

Genetic Diversity of several Inbred Sweet Corn Lines for the Main Characters of the Ear

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Abstract

The genetic diversity of the inbred lines used in hybrid formula is a major component of the final success of sweet corn commercial hybrids. The purposes of the presented paper were to identify and prognosticate the performance of 'Sugary 1' sweet corn inbred lines, on the basis of their variability expressed at phenotypic and genotypic levels. In this respect 18 inbred "su" lines, developed at the Turda (Romania) Agricultural Research and Development Station (ARDS) were studied concerning the phenotypic and genotypic diversity of ear weight, ear length, no. of rows/ear and depth of kernels. The results obtained have shown that T152su, T339su, TA28su, TD10su, TA26su, TC209su lines have registered high values for the phenotypic expression for the studied characters. T339su, TA28su transmit positive additive genetic effects for the studied characters. The most obvious differences at the non additive genetic level were found in T339su with T244su, T193Asu with T233su, TC209su, TA27su with T244su, TC209su and T152su with TC209su.

Keywords: sweet corn, inbred lines, genotypic, phenotypic diversity

Introduction

In sweet corn breeding programs ear characters are of utmost importance (ear length, no. of rows/ear, no. of kernels/row, depth of kernel as well as the quality of the final product expressed by the uniformity of technological maturity, kernel content in starch, protein, dextrin etc.) (Huelsen, 1954; Hansen *et al.*, 1977; Kaukis and Davis, 1986; Has *et al.*, 1994; Has and Cabulea, 1998, 2000; Has, 1999).

In the sweet corn breeding program, developed at Turda ARDS, new "su" lines were tested in crossing networks in order to identify valuable genitors for ear characters specific to sweet corn (Has and Cabulea, 1998). Such valuable inbred lines can already be found in the newly released Romanian sweet corn hybrids such as Dulcin, Prima, Estival and Deliciul verii (Has *et al.*, 1999).

Materials and methods

The biological material consisted of 18 sweet corn inbred lines (Tab. 1), 'Sugary 1' type, which were used in a cyclic system of crossing with tree testers (3 x 15). Previously, these lines were tested for two years (2005 and 2006) at Turda ARDS, in an experiment organized in randomized blocks with four replications.

All observations and measurements were performed at technological maturity of ears, on 10 plants and 10 ears/plot, resulting 40 plants and 40 ears/line/year. Four of the main ear characters are discussed in this paper: ear weight, ear length, no. of kernel rows/ear and depth of kernel.

For these quantitative traits under study the genetic diversity of the tested lines was estimated on the basis of their general (GCA) and specific (SCA) combining ability for each interlineal combination and for the whole factorial system of crossing.

The polygenic diversity was estimated by computing the additive effects \hat{g}_m or $\hat{g}_n = X_{m/n} - \bar{X}$,

where $X_{m/n}$ is the mean of the m or n parent and \bar{X} is the mean of all values of the factorial system.

The non additive genetic effects (\hat{s}_{mn}) was computed using the relation: $\hat{s}_{mn} = X_{mn} - \bar{X} - (\hat{g}_m + \hat{g}_n)$,

where \hat{s}_{mn} is the genetic effect of interaction of the two (m and n) parents. The levels of genetic differentiation (intra and interallelic) and the sum of these specific effects was used ($\sum \hat{S}_{ij}$).

Results and discussion

The mean values of the analyzed characters in the two experimental years are displayed in Tab. 2. It is quite evident that the tested sweet corn inbred lines were significantly different from each other and from the mean of the

Tab. 1. Sweet corn „su1’ Inbreed lines tested in Turda ARDS(Romania), 2005-2006

Nr. crt.	Line	Pedigree/ Origin	Nr. crt.	Line	Pedigree/ Origin	Nr. crt.	Line	Pedigree/ Origin
1	T152su	T152 x sursa su1	7	TD101su	Aux 5651-SUA	13	TA28su	Golden Beauty/SUA
2	T193Asu	T 1602 x sursa su1	8	T345Rsu	1700tt x sursa su1	14	TA22su	Q206/Canada
3	T209su	A4951 x sursa su1	9	T346su	A508 x sursa su1	15	TA21su	Q206/Canada
4	T339Rsu	EB159-2x sursa su1	10	TA25su	Reward-SUA	16	T233su	T285 x sursa su1
5	LC153su	LCA Delicios	11	TA26su	Reward-SUA	17	T244su	T244 x sursa su1
6	LC154su	LCB Delicios	12	TA27su	Reward-SUA	18	TC209su	Received from R. Moldova

experiment for all the considered characters. Thus, the ear weight showed a mean value of 85.86 g with the amplitude of variation comprised between 61.65 g (TA21su) and 115.78 g (TA28su). The same obvious variation was noted for the ear length (11.38-16.90 cm) and the no. of kernel rows/ear (9.36 in T193 Asu-19.62 in TA 26 su).

Considering the fact that, in Romania, sweet corn is still destined mainly for fresh consumption (boiled ears), the depth of kernels in the tested lines has been estimated, being comprised between 0.4 cm (T152 su) and 0.89 cm (TA 27 su and TA 28 su). According to Tracy (1994),

sweet corn ears should present small and profound kernels for fresh consumption.

Data in Tab. 3 show the GCA of the tested lines or the differences among these lines determined by the homozygote loci with cumulative effects.

Based on results presented in Tab. 3 it can be stated that the tested sweet corn inbreed lines can be used as sources of valuable genes which are additively transferred to hybrids, as follows:

- the ear weight (yield element) is additively and positively transmitted in the higher degree by TC 209 su, T339Rsu, LC153su, T346su, TA25su, TA27su;
- T209su, T339Rsu and TD101su, are valuable parental lines for a long ear while T346su, LC154su and T152su determine a shorter year in hybrids;
- for a large number of kernel rows/year TA26su, TA-27su, LC153su, TA25su and T193Asu are recommended as parental lines while LC154su, TA22su, T152su, T209su, TD101su and TA21su showed negative additive effects in the transmission of these traits to hybrids.

The non additive effects in transmission of the tree tester used in the cyclic system of crossing in Turda, for the ear characters under study, are presented in tab. 4 and 5. It can be observed that the highest values of non additive effects were found:

- T233 in combination with T193A (27.55), T346 (17.95), TA21(12.78);
- T244 in combination with T339R (14.29), TA27 (6,87), TA28 (15.14);
- TC209 in combination with T193A (20.24), T152 (14.61), TA27 (8.14), TA25 (7.39).

For ear weight, the highest value of non additive effects were used in the following combinations: T233 and T193A, TC 209 x T193 A and T233 x T346 while for ear length the largest non additive effects were found in T233 x T193 A, T244 x T209 and T244 x T339R. The combination T244 x TA 27 was the only one in which a high value of non additive effects was found while for the depth of kernel three combinations showed high values of non additive effects: T233 X lc 153 (-0.49), T233 x T346 (-0.50) and T209 x T339 R (-0.52).

Tab. 2. Phenotypic expression (mean values) of four ear and kernel quantitative characters of importance in sweet corn breeding, Turda (Romania), 2005-2006

Line	Ear weight (g)	Ear length (cm)	No. of kernel rows	Kernel depth (cm)
T152su	87.93	15.88***	12.55 ⁰⁰⁰	0.40 ⁰⁰⁰
T193Asu	80.75	12.65	9.36 ⁰⁰⁰	0.61
T209su	87.11	13.50	12.94 ⁰⁰	0.68
T339Rsu	87.95	16.90***	16.40 ***	0.69
LC153su	80.60	11.47 ⁰⁰⁰	17.77 ***	0.52 ⁰⁰⁰
LC154su	71.87 ^o	13.40	11.35 ⁰⁰⁰	0.76
TD101su	82.70	16.44***	12.13 ⁰⁰⁰	0.75
T345Rsu	89.96	13.46	14.59	0.74
T346su	81.69	16.19***	14.10	0.56 ⁰⁰
TA25su	90.48	12.12 ⁰⁰	15.92 **	0.62
TA26su	78.32	12.04 ⁰⁰	19.62 ***	0.84**
TA27su	90.06	14.53	15.55 *	0.89***
TA28su	115.78***	11.38 ⁰⁰⁰	14.65	0.89***
TA22su	89.79	12.21 ⁰⁰	10.75 ⁰⁰⁰	0.82**
TA21su	61.65 ⁰⁰⁰	11.61 ⁰⁰⁰	12.24 ⁰⁰⁰	0.69
T233su	87.27	12.71	16.68 ***	0.57 ⁰⁰
T244su	90.03	13.35	13.01 o	0.83**
TC209su	91.56	16.07***	18.34 ***	0.52 ⁰⁰⁰
Mean of experiment	85.86	13.66	14.33	0.69
LSD5%	11.9	1.03	1.02	0.09
LSD1%	15.8	1.37	1.36	0.12
LSD0,1%	20.36	1.76	1.75	0.16

Tab. 3. Additive genetic effects (\hat{g}) for 18 sweet corn inbred lines tested at Turda ARDS (Romania) in 2005 and 2006 in a cyclic crossing system (3x15)

Line	Ear weight	Ear length	No. of kernel rows	Kernel depth	Line	Ear weight	Ear length	No. of kernel rows	Kernel depth
T152su	-7.45	0.38	-1.6	-0.08	TA25su	6.37	-0.57	1.83	-0.02
T193Asu	-22.85	-1.54	0.3	-0.13	TA26su	-0.31	-0.96	3.65	0.02
T209su	-0.17	2.24	-1.65	-0.08	TA27su	9.52	-0.3	2.76	-0.05
T339Rsu	12.76	1.4	-0.36	0.42	TA28su	5.51	-1.5	-0.02	-0.01
LC153su	18.66	-0.34	1.84	-0.34	TA22su	1.69	-0.35	-2.35	-0.07
LC154su	-8.24	0.39	-2.32	-0.11	TA21su	-1.96	-0.58	-0.8	0.15
TD101su	-7.6	1.34	-0.96	-0.16	T233su	-6.52	-0.86	-0.02	-0.19
T345Rsu	-8.46	-0.03	-0.31	-0.02	T244su	-10.67	-0.51	-0.73	0.10
T346su	2.53	0.4	-0.03	0.48	TC209su	17.19	1.38	0.75	0.09

Tab. 4. Non additive genetic effects (\hat{s}_{mn}) of the sweet corn inbred lines tested in cyclic crosses in Turda (Romania), 2005-2006 (T233 x 15 lines; T244 x 15 lines)

Combination T233 x	Ear weight	Ear length	No. of kernel rows	Kernel depth	$\Sigma\hat{s}_{ij}$	Combination T244 x	Ear weight	Ear length	No. of kernel rows	Kernel depth	$\Sigma\hat{s}_{ij}$
T152su	-9.90	-0.47	0.01	-0.10	-10.46	T152su	-4.21	-0.02	-0.06	0.13	-4.16
T193Asu	25.12	2.11	0.20	0.12	27.55	T193Asu	-44.42	-2.77	-0.15	-0.46	-47.8
T209su	-0.42	-0.36	0.07	-0.01	-0.72	T209su	3.17	1.13	0.05	0.00	4.35
T339Rsu	-0.19	-0.74	-0.22	-0.32	-1.47	T339Rsu	11.61	1.61	0.24	0.83	14.29
LC153su	-0.06	0.25	0.29	-0.49	-0.01	LC153su	-0.43	0.04	-0.89	0.16	-1.12
LC154su	1.67	-0.03	0.28	0.08	2.00	LC154su	-0.36	0.00	0.12	-0.03	-0.27
TD101su	-2.11	-0.30	0.46	0.15	-1.80	TD101su	0.73	0.48	-0.54	-0.03	0.64
T345Rsu	-7.23	0.17	-0.41	0.00	-7.47	T345Rsu	6.40	-0.72	0.24	0.06	5.98
T346su	17.88	0.41	0.16	-0.50	17.95	T346su	-0.20	-0.29	0.33	0.22	0.06
TA25su	-14.66	-0.28	-0.83	0.22	-15.55	TA25su	8.32	-0.27	0.18	-0.09	8.14
TA26su	-17.43	-0.03	0.87	0.20	-16.39	TA26su	11.54	-0.02	-0.83	-0.08	10.61
TA27su	-12.64	-0.88	-1.58	0.08	-15.02	TA27su	5.25	0.41	1.46	-0.25	6.87
TA28su	4.38	-0.33	0.06	0.22	4.33	TA28su	0.98	0.51	0.13	-0.04	1.58
TA22su	3.56	0.24	0.25	0.21	4.26	TA22su	0.37	-0.18	0.01	-0.08	0.12
TA21su	12.05	0.22	0.40	0.11	12.78	TA21su	1.23	0.09	-0.28	-0.36	0.68

Tab. 5. Non additive genetic effects (\hat{s}_{mn}) of the sweet corn inbred lines tested in cyclic crosses in Turda (Romania), 2005-2006 (TC209 X 15 lines)

Combination	Ear weight	Ear length	No. of kernel rows	Kernel depth	$\Sigma\hat{s}_{ij}$
TC209 x T152su	14.11	0.48	0.05	-0.03	14.61
TC209 x T193Asu	19.30	0.66	-0.05	0.33	20.24
TC209 x T209su	-2.75	-0.77	-0.12	0.01	-3.63
TC209 x T339Rsu	-11.42	-0.88	-0.02	-0.52	-12.84
TC209 x LC153su	0.49	-0.28	0.60	0.32	1.13
TC209 x LC154su	-1.31	0.02	-0.40	-0.06	-1.75
TC209 x TD101su	1.38	-0.19	0.08	-0.12	1.15
TC209 x T345Rsu	0.83	0.56	0.17	-0.06	1.5
TC209 x T346su	-17.68	-0.11	-0.49	0.27	-18.01
TC209 x TA25su	6.34	0.54	0.65	-0.14	7.39
TC209 x TA26su	5.89	0.06	-0.04	-0.12	5.79
TC209 x TA27su	7.39	0.46	0.12	0.17	8.14
TC209 x TA28su	-5.36	-0.19	-0.19	-0.18	-5.92
TC209 x TA22su	-3.93	-0.06	-0.26	-0.14	-4.39
TC209 x TA21su	-13.28	-0.30	-0.12	0.24	-13.46

Conclusions

The following sweet corn inbred lines proved to be valuable by showing highest values of ear weight and other important ear traits:

- T152su and T101su for ear length;
- T339Rsu for ear weight, ear length, no of kernel row/ear;

- TA28su, for ear weight and kernel depth;

- TA26su, for no of kernel rows/ear and kernel depth;

- TC209su, for ear length and no of kernel rows/ear.

T339Rsu, LC153su, T346su, TA27su and TA28su are the sweet corn inbred lines which are additively transferred to hybrids high values of ear weight, ear length, no of kernel/ear and kernel depth.

The highest values of non additive effects for all four characters under study were found in the following crosses:

- T233su in combination with T193Asu, T346su and TA21su;

- T244su in combination with T339Rsu, TA27su, TA28su;

- TC209su in combination with T193Asu, T152su, TA27su, TA25su.

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