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Variability For Grain Yield, its Components and Quality Traits in a Sweet Corn Population

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Abstract

One hundred S_1 families were developed from an open pollinated population of sweet corn. The estimates of genetic variance and broad-sense heritability were significant for all the yield and quality traits. The maximum estimate of broad-sense heritability was for number of grain rows per cob ($h^2 = 0.84$). Significant and positive estimates of genetic correlations were noted for cob length in combination with number of grains per row ($r = 0.75$). Similarly, among quality traits, sweetness and sweet flavour showed positive and significant genetic correlation ($r = 0.82$).

Introduction

Sweet corn is one of the most popular vegetables grown in the United States. It currently ranks second in farm value for processing and fourth for fresh-market among vegetable crops. Sweet corn is used as fancy maize and little research work has been conducted on its improvement. In Pakistan, research work for the improvement of sweet corn through mass selection has been done (Tanveer, 1989). Whereas Younas (1989) compared half-sib, full-sib and S_1 family selection for improving an open-pollinated sweet corn population. Georgiev and Mukhtanov (1980) reported that in west corn grain moisture content at harvest was positively correlated with cob length ($r = 0.61$) and grain yield $r = 0.43$). However, negative correlations between silking and plant height and silking and grain yield per plant were observed (Bejarano *et al.*, 1992).

The progress in any of the plant breeding programme depends primarily upon genetic diversity and the effectiveness of selection procedure involved.

Recurrent S_1 family selection based upon an index of economically important primary characters and correlated secondary characters has proven very effective in maize population improvement (West *et al.*, 1980).

With similar considerations in view, present study was conducted on an open-pollinated sweet corn population. The objectives of this study were (i) to determine genetic variability among S_1 families of sweet corn population and to obtain the estimates of genetic and environmental variances for various grain yield and quality traits. (ii) To calculate the broad-sense heritabilities of S_1 families for these traits. (iii) to estimate the genetic and phenotypic correlation coefficients among and between yield and quality traits.

Materials and Methods

The experimental material used in this study consisted of a random sample of 100 S_1 families derived from an open-pollinated population of sweet corn by selfing the S_0 plants at random. These S_1 families were planted during 1996 at the experimental area of the Department of Plant Breeding

and Genetics, University of Agriculture, Faisalabad. A modified randomized complete block design with three replications was used, where each block contained 25 S_1 families. The experimental unit consisted of a single row plot of 3.5 m length with plants spaced 30 cm apart and having 60 cm distance between rows. The agronomic characters measured on plot mean basis were days to silking, plant height (cm), cob length (cm), cob diameter (cm), number of grain rows per cob, number of grains per row, 100-grain weight (g) and grain yield per plant (g). Two random plants from each plot were selected for organoleptic evaluation of quality traits as described by Marshall (1987) like seed quality, pericarp tenderness, sweetness, sweet flavour, shank softness and shank wetness. A separate analysis of variance and covariance of all plant traits and pairs of traits was carried out for S_1 families of sweet corn population by following the procedures described by Steel and Torrie (1984).

The stand establishment of S_1 families in sweet corn population was erratic. Therefore, a simple linear regression analysis was performed prior to the statistical analyses for all the agronomic traits on the number of plants per plot. All the agronomic traits except days to silking were found significantly affected by plant stand. Hence these traits were adjusted by using the following equation as described by Le Clerg *et al.* (1962):

$$Y' = Y - b(X - \bar{X})$$

where,

Y' = the adjusted value of the Y trait

Y = the observed value of the Y trait

b = the regression coefficient of Y on X
and

$(X - \bar{X})$ = the deviation of number of plants in the plot from the overall average number of plants

The genetic components of variance and covariance were calculated as outlined by Robinson *et al.* (1951). Phenotypic variances and covariances were calculated by dividing S_1 families mean squares and S_1 families mean cross products

Asghar and Mehdi: Variability, grain yield and its components, quality traits.

Table 1: Mean squares from the analyses of variance of grain yield and its components among S₁ families of sweet corn population

SOV	df	DSLK	PLHT	CLEN	CDIA	RCOB	GROW	GRWT	GYLD
Blocks	3	139.08	1510.83	0.31	4.11	7.41	59.83	19.09	153.41
Reps/Blocks	8	69.50	1197.90	20.13	3.32	1.15	142.10	15.73	786.65
Fam/Blocks	96	33.81**	392.89**	7.66**	1.51**	4.28**	41.48**	10.58**	141.89**
Error	192	14.22	128.09	2.11	0.60	0.68	14.12	2.39	87.88

DSLK = days to silking, PLHT = plant height (cm), GLEN = cob length (cm), CDIA = cob diameter (cm), RCOB = number of grain rows per cob, GROW = number of grains per row, GRWT = 100-grain weight (g) and GYLD = grain yield per plant (g)

** = Significant at 0.01 probability level

Table 2: Mean squares from the analyses of variance of quality traits among S₁ families of sweet corn population

Soy	df	SOLT	PTEN	SWTN	SWTF	SHKS	SHKW
Blocks	3	0.44	0.46	0.32	0.72	0.65	0.43
Reps/Blocks	8	1.50	0.41	0.14	0.16	0.28	0.29
Fams/Blocks	96	0.60**	0.40*	0.37**	0.33*	0.61**	0.54**
Error	192	0.33	0.28	0.23	0.22	0.28	0.28

SOLT = Seed quality, PTEN = pericarp tenderness, SWTN = sweetness, SWTF = sweet flavour, SHKS = shank softness and SHKW = shank wetness

** = Significant at 0.05 and 0.01 probability levels, respectively

Table 3: Mean, range and coefficients of variation (GCV% and PCV%) for agronomic traits among S₁ families of sweet corn population

Trait #	Mean	Range			Coefficients of variation	
					GCV%	PCV%
DSLK	61.77	51.0	-	75.02	5.14	5.43
PLHT	88.59	52.9	-	139.3	10.61	12.92
CLEN	10.92	3.0	-	18.3	12.46	14.63
CDIA	10.25	6.2	-	12.5	5.38	6.93
RCOB	12.20	8.8	-	16.7	8.97	6.79
GROW	21.49	2.3	-	35.3	14.05	17.30
GRWT	11.47	3.2	-	18.9	14.40	16.37
GYLD	25.42	2.6	-	65.6	16.68	27.05

= DSLK = days to silking, PLHT = plant height (cm), CLEN = cob length (cm), CDIA = cob diameter (cm), RCOB = number of grain rows per cob, GROW = number of grains per row, GRWT = 100-grain weight (g) and GYLD = grain yield per plant (g)

Table 4: Mean, range and coefficients of variation (GCV% and PCV%) for quality traits among S₁ families of sweet co population

Trait #	Mean	Range			Coefficients of variation	
					GCV%	PCV%
SOLT	0.82	0.0	-	2.0	36.84	54.48
PTEN	0.80	0.0	-	2.0	25.52	45.81
SWTN	0.85	0.0	-	2.0	25.17	41.39
SWTF	0.85	0.0	-	2.0	22.01	38.68
SHKS	1.09	0.0	-	2.0	30.50	41.41
SHKW	0.78	0.0	-	2.0	38.43	54.81

= SALT = Seed quality, PTEN = pericarp tenderness, SWTN = sweetness, SWTF = sweet flavour, SHKS = shank softness and SHKW = shank wetness

Asghar and Mehdi: Variability, grain yield and its components, quality traits.

Table 5: Estimates of genetic variance, environmental variance and broad-sense heritability for agronomic traits among S₁ families of sweet corn population

Traits#	σ^2_g	σ^2_e	h^2
DSLK	6.5309 ± 1.6804	4.7395	0.5795 ± 0.1491
PLHT	88.2668 ± 19.2048	42.6967	0.6740 ± 0.1466
GLEN	1.8511 ± 0.3718	0.7033	0.7247 ± 0.1456
CDIA	0.3041 ± 0.0748	0.2001	0.6033 ± 0.1484
RCOB	1.1985 ± 0.2051	0.2269	0.8402 ± 0.1438
GROW	9.12312 ± 2.4163	4.7053	0.6597 ± 0.1747
GRWT	2.7280 ± 0.5100	0.7969	0.7739 ± 0.1447
GYLD	17.9698 ± 7.3738	29.2948	0.3802 ± 0.1561

= DSLK = days to silking, PLHT = plant height (cm), GLEN = cob length (cm), CDIA = cob diameter (cm), RCOB = number of grain rows per cob, GROW = number of grains per row, GRWT = 100-grain weight (g) and GYLD = grain yield per plant (g)

Table 6: Estimates of genetic variance, environmental variance and broad-sense heritability for quality traits among S₁ families of sweet corn population

Traits#	σ^2_g	σ^2_e	h^2
SALT	0.0908 ± 0.0308	0.1104	0.4515 ± 0.1532
PTEN	0.0419 ± 0.0215	0.0931	0.3104 ± 0.0531
SWTN	0.0456 ± 0.0193	0.0777	0.3698 ± 0.1565
SWTF	0.0354 ± 0.0173	0.0739	0.3239 ± 0.1583
SHKS	0.1103 ± 0.0305	0.0930	0.5425 ± 0.1500
SHKW	0.0894 ± 0.0276	0.0925	0.4915 ± 0.1517

= SALT = Seed quality, PTEN = pericarp tenderness, SWTN = sweetness, SWTF = sweet flavour, SHKS = shank softness and SHKW = shank wetness

with number of replications, respectively. The genetic and phenotypic covariances were calculated separately among and between agronomic and quality traits. The genotypic and phenotypic coefficients of variation for a character were calculated as the square root of the genotypic and phenotypic variances divided by the mean. The estimates of broad-sense heritability on S₁, family mean basis were calculated for each trait in sweet corn population with the formula:

$$h^2 (BS) = \sigma^2_g / \sigma^2_p$$

Where σ^2_g and σ^2_p are the estimates of genetic and phenotypic variances, respectively.

The estimates of genetic correlation were calculated for all pairs of traits among and between agronomic and quality traits in sweet corn population by using the formula:

$$r_{g_{xy}} = \frac{\sigma_{g_{xy}}}{\sqrt{\sigma^2_{g_x} \cdot \sigma^2_{g_y}}}$$

Where,

$\sigma^2_{g_x}$ = the family genetic variance for trait X

$\sigma^2_{g_y}$ = the family genetic variance for trait Y

$\sigma_{g_{xy}}$ = the genetic covariance between trait X and Y

The phenotypic correlation coefficients were similarly calculated using phenotypic variances and covariances

estimates, respectively. The estimates of broad-sense heritability and genetic correlation coefficients were considered significant if their absolute value exceeded twice of their respective standard error.

Results and Discussion

The objective of various breeding programmes being conducted by breeders is to improve grain yield and quality of the crop. The measurement and evaluation of variability is essential in order to draw meaningful conclusions from a given set of observations (Mehdi and Khan, 1994). The genetic variability of a metric trait can be studied through the use of various statistical parameters like range, variance components and coefficient of variation.

Range, mean, genotypic coefficient of variation (GCV%) and phenotypic coefficient of variation (PCV%) among S₁ families of sweet corn population revealed the presence of sufficient amount of genetic variation in the population for all the agronomic and quality traits (Table 3 and 4).

The variation among families for all the traits showed promise for the improvement of population. Mean squares from the analyses of variance for grain yield, its components and quality traits measured from S₁ progenies in sweet corn population are given in Table 1 and 2. The results showed highly significant differences among S₁ families for all the agronomic traits. Fountain and Hallauer (1996) also found significant differences among S₁ progenies within maize population for most of the traits.

Table 7: Estimates of genetic correlation coefficients for agronomic and quality traits among S_i families of sweet corn population

Trait#	PLHT	CLEN	CDIA	RCOB	GROW	GRWT	GYLD	SALT	PTEN	SWTN	SWTF	SHKS	SHKW
DSLK	0.161*	0.355	0.337	0.265	0.474	-0.567	0.166	0.247	-0.082	0.320	0.649	0.315	-0.142
PLHT		0.457	0.189	0.040	0.469	-0.138	0.399	0.531	-0.128	0.191	0.253	-0.140	0.241
CLEN			0.163	-0.283	0.755*	0.066	0.625	0.292	-0.227	0.208	0.028	0.180	0.061
CDIA				0.508	-0.071	0.213	0.407	0.203	-0.128	0.130	0.191	0.070	0.076
RCOB					-0.357	-0.422	0.052	0.218	0.152	-0.290	-0.233	0.153	-0.377
GROW						-0.314	0.521	0.309	0.041	-0.262	0.166	0.157	-0.044
GRWT							0.213	-0.256	-0.214	-0.020	-0.122	-0.259	0.354
GYLD								0.574	-0.288	0.280	0.098	0.106	0.066
SOLT									-0.058	-0.036	0.279	0.210	0.061
PTEN										-0.714	-0.730	-0.115	-0.345
SWTN											0.821*	-0.083	0.167
SWTF												-0.186	0.414
SHKS													-0.721

= DSLK = days to silking, PLHT = plant height (cm), CLEN = cob length (cm), CDIA = cob diameter (cm), RCOB = number of grain rows per cob, GROW = number of grains per row, GRWT = 100-grain weight (g), GYLD = grain yield per plant (g), SOLT = Seed quality, PTEN = pericarp tenderness, SWTN = sweetness, SWTF = sweet flavour, SHKS = shank softness and SHKW = shank wetness
 + = Genetic correlation coefficients differ significantly from zero as its magnitude exceeded twice its standard error

Table 8: Estimates of phenotypic correlation coefficients for agronomic and quality traits among S_i families of sweet corn population

Trait#	PLHT	CLEN	CDIA	RCOB	GROW	GRWT	GYLD	SALT	PTEN	SWTN	SWTF	SHKS	SHKW
DSLK	0.161*	0.175*	0.131	0.157*	0.203	-0.483**	-0.118	0.092	-0.035	0.181*	0.316**	0.007	-0.107
PLHT		0.403**	0.237**	0.038	0.386	-0.003	0.372**	0.322**	-0.043	0.104	0.111	-0.048	0.102
CLEN			0.295**	-0.185**	0.758*	0.124	0.572**	0.185**	-0.029	0.164*	0.062	0.099	0.072
CDIA				0.469**	0.168	0.260*	0.494**	0.139	-0.103	0.112	0.123	0.011	0.087
RCOB					-0.209	-0.333**	0.084	0.144**	0.065	-0.170*	-0.131	0.065	-0.196*
GROW						-0.224**	0.565**	0.196**	-0.047	0.198**	0.110	0.123	0.037
GRWT							0.306	-0.088	-0.095	0.010	-0.031	-0.135	0.207
GYLD								0.296**	-0.197**	0.163*	0.069	0.021	0.116
SOLT									0.189	-0.117*	0.005	0.282**	-0.119
PTEN										-0.622**	-0.607**	0.237**	-0.424**
SWTN											0.803**	-0.079	0.186**
SWTF												-0.078	0.240**
SHKS													-0.747**

= DSLK = days to silking, PLHT = plant height (cm), CLEN = cob length (cm), CDIA = cob diameter (cm), RCOB = number of grain rows per cob, GROW = number of grains per row, GRWT = 100-grain weight (g), GYLD = grain yield per plant (g), SOLT = Seed quality, PTEN = pericarp tenderness, SWTN = sweetness, SWTF = sweet flavour, SHKS = shank softness and SHKW = shank wetness
 *, **, *** = Significant at 0.05 and 0.04 probability levels, respectively

Asghar and Mehdi: Variability, grain yield and its components, quality traits.

Highly significant differences were also observed among S_1 families for all quality traits (Table 2). However, pericarp tenderness and sweet flavour scores showed significant differences. Our results are in conformity with the research findings of Winter *et al.* (1955). Whereas Schmidt and Tracy (1988) found highly significant differences among pericarp tenderness scores.

The estimates of genetic variance were significant for all the agronomic and quality traits as their absolute magnitude exceeded twice their respective standard errors. These statistics revealed that significant genetic variability existed among S_1 families of sweet corn population evaluated. The estimates of genotypic variance were smaller than their respective phenotypic variances. Our results are consistent with the findings of Walters *et al.* (1991), Funduiana (1976) and Zieger (1987).

The estimates of genetic variance and broad-sense heritability for agronomic and quality traits are given in Table 1 and 2. Grain yield is the most economically important trait in maize but often has the low heritability of all the traits. In our study, the value of broad-sense heritability for grain yield was 0.38. The maximum estimates of broad-sense heritability were noted for number of kernel rows per cob among yield components and shank softness among quality traits on sweet corn population (Table 5 and 6). Most of the agronomic traits in sweet corn population appeared more easily heritable than quality traits. Estimates of genetic correlations were greater than their respective phenotypic correlations for most of the agronomic and quality traits. Among yield components the estimate of genetic correlation between cob length and number of grains per row was positive and significant (Table 7). Likewise, grain yield showed positive and significant estimate of phenotypic correlation with almost all the agronomic traits except days to silking and number of grain rows per cob (Table 8). Similarly among quality traits, the significant estimate of genetic correlation was found only between sweetness and sweet flavour. No significant and positive estimate of genetic correlation was obtained between agronomic and quality traits. However, grain yield showed significant and positive phenotypic correlations with seed quality and sweetness and negative with pericarp tenderness. Positive and significant estimates of phenotypic correlations existed between sweetness and days to silking, cob length, number of grains per row and 100-grain weight. Sweetness showed significant and negative estimate of phenotypic correlation in combination with pericarp tenderness.

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