

Genetic Inheritance of Some Important Characters of Sweet Corn

Voichita HAS¹⁾, Ioan HAS^{1), 2)}

¹⁾ *Agricultural Research Station Agriculturii 27, Turda, Romania; hasvoichita@yahoo.com*

²⁾ *University of Agricultural Sciences and Veterinary Medicine, Manastur 3-5, Cluj-Napoca, Romania; ioanhas@yahoo.com*

Abstract

Ten early sweet corn inbred lines were studied for estimating components of genetic variance and heritability, using a factorial (m.n + n.m) mating design with reciprocal combinations. The genotype × years interactions (G × Y) influenced the expression of the most traits emphasize. submitting the importance of their evolution in different years. The additive effect values for yield components were highly significant in the genotypes studied here. Specific combining ability (SCA) variance was larger than general combining ability (GCA) variance for kernel chemical composition and pericarp thickness. The predominance of SCA effects indicates that the pattern of carbohydrate accumulation in a hybrid depended upon the particular interaction of inbred lines involved in the crosses. Reciprocal (R) hybrids differences were detected for all kernel composition analysed. These differences should be attributed to an interaction of cytoplasm × nuclear genome (R). The narrow-sense heritability estimate (h^2) respectively the proportion of variance components to phenotypic variance for some ear traits are presented here. Genetic correlations among twenty traits submitted an unfavourable genetic correlation between sucrose-row number, silking data-total sugar and total sugar-ear weight that suggest the difficulties in obtaining early sweet corn hybrids high yielding with a good quality.

Keywords: sweet corn, genetic inheritance, heritability, correlations

Introduction

Sweet corn (*Zea mays* L.) is a popular crop in USA and Europe. In Romania the areas planted with sweet corn have increased considerably during the last ten years. The nutritive value of sweet corn and the many different ways of using the ears and kernels, also determined an extension of this plant.

Yield gains due to the genetic improvement have been smaller in sweet corn than in field corn. Sweet corn breeders have often focused on improving quality and ear appearance, rather than on enhancing yield (Tracy, 1993). Moreover, all commercial sweet corn hybrids are based on one or more defective endosperm mutants, and production of high quality seed is more difficult for sweet corn than for most types of corn (Tracy, 1994). Additionally, the narrow genetic base of sweet corn may limit genetic gains for yield. Sweet corn (eating) quality is a very complicated trait because of the effects of the individual gene influencing this trait, which is difficult to isolate and quantify. The polygenic nature of this trait has directed the breeding efforts towards the development of new sweet corn hybrids with improved eating quality and favourable ear and kernel traits (Hansen et al., 1977; Kaukis and Davis, 1986; Tracy, 1994; Has and Cabulea, 1996; Has et al., 2000; Has, 2000, 2007).

An extensive sweet corn breeding programme has been started, some years ago (1980) at the Agricultural Research Station, Turda, Romania, aimed at producing local superior hybrids with a short growing season and high quality yield.

Advanced breeding inbred lines have been developed from local sources as well as imported germplasm. The present study is a part of the programme of testing of new inbred lines. The aim of the study were to estimate genetic variances involved in the inheritance of: yield, kernel chemical composition, ear and kernel characteristics, vegetative and physiological plant traits; to observe the expression of some sweet corn traits in different environmental conditions; to estimate heritability of some of the important plant traits in the hybrids and to determine correlations among those traits.

Materials and methods

Ten early sugary-1 inbred lines that were developed at the Agricultural Research Station Turda, Romania (Tab. 1).

Tab. 1. Origin and genealogy of the sweet inbred lines used in the Design 2 experiment

No.	Inbred line	Pedigree / Origin	Genealogy
1.	SW 87	SUA	n.a.
2.	TA 22 su	Q 206 - Canada	3603-1-1-7-
3.	TA 27 su	Reward - SUA	5103-6-3-5
4.	TA 28 su	Golden Beauty - SUA	7188-1-1-3-
5.	TD 103 su	How Sweet It Is - SUA	7208-1-1-1-
6.	TA 25 su	Reward - SUA	3610-2-4-1-
7.	TA 26 su	Reward - SUA	5093-1-1-1-
8.	TD 101 su	Aux 5651 - SUA	3607-2-1-3-
9.	TD 282 su	Silver Queen - SUA	3870-10-2-1-
10.	TD 102 su	Aromatnaja - R.Moldova	7208-3-1-1-

They were crossed in an incomplete diallel with reciprocals of 30 single cross hybrids using a factorial (m,n + n,m) (m = inbred lines used as mother; n = inbred lines used as father and reciprocals) mating design. Data for morphological and field performance were collected during the summer of two years at the A.R.S. Turda. Complete block designs were used with three replications both inbred lines and hybrids. The plot consisted of four rows, 5.0 m long with 70 cm between the rows. Plant densities averaged 40.000 plants/ha in each experiment. Ten plants were selected at random from each plot at harvest (at 21 days after silking date) and they were measured (22 traits / plant). Data collected involved: 1. ear traits: ear weight, husk weight, ear length, row number; 2. kernel chemical composition: sucrose, total sugar, phytoglycogen, starch, protein, fats, dry matter; 3. vegetative and physiological plant traits. For estimating components of genetic variance it was used Design 2 of Comstock and Robinson (1952) adapted by Cabulea et al. (1994). which permitted us to partition the genotypes into: additive gene action (GCA), non-additive gene action (SCA), cytoplasmic (maternal) effects, reciprocal effects (nucleo - cytoplasmic interaction) and their interactions with the years. The variance of the observed values of phenotypic variance (Vp), can be partitioned into different components:

$$V_p = V_A + V_{AE} + V_e$$

$$H^2 = \frac{s_G^2}{s_G^2 + s_{G \times E}^2 + s_e^2}$$

A broad-sense heritability (H %) was estimated as (Sprague, 1967):

where: σ_G^2 = total genetic variance; σ_A^2 = additive genetic variance; σ_E^2 = environmental variance.

Narrow-sense heritability (h^2) was estimated as (Kriebel et al., 1972):

$$h^2 = \frac{2s_A^2}{2s_A^2 + s_N^2 + s_{Cit.}^2 + s_{R.c.}^2 + s_{A \times E}^2 + s_{N \times E}^2 + s_{Cit \times E}^2 + s_{R.c \times E}^2 + s_e^2}$$

where: σ^2 is estimate of: (A) additive effects, (NA) non-additive effects, (A×E) additive effects environment, (NA×E) non-additive effects × environment, (Cit.) maternal effects, (Cit.×E) maternal effects × environment, (Rec.) reciprocal interactions, (Rec. ×E) reciprocal interactions × environment, (e) environmental variance.

The model for the general combining ability effects (\hat{g}_m ; \hat{g}_n) analysis is:

where: \hat{g}_m ; \hat{g}_n = general combining ability effects for m or n inbred lines; Σ = overall sum;

$$\hat{g}_m = \frac{\sum m}{m} - \frac{\sum \cdot}{m \cdot n} \quad (\text{Cabulea, 1975})$$

Relationships among all traits were computed using simple genotypic correlation coefficients based on the formula (Ceapoiu, 1968):

$$r = \frac{\sum_{i=1}^n (x_i - \bar{x})(y_i - \bar{y})}{\sqrt{\sum_{i=1}^n (x_i - \bar{x})^2 \sum_{i=1}^n (y_i - \bar{y})^2}}$$

r = correlation between the traits x and y; x_i = variance of x_i and y_i = variance of y_i

Genetic correlation coefficients were analyzed among 20 traits.

Results and discussion

Hybrid (G) and year × hybrid (G × Y) interactions were significant or highly significant for all ear traits. Years (Y) were significant for all traits (Tab. 2). Both additive (GCA) and non-additive (SCA) genetic effects were significantly involved in the inheritance of most characters except some of the ear and kernel characteristics. The highly significant GCA mean squares (A_m , A_n) for yield components point to the importance of additive gene action in the genotypes and traits studied here: ear length, row number, ear and husk weight (Tab. 2). Though maternal effects (M_m , M_n) involved in the inheritance of ear and husk weight had a poor value they would be used as a source of the ear weight improvement. Both SCA variance and reciprocal effects (R) were significant for traits related to quality, such as: ear length, row number, kernel depth according to the results of Hansen and Baggett (1977) for ear traits. Interactions of additive gene actions with years ($A_m \times Y$, $A_n \times Y$) were significant for: ear and husk weight, ear length, row number. Non-additive gene action × year was significant for all ear and kernel characters.

SCA (non-additive gene action) variance was larger than GCA variance for kernel chemical composition (Tab. 3). The predominance of SCA effects indicates that the pattern of carbohydrate accumulation in a hybrid depended upon the particular interaction of the su inbred lines involved in these crosses. Similar results were obtained by Michaels and Andrew (1986). Tracy (1994). Azanza et al. (1996) as well. Reciprocal hybrid differences were also detected for all analysed components of the kernel chemical composition. These differences have been attributed to "plasmon - sensitive genes" in which an interaction between the cytoplasm and genome occurs, this opinion also being supported by some authors: Hansen and Baggett (1977), Kaukis and Davis (1986), Tracy (1994).

The proportion of variance components to phenotypic variance and heritabilities for some ear traits are presented in Tab. 4. Additive variance was the major component of

Tab. 2. Genetic variances (s^2) involved in the expression of ear and kernel characteristics in sweet corn hybrids

Source of variation	DF	Weight		Ear length	Row number	Ear shape	Kernel depth	Eating quality
		ear	husk					
TOTAL	547							
YEARS (Y)	1	38250.83**	12229.06**	8.61*	2.36**	8.61**	13.86*	12.66**
REPLICATION	2	262.84	306.42	0.80	0.35	1.02	5.49	5.97
ERROR (a)	2	79.91	220.25	0.43	0.36	1.12	3.81	0.17
GENOTYPES (G)	87	2490.48**	1029.45**	10.09**	17.98**	5.15**	5.76**	2.30**
-Additive actions (Am)	(11)	9672.33**	3114.74**	31.63**	58.47**	16.57**	10.99	3.45
-Additive actions (An)	(10)	6112.29**	3075.17**	41.67**	77.19**	20.53**	19.74**	4.08
-Non-additive actions (NA)	(20)	1854.22**	848.10**	1.35**	3.95**	1.42**	5.08**	2.27**
-Differences m/n	(5)	322.89	111.26	3.05*	2.62	0.38	4.33*	4.13**
-Maternal effects (Mm)	(11)	171.67	268.21**	1.06	1.62	1.13	1.28	2.21
- Maternal effects (Mn)	(10)	541.54**	289.81**	3.75	0.77	0.76	2.04	0.97
Reciprocal effects (R)	(20)	157.55	59.08	1.09**	1.56**	0.54	1.27*	1.05**
G × Y	87	1480.66**	333.71**	2.32**	3.26**	0.82**	6.52**	1.75**
- Am × Y	(11)	4611.29**	859.99*	8.20**	8.49**	1.79	17.32	3.08
- An × Y	(10)	3933.88*	485.81	4.71**	8.40**	1.13	9.33	2.55
NA × Y	(20)	1522.78**	339.50**	1.01**	1.37**	0.96**	7.57**	1.02**
- m/n × Y	(5)	239.63	213.12	0.41	1.21	1.24**	4.10	1.20**
- Mm × Y	(11)	84.69	95.95	0.68	2.37	0.52	3.12	1.96
- Mn × Y	(10)	307.73	222.88	0.64	2.07	0.20	3.13	2.29
- R × Y	(20)	154.58	178.74	1.42	1.28**	0.38	2.29**	1.08**
ERROR (b)	368	91.23	133.70	0.36	0.34	0.51	0.80	0.21

*, ** Significant at the 0.05 and 0.01 levels of probability, respectively.

phenotypic variance, for ear length ($\sigma^2 A / \sigma^2 P = 53\%$), row number ($\sigma^2 A / \sigma^2 P = 58\%$), Additive variance components were relatively low for most of the characteristics ($VA / VP = 8 - 32\%$): kernel depth, eating quality, ear weight. The relatively high ratio of additive x environment variance to phenotypic, variance resulted in large differences between $\sigma^2 A / \sigma^2 P$ (narrow sense heritability parameters) on $H\%$ (broad sense heritability parameters) for ear weight and kernel depth.

Significance of additive × environment variances, especially for ear weight and kernel depth, indicated the need

to evaluate these interactions in multiple environments which are representative of the area in which the genotypes are to be grown. The characters of ear length, row number of kernels per ear, number of branches/tassel and silking data showed high heritability value. Meanwhile, the characters of ear weight, husk weight, kernel depth, cob diameter, eating quality showed moderate to low heritability value. Similar results were obtained by Hansen et al (1977), Saleh et al. (2002), Eltahir et al (2003), Sujiprihati et al (2005), Kumari et al (2006), Nigussie and Saleh (2007), Rea et al (2007). For most other traits, additive

Tab. 3. Genetic variances (s^2) involved in the expression of kernel quality of sweet corn hybrids

Source of variation	DF	Kernel contents in:						
		Dry matter	Total sugar	Sucrose	Phytoglycogen	Starch	Protein	Fats
TOTAL	179							
REPLICATION	5	1.66	0.10	0.001	0.001	0.25	0.01	0.01
GENOTYPES	87	14.56**	30.31**	2.27**	7.77**	45.56**	2.27**	0.67**
-additive actions (Am)	(11)	25.20	79.65	4.31	7.36	70.94	5.36*	1.47
-additive actions (An)	(10)	25.25	38.74	3.28	22.62	66.11	1.09	0.48
-non-additive actions (NA)	(20)	12.92**	39.31**	3.27**	6.15**	45.21**	2.09**	0.74**
-differences m/n	(5)	11.86**	9.85**	1.16**	3.04**	6.27**	1.37**	0.29**
-maternal effects (Mm)	(11)	11.97	12.72	0.98	2.76	27.98	1.55	0.41
-maternal effects (Mn)	(10)	6.47	5.96	0.83	5.44	26.29	1.54	0.75
-reciprocal effects (R)	(20)	11.13**	16.94**	1.34**	7.29**	50.83**	2.32**	0.44**
Error	87	0.27	0.09	0.001	0.001	0.35	0.001	0.01

*, ** Significant at the 0.05 and 0.01 levels of probability, respectively.

Tab. 4. Proportion of variance components to phenotypic variance, heritability and correlation coefficients ("per se") between parental inbreds and F₁ crosses in a factorial system

Nr. crt.	Trait	Parameters					h ² (%)	H (%)	Correlation coefficient (r)
		σ_A^2 / σ_F^2	$\sigma_A^2 \times E / \sigma_F^2$	$\sigma^{2NA} / \sigma_F^2$	$\sigma^{2NA \times E} / \sigma_{2F}$	$\sigma_{2e} / \sigma_{2F}$			
1.	Ear weight	21	22	19	32	6	29	61	0.53**
2.	Husk weight	24	9	25	14	28	38	69	0.49**
3.	Ear length	53	19	6	8	14	58	79	0.89**
4.	Row number	58	14	13	8	7	65	83	0.88**
5.	Kernel depth	10	19	15	41	15	15	44	0.09
6.	Cob diameter	22	8	3	27	40	33	57	0.61**
7.	Ear shape	44	6	9	9	32	44	79	0.22**
8.	Eating quality	12	8	29	23	18	16	54	-
9.	No. tillers / plant	40	13	5	16	26	50	71	0.86**
10.	No. ears / plant	17	18	18	12	35	24	44	0.56**
11.	No. branches / tassel	73	5	9	9	4	81	93	0.89**
12.	GDUs from sowing to silking	62	11	14	3	10	70	87	0.60**
"r" P 5%								0.36	
P 1%								0.46	

effects were consistent over the years and showed little changes.

Highly significant positive correlations between parental inbreds and F₁ hybrids for the same traits were found in: ear length, row number, tillers / plant. This suggests

that it is possible to develop valuable sweet corn hybrids if parental inbreds with valuable traits will be crossed, respectively inbred lines with long ear ($r = 0,89^{**}$) or with a high number of kernel rows ($r = 0,88^{**}$), number of tillers per plant ($r = 0,86^{**}$), growing season from sowing to silk-

Tab. 5. Correlation coefficients between additive genetic effects (r_g)

Trait	1. S	2. TS	3. Ph	4. S	5. P	6. F	7. DM
Kernel chemical composition							
1.Sucrose (S)	-	0.10	-0.05	0.02	-0.35	0.30	0.03
2.Total sugar (TS)		-	0.25	-0.41*	0.53**	-0.05	-0.57**
3.Phytglycogen (Ph)			-	-0.13	0.33	-0.27	-0.52**
4.Starch (S)				-	-0.39*	0.20	0.19
5.Protein (P)					-	0.25	-0.35
6.Fats (F)						-	0.36*
7.Dry matter(DM)							-
Ear and kernel traits							
Ear weight	-0.06	-0.38**	-0.03	0.59**	-0.28	0.20	0.12
Husk weight	0.27	-0.15	0.15	0.15	-0.12	0.11	-0.30
Ear length	-0.08	-0.33	-0.64**	0.22	-0.28	0.20	0.02
Row number	-0.41**	-0.15	0.16	0.07	0.36*	-0.37*	0.26
Kernel depth	-0.16	0.11	0.27	-0.15	0.22	-0.25	0.15
Plant traits							
Plant height	0.27	0.18	-0.11	0.01	-0.35	0.40*	-0.01
Ear height	0.13	0.09	-0.19	-0.01	-0.31	0.22	0.09
Leaf area	0.35	0.32	-0.22	-0.11	-0.34	0.28	0.07
No. leaves / plant	0.16	0.36*	0.17	-0.27	-0.16	0.04	0.20
No. branches / tassel	0.06	-0.01	-0.04	-0.01	-0.16	0.13	0.21
No. ears / plant	0.07	0.12	-0.01	-0.12	-0.23	0.19	0.20
No. tillers / plant	-0.29	-0.29	-0.30	0.37*	0.18	-0.19	0.17
Growing season							
GDUs: sowing - silking	-0.43**	0.17	0.11	-0.09	0.16	-0.33	-0.52**

*. ** - indicates significance at $P < 0.05$ and $P < 0.01$ respectively; * - indicates significance both for the genetic (r_g) and phenotypic (r_P) correlation coefficients

ing ($r = 0,60^{**}$). A similar result was obtained by Kumari et al. (2006).

Results on correlations between additive genetic effects ($r\hat{g}$) analysis among ear and plant traits and kernel chemical composition are presented in Tab. 5. The existence of unfavourable genetic correlations has been observed between: sucrose-row number ($r\hat{g} = - 0,41^{**}$), total sugar – ear weight ($r\hat{g} = - 0,38^*$), phytoglycogen – ear length ($r\hat{g} = - 0,64^{**}$) indicating the difficulty of simultaneous improvement of sweet corn hybrids for both yield ability and kernel quality, according to the results of Saleh et al. (2002),

Conclusions

The highly significant of GCA mean squares for the most traits indicates the importance of additive gene action in the genetic material studied here. SCA effects were significant for kernel chemical composition, kernel depth, eating quality, indicating nonadditive gene action for these attributes, although each attribute appeared to be affected to a relatively greater extent by additive gene effect.

The existence of unfavourable genetic correlations that has been observed indicates the difficulty of simultaneous improvement of early sweet corn hybrids for both yield ability and kernel quality.

References

- Azanza, F., Avri Bar-Zur and J. A. Juvik (1996). Variation in sweet corn. kernel characteristics associated with stand establishment and eating quality. *Euphytica*. 87:7-18.
- Cabulea, I. (1975). Metode statistice pentru analiza componentelor genetice ale variabilitatii continue. *Prob. Genet. Teor. Aplic.* VII: 391-421.
- Cabulea, I., V. Has and I. Has (1994). Research regarding to genetic diversity of cytoplasm and nuclear - cytoplasmic interactions in maize. *Contributii ale cercetarii stiintifice la dezvoltarea agriculturii* V:85-104.
- Ceapoi, N. (1968). Modele statistice aplicate in experientele agricole si biologice. Chapter 5: Analysis of correlations: 172-196. Ed. Agro-Silvica. Bucuresti.
- Eltahir, S. A., G. B. Saleh. Z. B. Wahab and A. A. Rahim (2003). Performance, heritability and correlation studies on varieties and population cross of sweet corn. *Asian Journal of Plant Sciences*. 2:756-760.
- Hansen, L. A. and J. R. Baggett (1977). Reciprocal differences for plant and ear characteristics in sweet corn. *Hort Science*. 12:60-62.
- Hansen, L. A., J. R. Baggett and K. E. Rowe (1977). Quantitative genetic analysis of ten characteristics in sweet corn. *J. Amer. Soc Hort. Sci.* 102:158-162.
- Has, V. and I. Cabulea (1998). Genetic inheritance of some quantitative characters in sweet corn. *Cercetari de genetica vegetala si animala*. V:41-55.
- Has, V. (2000). Research regarding to the inheritance of some quantitative and quantitative characters in sweet corn. Ph. thesis.
- Has, V., I. Cabulea, I. Has, A. Rotari, S. Musteata (2000). Genetic inheritance of quality in sweet corn. *Cercetari de genetica vegetala si animala*. VI.
- Has, V. (2007). Genetic analysis of some yield components and kernel quality in sweet corn. *Recent Progress in Medicinal Plants. Natural Products II*. (India). Studium Press LLC. U.S.A. 18:437-452.
- Kaukis, K. David and W. Davis (1986). Sweet corn breeding. *Breeding vegetable crops*:475-519.
- Kriebel, H. B., G. Namkoong and R. A. M. Usanis (1972). Analysis of genetic variation. in 1-, 2- and 3 year old eastern white pine in incomplete diallel cross experiments In: *Silvae Genetic*.
- Kumari, J., R. N. Gadag and G. K. Jha (2006). Heritability and correlation studies in sweet corn for quality traits, field emergence and grain yield. *MNL* 80: 18-19.
- Nigussie, M. and G. Saleh (2007). Genetic variability and heritability within sweet corn (*Zea mays* L. *saccharata*) breeding populations. *Malaysian Applied Biology* 36:15-20.
- Rea, R. A., C. E. Watson and F. M. Davis (2007). Heritability and correlation among some selected morphological traits and their relationship with fall armyworm damage in sweet corn. *J. Econ Entomol.* 100(6):1887-1895.
- Saleh, G. B., S. A. S. Alawi and K. Panjaitan (2002). Performance, correlation and heritability studies on selected sweet corn synthetic populations. *Pakistan Journal of Biological Sciences*. 5(3):251-254.
- Sprague, G. F. (1967). Quantitative genetics in plant improvement. In *Plant Breeding*: 315-354. A Symposium held at Iowa State Univ. Ames. Iowa.
- Sujiprihati, S., M. Syukur and R. Yuniarti (2005). Estimation of genetic variability and heritability of some vegetative characters and yield of sweet corn. *Jurnal Agrotropika (Indonesia)* 10(2):75-78.
- Tracy, W. F. (1993). Sweet corn: 777-807. In: G. Kalloo and B. O. Bergh (Eds.) *Genetic improvement of vegetable crops*. Pergamon. Oxford. U. K.
- Tracy, W. F. (1994). Sweet Corn: 147-187. *Speciality types of maize* CRC. Boca Raton. FL.