Study of the genetic similarity / divergence and genetic value of maize inbred lines *(Zea mays L.)*

(SUMMARY OF PhD THESIS)

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INTRODUCTION

Maize is a cereal with a large production capacity, but also with a wide range, being less influenced by climate change. More moreover, it has a high resistance to drought, heavy rains, but also to diseases and pests, and agrotechnical and harvesting works can be fully mechanized (HAŞ et al., 2018).

The biological potential of maize production has reached such levels that some scientists are becoming skeptical about the future possibilities of increasing it. Thus, some researchers come to the opinion "that new creations will result from a progressive improvement of agronomic traits rather than from the increase of productive potential"(CRISTEA., 2004).

The diversity of pedoclimatic conditions in the northern half of our country makes it necessary to cultivate a wider range of hybrids, from the very early to the group of semi-early hybrids.

The dynamics of the integration processes in the European seed market oblige the local breeders to respond to the intensive cultivation conditions, but at the same time to take into account the socio-economic conditions of the farmers in this part of the country (HAŞ, 2003). Compared to other areas of the country, Transylvania raises some particular problems for the maize crop due to the lower thermal regime, the relatively shorter frost-free interval, the climatic diversity, the diverse relief and the soils often with different peculiarities even from one soil. to another (CĂBULEA et al., 1982). Therefore, in order to carry out this research, maize genotypes belonging to FAO groups 300-400 were used, these genotypes having a lower production capacity, compared to the late ones.

1. Structure of the doctoral thesis

The doctoral thesis comprises a total of 168 pages and has been structured into two parts, The Current State of Knowledge and Personal Contribution. The current state of knowledge comprises 54 pages.

The second part of the thesis totals a number of 114 pages, structured in 8 chapters, which presents the objectives pursued, the particularities of the natural environment, the results obtained and discussions, conclusions and recommendations based on the results obtained, as well as its originality and innovative constructions. The thesis includes a total of 56 tables, 7 figures, 7 annexes, and 139 bibliographic titles.

2. Research objectives

Phenotypic diversity and especially the genetic diversity of parental forms is one of the determining causes of the expression of heterosis in the hybrids. Research problems regarding genetic diversity and / or the degree of relatedness inbred lines created from the same source of initial material are insufficiently argued in the literature, and their solution requires experiments with biological material appropriate to current early maize breeding programs.

Through the research objectives of this thesis (research project) it is assumed to get to know some aspects regarding the identification of diversity and / or the degree of kinship existing at a set of inbred lines created at the Agricultural Research-Development Station, Turda, thus allowing crossings logical, based on the heterotic model of parental forms.

Research objectives

The priority objectives that need to be studied in the direction of assessing genetic diversity or the degree of similarity are the following:

1. Phenotypic (intra-population) evaluation of quantitative characters, in expressing the diversity and / or similarity of sister inbred lines, respectively, created from the same sources of initial material.

2. Evaluation of the determinism of quantitative characters in the expression of genetic diversity / similarity and the value of improvement, of sister inbred lines, with common origin.

3. Analysis of the diversity / molecular similarity of inbred lines, with a common origin of corn

4. Evaluation and classification of heterotic diversity/similarity of inbred maize lines, by classical breeding methods and by analysis with molecular markers.

5. Analysis of the possibilities for improving the strategy for creating inbred lines and genetic improvement of maize

3. Material and method

In the analysis of the degree of diversity or similarity, between the inbred lines created from the same initial material, the following groups of lines were studied:

–Study of phenotypic variability (CV %) of 136 inbred lines, included in 10 groups (annex 1), according to the common origin of the initial material from which they were created:

- 65 inbred lines obtained from 5 synthetic populations:

1. Tu SRR 3D (4I) - 10 lines;
2. Syn. Low Temperature Resistant (SRTS) - 16 lines;
3. SRR DCT (2I) - 9 lines;
4. You SRR Comp. B (Comp. A) - 19 lines;
5. You SRR Comp. A (Comp. B) - 11 lines;

- 71 inbred lines created from 5 hybrid populations**:**

1. Raissa - 39 lines;
2. HST 6453 - 12 lines;
3. HST 5743 - 6 lines;
4. Mona - 7 lines;
5. Desc. BK - 8 lines

I. The following groups of germplasm were analyzed

- 7 parental inbred lines, created from the Mona hybrid population and 4 inbred lines - tester, 2 tester lines are (possible) the parental forms of the original hybrid Mona and 2 tester lines are genetically different belonging to other germplasm groups;

- 8 parental inbred lines created from the hybrid population Raissa and 4 inbred lines - tester, belonging to different germplasm groups;

- **8 parental inbred lines** of which: 4 lines created from Tu SRR Comp A (Comp B) and 4 lines created from Tu SRR Comp B (Comp A)

II. Simple hybrids experienced in cyclic systems or in diallel systems.

- 21 simple hybrids made by diallel crossing system p (p-1) / 2 type dialel system, the 7 parental inbred lines created from the Mona hybrid population, respectively 7 (7-1) / 2;
- 28 simple hybrids made by factorial crossing system m x n, the 7 parental inbred lines from the Mona hybrid population, and 4 tester – inbred lines (7 x 4)
- 32 simple hybrids made by factorial crossing system m x n, the 8 parental inbred lines from the Raissa hybrid population, and 4 inbred lines - tester (8 x 4)
- 56 simple hybrids made by diallel crossing system p (p-1) with direct and reciprocal crossing, of the 8 parental inbred lines (4 lines obtained from the synthetic population Tu SRR Comp. A and 4 lines created from the synthetic population Tu SRR Comp. B, respectively 8 (8 - 1).
- the 30 inbred lines created at ARDS Turda were genetically analyzed with 84 molecular markers of the SSR type.

Diversity estimation was performed by several methods grouped in to:

1. Evaluation of the diversity/similarity of some inbred lines al the level of phenotypic methods based on biometric analysis, analysis of variances, analysis of correlations between inbred lines;
2. Evaluation of the diversity/similarity of some inbred lines al the level of genetic methods based on the analysis of factorial and diallel crossing systems with the determination of genetic variants, genetic effects (additive, non-additive) of the intensity of heterosis in hybrids, and analysis of correlations at the level of genetic effects.
3. Genetic methods based on analysis with molecular markers of SSR type.

4. Results and discussions

4.1. Results obtained, regarding the study of inbred lines of common origin, Mona hybrid population

The characterization of a genotypic structure as part of a population or family can be performed by biometrical and summing multivariable data of quantitative and / or qualitative type.

The use of phenotypic differences as an indicator of diversity can provide information on the possible prognosis of hybrid combinations, with a more intense expression of heterosis due to the association of complementary characters.

In order to evaluate the production potential, the resistance to breaking and falling, as well as the vegetation period expressed at harvest by the dry matter in the grains, a series of determinations were performed on the plots (table 4.1).

The production potential expressed by grain yeld expressed on average values between 2049 kg / ha for the line (TD 234) and 4576 kg / ha (TD 236), the average genotypes being 3779 kg / ha.

Among the sister lines, with higher grain yield ability being TD 236 (4576 kg / ha), TD 238 (4553 kg / ha), TD 237 (4169 kg / ha).

Regarding the vegetation period, expressed by the dry matter in the grains at harvest, there were differences between the inbred lines, TD 236 (80.3%) was proved to be significantly later than the general average, and line TD 234 (87.1) showed to be significantly earlier than the sister lines.

The breaking and falling resistance, represented by the percentage of erect plants at harvest, was expressed in values between 73.4% (TD 234) and 82.9% (TD 235). There were no significant differences between the seven related lines in terms of breaking strength.

Table 4.1

***Some per se traits of the seven studied inbred lines* for production characters**

Nr. crt.	Character	Lines p(p-1)/2								LSD 5 %
		TD 233	TD 234	TD 235	TD 236	TD 237	TD 238	TD 239	Media Average	
1	Grain yield (kg/ha)	4026	2049	3945	**4576**	4169	**4553**	3135	3779	608
2	Dry matter (%)	82.4	**87.1**	82.6	80.3	82.7	83.9	82.2	83.0	1.6
3	Unbroken plants (%)	78.5	73.4	82.9	78.8	80.1	79.7	77.7	78.7	6.1
4.	Weight of 1000 grains (g)	233	178	227	221	**243**	216	**277**	228	14
5.	Percentage of grains / cobs (%)	79.4	73.4	73.3	80.1	77.6	81.0	75.7	77.2	4.2
6.	Weight hectoliter (kg/cm^3)	62.4	60.3	61.0	**67.6**	63.3	**66.9**	66.2	64.0	2.9
7.	Weight cob (g)	80.3	47.0	**109.3**	**100.5**	**90.6**	84.4	72.7	83.5	6.0
8.	Grain weight (g)	66.8	37.2	**88.2**	**85.8**	**74.6**	69.9	58.2	68.7	3.9
9.	Length cob (cm)	12.9	11.8	**15.6**	**15.2**	**14.2**	13.7	12.0	13.6	0.5
10.	Number of rows (nr.)	13.9	11.2	**16.7**	**17.0**	12.7	13.8	12.3	13.9	0.5
11.	Num. of grains / row (nr.)	25.5	20.8	**27.7**	**27.8**	**28.3**	**27.0**	21.7	25.5	1.3
12.	Bob depth (cm)	0.72	0.47	**0.74**	0.67	0.70	0.68	0.66	0.7	0.04

Table 4.2

Additive genetic effects ($\hat{g}$) to 7 inbred lines in a system of diallel crossings p(p-1)/2 for yield characters (Turda, 2013-2014)

No. crt.	Character	Lines p(p-1)/2							DL (LSD) 5 %
		TD 233	TD 234	TD 235	TD 236	TD 237	TD 238	TD 239	
1.	Grain yield (kg/ha)	-62	-241	-620	**2097**	-310	-304	-561	506
2.	Dry matter (%)	0.1	0.3	0.3	-0.6	-0.3	-0.1	0.4	0.5
3.	Weight of 1000 grains (g)	-6,1	-12,6	-3,2	**29,2**	2,7	-2.9	-7.1	11
4.	Ear weight (%)	5.25	-2.22	-13.23	**28.98**	-0,13	-8,91	-9.73	5.97
5.	Grain weight (g)	5.05	-0.99	-11.35	**23.73**	1.50	-6.62	-8.32	5.04
6.	Ear length (cm)	0.64	-0.02	-0.94	**0.45**	0.29	-0.19	-0.23	0.39
7.	No. rows (nr.)	-0.07	0.10	-0.24	0.60	-0.07	-0.24	-0.07	0.80
8.	No. grains/ row (nr.)	1.86	0.49	-1.53	**1.25**	-0.93	-0.15	-0.98	1.15

Genetic evaluation In the diallel crossing system of the seven inbred sister lines, created from the Mona hybrid population: TD 236 was the only line that proved to possess many favorable genes with additive inheritance.

4.2. Variability of phenotypic characters in inbred lines, created from the hybrid population - Raissa, parental forms (m)

The large number of inbred lines created from the same initial material, as well as its phenotypic diversity led us to study the extent to which phenotypic differences are found in the degree of kinship, or genetic differentiation, between lines with the same origin.

For this study, 8 sister lines were selected, out of a total of 39 inbred lines created from the Raissa hybrid population.

Table 4.3

Some per se traits of the seven studied inbred lines

a) production characters

Nr. crt	Character	Sister lines									LSD 5 %
		TE 202A	TE 229	TD 350	TD 352	TD 364	TE 317	TE 318	TE 341	Media	
1	GY (kg/ha)	4375	4633	4844	5089	5040	5807	5138	5317	5030	530
2	DM (%)	85.3	85.7	85.9	85.6	83.6	83.3	77.9	83.9	83.9	0.7
3.	UP (%)	72.6	82.9	73.9	77.7	75.4	72.6	81.3	74.9	76.4	5.8
4.	MMB (g)	262	239	190	211	216	202	272	213	226	11
5.	RB (%)	81.1	77.8	80.0	81.2	82.6	84.3	83.7	82.3	81.6	3.6
6.	MH (kg/cm^2)	65.7	67.1	73.8	70.4	71.7	70.5	68.2	71.5	69.9	9.2
7.	WC (g)	101	90	101	96	120	101	106	115	104	9
8.	GW (g)	81.8	69.2	80.5	79.9	98.3	85.0	89.2	94.1	84.8	7.8
9.	LC (cm)	14.7	11.8	14.7	14.0	14.2	14.4	11.5	14.6	13.7	0.5
10.	NR (nr.)	14.6	16.4	16.6	15.0	15.0	17.6	19.0	15.3	16.2	0.8
11.	NGR (nr.)	27.5	24.1	31.3	28.8	30.1	26.5	19.5	30.2	27.3	2.8
12.	PN (%)	0.7	0.7	0.6	0.7	0.8	0.8	0.9	0.7	0.74	0.1

Most researchers (SPRAGUE, 1966; HALLAUER and MIRANDA, 1981; CĂBULEA, 1987; SARCA, 2004) believe that in order to achieve effective heterosis, diversity must exist either due to genealogy or as a result of the process of improvement, and its manifestation depends on the genetic diversity of the parents, ie the more they are complementary from a phenotypic point of view, the more intense the heterosis could be in the first hybrid generation.

Genetic evaluation.

The analysis of the genetic value of the eight sister lines from the Raissa hybrid population, in the cyclic crossing system with four testers, allowed highlighting the additive genetic differences between the analyzed lines, regarding the transmission of production elements: TE 317 line (a large number of rows of grains and deep grain), line TE 318 (a large number of rows of grains), TD 364 (deep grain) TE 202A (long cob).

Table 4.4

Diversity / genetic kinship of sister inbred lines (Raissa) m = 8, at the level of additive loci in the cyclic cross system m x n (8 x 4) for yield characters (Turda, 2012-2014)

Character	Lines								LSD 5 %
	TE 202 A	TE 229	TD 350	TD 352	TD 364	TE 317	TE 318	TE 341	
Grain yield (kg/ha)	279.9	**471.7**	-583	-649.4	-57.8	-46.3	**481.6**	103.3	853.5
Dry matter (%)	1.18	-1.03	1.08	0.87	-0.58	-1.04	-0.40	-0.08	4.57
Unbroken plants (%)	0.63	-0.40	-0.50	-0.24	-0.09	-2.83	2.94	0.49	5.78
Weight of 1000 grains (g)	-0.7	**5.4**	**5.4**	1.4	-10.6	-6.2	3.6	1.7	9.46
Weight cob (g)	**7.63**	**7.75**	-16.83	-12.34	3.39	-1.68	**10.15**	1.93	15.65
Grain weight (g)	**7.96**	3.32	-14.46	-8.94	5.90	-3.87	**6.63**	3.47	19.12
Length cob (cm)	**1.16**	-0.30	-0.31	-0.61	0.05	0.33	-0.41	0.07	0.61
Number of rows (nr.)	-0.74	-0.35	-0.37	-0.57	-0.73	**1.28**	**1.71**	-0.22	0.68
Number of grains / row (nr.)	**1.15**	-0.22	-0.86	0.22	0.16	-0.11	-0.64	0.30	1.73
$\Sigma\hat{g}$	298.2	485.9	-609.9	-669.6	-60.3	-60.4	505.2	111.0	-

4.3. Results obtained in the experimental system regarding the study of inbred sister lines created from Tu SRR Comp. A and lines created from Tu SRR Comp. B

In the present study, the following inbred lines were used as constant lines: TD 337, TA 422, TA426 and TA428 from Tu SRR Comp. A; TC 385 A, TC384 A, TC 398 and TC399 of Tu SRR Comp. B.

Table 4.5

Some per se traits of the eight studied inbred lines

Nr. crt.	Character	Heterotic group BSSS					LSD 5 %
		TD 337	TA 426	TA 428	TA 422	Media	
1.	Grain yield (kg/ha)	**4361**	**4819**	3855	1855	**3722**	478
2.	Dry matter (%)	**82.3**	73.3	75.8	**83.7**	**78.7**	1.7
3.	Unbroken plants (%)	80.7	81.4	76.0	72.8	**77.7**	5.5
4.	Weight of 1000 grains (g)	204	**230**	**256**	155	**211**	12.
5.	Percentage of grains / cobs (%)	73.5	75.4	74.2	72.0	**74**	3.6
6.	Weight hectoliter (kg/cm^3)	**68.9**	58.8	59.2	57.2	**61**	2.7
7.	Weight cob (g)	107	**123**	101	66	**99**	8.2
8.	Grain weight (g)	85	**102**	85	49	**80**	7.2
9.	Length cob (cm)	**15.7**	14.4	13.5	15.1	**14.5**	0.7
10.	Number of rows (nr.)	16.3	**20.8**	18.4	17.1	**18**	0.6
11.	Num. of grains / row (nr.)	27.9	28.7	25.3	28.3	**27.5**	1.6
12.	Bob depth (cm)	0.68	**0.85**	**0.84**	0.63	**0.75**	0.06
Nr. crt.	Character	Heterotic group Lancaster					LSD 5 %
		TC 385A	TC 384A	TC 398	TC 399	Media	
1.	Grain yield (kg/ha)	**5267**	3821	4067	3448	**4151**	478
2.	Dry matter (%)	79.8	79.4	78.1	79.9	**79.3**	1.7
3.	Unbroken plants (%)	80.4	78.4	74.5	80.3	**78.0**	5.5

4.	Weight of 1000 grains (g)	258	**280**	230	**273**	**260**	12.
5.	Percentage of grains / cobs (%)	**79.9**	75.1	74.9	72.8	**76**	3.6
6.	Weight hectoliter (kg/cm³)	65.2	66.2	64.2	65.3	**65**	2.7
7.	Weight cob (g)	**114**	100	98	89	**100**	8.2
8.	Grain weight (g)	**96**	**81**	**81**	71	**65**	7.2
9.	Length cob (cm)	**17.1**	14.9	**16.9**	14.8	**16**	0.7
10.	Number of rows (nr.)	13.6	13.8	**15.8**	11.9	**14**	0.6
11.	Num. of grains / row (nr.)	**32.5**	27.5	28.4	25.0	**28.5**	1.6
12.	Bob depth (cm)	0.71	0.73	0.71	0.68	**0.70**	0.06

The analysis of the data regarding the “per se” differentiation of the lines created from the two synthetics, regarding the production elements with values significantly higher than the average, the following lines created from can be noticed:

- Tu SRR Comp A (Comp B): TA 426 (for grain production, MMB, cob and grain weight, number of grain rows, grain depth) and TD 337 (for grain production, precocity, hectolitre mass, length ear);

- Tu SRR Comp B (Comp A): TC 385A (for grain production, MMB, cob and grain weight, cob length, number of grains / row).

4.4. Study on the genetic diversity / kinship of maize germplasm from SCDA Turda using SSR type molecular markers

The genetic distance values confirm the existing information in the pedigree for lines TD233, TD234, TD235, TD237, TD238 and TD239, as an example, all these lines come from the same original material, the hybrid population Mona. Although most of the lines created from the Mona hybrid population are part of the same family, so they are registered with a very little differentiated pedigree, they are closely related to the parent line of the Mona hybrid, respectively they are part of the heterotic Iodent group (Fig. 4.1). A single line TD 236 is genetically differentiated from the mother line and is genetically similar to the father line (TC 177), belonging in proportion of 40% to the heterotic group Flint European. This genetic differentiation of the TD 236 line highlighted with the help of SSR molecular markers, confirms the results obtained by the high level of intensity of heterosis, at the intersection of the TD 236 line with the sister lines.

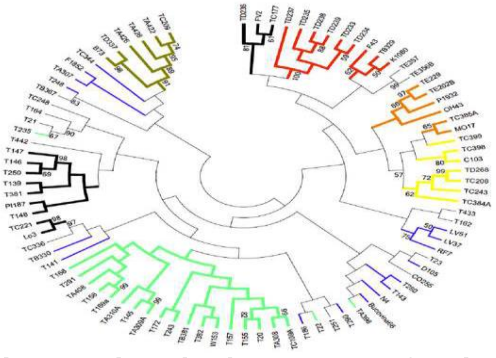

Fig. 4.1 The existing phylogenetic relationships between a group of 90 inbred lines (NJ tree).
(by: Şuteu et al., 2013)

5.Conclusions and recommendations

The phenotypic expression of quantitative traits in inbred maize lines is specific to each trait in relation to the interaction between the genetic basis of the trait (number of genes, mode of action and their relative state) and the environmental conditions faced by the genotype.

The analysis of the quantitative characters at the studied lines revealed both a considerable diversity of their expression media and the existence for each character of some genotypes significantly superior or inferior to the general average.

The phenotypic evaluation of the differentiation or kinship between the sister inbred lines was estimated by calculating the differentiation or similarity of the phenotypic characters, by the synthetic selection index, as well as by the correlations between the phenotypic characters.

6.Originality and innovative contributions of the thesis

The originality of the doctoral thesis "**Study of genetic similarity/divergence and genetic value of some maize inbred lines (*Zea mays L.)***" derives from the establishment of research objectives, designed to complement the literature, less rich in our country.

The biological material studied in the respective research (136 lines with common origin obtained from 10 different initial materials), as well as the experimental methods bring a note of originality, considering the area where this biological material is cultivated, and the results obtained to clarify whether the existing phenotypic differentiation between the lines studied also exists at the level of genetic determinism of some characters of agronomic interest.

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