (100 grains weight in g.)	17.39	19.19
8.	Germination %	0.23	0.99
9.	Shoot length(cm)	38.22	38.41
10.	Root length(cm)	24.16	24.29
11.	Seedling fresh weight(g)	24.03	24.38
12.	Seedling dry weight(g)	15.41	15.49

Table 2: Heritability and Genetic advance for 12 characters in Sweet corn

S. N.	Character	Heritability coefficient	Heritability percent	Genetic advance	Genetic advance over mean
1.	Plant height(cm)	0.942	94.2	19.70	13.88
2.	Rows per cob	0.521	52.1	2.31	18.24
3.	Cob diameter(cm)	0.954	95.5	2.02	27.40
4.	No. of kernels	0.993	99.3	177.48	59.49
5.	Weight of cob with husk(gm)	0.982	98.2	107.89	36.69
6.	Weight of cob without husk(gm)	0.994	99.4	91.52	33.48
7.	Seed index (100 grains wt. in gm)	0.821	82.1	4.79	32.47
8.	Germination %	0.161	16.1	1.21	1.24
9.	Shoot length(cm)	0.993	99.3	5.13	78.44
10.	Root length (cm)	0.995	99.5	7.20	49.51
11.	Seedling fresh weight (gm)	0.971	97.1	6.23	48.78
12.	Seedling dry weight (gm)	0.992	99.2	0.10	33.33

Table 3: Genotypic and Phenotypic correlation coefficient among 12 characters for seed yield quality traits in Sweet corn

Character	Plant height (cm)	Rows per cob	Cob diameter (cm)	Number of kernels	Weight of cob with husk (g)	Weight of cob without husk (g)	Seed index (100 grains weight in g.)	Germination %	Shoot length (cm)	Root length (cm)	Seedling fresh weight (g)	Seedling dry weight (g)
Plant height(cm)	1.00	-0.502	0.306	0.221	0.015	0.012	-0.455	0.280	-0.360	-0.227	0.402	-0.305
Row per cob	-0.387	1.00	-0.336	-0.428	-0.060	-0.042	0.263	1.555	0.355	0.346	-0.335	0.047
Cob diameter(cm)	0.297	-0.241	1.00	0.122	-0.066	-0.378	-0.004	0.219	0.032	-0.201	-0.005	0.096
No. of kernels	0.214	-0.323	0.120	1.00	-0.156	0.160	-0.066	-0.251	-0.062	-0.087	0.064	0.100
Weight of cob with husk(g)	0.011	-0.021	-0.061	-0.156	1.00	0.161	0.048	-0.541	0.183	-0.035	-0.339	0.075
Weight of cob without husk(g)	0.011	-0.043	-0.366	0.160	0.156	1.00	0.063	-0.402	0.089	0.289	0.149	0.354
Seed index (100 grains weight in g.)	-0.383	0.173	0.013	-0.062	0.038	0.051	1.00	0.252	0.434	0.459	-0.230	0.450
Germination %	-0.081	-0.208	0.003	0.034	0.138	0.084	0.099	1.00	-0.257	-0.212	-0.943	0.299
Shoot length(cm)	-0.348	0.264	0.025	-0.061	0.174	0.085	0.396	0.045	1.00	0.513	-0.065	-0.288
Root length(cm)	-0.214	0.247	-0.199	-0.090	-0.035	0.284	0.418	0.077	0.509	1.00	0.306	-0.164
Seedling fresh weight(g)	0.383	-0.245	-0.017	0.063	-0.339	0.155	-0.214	0.208	-0.063	0.304	1.00	-0.453
Seedling dry weight(g)	-0.300	0.012	0.087	0.100	0.071	0.350	0.395	-0.115	-0.286	-0.164	-0.466	1.00

Table 4a: Genotypic path matrix of Seedling dry weight (gm)

Character	Plant height (cm)	Rows per cob	Cob diameter (cm)	Number of kernels	Weight of cob with husk (g)	Weight of cob without husk (g)	Seed index (100 grains weight in g)	Germination %	Shoot length (cm)	Root length (cm)	Seedling fresh weight (g)
Plant height (cm)	-0.477	0.240	-0.146	-0.105	-0.007	-0.006	0.217	-0.133	0.172	0.108	-0.192
Row per cob	-0.069	0.139	-0.046	-0.059	-0.008	-0.005	0.036	0.216	0.049	0.048	-0.046
Cob diameter(cm)	0.149	-0.163	0.486	0.059	-0.032	-0.184	-0.002	0.106	0.015	-0.097	-0.002
No. of kernels	0.025	-0.049	0.014	0.114	-0.017	0.018	-0.007	-0.028	-0.007	-0.010	0.007
Weight of cob with husk (g)	0.002	-0.008	-0.009	-0.023	0.147	0.023	0.007	-0.079	0.027	-0.005	-0.050
Weight of cob without husk (g)	0.008	-0.027	-0.244	0.1032	0.1039	0.644	0.040	-0.259	0.057	0.186	0.096
Seed index (100 grains weight in g.)	-0.253	0.147	-0.002	-0.036	0.027	0.035	0.557	0.140	0.241	0.256	-0.128
Germination %	0.017	0.094	0.013	-0.015	-0.032	-0.024	0.015	0.060	-0.015	-0.012	-0.057
Shoot length(cm)	0.250	-0.247	-0.022	0.043	-0.127	-0.062	-0.302	0.178	-0.695	-0.357	0.045
Root length(cm)	0.060	-0.092	0.053	0.023	0.009	-0.077	-0.122	0.056	-0.137	-0.267	-0.081
Seedling fresh weight(g)	-0.017	0.014	0.0002	-0.002	0.014	-0.006	0.010	0.040	0.002	-0.013	-0.043
Seedling dry weight(g)	-0.305	0.047	0.096	0.100	0.075	0.354	0.450	0.299	-0.288	-0.164	-0.453
Partial R ²	0.145	0.006	0.046	0.0115	0.0111	0.228	0.250	0.018	0.201	0.043	0.019

Table 4b: Phenotypic path matrix of Seedling dry weight (gm)

Character	Plant height (cm)	Rows per cob	Cob diameter (cm)	Number of kernels	Weight of cob with husk (g)	Weight of cob without husk (g)	Seed index (100 grains weight in g)	Germination %	Shoot length (cm)	Root length (cm)	Seedling fresh weight (g)
Plant height(cm)	-0.449	0.174	-0.133	-0.096	-0.0052	-0.0051	0.172	0.036	0.156	0.096	-0.172
Row per cob	-0.010	0.027	-0.006	-0.009	-0.0006	-0.0012	0.0048	-0.0058	0.0074	0.0069	-0.0069
Cob diameter(cm)	0.126	-0.102	0.426	0.051	-0.026	-0.156	0.005	0.001	0.0109	-0.085	-0.007

No. of kernels	0.013	-0.019	0.007	0.061	-0.009	0.009	-0.003	0.002	-0.003	-0.005	0.003
Weight of cob with husk(g)	0.0007	-0.001	-0.004	-0.0102	0.064	0.0101	0.002	0.009	0.011	-0.002	-0.022
Weight of cob without husk(g)	0.006	-0.026	-0.223	0.098	0.095	0.610	0.031	0.051	0.052	0.174	0.094
Seed index (100 grains weight in g.)	-0.181	0.081	0.006	-0.029	0.018	0.024	0.473	0.046	0.187	0.198	-0.101
Germination %	0.014	0.036	-0.0006	-0.006	-0.024	-0.014	-0.017	-0.176	-0.008	-0.013	-0.036
Shoot length(cm)	0.221	-0.168	-0.016	0.039	-0.111	-0.054	-0.252	-0.028	-0.636	-0.324	0.040
Root length(cm)	0.032	-0.037	0.029	0.013	0.005	-0.042	-0.062	-0.011	-0.076	-0.149	-0.045
Seedling fresh weight(g)	-0.074	0.047	0.003	-0.012	0.065	-0.030	0.041	-0.040	0.012	-0.059	-0.193
Seedling dry weight(g)	-0.300	-0.012	0.087	0.100	0.071	0.350	0.395	-0.115	-0.286	-0.164	-0.446
Partial R ²	0.135	0.0004	0.037	0.006	0.004	0.214	0.187	0.020	0.182	0.024	0.086

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