

## ANALYSIS OF THE DEGREE OF PHENOTYPIC AND GENETIC DIVERSITY AMONG MAIZE INBRED LINES DERIVED FROM THE SAME HYBRID

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**Abstract.** *The paper aims to appreciate the degree of relationship / differentiation of lines created from a single source of original material. Relatively limited research has been done with related inbred lines (Musteață and Mistreț, 2002), which at the present stage predominates in the maize improvement programs. Differentiating the sister lines, made from a single source of source material and related lines from various sources with common genitors, allows for their identity to be identified, a necessary element in the selection and hybridization process. Differentiating the sister lines, made from a single source of original material and related lines originating from various sources with common genitors, allows the determination of their identity, a necessary element in the selection and hybridization process. Determination of the degree of similarity was done by various methods: the pedigree of the lines, morphological characters, heterosis (production and production elements) and general combining ability. There were studied 7 inbred lines of common origin, among which crosses of type (4) p (p-1) / 2 diallel were made. Both parental lines and crosses were studied at SCDA Turda, within the maize amelioration laboratory in the year 2016. At the parental lines, 22 phenotypic characters were studied after the UPOV system. From the heterosis calculation made from the crossing of the 7 lines (of common origin), heterosis values > 90% result for: grain production, ear weight, grain weight, insertion height and foliar surface. The purpose of this paper is to assess the degree of similarity of the lines created from a single source of the original material, which has allowed the establishment of their identity, a necessary element in the selection and hybridization process.*

**Key Words:** *similarity, heterosis, inbred lines*

### INTRODUCTION

Inbred lines, as uniform and consistent descendants after several successive generations self-pollinations and phenotypic character selection, primarily requires the genetic potential of performing high-performance hybrids.

The value of the lines is ultimately determined by the combining ability. Phenotypic diversity and, in particular, the genetic diversity of parental forms are one of the determinant causes of heterosis expression in maize hybrids.

Obtaining inbred lines from earlier materials of more complicated genealogical origin has created difficulties in trying to classification of these genotypes in to germplasm groups.

The effectiveness of methods for differentiating the selection material is sufficiently analyzed in the literature (J. SMITH, O. SMITH, 1989A; 1989B; O. SMITH ET AL., 1990; 1991).

Relatively limited research has been done with related inbred lines (MUSTEAȚĂ AND MISTREȚ, 2002; BRUMĂ, 2012, 2013), which currently predominates in maize improvement programs.

Differentiating sister lines, made from a single source of original material and lines related to coming from different sources with common genres, requires the establishment of their identity, element determinant in the selection and hybridization process.

Elaboration of comparative indices of appreciation of the distinctiveness, determination of the differentiation threshold a sister lines and related lines have become a serious impediment to improvement (BRUMĂ, 2013).

In this paper we have proposed to present the research on the evaluation similarity / distinctive to a set of related lines, created from the same source of original material.

### MATERIAL AND METHOD

For the realization of the mentioned objective, 7 related inbred lines were obtained from the same initial material, respectively the hybrid population (TC 177 x TB 329), the lines come from the same family and have differentiated during the selection process.

Table 1

Biological material - the pedigree of the inbred lines used in the cross-breeding system

Nr. crt.	Inbred line	Origin	Genealogy
Inbred line - studied			
1.	TD 233	Hybrid population of (TC 177 x TB 329)	3309-1-4-3-1-1
2.	TD 234		3309-1-5-3-1-1
3.	TD 235		3309-4-2-4-1-1
4.	TD 236		3309-5-1-1-3-1
5.	TD 237		3309-5-4-2-2-2-1
6.	TD 238		3309-4-6-1-2-1
7.	TD 239		3309-4-2-1-1-1

The biological material used was represented by inbred lines parental forms and simple hybrids F 1 made in cross-breeding systems dialel of the type (4) p(p-1)/2 (Căbulea, 1975), respectively 7 inbred lines, 21 experienced hybrids, 1 year and 4 repetitions.

Field experiments of hybrids were conducted at SCDA Turda in 2016, according to the model of randomized blocks with 4 repetitions, parcel size of 7.0 m<sup>2</sup>, density of 60.000 plants / ha.

Average data has been processed and used for:

- evaluation of the degree of phenotypic relationship / differentiation,
- variance analysis,
- evaluation of heterosis expression.

Estimation of phenotypic heterosis was performed after Hallauer and Miranda (1981):

$$H \% = \frac{F_1 - \frac{P_1 + P_2}{2}}{\frac{P_1 + P_2}{2}} \times 100$$

H% = percentage expression of heterosis;

F1 = the value of the berry production of F1 hybrids;

P1 + P2 = mean value of parental inbred lines P1 and P2.

**RESULTS AND DISCUSSIONS**

From variance analysis for important agronomic characters, it can be observed that there are significant positive differences in the genotypes studied for the characters: grain production and percentage of broken plants and distinct significant differences provided by sample F in characters such as: weight of the ear, length and the percentage of dry matter.

*Table 2*

Variance analysis for phenotypic characters of related inbred lines, Turda, 2016  
a) for the elements of production

Source of variability	GL	Grain yield			Dry matter			Plants no broken		
		s <sup>2</sup>	Sample F	Signify.	s <sup>2</sup>	Sample F	Signify.	s <sup>2</sup>	Sample F	Signify.
TOTAL	20	9754757			75.41			1926.31		
Repetition	2	260443			2.01			4.74		
Genotypes (G)	6	6106825	3.60	*	63.81	13.32	**	1353.45	4.76	*
Error G	12	3387490			9.58			568.11		

Source of variability	GL	Cob weight			Grain weight			Cob length		
		s <sup>2</sup>	Sample F	Signify.	s <sup>2</sup>	Sample F	Signify.	s <sup>2</sup>	Sample F	Signify.
TOTAL	20	1995.05			1474.76			31.39		
Repetition	2	28.91			31.34			0.20		
Genotypes (G)	6	1502.27	6.47	**	1039.23	5.14	**	29.55	36.21	**
Error	12	463.86			404.18			1.63		

From the variance analysis for the phenotypic characters of the inbred lines it can be seen in Table 3 that there are distinctly significant differences in the genotypes studied in all the analyzed characters respectively: number of grains per row, number of rows of grains, grain depth, height of the plant, insertion height a maize cob and leaf length.

*Table 3*

Variance analysis for the phenotypic characters of the inbred lines, Turda, 2016  
b) for plant elements and vegetative characters of the plant

Source of variability	GL	Number of grains per row			Number of rows			Depth grain		
		s <sup>2</sup>	Sample F	Signify.	s <sup>2</sup>	Sample F	Signify.	s <sup>2</sup>	Sample F	Signify.
TOTAL	20	150.24			15.06			0.0723		
Repetition	2	2.96			0.19			0.0009		
Genotypes(G)	6	118.88	8.37	**	11.44	6.67	**	0.0507	4.89	**
Error G	12	28.39			3.42			0.0207		

Source of variability	GL	Plant height			Insertion height			Leaf length		
		s <sup>2</sup>	Sample F	Signify.	s <sup>2</sup>	Sample F	Signify.	s <sup>2</sup>	Sample F	Signify.

TOTAL	20	3346.82			1220.55			306.19		
Repetition	2	15.61			4.96			8.59		
Genotypes (G)	6	2828.02	11.24	**	1099.75	18.98	**	271.31	20.64	**
Error G	12	503.18			115.83			26.28		

The analysis of the production elements in the related lines studied is shown in Table 4. There can be noticed the existence of distinctly significant differences between the TD line 236 and the rest of the lines studied in the weigh cob.

As for the weight of the grains, it can be seen that there are also significant differences between the lines TD 236 and the rest of the lines. At the length of the cob, the line TD 233 is distinguished with very significant differences compared to the other lines studied and TD 236 line with very significant negative differences, but also the line TD 235 with distinct significant negative differences.

Table 4

Phenotypic differentiation of related inbred lines for some elements of production

Inbred line	Cob weight			Grain weight			Cob length		
	%	% to control	Difference	%	% to control	Difference	%	% to control	Difference
Mean-mt	84.9	100	0.00	69.8	100.0	0.00	13.4	100.0	0.00
TD 233	95.8	112	10.8	78.1	111.9	8.28	15.0	112.3	1.65***
TD 234	91.1	107	6.1	76.2	109.2	6.41	13.7	102.4	0.31
TD 235	89.8	106	4.9	74.4	106.6	4.61	12.1	90.9	-1.22 <sup>00</sup>
TD 236	67.4	79	-17.6 <sup>00</sup>	56.5	80.9	-13.32 <sup>0</sup>	11.3	84.4	-2.09 <sup>000</sup>
TD 237	81.5	96	-3.5	63.6	91.2	-6.15	13.2	98.6	-0.19
TD 238	83.9	99	-1.1	69.6	99.7	-0.19	14.1	105.8	0.78 <sup>+</sup>
TD 239	85.1	100	0.18	70.1	100.5	0.35	14.1	105.6	0.75 <sup>+</sup>
DL P=5%			11.07			10.33			0.66
DL P=1%			15.53			11.50			0.92
DL P=0.1%			21.93			20.47			1.30

Regarding the vegetative characters and the height of the plant, line TD 233 and line TD 237 are marked by a significantly positive height compared to other sister lines, and the lines TD 235 and TD 239 have a negative height compared to the other lines.

In terms of height of insertion, the TD line 236 and TD 237 have a significant positive height relative to the other lines studied and the lines TD 235 and TD 239 differ by a negative signaling height.

For leaf length, line TD 237 differs from the other significantly positive, and line TD 233 differs significantly positive, and line TD 236 is very significantly negative.

Table 5

Phenotypic differentiation of related inbred lines for vegetative characters of the plant

Inbred lines	Plant height			Insertion height			Leaf length		
	%	% to control	Difference	%	% to control	Difference	%	% to control	Difference
Mean-mt	152.9	100.0	0.00	38.8	100.0	0.00	61.9	100.0	0.00
TD 233	166	108.6	13.1 <sup>*</sup>	38.9	100.4	0.15	64.7	104.5	2.81 <sup>*</sup>
TD 234	154.3	100.9	1.4	33.3	86.0	-5.45	59.4	95.9	-2.52
TD 235	133.9	87.6	-19.0 <sup>00</sup>	31.9	82.3	-6.85 <sup>0</sup>	60.3	97.3	-1.66
TD 236	152.6	99.8	-0.27	50.9	131.3	12.15 <sup>***</sup>	55.9	90.2	-6.06 <sup>000</sup>
TD 237	168.4	110.2	15.53 <sup>*</sup>	48.5	125.0	9.69 <sup>**</sup>	67.9	109.6	5.94 <sup>***</sup>
TD 238	154.8	101.3	1.93	34.8	89.7	-3.98	62.3	100.6	0.34
TD 239	140.1	91.7	-12.73 <sup>0</sup>	33.1	85.3	-5.71 <sup>0</sup>	63.1	101.8	1.14
DL P=5%			11.53			5.53			2.63
DL P=1%			16.18			7.76			3.70
DL P=0.1%			22.84			10.96			5.22

Phenotypic character analysis by height correlations is shown in Table 6, and TD 234 is significantly different from TD 235 ( $r = -0.74^{**}$ ) and TD 238 ( $r = 0.52^{*}$ )

Table 6

Phenotypic character analysis by means of correlations, of the 7 related plant height lines

Inbred lines	TD 233	TD 234	TD 235	TD 236	TD 237	TD 238	TD 239
TD 233	1.00						
TD 234	0.30	1.00					
TD 235	-0.06	-0.74 <sup>**</sup>	1.00				
TD 236	-0.36	-0.08	-0.19	1.00			
TD 237	0.04	0.08	0.02	-0.29	1.00		
TD 238	-0.39	-0.52 <sup>*</sup>	0.39	0.36	-0.25	1.00	
TD 239	-0.04	0.18	-0.06	-0.38	0.15	-0.27	1
DL P (5%)	0.51						
DL P (1%)	0.64						

The analysis of phenotypic characters with correlations for the height of insertion of the ear are presented in Table 7, and the TD line 236 remarkably resembles the line TD 237 ( $r = 0.80^{**}$ ).

*Table 7*

Phenotypic character analysis by means of correlations, of the 7 related lines for the height of the ear

Inbred lines	TD 233	TD 234	TD 235	TD 236	TD 237	TD 238	TD 239
TD 233	1.00						
TD 234	-0.17	1.00					
TD 235	-0.03	0.23	1.00				
TD 236	-0.05	0.29	-0.08	1.00			
TD 237	0.01	0.18	-0.14	0.80**	1.00		
TD 238	0.26	-0.21	-0.16	-0.45	-0.49	1.00	
TD 239	0.04	-0.02	0.41	-0.45	-0.37	0.31	1.00
DL P (5%)	0.51						
DL P (1%)	0.64						

From the analysis of phenotypic characters with correlations for panicle length are presented in table 8, and the TD line 238 differs significantly from the line TD 239 ( $r = 0.51$  \*).

*Table 8*

Phenotypic character analysis by means of correlations, of the 7 related lines for panicle length

Inbred lines	TD 233	TD 234	TD 235	TD 236	TD 237	TD 238	TD 239
TD 233	1.00						
TD 234	-0.41	1.00					
TD 235	-0.19	-0.18	1.00				
TD 236	-0.01	0.04	0.01	1.00			
TD 237	-0.18	0.04	-0.32	0.59*	1.00		
TD 238	0.31	-0.02	0.25	0.34	-0.26	1.00	
TD 239	-0.20	0.10	-0.36	-0.28	0.33	-0.51*	1.00
DL P (5%)	0.51						
DL P (1%)	0.64						

From the analysis of the phenotypic characters with correlations for the number of panical axes are presented in table 9 two cases of similarity, the line TD 235 is remarkably similar to the line TD 236 ( $r = 0.54$  \*) and the TD line 234 resembles the line TD 235 ( $r = 0.59$ ).

*Table 9*

Phenotypic character analysis by means of correlations, of the 7 related lines for the number of panicles

Inbred lines	TD 233	TD 234	TD 235	TD 236	TD 237	TD 238	TD 239
TD 233	1.00						
TD 234	-0.05	1.00					
TD 235	0.17	-0.34	1.00				
TD 236	-0.19	-0.47	0.54*	1.00			
TD 237	-0.01	-0.29	-0.09	-0.23	1.00		
TD 238	0.43	-0.01	0.10	0.05	-0.08	1.00	
TD 239	0.23	0.10	0.04	0.14	-0.07	0.59*	1.00
DL P (5%)	0.51						
DL P (1%)	0.64						

From the phenotypic character analysis with row / ear correlation correlations are presented in table 10, there is a significant similarity between TD 233 and TD 236 ( $r = 0.87$  \*\*) but also a significant differentiation between TD 234 and TD 235 ( $r = -0.65$  \*\*)

Table 10

Phenotypic character analysis by means of correlations, of the 7 related lines for the number rows of kernels on the cob

Inbred lines	TD 233	TD 234	TD 235	TD 236	TD 237	TD 238	TD 239
TD 233	1.00						
TD 234	0.23	1.00					
TD 235	-0.23	-0.65**	1.00				
TD 236	0.87**	0.26	-0.26	1.00			
TD 237	0.46	-0.06	0.20	0.15	1.00		
TD 238	0.29	0.37	-0.16	0.05	0.29	1.00	
TD 239	0.00	0.00	0.00	0.00	0.00	0.26	1.00
DL P (5%)	0.51						
DL P (1%)	0.64						

From the analysis of the ear type by correlation for the diameter of the rash are presented in table 11, there is a significant similarity between TD 239 and TD 236 ( $r = 0.56^*$ ) but also a significant differentiation from line TD 238 ( $r = -0.51^*$ ) the same differentiation is also observed between line TD 236 and TD 238 ( $-0.57^*$ ).

Table 11

Phenotypic character analysis by means of correlations, of the 7 related lines for diameter cobs

Inbred lines	TD 233	TD 234	TD 235	TD 236	TD 237	TD 238	TD 239
TD 233	1.00						
TD 234	0.32	1.00					
TD 235	-0.07	-0.27	1.00				
TD 236	-0.09	0.28	0.03	1.00			
TD 237	0.40	0.14	0.49	-0.14	1.00		
TD 238	0.17	-0.45	-0.10	-0.57*	0.01	1.00	
TD 239	-0.24	0.56**	-0.45	0.26	-0.22	-0.51*	1.00
DL P (5%)	0.51						
DL P (1%)	0.64						

From the analysis of the phenotypic variation of the seven lines of common origin, the low values are observed, which underlines their phenotypical similarity except for some characters such as grain production, the percentage of unframed plants, the height of the ear and the number of panicle ramifications where the value of the coefficient of variation has mean values between (10-20%).

Table 12

Analysis of variability parameters for some phenotypic characters at related inbred lines

Parameters	Coefficient of variation CV (%)	Mean	Minimum value	Maximum value	Standard deviation	Standard error	Number of cases
Grain yield	15	3834	3057	4673	583	220	7
Plants broken	14	61	50	73	9	3	7
Grain weight	11	70	57	78	8	3	7
Length cob	10	13	11	15	1.3	0.48	7
Number of grains per row	9	27	24	32	2.6	0.96	7
Insertion height	20	39	32	51	7.9	2.99	7
Length panicol	14	28	22	33	3.9	1.49	7
Main spindle length panicol	15	20	15	24	3.2	1.21	7
Number ramifications panicol	15	5	4	7	0.8	0.29	7

CV >10% - small variation  
 CV = 10-20% - medium variation  
 CV < 20% - large variation (by Ceapoiu, 1967)

From the analysis of variants in the dialectic crossing system, it is evident that between the genotypes under study there are distinctly significant differences with respect to the important agronomic characters.

*Table 13*

Analysis of variants for some elements of production, dialel cross p (p-1) / 2, Turda, 2016  
 a) for important agronomic characters

Source of variability	G L	Grain yield			Dry matter			Plants no broken		
		s <sup>2</sup>	Sampl e F	Signify .	s <sup>2</sup>	Sampl e F	Signify .	s <sup>2</sup>	Sampl e F	Signify .
TOTAL	83	19078280			103.66			4456.16		
Repetiþion	3	5547796			7.68			977.23		
Genotypes(G )	20	16618650	26.17	**	65.23	6.36	**	1920.66	3.69	**
Erorr G	30	19048490			30.74			1558.26		

Source of variability	G L	1000 grain weight			Yield			Hectoltric mass		
		s <sup>2</sup>	Sampl e F	Signify .	s <sup>2</sup>	Sampl e F	Signify .	s <sup>2</sup>	Sampl e F	Signify .
TOTAL	83	59994.75			1414.60			234.58		
Repetiþion	3	1257.88			49.05			8.67		
Genotypes(G )	20	4947.80	16.03	**	611.34	2.43	**	118.15	3.29	**
Erorr G	30	9258.07			754.19			107.75		

From the variance analysis of the dialectic crossing system, it is apparent that there are distinctly significant differences in genotypes between the production elements.

*Table 14*

Analysis of variants for the production elements of dialel cross p (p-1) / 2, Turda, 2016  
 b) for production characters

Source of variability	G L	Weight cobs			Weight grain			Length cobs		
		s <sup>2</sup>	Sampl e F	Signify .	s <sup>2</sup>	Sampl e F	Signify .	s <sup>2</sup>	Sampl e F	Signify .
TOTAL	83	34004.68			22696.87			51.52		
Repetiþion	3	114.14			126.87			0.03		
Genotypes(G )	20	31896.41	47.98	**	21145.95	44.54	**	43.20	15.63	**
Erorr G	30	1994.12			1424.04			8.28		



Source of variability	GL	Cob diameter			Number of grains per row			Number of rows of grains		
		s <sup>2</sup>	Sample F	Signify.	s <sup>2</sup>	Sample F	Signify.	s <sup>2</sup>	Sample F	Signify.
TOTAL	83	4.62			298.91			38.17		
Repetition	3	0.01			0.86			0.21		
Genotypes(G)	20	4.10	24.08	**	222.81	8.88	**	20.46	3.51	*
Error G	30	0.51			75.23			17.49		

From the analysis of the variants in the dialectic crossing system it is evident that between genotypes studied there are distinctly significant differences in vegetative characters of the plant.

Table 15

Variation analysis for plant vegetative characters, dialects p (p-1) / 2, Turda, 2016  
b) for vegetative characters of the plant

Source of variability	G L	Plant height			Height insertion			Total leaf		
		s <sup>2</sup>	Sampl e F	Signify .	s <sup>2</sup>	Sampl e F	Signify .	s <sup>2</sup>	Sampl e F	Signify .
TOTAL	83	33414.18			22696.87			19.82		
Repetition	3	109.41			126.87			3.11		
Genotypes(G)	20	31377.61	48.84	**	21145.95	44.54	**	11.29	6.25	**
Error G	30	1927.15			1424.04			5.41		

Source of variability	G L	Leaf length			Leaf width			Foliar surface		
		s <sup>2</sup>	Sampl e F	Signify .	s <sup>2</sup>	Sampl e F	Signify .	s <sup>2</sup>	Sampl e F	Signify .
TOTAL	83	1063.21			50.58			286539.30		
Repetition	3	292.12			3.10			56354.38		
Genotypes(G)	20	519.92	6.21	**	40.30	16.83	**	178890.10	10.46	**
Error G	30	251.15			7.18			51294.76		

The value of the genetic effects (g) of the 7 related lines shows that there is significant differentiation between them, even if they originate from the same initial material in the transmission of one character.

- the TD 236 line has a significantly higher transmission capacity of the following characters: grain production, 1000 grain mass, ear weight, ear length, number of rows, plant height, ear height, leaf length and foliar surface.

- line TD 233 is characterized by the generally significant transmission capacity of the dry matter percentage, the length of the ear and the number of grains / row.

Table 16

The additive genetic effects (g), of the related inbred lines, within the p (p-1) / 2 dialects, Turda 2016

a) for production production characters

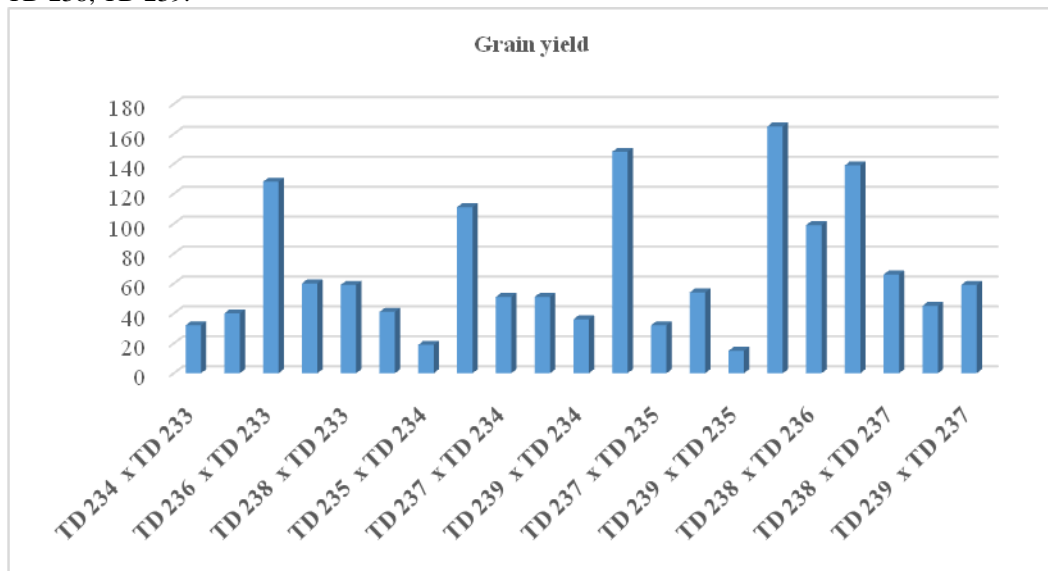
Caracters	Lines							DL 5 %
	TD 233	TD 234	TD 235	TD 236	TD 237	TD 238	TD 239	
Grain yield	40.9	32.9	-296.9	1898.6	-579.6	-822.1	-273	797

Dry matter	2.2	2.3	2.3	1.2	1.2	-11.8	2.7	1.01
Weight of 100 grains	-1.4	-10.9	5.3	39.8	10.1	-41.7	-1.2	17.5
Weight cob	4.7	-0.3	-9.5	29.9	2.9	-21.6	-6.1	8.1
Length cob	0.6	0.1	-0.4	0.8	0.6	-2.2	0.3	0.5
Number of rows	0.2	0.4	0.1	0.9	0.2	-2.1	0.2	0.8
Number of grains / row	1.7	1.2	0.4	0.4	0.4	-4.1	0.1	1.6

b) for the characters of the plant

Characters	Lines							DL 5 %
	TD 233	TD 234	TD 235	TD 236	TD 237	TD 238	TD 239	
Plant height	4.7	-0.1	-9.3	29.7	2.7	-21.5	-6.1	8.0
Height cob	5.0	0.4	-7.8	24.0	0.9	-16.8	-5.6	6.9
Leaf length	0.9	-0.2	1.4	4.3	3.3	-10.7	1.1	2.9
Width of the leaf	0.1	0.1	-0.1	0.3	0.4	-0.9	0.1	0.5
Foliar surface	1.6	-3.9	-14.4	74.6	18.1	-64.7	-11.5	41.4
Number of branches panicol	0.0	-0.4	-1.2	4.8	-1.2	-2.0	0.0	1.5
Plants broken	0.5	3.5	-1.0	6.7	2.2	-11.8	-0.3	7.2

The heterosis calculated for grain production clearly shows the likeness of the sampling of the 7 related lines obtained from the same initial material. The highest value of heterosis was recorded in hybrid combinations having the TD 236 constant line, therefore this line is most genetically differentiated from the other 6. Instead, the TD line 235 has achieved the lowest values of heterosis, so this line is the closest to the lines: TD 233, TD 234, TD 237, TD 238, TD 239.

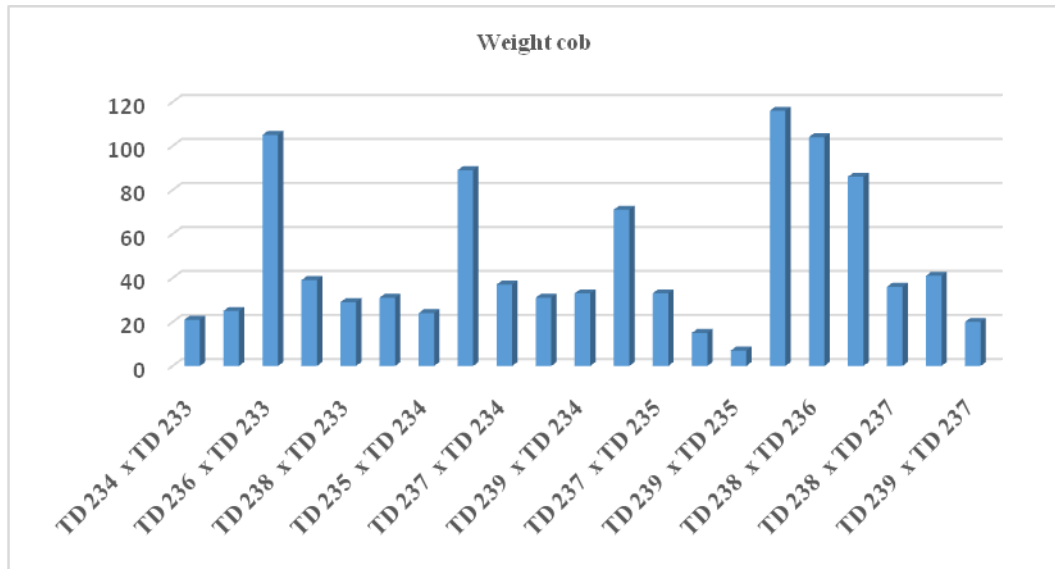


Grouping of heterosis-based lines:

- 1) similar - H% <30
  - 2) genetically similar - H% = 30-70%;
  - 3) genetically removed - H% = 70-90%
  - 4) from alternative groups - H% > 90%
- (by Musteață and Mistreț, 2009)

Fig. 1. Heterosis (%) for production capacity

The heterosis calculated for the weight of the ear is the most obvious resemblance to the sampling of the 7 related lines obtained from the same initial material. The highest value of heterosis was recorded in hybrid combinations having the TD 236 constant line, therefore this line is most genetically differentiated from the other 6. Instead, the TD line 235 has achieved the lowest heterosis values, so this line is the closest to the lines: TD 233, TD 234, TD 237, TD 238, TD 239.

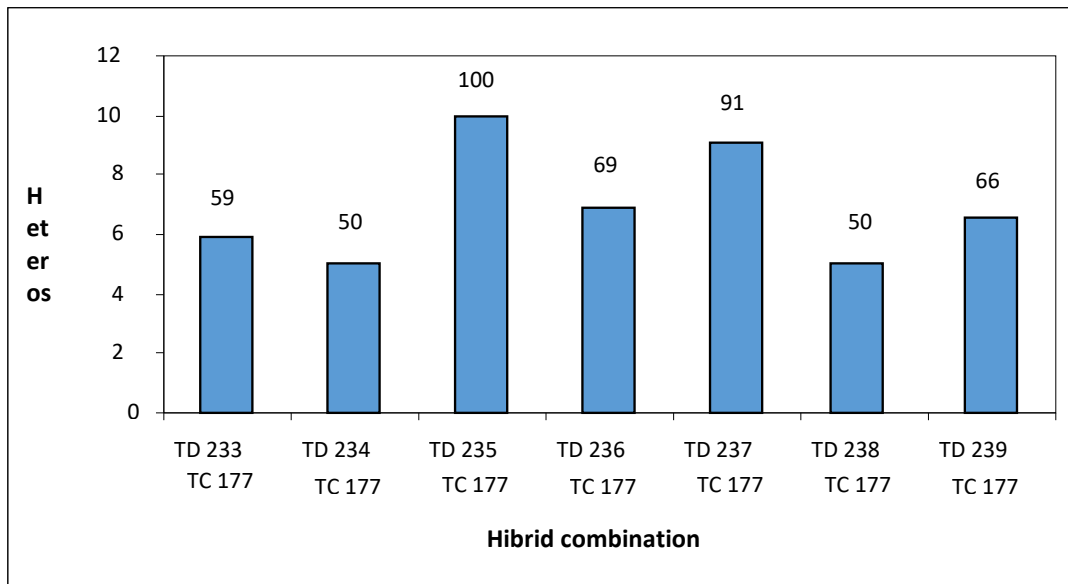
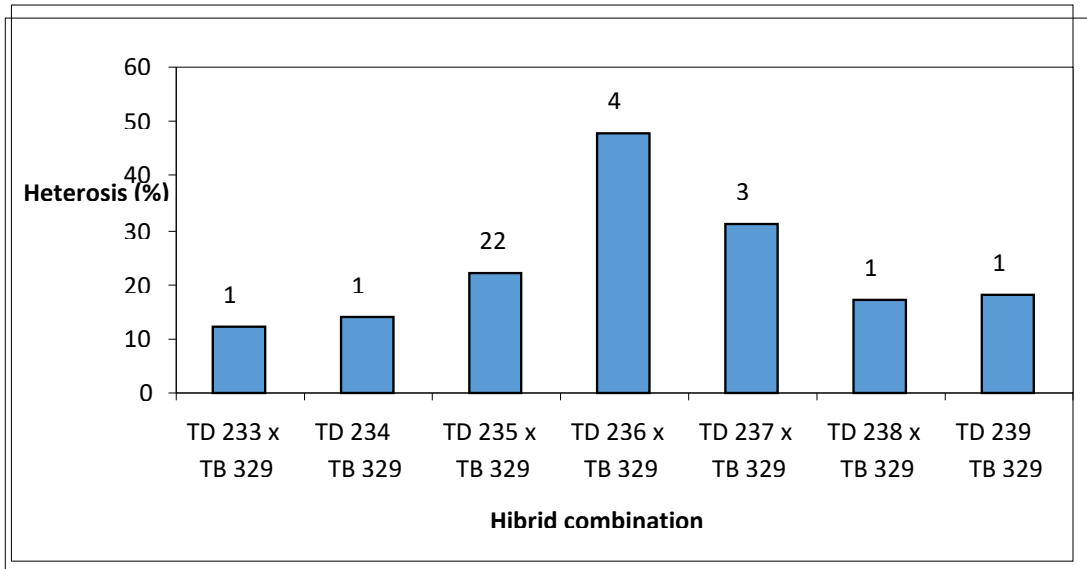


Grouping of heterosis-based lines:

- 1) similar - H% <30
  - 2) genetically similar - H% = 30-70%;
  - 3) genetically removed - H% = 70-90%
  - 4) from alternative groups - H% > 90%
- (by Musteață and Mîstreț, 2009)

Fig.2. Heterosis (%) for the weight cob

The heterosis calculated in the case of crosses between the seven sister lines and line A of the initial material has low values of 12-48%, therefore the seven sister lines are genetically close to line A. The value of heterosis for the hybrid combinations made between the 7 related lines and line B of the starting material, has values greater than 50-100%. It can be argued that in the process of selection of the seven sister lines were followed the characteristics of line A, from the composition of the original material.



Grouping of heterosis-based lines:

- 1) similar - H% <30
  - 2) genetically similar - H% = 30-70%;
  - 3) genetically removed - H% = 70-90%
  - 4) from alternative groups - H% > 90%
- (by Musteață and Mistreț, 2009)

Fig.3. Heterosis (%) for production capacity

## CONCLUSIONS

- 1) From the analysis of variance for the phenotypic characters of the 7 inbred lines - parental forms taken into study, it appears that between the lines there are distinctly significant differences, both for the elements of the production capacity and for the vegetative characters of the plant.
- 2) From the analysis of phenotypic characters it can be seen that the TD line 236 differs significantly for most of the analyzed characters, especially through the production elements, but also by the vegetative characters.
- 3) The values of the phenotypical correlations reveal the existence of some - significant similarities between the lines TD 236 with TD 237, TD 233, TD 235; TD 239 with TD 234, TD 238; - significant differences between TD 238 lines with TD 234, TD 236, TD 239; TD 234 with TD 235.
- 4) The phenotypic variation of the 7 lines of common origin has mean values (between 10-20%).
- 5) From the analysis of variants in the dialectic crossing system, it appears that between genotypes studied there are distinctly significant differences in production elements and phenotypic characters.
- 6) The genetic value ( $\hat{g}$ ) of the 7 related lines reveals that there is significant genetic differentiation between them, even if they originate from the same material initially, in the transmission of characters:
  - TD 236 has the overall significant transmission capacity of five of the seven studied elements of production; the same situation in the vegetative characters of the plant.
- 7) The highest value of heterosis (H%) was achieved in hybrid combinations having the TD 236 constant line, therefore, this line is most genetically differentiated from the other 6 related lines. Instead, line TD 235 has achieved the lowest heterosis values, so this line is closest to the lines: TD233, TD234, TD237, TD 238, TD 239.
- 8) The heterosis calculated in the case of crosses between the seven sister lines and line A of the initial material has low values of 12-48%, therefore the seven sister lines are genetically close to line A. The value of heterosis for the hybrid combinations made between the 7 related lines and line B of the starting material, has values greater than 50-100%. It can be argued that in the process of selection of the seven sister lines, the characters specific to line A, from the component of the original material, were followed.

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