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Genetic variability, association and contribution of different characters towards grain yield in sweet corn (*Zea mays* var. *saccharata*) in North Western Hills

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ABSTRACT

A set of 21 single-cross sweet corn hybrids was evaluated for yield and yield contributing traits. Analysis of variance revealed presence of significant genetic variation for grain all the traits studied viz., cob length, cob girth, number of kernel rows, number of kernels per row, shelling percentage, 100-grain weight and grain yield. Phenotypic coefficients of variation (PCV) for all the traits were higher in magnitude compared to genotypic coefficients of variation (GCV), indicating the environmental influence on the traits. Moderate level of GCV observed for the number of kernel rows (11.56%), 100-grain weight (10.03%) and grain yield (17.98%) suggested sufficient variability and thereby scope for genetic improvement through selecting for these traits. Cob length, cob girth, number of kernel rows and 100-grain weight exhibited high heritability. High heritability coupled with moderate genetic advance as per cent of mean observed for cob length, number of kernel rows and 100-grain weight indicated that direct selection for these traits can be effective for grain yield improvement. Grain yield exhibited positive and significant correlation with all the traits studied. The number of kernel rows, number of kernels per row and 100-grain weight had a positive direct effect on total yield per plant. Correlation and path analysis indicated that selection for number of kernel rows, number of kernels per row and 100-grain weight would be more promising for the improvement of grain yield in sweet corn.

1. Introduction

Sweet corn (*Zea mays* var. *saccharata*) has emerged as an important cash crop in India on account of its shorter growing period and year round demand. It is amenable to processing and preservation and yields green fodder as well. Sweet corn is popular as a specialty corn for having a sweeter flavor than field corn (Bian *et al.*, 2015). India ranked 9th with export value of 23.42 million US\$ and is exporting sweet corn to global market including developed countries such as, Netherlands, France, USA, China and United Kingdom (FAOSTAT 2020).

Sweet corn is harvested at milky ripening stage, generally at 20-24 days after pollination and marketed as fresh or in canned form (Khanduri *et al.*, 2011; Mehta *et al.*, 2017). The demand of sweet corn has increased tremendously in the last few years primarily due to urbanization, increased consumption and availability of organized food processing industries (Lertrat and Pulam, 2007). Among various recessive mutations responsible for enhancing sweetness in maize, *shrunk2(sh2)*, *sugary1(su1)* and *sugary enhancer1(se1)* are commonly used for development of sweet corn cultivars. The *sh2*-based accumulates extra sugar in place of starch and popularly known as 'super sweet' or extra sweet corn'. The content of

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sucrose or reducing sugars is about six fold higher than the normal corn at the milky ripening stage (Feng *et al.*, 2008; Khanduri *et al.*, 2010). Recessive mutation of *Su1* gene is responsible for accumulation of three fold more reducing sugar and ten times more water-soluble polysachharides (WSP), i.e., phytoglycans rather than starch, due to which kernels become plumpy and attractive, at harvest maturity (Fisher and Boyer, 1983).

The understanding of the genetic variability is the prerequisite of any successful breeding programme (Sankar *et al.*, 2006). The simple parameters of variability (PCV, GCV and GA) are useful in detecting the amount of genetic variation present in the material. The efficiency of selection along with genetic variability can be utilized through the estimates of heritability and genetic advance (Bilgin *et al.*, 2010). Only the heritable variation present in the material responds to selection. The heritability estimates coupled with genetic advance would be useful in predicting the best genotype for yield and its attributing traits (Singh *et al.*, 2011). Since yield is a polygenic trait, so improvement of contributing traits is imperative (Reddy *et al.*, 2013). Character association studies helps to understand the cause and effect relationship of two or more traits and for this correlation and path studies are important for improving the efficiency of crop improvement programmes.

In sweet corn only a limited choice of high yielding sweet corn hybrids is available to the farmers and therefore there is a need to widen this range in order to be able to cater to diverse regional and seasonal growing requirements. Higher grain yield is an important breeding objective in sweet corn also besides grain quality that includes grain size, colour, texture, flavour and TSS. Selection for yield is often difficult in crop breeding because of its complex architecture, polygenic inheritance and composite nature. Dissection of complex composition of the yield trait therefore is important to understand the relationship among its constituent traits. There is less understanding of such information in sweet corn compared to normal corn. Hence, the present study was designed to obtain the information on variability, character association and path analysis of sweet corn hybrids.

2. Material and Methods

The experiment material used in the study comprised of a set of 20 single-cross sweet corn hybrids and one check Sugar 75 (private sector hybrid). The experiment was conducted in a randomized block design (RBD) with three replications at ICAR-VPKAS, Experimental Farm, Hawalbagh (1250 m amsl, latitude 29° 36' N, longitude 79° 40' E). The plot size comprised of two rows of 3m length. Row-to-row spacing was kept at 60 cm and plant-to-plant spacing was maintained at 25 cm so as to have a final stand of 12 plants per row. Recommended package of practices was followed to obtain a good crop. The ears were harvested at early dough-stage and observations on seven traits viz., cob length (cm), cob girth (cm), number of kernel rows, number of kernels per row, shelling (%), 100-grain weight (g) and grain yield (g) were recorded on two cobs selected at random from each genotype in each replication. Standard statistical procedure was followed to analyse the experimental material for the presence of variability and coefficient of variation according to Burton and Devane, 1953. Heritability and genetic advance was estimated following the method suggested by Jonson *et al.*, 1955. Path analysis was worked out by genotypic correlation coefficient as suggested by Wright, 1921 and elaborated by Dewey and Lu, 1959. The statistical analysis was performed by statistical software INDOSTAT v8.0.

3. Results and Discussions

Analysis of variance revealed significant differences among the 21 sweet corn hybrids for grain yield and its attributes (Table 1).

The presence of substantial genetic variation among genotypes suggested scope for improvement in these traits through selection. Similar genetic variation for the traits was observed in sweet corn in earlier studies (Niji *et al.*, 2018, Stansulos *et al.*, 2019). The descriptive statistics for the studied traits has been presented in the Table 2.

Genetic variability study revealed that the phenotypic coefficient of variation (PCV) was higher in magnitude than the genetic coefficient of variation (GCV) for all the traits (Table 3).

Table 1. Analysis of variance of yield and contributing traits

Source		Mean squares						
Character	d.f	Length	Girth	Rows	Kernels/row	Shelling (%)	100-grain wt	Grain yield
Replication	2	1.81	0.22	1.24	9.20	8.62	8.48	2.78
Treatment	20	7.10**	2.82**	9.50**	49.92**	42.99**	39.22**	3192.23**
Error	40	0.96	0.45	1.26	11.49	8.63	6.24	587.07

Table 2. Simple parameters of variability

Parameters	Length	Girth	Rows	Kernels/row	Shelling (%)	100-grain wt	Grain yield
Mean	17.99	15.25	14.34	36.32	74.68	33.07	163.90
C.D.	1.63	1.11	1.86	5.62	4.87	40.13	4.14
SE(m)	0.57	0.39	0.65	1.96	1.69	13.99	1.44
SE(d)	0.80	0.55	0.92	2.77	2.39	19.78	2.04
C.V.	5.45	4.38	7.82	9.34	3.93	14.78	7.55

Table 3. Estimation of genetic parameters for morphological characters of twenty-one maize genotypes

Characters	Range	Heritability (%)	GCV (%)	PCV (%)	GA (%)
Cob length	15.55-21.10	67.99	7.95	9.64	13.50
Cob girth	13.87-17.75	63.90	5.83	7.29	9.60
Rows per cob	11.67-18.33	68.59	11.56	13.96	19.72
Kernels/row	28.00-44.00	52.71	9.86	13.58	14.74
Shelling (%)	64.24-78.95	57.01	4.53	6.00	7.04
100-grain wt	24.55-39.97	63.80	10.03	12.55	16.50
Grain yield	102.15-238.66	59.66	17.98	23.28	28.61

This indicated the influence of environmental factors on the expression of these traits. Similar trend was reported for sweet corn (Alan *et al.*, 2013, Niji *et al.*, 2018) and normal corn (Sesay *et al.*, 2016, Jilo *et al.*, 2018). Moderate level for GCV was recorded for grain yield (17.98%), number of kernel rows (11.56%) and 100-grain weight (10.03%) suggesting that these traits were predominantly under genetic control. Thus the selection for these traits can be carried out efficiently in sweet corn improvement programs. Moderate GCV and PCV for 100-grain weight (Hefny, 2011), number of kernels per row (Alake *et al.*, 2008) and number of kernel rows (Alan *et al.*, 2013, Jilo *et al.*, 2018) have been reported in the previous studies

Estimation of heritability revealed that heritable portion of variability was present for all traits and ranged from 52.71% to 68.59% for number of kernels per row and number of kernel rows, respectively (Table 3). High magnitude of heritability was estimated for number of kernel rows (68.59%), cob length (67.99%), girth (63.90%) and 100-grain weight (63.80%). In contrast, moderate level of heritability was recorded for grain yield (59.66%), shelling per cent (57.01%) and number of kernels per row (52.71%). The knowledge of heritability estimates for a particular trait helps the plant breeder to decide the selection procedure in the segregating generations (Li and Yang, 1985). However, the effectiveness of selection is mainly based on the coupled effects of higher genetic gain with heritability (Nyquist, 1991). The values of genetic advance ranged from 7.04% for shelling per cent to 28.61% for grain yield (Table 3). Moderate heritability coupled with a high genetic gain was observed for grain yield. Similar trend of moderate heritability with high genetic advance was reported in normal corn (Rajesh *et al.*, 2013; Sesay *et al.*, 2016) and sweet corn (Niji *et al.*, 2018). On the other hand, traits like cob length, number of kernel rows, number of kernels per row and 100-grain weight showed high heritability with moderate genetic advance, indicating the presence of both additive and non-additive gene effects and suggesting that superior phenotypic performance for these traits may be achieved through careful selection. Rajesh *et al.*, 2013 reported moderate heritability with moderate GA estimates for number of kernels per row and 100-grain weight. High to moderate heritability with low genetic advance was observed for cob girth and shelling %, respectively, suggesting that direct selection for these traits is unlikely to be rewarding due to non-additive gene

action and environmental influence on these traits. Similar results were reported by Vashistha *et al.*, 2013. However, Johnson *et al.*, 1955 suggested that simultaneous consideration of heritability and GA estimates, high heritability may not be always associated with high genetic gain. The estimates of heritability and genetic advance indicated that the studied traits were governed by non-additive gene action among the tested genotypes and thus heterosis breeding, progeny testing and family selection could be employed for the improvement of such traits.

Correlation coefficient determines the mutual relationship among the contributing traits and helps in deciding the component trait on which selection could be based for the genetic improvement of the grain yield. Only the genotypic component is the heritable component of the association among two traits. However, the phenotypic component includes both genotypic and environmental effects. Hence significant phenotypic correlation without significant genotypic correlation has no importance in the improvement of the trait. The character association studies revealed that at the genotypic level the grain yield had a highly significant ($P < 0.01$) and positive association with cob length (0.945), girth (0.909), number of kernels per row (0.841), number of kernel rows (0.671), shelling % (0.387) and 100-grain weight (0.392) (Table 4).

Association of grain yield with all other traits was found significant and positive at the phenotypic level also. Niji *et al.*, 2018 reported the significant and positive association of grain yield with cob length, cob girth, 100-grain weight and number of kernel rows in sweet corn. Among yield contributing traits, cob length and cob girth were observed to exhibit highly significant positive association with grain yield per plant. A similar kind of association has been reported by Beulah *et al.*, 2018 in normal corn and Prakash *et al.*, 2019 in sweet corn.

Shelling percentage exhibited a positive and significant association with cob length and number of kernels per row. The number of kernels per row had a positive and significant association with cob length. This indicated the role of cob length in selection of high yielding genotypes. Asghar *et al.*, 1999 reported positive significant association of cob length with number of kernels per row in sweet corn. 100-grain weight showed a significant positive association with cob length and cob girth, whereas the number of kernel rows exhibited a significant negative association with 100-grain weight.

Table 4. Correlation Coefficients of different morphological traits of 21 maize genotypes at the phenotypic and genotypic level

Characters	Correlation	Girth	Rows	Kernels/row	Shelling (%)	100-grain wt	Grain yield
Length	rP	0.654**	0.605**	0.677**	0.215NS	0.228NS	0.795**
	rG	0.848**	0.754**	0.749**	0.364**	0.268*	0.945**
Girth	rP		0.692**	0.505**	0.097NS	0.442**	0.836**
	rG		0.722**	0.701**	-0.003NS	0.347**	0.909**
Rows	rP			0.352**	0.069NS	-0.132NS	0.598**
	rG			0.563**	0.097NS	-0.284*	0.671**
Kernels/row	rP				0.211NS	0.108NS	0.628**
	rG				0.431**	-0.005NS	0.841**
Shelling (%)	rP					0.261*	0.442**
	rG					0.072NS	0.387**
100-grain wt	rP						0.517**
	rG						0.392**

Table 5. Partitioning of direct and indirect effects of morphological characters of 21 maize genotypes at genotypic level by path coefficient analysis

Characters		Length	Girth	Rows	Kernels/ row	Shelling (%)	100-grain wt	Grain yield
Length	P	0.26853	0.22736	0.09892	0.09099	0.05297	0.05579	0.795**
	G	-5.42189	-11.9856	10.10961	6.62837	-1.29856	2.91321	0.945**
Girth	P	0.17574	0.3474	0.11323	0.06777	0.02396	0.10814	0.836**
	G	-4.59853	-14.1316	9.67069	6.19778	0.00907	3.76147	0.909**
Rows	P	0.16235	0.24041	0.16362	0.04729	0.01692	-0.0323	0.598**
	G	-4.09005	-10.1975	13.40159	4.98286	-0.34622	-3.07946	0.671**
Kernels/row	P	0.18192	0.17529	0.0576	0.13431	0.05197	0.02644	0.628**
	G	-4.06249	-9.90062	7.54865	8.84637	-1.53778	-0.05289	0.841**
Shelling (%)	P	0.05763	0.03373	0.01122	0.02828	0.24683	0.06391	0.442**
	G	-1.97119	0.03588	1.29904	3.80868	-3.57178	0.78616	0.387**
100-grain wt	P	0.06124	0.15357	-0.0216	0.01451	0.06448	0.24464	0.517**
	G	-1.45561	-4.89859	-3.80324	-0.04312	-0.25877	10.8512	0.392**

These results were consistent with the observation of earlier workers (Niji *et al.*, 2018, Prakash *et al.*, 2019). As 100-grain weight is an important trait in determining grain yield of maize, the selection for these correlated traits could be beneficial in identifying the high yielding lines.

Path analysis revealed that highest direct and positive effect on grain yield was exhibited by the number of kernel rows, followed by 100-grain weight and number of kernels per row (Table 5).

Similar results were reported by Prakash *et al.* (2019). This indicated that number of kernel rows and 100-grain weight were the major traits in determining higher grain yield. The indirect effects suggest forming indices concerned for improving the grain yield. Cob length and cob girth showed a positive effect on grain yield via shelling %. Thus the traits number of kernel rows, number of kernels per row, 100-grain weight and shelling % are important traits for improving grain yield of sweet corn.

4. Conclusions

The sufficient amount of genetic availability was available for grain yield and its attributes. High heritability coupled with moderate genetic advance as per cent of mean for cob length, number of kernel rows and 100-grain weight indicated that direct selection for these traits can be effective for yield improvement. The number of kernel rows, number of kernels per row and 100-grain weight had a positive direct effect on total yield per plant. Correlation and path analysis indicated that selection for number of kernel rows, number of kernels per row and 100-grain weight would be more promising for the improvement of grain yield in sweet corn. Selection for these characters may, therefore, be practiced for improving the grain yield in sweet corn.

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