

# GENETIC ANALYSIS OF SOME YIELD COMPONENTS AND KERNEL QUALITY IN SWEET CORN

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## ABSTRACT

Ten *sugary-1* inbreds developed at the Agricultural Research Station of Turda were chosen for this study. They were crossed using the factorial ( $m \cdot n + n \cdot m$ ) mating design with reciprocal combinations in order to estimate GCA and SCA for inheritance of some ear and kernel characteristics. Genotype x year interactions influenced the expression of the most traits, emphasizing the importance of their evaluation in different years. The highly significant GCA mean squares for yield components point to the importance of additive gene action in the genotypes under study. The significant SCA effects for all traits point to nonadditive gene action as well, although on a basis of comparative mean squares, additive gene action appears the most important. SCA variance was larger than GCA variance only for kernel chemical compositions and pericarp thickness. The predominance of SCA effects indicates that the pattern of carbohydrate accumulation in a hybrid depends upon the specific interaction of parental inbreds involved in the crosses. Reciprocal hybrid differences were detected for all kernel composition analysed. These differences should be attributed to an interaction of cytoplasm x nuclear genome. The unfavourable genetic and phenotypic correlation coefficients between sucrose - row number, total sugar - ear weight suggest that in breeding programmes is difficult enough to obtain high yield sweet corn hybrids with good quality.

**Key words:** additive genetic effects, breeding genetic variance, heritability, sweet corn.

## INTRODUCTION

In Europe, as well as in Romania, the areas cultivated with sweet corn have increased considerably, during the last ten years. Sweet corn nutritive value and many different ways of using the ears and kernels, determined also an extension of this plant to all continents.

Yield gains due to the genetic improvement have been smaller in sweet corn than in field corn. Sweet corn breeders have often focused on the quality improvement and ear appearance, rather than on enhancing yield (Tracy, 1990b; Cartea et al., 1996). 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 yield genetic gains.

Sweet corn edible quality is a very complex trait because of the effects of individual genes influencing this trait, which is difficult to isolate and quantify. The polygenic nature of this trait has constrained the breeding efforts to be directed towards the development of new sweet corn hybrids with improved edible quality and favourable ear and kernel traits (Huelssen, 1954; Wann et al., 1971; Hansen et al., 1977; Kaukis and Davis, 1986; Tracy, 1993, 1994; Ha<sup>o</sup> et al., 1994; Wong et al., 1994; Ha<sup>o</sup> and Căbulea, 1998; Ha<sup>o</sup>, 1999).

Sometimes, the breeders' opinions with regard to gene action involved in the control of some sweet corn traits are different, such as:

- according to some researchers, the kernel carbohydrate content control could be oligogenic (Creech, 1965, 1968; Soberalske and Andrew, 1978; Juvik et al., 1983; Wong et al., 1994) while according to other authors the control of this trait could be oligo-poligenic (Michaels and Andrew, 1986; Ha<sup>o</sup> et al., 1994; Azanza et al., 1996a, 1996b; Ha<sup>o</sup>, 1999);

- according to some authors, sugar concentration in kernel could be more influenced by genotype x environment interaction (Wong et al., 1994), but Michaels and Andrew (1986) and Azanza et al. (1996a) considered that the contribution of endosperm gene could be more important as compared to the environment;

- in the sucrose and phytoglycogen accumulation in kernel, the additive gene action could be significant, according to Rosenbrook and Andrew (1971), while Michaels and Andrew (1986) considered that nonadditive gene interactions could be involved in the determinism of sucrose accumulation in kernel;

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- the ear weight and grain yield per plant, according to Stuber et al. (1987), Tracy (1994), Ordas et al. (1994) were supposed to be determined by gene actions, preponderantly by dominance and overdominance, whereas Hunter and Gamble (1968), Hansen and Baggett (1977), Ha<sup>o</sup> and Căbulea (1998), Ha<sup>o</sup> (1999) appreciated that the cytoplasmic effects and even nucleo-cytoplasmic interactions could be also very important;

- some authors considered that the yield heterosis is the result of dominance and overdominance or that it could be an effect of very different heterotic group crosses (Huelsen, 1954; Galinat, 1971; Kaukis and Davis, 1986; Tracy, 1990a; Ordas et al., 1994) although according to others, sweet corn variability is not satisfactory, because the sweet corn germplasm is divided only in four origin groups;

- the most important source of sweet corn variability may be the field corn (Tracy, 1990b; Treat and Tracy, 1993; Căbulea et al., 1994b; Hady et al., 1994; Cartea et al., 1996; Malvar et al., 1997) but there are doubts, because, at the same time, both field corn germplasm and defective traits such as thick pericarp and unfavourable taste could be transferred (Kaukis and Davis, 1986; Hady et al., 1994; Ha<sup>o</sup> et al., 1994; Brewbaker et al., 1996).

For the development of our own opinion we focused our investigation at the Agricultural Research Station Turda, on the following objectives:

- 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 under different environmental conditions;

- to estimate linkages and pleiotropic effects of *su* gene to quantitative characters;

- to estimate phenotypic and genotypic correlation coefficients among traits.

## MATERIALS AND METHODS

We collected our data from two experiments. In the first experiment we used ten *sugary* inbreds (Table 1) which were crossed in an

incomplete diallel with reciprocals of 6 F<sub>1</sub> hybrids. The diallel hybrids and their parental inbreds were grown in two years, 1994 and 1995, at Turda.

In the second experiment we used six *sugary* inbreds (three of them with sugary cytoplasm and three with field corn cytoplasm) (Table 2). These parental inbreds were crossed in a cyclic system with reciprocals. The 16 hybrids resulted were grown in the years 1996 and 1997, at Turda.

Table 1. Pedigree and genealogy of sweet inbreds used in design 2 experiment, conducted at Turda in 1994-1995

Inbreds	Pedigree/Origin	Genealogy
SW 87	USA	-
TA 22su	Q 206- Canada	3603-1-1-7-
TA 27su	Reward- USA	5103-6-3-5
TA 28su	Golden Beauty- Canada	7188-1-1-3-
TD 103 su	How Sweet It Is- USA	7208-1-1-1-
TA 25 su	Reward- USA	3610-2-4-1-
TA 26 su	Reward - USA	5093-1-1-1-
TD 101 su	Aux 5651- USA	3607-2-1-3-
TD 282 su	Silver Queen- USA	3870-10-2-1-
TD 102 su	Aromatnaja- R. Moldova	7208-3-1-1-

Table 2. Pedigree and genealogy of sweet inbreds used in the cyclic experiment conducted at Turda in 1996-1997

Inbred lines with <i>sugary 1</i> cytoplasm		
Inbreds	Pedigree/Origin	Genealogy
TA 26 su	Reward-USA	5093-1-1-1-
TA 28 su	Golden Beauty-Canada	7188-1-1-3-
TD 101 su	Aux 5651-USA	3607-2-1-3-
Inbred lines with field corn cytoplasm		
T 193 A su	T 160 x su source-Turda	1283-2-1-3-
T 209 su	A 495 <sup>1</sup> x su -1 source-Turda	1118-1-3-3-
T 244 su	T 244 x su -1 source-Turda	1140-1-1-1-

The collected data included 25 traits in the first system and 32 traits in the second system such as:

1. ear traits: ear weight, husk weight, ear length, row number, cob diameter, ear shape, husk length, tip fill, flag leaves length;

2. kernel characteristics: kernel depth, pericarp thickness, pericarp weight, edible quality;

3. kernel chemical composition: sucrose, total sugar, phytoglycogen, starch, protein, fats, dry matter;

#### 4. vegetative and physiological plant traits: 12 traits.

For analysis of variance and genetic variances we used a factorial ( $m \cdot n + n \cdot m$ ) mating design [ Design 2 of Comstock and Robinson (1952), adapted by Căbulea et al. (1994)] which permitted us to partition the genotypes into: additive gene action (GCA), nonadditive interaction (SCA), cytoplasmic (maternal) effects, reciprocal effects (nucleo-cytoplasmic interaction) and their interactions with years.

The variance of the observed values of phenotypic variance ( $V_p$ ), can be partitioned into different components:  $V_p = V_A + V_{AE} + V_e$ . A narrow sense heritability is estimate as  $V_A / V_P$  (Kriebel et al., 1972) and broad sense heritability ( $H_B$ ) can be estimated as  $H_B = (V_A + V_{AE}) / V_P$  (Sprague, 1967).

The genetic additive effects ( $r_G$ ) and phenotypic ( $r_p$ ) correlation coefficients were estimated among all traits.

## RESULTS AND DISCUSSIONS

Hybrid (G) effects and year x hybrid (G x Y) interactions were significant or highly significant for all ear traits. Years (Y) were significant for all traits (Table 3). Both additive (GCA) and non-additive (SCA) genetic effects were significantly involved in the inheritance of the most characters excepting some of 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 genotypes and traits under study: ear length, row number, ear and husk weight, husk length (Tables 3 and 4).

Although maternal effects (Mm, Mn) involved in the inheritance of ear and husk weight had a poor value they could be used as a source of ear weight improvement. Both SCA variance and reciprocal effects (R) were significant for quality traits, such as ear length, row number, kernel depth, pericarp thickness and weight, in accordance with the results of Hansen and Baggett (1977) for ear traits and with the results of Tracy (1990a, 1990b) for vegetative plant traits.

The interactions of additive gene action 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 x year ( $NA \times Y$ ) interaction was significant for all ear and kernel traits.

SCA (non-additive interaction) variance was larger than GCA variance for kernel chemical composition, pericarp thickness and pericarp weight (Table 4). The predominance of SCA effects indicates that the pattern of carbohydrate accumulation in a hybrid depends upon the particular interaction of the *su* inbreds involved in these crosses. Similar results were obtained by Michaels and Andrew (1986), Tracy (1994), Wong et al. (1994), Azanza et al. (1996a, 1996b), too.

Table 3. Genetic variances ( $s^2$ ) involved in ear and kernel characteristic expression (Turda 1994-1995)

Source of variation	DF	Weight		Ear length	Row number	Ear shape	Kernel depth	Edible quality
		ear	husk					
TOTAL	547							
YEARS (Y)	1	38250.83**	12229.06**	8.61*	2.36**	8.61**	13.86*	12.66**
REPLICATIONS	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)	15	2490.48**	1029.45**	10.09**	17.98**	5.15**	5.76**	2.30**
- additive actions ( $A_m$ )	(3)	9672.33**	3114.74**	31.63**	58.47**	16.57**	10.99	3.45
- additive actions ( $A_n$ )	(1)	6112.29**	3075.17**	41.67**	77.19**	20.53**	19.74**	4.08
- nonadditive actions (NA)	(3)	1854.22**	848.10**	1.35**	3.95**	1.42**	5.08**	2.27**
- differences m/n	(1)	322.89	111.26	3.05*	2.62	0.38	4.33*	4.13**
- maternal effects (Mm)	(3)	171.67	268.21**	1.06	1.62	1.13	1.28	2.21
- maternal effects (Mn)	(1)	541.54**	289.81**	3.75	0.77	0.76	2.04	0.97
- reciprocal effects (R)	(3)	157.55	59.08	1.09**	1.56**	0.54	1.27*	1.05**
GENOTYPES x YEARS (G x Y)	15	1480.66**	333.71**	2.32**	3.26**	0.82**	6.52**	1.75**
- $A_m \times Y$	(3)	4611.29**	859.99*	8.20**	8.49**	1.79	17.32	3.08
- $A_n \times Y$	(1)	3933.88*	485.81	4.71**	8.40**	1.13	9.33	2.55
- $NA \times Y$	(3)	1522.78**	339.50**	1.01**	1.37**	0.96**	7.57**	1.02**
- m/n x Y	(1)	239.63	213.12	0.41	1.21	1.24**	4.10	1.20**
- Mm x Y	(3)	84.69	95.95	0.68	2.37	0.52	3.12	1.96
- Mn x Y	(1)	307.73	222.88	0.64	2.07	0.20	3.13	2.29

Table 4. Genetic variances ( $s^2$ ) involved in the expression of some kernel and ear characteristics of sweet corn (Turda, 1997)

Source of variation	DF	Pericarp thickness	Pericarp weight	Tip fill	Husk length	Flag leaves length	Plant susceptibility to <i>Aphis</i> sp.	Biotest for kernel susceptibility to <i>Fusarium moniliforme</i>
TOTAL	47							
REPLICATIONS	2	172.40	0.37	0.04	0.07	2.08	114.38	54.87
GENOTYPES	15	3325.52**	6.37**	2.31**	20.61**	34.14**	752.81**	125.03**
-additive actions (Am)	(3)	3122.74	4.70	0.85	6.72**	28.22	1687.72	295.34*
-additive actions (An)	(1)	1354.69	2.43	25.23**	248.21**	376.88**	210.13	463.64*
-non-additive actions (NA)	(3)	2404.69**	18.39**	0.57	0.40	7.57	1661.97**	30.58
-differences m/n	(1)	5742.19**	0.80*	1.84*	1.02*	0.46	512.00*	11.19
-maternal effects (Mm)	(3)	4156.08	3.45	0.55	0.41	2.27	150.30*	26.44
-maternal effects (Mn)	(1)	379.69	5.07	0.48	0.48	2.66	50.00	23.13
-reciprocal effects (R)	(3)	4451.91**	2.54**	0.40	0.28	5.98	6.69	106.80
Error	30	79.06	0.19	0.31	0.21	3.45	106.19	44.80

The reciprocal hybrid differences were detected also for all analysed components of kernel chemical composition. These differences have been attributed to "plasmon-sensitive genes" in which an interaction between the cytoplasm and genome occurs, this opinion being supported also by : Huelsen (1954), Hansen and Baggett (1977), Kaukis and David (1986), Tracy (1994).

The components of variance for GCA and SCA for each trait from 1994-1995 experiment are presented in tables 3 and 5 and from 1996-1997 experiment in table 4. The proportion of variance components to phenotypic variance and heritabilities for some ear traits are presented in table 6. Additive variance was the major component of phenotypic variance, for ear length ( $\sigma^2_A / \sigma^2_P = 53\%$ ) and row number ( $\sigma^2_A / \sigma^2_P = 58\%$ ). Additive variance components were relatively low for most other characteristics ( $V_A / V_P = 8-32\%$ ): kernel depth, edible 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 HB (broad sense heritability parameters) for ear weight and kernel depth. Significance of additive x environment variances, especially for ear weight and kernel depth, indicated the need to evaluate these interactions in multiple environments representative for the area in which the genotypes are to be grown. For most other traits, additive effects were consistent over years and showed little changes.

Highly significant positive correlations between parental inbreds and F<sub>1</sub> 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 favourable traits will be crossed, respectively inbreds 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 silking ( $0.60^{**}$ ). Phenotypic and genetic correlations among 20 traits for sweet corn were studied in this paper (Table 7).

Table 5. Genetic variances ( $s^2$ ) involved in sweet corn kernel quality expression (Turda, 1994-1995)

Source of variation	DF	Dry matter	Total sugar	Sucrose	Phytoglycogen	Starch	Protein	Fats
TOTAL	179							
REPLICATIONS	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

**Table 6.** Proportion of variance components to phenotypic variance, heritabilities and correlation coefficients (*per se*) between parental inbreds and F<sub>1</sub> crosses in a cyclic system

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

$$1) \quad h^2 = \frac{2s_A^2}{2s_A^2 + s_{NA}^2 + s_{Cit.}^2 + s_{Rec.}^2 + s_{A \cdot E}^2 + s_{NA \cdot E}^2 + s_{Cit \cdot E}^2 + s_{Rec \cdot E}^2 + s_e^2} \quad (\text{after Kriebel et al., 1972})$$

$s_A^2$  and  $s_{NA}^2$ ;  $s_{A \cdot E}^2$  and  $s_{NA \cdot E}^2$  = variances for additive, non-additive, additive x environment, non-additive x environment.

$s_{Cit.}^2$ ,  $s_{Rec.}^2$ ,  $s_{Cit \cdot E}^2$ ,  $s_{Rec \cdot E}^2$  = variances for maternal, reciprocal, maternal x environment, reciprocal x environment

$s_F^2$  = phenotypic variance;  $s_e^2$  = variance for residual

$$2) \quad H = \frac{s^2G}{s^2G + s^2G \cdot E + s^2e} \quad (\text{after Sprague, 1967})$$

**Table 7.** Correlation coefficients between additive genetic effects ( $r_G$ ) involved in kernel chemical composition and other characteristics (Turda, 1994-1995)

Traits	S/1	TS/2	Ph/3	S/4	P/5	F/6	DM/7
<b>Kernel chemical composition</b>							
1. Sucrose (S)	-	0.10	-0.05	0.02	-0.35	0.30	0.03
2. Total sugar (TS)		-	0.25	<u>-0.41*</u>	<u>0.53**</u>	-0.05	<u>-0.57**</u>
3. Phytoglycogen (Ph)			-	-0.13	0.33	-0.27	-0.52**
4. Starch (S)				-	<u>-0.39</u>	0.20	0.19
5. Protein (P)					-	0.25	-0.35
6. Fats (F)						-	0.36*
7. Dry matter (DM)							-
<b>Ear and kernel traits</b>							
Ear weight	-0.06	<u>-0.38</u>	-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	<u>-0.41**</u>	-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
<b>Plants traits</b>							
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	<u>0.36*</u>	0.17	-0.27	-0.16	0.04	0.20
No. branches/ tassels	0.06	<u>-0.01</u>	-0.04	-0.01	-0.16	0.13	0.21
No. ears/plant	0.07	<u>0.12</u>	-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 genetic ( $r_G$ ) and phenotypic ( $r_p$ ) correlation coefficients

The existence of unfavourable genetic correlations between sucrose - row number (-0.41\*\*), total sugar - ear weight (-0.38\*\*), phytoglycogen - ear length (-0.64\*\*) were ob-

served indicating the difficulty of simultaneous improvement of sweet corn hybrids for both yield ability and kernel quality.

## CONCLUSIONS

The highly significant GCA mean squares for many traits indicate the importance of additive gene action in the genetic material studied here.

SCA effects were significant for kernel chemical composition, kernel depth, pericarp thickness, pericarp weight, edible quality, indicating nonadditive gene action for these traits although each trait appeared to be affected to a relatively greater extent by additive gene effects.

Maternal effects involved in the inheritance of ear and husk weight had a poor value but they could be used as source of ear weight improvement.

Reciprocal hybrid differences detected for all traits related to ear and kernel quality, such as ear length, row number, kernel depth, pericarp thickness and pericarp weight, edible quality, kernel chemical composition, could be used as sources of quality improvement.

Statistically significant correlation coefficients among *per se* values of parental inbreds and their additive effects support the feasibility of phenotypic selection of some traits.

The existence of some unfavourable genetic (additive effects) correlations between yield and quality indicates the difficulty of simultaneous improvement of sweet corn hybrid for both yield and kernel quality.

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**Table 1. Pedigree and genealogy of sweet inbreds used in Design 2 experiment, conducted at Turda in 1994-1995**

Inbreds	Pedigree/Origin	Genealogy
SW 87	USA	-
TA 22su	Q 206 - Canada	3603-1-1-7-
TA 27su	Reward- USA	5103-6-3-5
TA 28su	Golden Beauty - Canada	7188-1-1-3-
TD 103 su	How Sweet It Is- USA	7208-1-1-1-
TA 25 su	Reward- USA	3610-2-4-1-
TA 26 su	Reward - USA	5093-1-1-1-
TD 101 su	Aux 5651- USA	3607-2-1-3-
TD 282 su	Silver Queen- USA	3870-10-2-1-
TD 102 su	Aromatnaja- R.Moldova	7208-3-1-1-

**Table 2. Pedigree and genealogy of sweet inbreds used in the cyclic experiment conducted at Turda in 1996-1997**

Inbred lines with <i>sugary 1</i> cytoplasm		
Inbreds	Pedigree/Origin	Genealogy
TA 26 su	Reward-USA	5093-1-1-1-
TA 28 su	Golden Beauty-Canada	7188-1-1-3-
TD 101 su	Aux 5651-USA	3607-2-1-3
Inbred lines with field corn cytoplasm		
T 193 A su	T 160 x su source-Turda	<b>1283-2-1-3-</b>
T 209 su	A 495 <sup>1</sup> x su -1 source- Turda	1118-1-3-3-
T 244 su	T 244 x su -1 source- Turda	1140-1-1-1-



**Table 3. Genetic variances ( $s^2$ ) involved in ear and kernel characteristic expression (Turda 1994-1995)**

Source of variation	DF	Weight ear	Weight husk	Ear length	Row number	Ear shape	Kernel depth	Edible quality
TOTAL	547							
YEARS (Y)	1	38250.83**	12229.06*	8.61*	2.36**	8.61**	13.86*	12.66**
REPLICATIONS	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)	15	2490.48**	1029.45**	10.09**	17.98**	5.15**	5.76**	2.30**
- additive actions (Am)	(3)	9672.33**	3114.74**	31.63**	58.47**	16.57**	10.99	3.45
- additive actions (An)	(1)	6112.29**	3075.17**	41.67**	77.19**	20.53**	19.74**	4.08
- nonadditive actions (Na)	(3)	1854.22**	848.10**	1.35**	3.95**	1.42**	5.08**	2.27**
- differences m/n	(1)	322.89	111.26	3.05*	2.62	0.38	4.33*	4.13**
- maternal effects (Mm)	(3)	171.67	268.21**	1.06	1.62	1.13	1.28	2.21
- maternal effects (Mn)	(1)	541.54**	289.81**	3.75	0.77	0.76	2.04	0.97
- reciprocal effects (R)	(3)	157.55	59.08	1.09**	1.56**	0.54	1.27*	1.05**
GENOTYPES x YEARS (G x Y)	15	1480.66**	333.71**	2.32**	3.26**	0.82**	6.52**	1.75**
- Am x Y	(3)	4611.29**	859.99*	8.20**	8.49**	1.79	17.32	3.08
- An x Y	(1)	3933.88*	485.81	4.71**	8.40**	1.13	9.33	2.55
- NA x Y	(3)	1522.78**	339.50**	1.01**	1.37**	0.96**	7.57**	1.02**
- m/n x Y	(1)	239.63	213.12	0.41	1.21	1.24**	4.10	1.20**
- Mm x Y	(3)	84.69	95.95	0.68	2.37	0.52	3.12	1.96
- Mn x Y	(1)	307.73	222.88	0.64	2.07	0.20	3.13	2.29
- R x Y	(3)	154.58	178.74	1.42	1.28**	0.38	2.29	1.08**
ERROR (b)	60	91.23	133.70	0.36	0.34	0.51	0.80	0.21

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**Table 4. Genetic variances ( $s^2$ ) involved in the expression of some kernel and ear characteristics of sweet corn (Turda, 1997)**

Source of variation	DF	Pericarp thickness	Pericarp weight	Tip fill	Husk length	Flag leaves length	Plant susceptibility to <i>Aphis</i> sp.	Biotest for kernel susceptibility to <i>Fusarium moniliforme</i>
TOTAL	47							
REPLICATIONS	2	172.40	0.37	0.04	0.07	2.08	114.38	54.87
GENOTYPES	15	3325.52**	6.37**	2.31**	20.61**	34.14**	752.81**	125.03**
-additive actions (Am)	(3)	3122.74	4.70	0.85	6.72**	28.22	1687.72	295.34*
-additive actions (An)	(1)	1354.69	2.43	25.23**	248.21**	376.88**	210.13	463.64*
-non-additive actions (NA)	(3)	2404.69**	18.39**	0.57	0.40	7.57	1661.97**	30.58
-differences m/n	(1)	5742.19**	0.80*	1.84*	1.02*	0.46	512.00*	11.19
-maternal effects (Mm)	(3)	4156.08	3.45	0.55	0.41	2.27	150.30*	26.44
-maternal effects (Mn)	(1)	379.69	5.07	0.48	0.48	2.66	50.00	23.13
-reciprocal effects (R)	(3)	4451.91**	2.54**	0.40	0.28	5.98	6.69	106.80
Error	30	79.06	0.19	0.31	0.21	3.45	106.19	44.80

**Table 5. Genetic variances ( $s^2$ ) involved in sweet corn kernel quality expression (Turda, 1994-1995)**

Source of variation	DF	drymatter	total sugar	sucrose	phytoglycogen	starch	protein	fats
TOTAL	179							
REPLICATIONS	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

**Table 6. Proportion of variance components to phenotypic variance, heritabilities and correlation coefficients**

**(per se) between parental inbreds and F1 crosses in a cyclic system**

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

**Table 7. Correlation coefficients between additive genetic effects ( $r_G$ ) involved in kernel chemical composition and other characteristics (Turda, 1994-1995)**

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Traits	S/1	TS/2	Ph/3	S/4	P/5	F/6	DM/7
<u>Kernel chemical composition</u>							
1. Sucrose (S)	-	0.10	-0.05	0.02	-0.35	0.30	0.03
2. Total sugar (TS)		-	0.25	<u>-0.41*</u>	<u>0.53**</u>	-0.05	<u>-0.57**</u>
3. Phytoglycogen (Ph)			-	-0.13	0.33	-0.27	-0.52**
4. Starch (S)				-	<u>-0.39</u>	0.20	0.19
5. Protein (P)					-	0.25	-0.35
6. Fats (F)						-	0.36*
7. Dry matter (DM)							-
<u>Ear and kernel traits</u>							
Ear weight	-0.06	<u>-0.38</u>	-0.03	0.59**	-0.28	0.20	0.12
Husk weight	0.27	<u>-0.15</u>	0.15	0.15	-0.12	0.11	-0.30
Ear length	-0.08	-0.33	<u>-0.64**</u>	0.22	-0.28	0.20	0.02
Row number	<u>-0.41**</u>	-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
<u>Plants traits</u>							
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	<u>0.36*</u>	0.17	-0.27	-0.16	0.04	0.20
No. branches/ tassel	0.06	<u>-0.01</u>	-0.04	-0.01	-0.16	0.13	0.21
No. ears/plant	0.07	<u>0.12</u>	-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	<u>-0.43**</u>	0.17	0.11	-0.09	0.16	-0.33	<u>-0.52</u>

\*,\*\* - indicates significance at  $P < 0.05$  and  $P > 0.01$  respectively

- - indicates significance both for genetic ( $r_G$ ) and phenotypic ( $r_P$ ) correlation coefficients