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ESTIMATION OF VARIABILITY PARAMETERS OF SOME QUALITATIVES COMPONENTS AT A SET OF SWEET CORN LINES FROM AGRICULTURAL RESEARCH AND DEVELOPMENT STATION TURDA

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Abstract

Sweet corn is a recent crop in Romanian agriculture, being cultivated more and more. Modern sweet corn, like all crops, is the product of its own evolution, in which human intervention was the first unconscious phase, becoming conscious over last two centuries. Knowledge of this development may be useful for forming the basis for planning for future improvement of this plant. Purpose of this study was to analyze inbred maize lines from germplasm collection from Turda Agricultural Research Center in terms of variability of some chemical components. Biological material was represented by 27 inbred lines of sugar-1 gene. Each variant was sown on four rows, an average of 40,000 pl/ha. Quality analyzes were performed using TANGO NIR spectro-photometer. Chemical parameters analysed were: protein content, starch, sugar, NDF (neutral detergent fibers) and NCGD (neutral cellulose digestibility). Between analyzed lines there is an important variability of sugar content.

***Key words**: lines, sugar, starch, sweet corn, variance.*

INTRODUCTION

Globally, sweet corn represents 7.7% of total vegetable consumption and ranks 2nd after tomatoes for US and Canada consumers (McMullen et al., 2009). Due to the high content of carbonates and other nutrients such as vitamins C, A, B_1, B_2, proteins, fats, starch, cellulose and mineral components (potassium, magnesium, calcium, phosphorus, iron, selenium, copper, nickel and chrom) and different uses for both fresh consumption and food industry, this species was quickly adopted worldwide (Hefny, 2011).

Recently, in U.S., use of high fructose syrup obtained from sweet corn and used as a sweetener gained a large market share (Revilla et al., 2005). Sweeteners made from sweet corn, belong to the best sweeteners class in US with a 52% market share due to their stability, high functionality and ease of use (Singh et al., 2014).

Sweet corn is one of the most recent crops in the landscape of Romanian agriculture, being cultivated more and more. Most of sweet corn production from Romania is obtained in the western part of the country and is not processed in the country, but taken to Hungary (www.agrointel.ro).

At Turda Agricultural Research Station, in 1971, a genetic improvement program was launched to obtain sweet corn on the basis of infusion of su1 recessive gene to a series of normal inbred lines. The obtained sugar lines were studied in a diaphragm crossing system, obtaining the general and specific combination capacity for the specific characters of sweet corn. Based on the behavior of studied inbred lines, the formula of DULCIN tri-linear hybrid was approved in 1988 (Căbulea et al., 1994; Has V., 2000).

Over past 15 years, Turda Agricultural Research Center has developed an intensive program to obtain new, early-quality inbred lines with superior qualities, which has led to recording of new genetic advances in amelioration of sweet corn.

As a result of using initial material from very early American and Canadian origins, the parental forms of PRIMA hybrid were obtained, approved in 1991 and considered the earliest hybrid from sweet corn hybrids experimented in CIOS network (Has et al., 1994).

Modern sweet corn, like all crops, is the product of its own evolution, in which human intervention was the first unconscious phase, becoming conscious over last two centuries (Srdić et al., 2012). Knowledge of this development may be useful for forming the basis for planning for future improvement of this plant (Lazcano et al., 2011).

It is important to know basic materials (varieties, populations) from which modern inbred lines have been extracted to retrieve lost characters during inbreeding (Kashiani et al., 2010). Sweet corn breeders have paid attention to varieties, both as starting material for inbred lines and as new sources of favorable alleles (Huelsen, 1954; Tracy, 1994). The one who dealt with study of varieties, their origins, role played in sweet corn evolution of was Walton C. Galinat (1971) in the study: "The Evolution of Sweet Corn".

Over the last 50 years, production gain in sweet corn, attributed to genetic gain, was modest compared to that obtained with ordinary corn (Letrat and Pulam, 2007). Important reasons for this could be:

- narrow genetic basis of sweet corn which, according to some authors, is largely derived from Northern Flint and which in its evolution has gone towards a severe narrowing of variability;
- non-Northern Flint germplasm, represented by Stowell's Evergreen and County Gentleman varieties, emerged through the introgression of sugary-1 gene in germplasm dentiformis (Revilla et al., 2009);
- excessive use of "Golden Bantam" type in creation of inbred lines (as a source of yellow endosperm and taste qualities). Current germ cell gene mutation contains, to a greater or lesser extent, genes of Golden Bantam genus in pedigree (Romay et al., 2013).

Following this study, analysis of inbred maize lines from Turda germplasm collection in terms of variability of some chemical components (sugar, starch, protein, NDF and NCGD) was proposed.

MATERIALS AND METHODS

Biological material was represented by 27 inbred lines of sugary-1 gene. Each variant was sown on four rows of 5 m in length and at a distance of 0.70 m corresponding to an average of 40,000 plants/ha. This group of lines was subjected to quality analysis, which was performed with the TANGO NIR spectrophotometer (Bruker Optik Gmbh, Ettingen, Germany).

From each line, self-pollinated cobs were selected to eliminate effects of alopolen sources involvement in the analyzed chemical components. Sweet corn cobs were analyzed at full maturity, being allowed to lose their moisture by natural drying in laboratory, after which grain samples were taken from each line. For each line of self-pollinated corn cobs that have been harvested, samples of about 50 grams of grains were harvested, which were subsequently ground using a WZ-1 knife mill (Sandkiewicz Instruments - Poland), and then sifted with a sieve.

Chemical parameters analyzed were: protein content, starch, sugar, NDF (neutral detergent fibers) and NCGD (neutral cellulose digestibility).

Based on variance analysis, some derived genetic parameters were also calculated:

$$\mathrm{V}G(Genetic\ variance) = \frac{\text{genotype variance} - \text{enviroment variance (residual)}}{\text{number of repetitions (R)}}$$

$VE(enviroment\ variance)$ = residual variance;
$VP\ (phenotypic\ variance) = VG\ \frac{\mathrm{VM}}{\mathrm{R}}$;

CVG% (Coefficient of genetic variation) $= \frac{\sqrt{VG}}{\mathrm{X}}$x100;

CVP% (Coefficient of phenotypic variation) = $\frac{\sqrt{VP}}{\mathrm{X}}$x100;

CVM% (Coefficient of environment variation) = $\frac{\sqrt{VM}}{\mathrm{X}}$x100

(Singh and Chaudhary, 1985);

H (Heritability in a broad sense) $= \frac{VG}{VP}$

(Falconer, 1971);

X = character average.

Generated results will be chemometrically processed using main component analysis and cluster analysis; such charts can provide valuable information about possible correlations between studied variables or samples composition, especially when working with large sets of values. Also, resulting clusters provide valuable insights into possible similarities between lines and also their grouping according to these similarities or differences.

RESULTS AND DISCUSSIONS

Chemical composition of maize lines studied is shown in Table 1.

Table 1. Chemical composition of a set of sweet corn lines (Turda, 2016)

Lines	NCGD (%)	NDF (%)	Protein (%)	Starch (%)	Sugar (%)
Ta su 21Q206	86.18	14.26	11.33	49.68	5.67
TA su 22	87.95	12.09	11.78	47.66	4.83
Tsu 152	88.07	15.55	13.26	49.94	6.67
Tsu 345R	86.67	16.71	12.09	45.83	6.70
TA 26	87.75	13.35	12.07	52.73	3.72
TA 27	87.79	12.51	12.53	53.65	2.16
TA 28	87.41	14.19	11.64	47.54	2.83
TD 101	88.66	15.80	9.30	53.25	6.52
TD 102	87.39	14.18	12.47	46.81	4.40
TA 28	87.11	15.38	12.52	50.62	3.73
TD 110	85.68	14.07	14.43	49.77	1.41
TVa 638	87.73	15.14	12.58	49.53	2.72
Tva 642	87.66	15.53	11.08	51.57	1.92
TVa 647	87.59	13.06	13.63	49.55	0.28
TV a 670	87.76	16.63	13.25	46.51	5.04
T su 209	84.64	19.17	12.41	44.88	5.26
T Su 233	86.54	14.89	13.43	45.83	4.07
T Su 244	85.35	17.84	12.06	38.94	6.03
P 51	84.06	14.95	12.80	44.73	6.66
LC 154/74	85.14	16.35	11.53	47.29	6.33
SW 87	83.76	16.07	14.80	42.31	4.85
TC 179 su	86.86	12.08	12.48	49.59	4.00
TD 111 su	87.93	12.95	10.66	50.86	4.78
TD 112 su	88.94	11,73	10.41	54.01	3.89
TD 113 su	85.75	15.15	18.19	27.44	4.01
TD 114 su	84.81	16.40	19.88	25.73	4.09
TD 115 su	87.24	12.52	10.31	51.50	3.68

Higher sugar content was found in Tsu 152 and Tsu 345R lines, which can indicate them as possible genres (only after being tested for combining ability) in amelioration of sugar content in sweet corn lines with a high yield but a lower sugar content. On the opposite side are Tva 642, TVa 647 and TD 110, which probably should be included in a sugar content improvement program if they are valuable under other aspects (cob production, precocity, cob size uniformity etc.).

Analyzing data in Table 2 led to the conclusion that there are considerable differences between analyzed lines with respect to sugar content, having highest C.V. of 39.2%, which suggests the existence of a great variability of this important taste characteristic. As a matter of fact, wide range of minimum and maximum values indicates a significant variation in sugar content.

Table 2. Variability parameters of protein content, starch, NCGD sugar and NDF at a set of sweet corn lines (Turda, 2016)

Indicators	CV (%)	Minimum	Maximum	Average	Standard deviation
Protein	17.4	9.3	19.88	12.70	2.21
Sugar	39.2	0.28	6.70	4.3	1.69
Starch	14.5	25.72	54.01	46.95	6.83
NDF	12.5	11.73	19.17	14.76	1.85
NCGD	1.6	83.76	88.94	86.75	1.4

CV% values reflect moderate variability within the group of lines analyzed for protein and starch content. Differences between minimum and maximum values of protein and starch content indicate an important variability of these components and the possibility of selecting valuable genres both as variants and as minus variants according to aims pursued by the breeder. Wide variation limits of the two components show existence of significant variations in the group of analyzed lines.

Lowest variability is recorded at neutral cellulose digestibility (NCGD) values. Reduced values of CV indicates a small fluctuation of these values around average. Therefore, we can say that there are no large differences in digestibility of cellulose between analyzed lines. This parameter is mainly used in fodder, for determination of formulas used for calculating of fodder energy values.

A moderate variability of studied parameters can also be noticed for neutral detergent fibers (NDF) represented by fractions of insoluble cell walls (hemicelluloses, celluloses, lignin, tannins etc.).

Generally, the two parameters, NDF and NCGD, are used to characterize food digestibility.

With higher protein content, lines in the HONEY group (TD 113 su and TD 114 su) stand out, with 19.88% protein and 19.8% respectively, as can be seen in Figure 1. Also known is the reverse relationship of sugar and protein, which is confirmed by this study, as protein content is reduced when sugar content is increased, with deviations (Figure 1).

Between the two important chemical components of sugar and starch there is a well-established logical correlation even though it is not statistically assured in present case, probably because of lower number of analyzed cases.

Large sample dispersion around the regression line suggests that there is insignificant interaction between the two variables and that choosing forms with lower starch content is not necessarily associated with a significant increase in sugar. A significant deviation that strengthens this negative relationship can be noticed within lines of the Honey group within the circle in Figure 2.

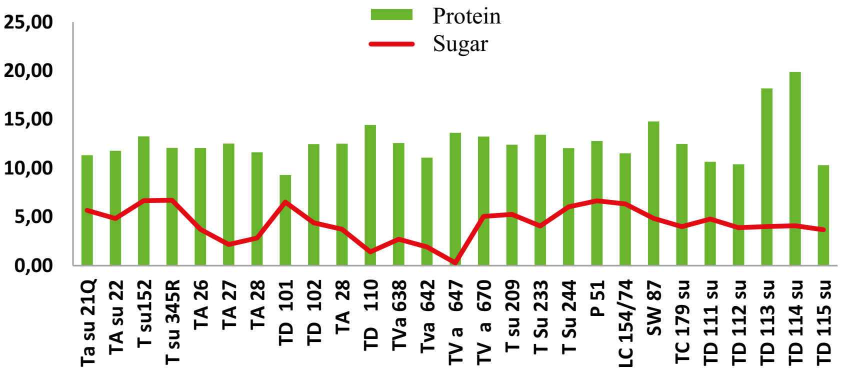

Figure 1. Protein and sugar content of 27 sweet corn lines (Turda, 2016)

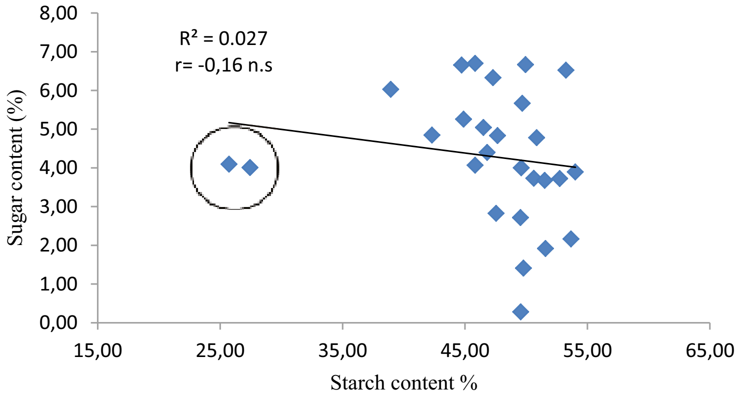

Figure 2. Correlation between sugar and starch content

Analyzing obtained data, between the analyzed lines there is an important variability of sugar content, values of sample F being very significant (Table 3). It can be stated with certainty that at the level of lines one can find some forms that included in hybridization programs can lead to the expression of a higher quality heterosis superior to parental forms. These lines are therefore of real use in improving the taste of sweet corn. Sugar content of sweet corn lines that directly influences their quality must be correlated with other factors such as cob production but also through other selection criteria.

Table 3. Analysis of the variance for sugar content in the 27 sweet corn lines

Variability source	SPA	GL	S^2	F
G	216.22	26	8.32	34.74***
R	7.03	2	3.52	
Error G	12.45	52	0.24	

Based on proposed calculation formulas from Singh (2014), genetic variation coefficients, environmental (residual) and phenotypic variation coefficients as well as broader heritability were calculated (after Nordby, 2008).

Analyzing data from Table 4, high values of genetic variation indicate the important contribution of genetic factor in obtaining sugar content. Obviously, phenotypic variance values are higher compared to those of genetic variance, suggesting major implications of the environment in accumulation of sugars in sweet corn. The coefficient of genetic variation indicates an important source of variability in sugar content that can be improved by amelioration, especially on the background of a high heritability index with high values of 0.57. Similar result were obtained by Haş and Haş in their study in 2009.

Table 4. Estimators of sugar content variability in analyzed sweet corn lines

Genetic Variance VG	Environment variance VM	Phenotypic variance VP	Coefficient of genetic variation CVG %	Coefficient of environment variation CVM%	Coefficient of phenotypic variation CVP%	H^2
Sugar content						
1.6	3.52	2.77	29.41	43.63	38.71	0.57

CONCLUSIONS

Use of sugary-1 (*su-1*) mutant gene for endosperm quality produces changes in the genetic determinism of carbohydrate synthesis.

Characters of sweet corn may be considered with complex determinism, both due to interactions between quality gene (*su-1*) of the endosperm and the polygenic complex on which it operates, as well as environmental conditions.

Higher heritability of transmitting sugar content makes recurrent selection during inbreeding very effective. Thus, improvement and fixation by individual selection of the quality character is very effective in the course of inbreeding.

Improving chemical composition of graines requires the combination of a set of procedures based on reciprocal recurrent selection, tandem selection with the requirement to control expression under various environmental conditions.

From the statistical analysis of the weight of the factors involved in the expression of the grain composition, contribution of genotype to environmental factors is predominant. Major share of genotype contribution in expressing grain quality suggests that sweet corn grain lines have relatively stable components in relation to environmental conditions.

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