Use of Genetic and Phenotypic Variability of Romanian Local Population Maize

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ABSTRACT

The continuous and significant loss of genetic variability in most crops, observed in recent years, has stimulated a growing interest in biodiversity conservation. Local germplasm represents valuable source of genetic variability in grain quality.

In this paper, aspects regarding the collection, study and conservation of local maize germplasm were followed. The germplasm was characterized in terms of phenotypic variability and potential for use in hybrid crosses. Subsequently, a series of crosses were made with inbred lines on various types of male-sterile cytoplasms, in order to observe their reaction.

The Agricultural Research and Development Station Turda had an impressive collection of local populations (over 1200 origins) but after selection only 376 remained, the rest being eliminated due to phenotypic similarity. Some of them were included in 20 synthetic populations created out of the desire to concentrate more valuable genes from local populations.

Following the study of the general and specific combining ability for several agronomic traits, some local populations were noted as valuable. The inbred lines obtained through selection from local populations were crossed with 4 elite lines, from different heterotic groups. The T291 inbred line, obtained from a local population from Mureş County, was the highest yielding.

Local germplasm (local population or derived inbred lines) generally exhibit good specific combining capacity for grain production in interaction with elite inbred lines.

Keywords: biodiversity, variability, germplasm, local populations, heterotic.

INTRODUCTION

The continuous and significant loss of genetic variability in most agricultural crops, observed in recent years, has stimulated increasing interest in biodiversity conservation (Duvick, 2005; Bernardo et al., 2009; Călugăr et al., 2023).

The high production potential, as well as the wide use of maize in numerous areas of human activity, places this species among the most extensive plants cultivated in Romania, ranking second in area after wheat, and first in production. This situation means that maize is given special attention, both by researchers and growers, especially since maize plays an important role in the food security of the ever-growing population (Cristea, 2004).

In all European maize-growing countries, the spread of hybrids with high grain yields has led to a gradual replacement of local populations (Lavergne et al., 1991; Bernardo et al., 2009; Has et al., 2009). Consequently, the genetic variability of the local cultivated maize germplasm has been reduced both in terms of the number of alleles and in terms of genetic diversity between hybrids (Reif et al., 2005). However, local germplasm represents an important source to explore for genetic variability in grain quality and a valuable material for improving production quality. The maize collection in the Suceava Genebank represents 32% of the entire Romanian national collection (Murariu et al., 2019).

To improve this plant, a genetic base as diverse as possible is needed so that specific heterosis can be achieved in the creation of

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maize hybrids. The diversity of local maize genotypes must also be preserved for future breeding work, but it is necessary to know it first. The Agricultural Research and Development Station Turda (ARDS) is one of the main agricultural research institutions in Romania, and maize breeding is one of the most important directions of its activity. The local maize germplasm collection at (ARDS) Turda is one of the most valuable at the national level, due to its diversity and significant number of genotypes. In 2023, this collection had 610 local populations originating from the pre-mountain areas of Transylvania, the Transylvanian Plateau area and the Mures basins, the Târnave basin and Moldavia.

The entire collection of local populations is maintained within the maize breeding laboratory at ARDS Turda, through SIB (sister and brother), once every 3-5 years, depending on germination capacity. A significant number of genotypes are also stored at the Suceava Gene Bank, long-term, at controlled temperatures.

The aim of this work is to analyze the variability existing in the collection of local maize populations within the ARDS Turda for some plant and cob traits.

MATERIAL AND METHODS

Biological material

The biological material was represented by 376 local populations originating from various perimontane areas of Transylvania, the Transylvanian Plateau area and the Mureş and Târnave basins area.

From the 376 local populations, 53 genotypes were selected and evaluated for the maintenance/restoration of pollen fertility by crossing them with 4 sources of cytoplasmic male sterility (male-sterile inbred lines - mother) and testing them the following year, by recording the number of plants that completely restored pollen fertility, those that

partially restored it, as well as those that were not restored, due to the lack of restoration genes, in the paternal genotypes.

In order to highlight the good behavior of inbred lines obtained from local populations and the transmission of production traits at an additive level in the creation of hybrids, 8 inbred lines from cycle I (lines obtained from local populations) and 4 tester lines from cycle II (elite lines) were factorially crossed.

Experimental design

Both the collection of local populations and the hybrids were tested between 2021-2023 in the experimental field within the maize breeding laboratory ARDS Turda, located in the north western part of Turda, Romania: and the maize breeding field is located on the upper terrace of the Aries River.

Both the local population collection and the hybrids were sown in early May at a density of 70,000 pl/ha using the Monoseed DT experimental field seeder (Wintersteiger). Each local population was sown in two rows of 5 m in length in a single replication. In the case of the hybrids, each plot was sown in two rows of 5 m in length with a harvestable area of 7 m². The plots were arranged in randomized blocks with replication.

In the experimental field, the same technology was used in all three years, a three-year rotation of soybean-winter wheatmaize. In the fall, plowing was done and in the spring, the soil was fertilized with complex fertilizer (N27:P13.5:K0 - 400 kg/ha raw material and a preparation of the seedbed with the combiner); during the vegetation period, two herbicides were applied (preemergence with 1.5 l/ha, using S-metolachlor as the active substance (960 g/L) and postemergence with 2.0 l/ha using tembotrione (44 g/L) and isoxadifen-ethyl (22 g/L) as active substances when the maize had 6-8 leaves), as maintenance work, one mechanical and one manual weeding was done and the harvesting was done manually.

No. crt.	No. crt. Inbred line Origin of inbred lines								
	Inbred lines studied (m)								
1	TC 316	S 54 (Pop. Smolice-Polonia) x Mo 17							
2	D 105	Populațion flint (I) from Southern Germany							
3	T 291	Population of Ungheni							
4	T 141	Population of Copșa Mică							
5	T 145	ICAR 54 x Romanian by Studina							
6	Т 139	Orange of Târgu-Frumos							
7	Т 157	Populațion of Dumbrăvioara							
8	T 164	Population of Batoş							
		Inbred lines tester (n)							
9	TA 367	F 32 x F 19							
10	TC 344	Selection commercial hybrid							
11	TC 385	Syn. SRR - Comp. B							
12	TE 356	Selection commercial hybrid							

Inbred lines used in the factorial breeding system m x n (8 x 4)

Statistical methods of data processing

Within the collection of local populations, the coefficient of variability was calculated for several analyzed characters according to the formula:

$$CV = s/m_x x 100$$

where:

s = standard deviation;

 $m_x = mean.$

Within the comparative culture with hybrids, the additive and non-additive effects involved in the genetic determinism of grain production were calculated using orthogonal and non-orthogonal decompositions for the factorial system (m x n) (Căbulea, 1975).

A complete evaluation of the genetic diversity that conditions the expression of quantitative traits was achieved by simultaneously considering both the diversity of expression of genes with additive actions (homozygous loci) and the differences in the mode of expression of intra-and interallelic interactions (dominance, epistasis).

At the level of quantitative traits, genetic diversity was estimated based on the general combining capacity (GCC) and the specific capacity (CSC) characteristic of each line, each interaction between lines, and for each crossing system (factorial or diallel).

The evaluation of polygenic diversity was carried out as follows:

- for the factorial system according to the formula (Căbulea, 1975):

where:

Xm and Xn - the sum of the values in which the parent "m" or "n" participates as a constant parent;

X.. - the sum of all the values in the factorial system.

- at the level of intra and interallelic interactions by calculating the non-additive gene effects (smn):

 $\hat{s}mn = Xmn - X.. - (\hat{g}m + \hat{g}n)$

RESULTS AND DISCUSSION

The local germplasm collection in Transylvania includes 376 local populations that were obtained by collecting by researchers of the maize breeding laboratory different perimontane from areas of Transylvania, the Transylvanian Plateau area and the Mures and Târnave basins. The distribution of these populations by counties of the previously mentioned areas is as follows: Cluj (77), Bistrița (34), Alba (47), Mureș (55), Hunedoara (41), Sibiu (25), Harghita (12), Brașov (13), Sălaj (11), Maramures (38), Satu Mare (23) (Figure 1).



Figure 1. Origin of local populations

Plant height and insertion height are important traits for mechanized harvesting (both for lines that are used as parental genotypes of maize hybrids, but also for hybrids). Plant height is of great importance because it determines the height that the hybrids will have. Another aspect related to plant height is the possibility of being used as silage. In our study, for this trait, the range of values is quite large, between 163 and 283. The coefficient of variation shows a medium variability for plant height (Table 1).

The insertion height has a high variability, the coefficient of variation having a value of 18.5, the values ranging between 50 and 136 cm. The insertion height, together with its uniformity, are important characteristics to follow in the choice of parental forms, due to the preparation of genotypes for mechanical harvesting.

Total leaf number is an important and determinant character of plant architecture in maize. Maize exhibits large natural variations in leaf number, with total leaf number ranging from 7 to 19 leaves in a collection of different maize landraces (Flint Garcia et al., 2005). The variation for total leaf number in our collection of landraces is between 10 and 17 (Table 1).

The number of panicle branches has a coefficient of variation of 23, indicating a high variability for this character, with values ranging from 8 to 52. Maize breeding trends in recent decades have been directed towards a plant ideotype that generally includes erect leaves, rigid stems and a low number of panicle branches, especially by reducing the number of branches (Mickelson et al., 2002; Brawbaker, 2015).

The length of the ear is a character whose coefficient of variation indicates a medium variation, the values being between 9 and 21 cm (Table 1), the majority having values between 12 and 15 cm.

The weight of the ear is the most important element in achieving a high production. The local populations from our collection have a coefficient of variation of 22.9, indicating a high variability, the values being between 37 and 192 grams (Table 1).

The number of grains per row is a character with a medium variability, with values between 22-42 grains/row.

The number of grain rows presents a medium variability, with values between 10 and 22 rows, this character having a high genetic determinism.

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	Plant height (cm)	Insertion height (cm)	Total number of leaves (no.)	Number of leaves above the ear (no.)	Number of panicle branches (no.)	Ear weight (g)	Ear length (cm)	Number of grain rows (no.)	Number of grain/row (no.)
Mean	217	78	12.7	4.7	21.9	113	16.2	13.1	33.7
Minimum	163	50.5	10.1	3.3	8.1	37.7	9.2	9.3	21.9
Maximum	283	136	17.3	6.6	52.1	192	21.4	21.2	42.5
Median (cm)	119	85	7.2	3.3	44	154	12.2	10.8	20.6
Standard deviation	22	14.6	1.2	0.6	5.04	25.8	1.9	12.4	3.7
Error	1.36	0.9	0.07	0.03	0.3	1.55	0.11	0.10	0.2
Confidence level (95%)	2.67	1.7	0.13	0.6	0.6	3.1	0.21	0.20	0.4
Coefficient of variation(cv%)	10.4	18.5	9.2	12.3	23.0	22.9	11.9	10.96	10.8

Table 1. Calculation of the coefficient of variation (CV) for some plant and ear traits - 376 local populations - 2021

Plant height is of great importance because it determines the height of the hybrids. Another aspect related to plant height is the possibility of using it as silage. In 2022, the amplitude between the minimum and maximum had higher values, respectively, 216 and 233. The coefficient of variation shows an average variability for plant height (Table 2).

The insertion height has a high variability, the coefficient of variation having a value of 22.3, the values varying between 31 and 132 cm. The insertion height, together with its uniformity, are important characteristics to follow in the choice of parental forms, due to the preparation of genotypes for mechanical harvesting.

Total leaf number is an important and determinant character of plant architecture in maize. Maize shows large natural variations in leaf number, with total leaf number ranging from 7 to 19 leaves in a collection of different maize landraces (Flint Garcia et al., 2005). The variation for total leaf number in our landrace collection is between 7 and 18 (Table 2).

The number of panicle branches has a coefficient of variation of 27, indicating a very high variability for this character, with values ranging from 4 to 30.

The length of the ear is a character whose coefficient of variability indicates a medium variation, most genotypes having values between 9 and 21 cm.

The weight of the ear is the most important element in achieving a high production. High variability in this character being due to the average values of the weight of the ear ranging between 55 and 255 grams (Table 2).

The number of grains per row is a character with a medium variability, with values between 22-42 grains/row.

The number of grain rows presents a medium variability, with values between 8 and 16 rows of grains, this character having a high genetic determinism.

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	Plant height (cm)	Insertion height (cm)	Total number of leaves (no.)	Number of leaves above the ear (no.)	Number of panicle branches (no.)	Ear weight (g)	Ear length (cm)	Number of grain rows (no.)	Number of grain/row (no.)
Mean	216	70	11.6	5.01	18.8	133	16.3	13.2	33.7
Minimum	216	31	6.5	3.5	4.3	55.3	9.2	8.0	21.9
Maximum	293	132	18.3	8.1	29.7	255	21.4	16.6	42.5
Median (cm)	153	101	11.8	4.6	25.4	202	12.2	8.6	20.6
Standard deviation	25.8	15.7	1.38	0.5	4.5	31	1.9	1.4	3.7
Error	1.5	0.89	0.07	0.03	0.25	1.7	0.11	0.07	0.2
Confidence level (95%)	2.89	1.76	0.15	0.05	0.50	3.4	0.21	0.15	0.4
Coefficient of variation(cv%)	11.97	22.3	11.9	10.5	27.8	22.9	11.9	10.2	10.8

Table 2. Calculation of the coefficient of variation (CV) for some plant and ear traits - 376 local populations - 2022

Within the collection of local populations, the genotypes with the flint x dent grain type dominate, but there is also a fairly high number of genotypes with flint and dent x flint grains, the fewest genotypes have the dent grain type (Table 3). Most local populations have grain color of different intensities of yellow, but dark yellow and normal yellow predominate. Regarding the color of the rachis, it was observed that most local populations have a white color (173), but the number of those with red rachis is not negligible (41).

Table 3. Classification of local populations according to grain type, grain color and rachis color - 376 local populations

Grain traits	Trait group	No of cases
	Flint	120
C	Flint x dent	173
Grain type	Dent x flint	65
	Dent	18
	Dark yellow	222
	Normal yellow	82
	Reddish yellow	12
	Dark yellow + Reddish yellow	23
	White	10
	Dark yellow + Normal yellow	2
Carlana 1an	Normal yellow + Reddish yellow	4
Grain color	Orange yellow	11
	Dark red	2
	Dark yellow + Orange yellow	1
	Dark yellow + Reddish yellow	1
	Reddish	4
	Normal yellow + White	1
	Dark yellow + White	1
	White	173
	Red	41
	White + Red	92
Deskie selen	Red + White	57
Rachis color	White + Red + Pink	6
	White + Pink	3
	Pink + Red	2
	Dark red	2

Following the analysis of the collection of local populations, 37 groups of possible combinations between grain type, grain color and rachis color were identified (Table 4). This analysis results in the largest group being represented by local populations with flint x dent grain, dark yellow and white rachis, which include 63 genotypes, followed by the group with indurated grain, dark yellow, white rachis (37) and flint type, normal yellow and white rachis with 30 genotypes. Other groups with a large number of genotypes are: flint x dent normal yellow grain - white rachis (22 local populations), flint x dent dark yellow grain - red rachis (14), dent dark yellow grain - red rachis (7), dent x flint dark yellow grain - white rachis (8).

Yellow color (normal or dark intensity) was found in all groups, regardless of the type of grain. In each of the four groups of grain type, the largest number of genotypes presents the dark yellow color of the grains, thus, in the flint group there are 74 populations with this color of grains, in the flint x dent group 141, in dent 15, and in dent x flint 52. In all groups, in second place in number of genotypes are those with the normal yellow color of the grains.

Table 4. Classification of local populations into groups according to grain type, grain color and rachis color - 376 local populations

Grain type	Grain color	Rachis color	No. populațions	Grain type	Grain color	Rachis color	No populations
Grain type Flint Flint x dent Dent		White	37			White	1
	Dark yellow	White + Red	22		NT	White + Red	1
		Red + White	10		Normal yellow	Red + White	1
		Red	5			Red	1
Flint		White	30		Dark red	Dark red	1
	Normal yellow	White + Red	6		White	White	1
		Red + White	3			White	8
	White	Wihte	6	Dont y flint	Dark vallow	White + Red	17
	Maron	Red	2	Dent x Innt	Dark yenow	Red + White	25
Grain type Flint Flint x dent Dent		White	63			Red	2
	Davis scall serv	White + Red	36		Normal vallow	White	1
		Red + Wihte	28			White + Red	4
		Red	14		Normai yenow	Red + White	1
rinn x deni		White	22			Red	1
	Normalization	White + Red	5		White	White	2
	Normai yenow	Red + Wihte	2		Redish	Red	1
		Red	2				
		White	3				
Dent	Deale and Herei	White + Red	3				
Dent	Dark yellow	Red + White	2				
Flint Flint x dent Dent		Red	7				

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Figure 2. Examples of grain type, grains colors and cob color

Regarding the additive and non-additive effects, among the 8 tested lines obtained from local populations, only the T 291 line had an additive gene effect (+1232.32 kg/ha); the TC 316 line also had a tendency to achieve a high additive effect; among the cycle II lines, the highest gene effect was

recorded in the inbred TE 356 line (+686.9 kg/ha), being statistically insignificant (Table 5). Significantly positive non-additive gene effects were recorded in the case of several hybrids, indicating the importance of non-additive gene effects in this type of crosses.

T 11 C	A 1 1	<	<u>~</u> `	1	11	a/		CC /	· 1	1.	.1	1 .		· ·	1	
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No. crt.	Linia ♀	TA 367	TC 344	TC 385 A	TE 356	ĝm
	Linia 👌					
1.	TC 316	271.4	564.2	608.2	1397.1**	710.2
2.	D 105	-60.80	231.9	276.0	1064.9*	378.0
3.	T 291	793.5	1086.3*	110.3**	1919.2**	1232.3**
4.	T 141	-928.90	-636.1	-592.1	196.8	-490.1
5.	T 145	-1175.00	-882.20	-838.10	-48.2	-736.1
6.	T 139	-1141.80	-849.00	-804.9	-16.0	-702.9
7.	Т 157	-253.60	39.2	83.29	872.2*	185.3
8.	T 164	-1015.60	-722.8	-678.7	110.2	-576.7
ĝn		-438.9	-146.1	-102.0	686.9	

LSD 5% = 837.24 LSD 1% = 1104.99 LSD 0.1% = 1422.46 The synthesis of the reaction of local populations to testing with three types of cytoplasmic male sterility (cms) is presented in (Table 6).

The reaction of local populations in interaction with a "cms T" source is presented in (Table 6): of the 52 populations tested, 16 (30.8%) maintained 100% male sterility. The local populations in which recessive genes for the maintenance of male sterility (cms) of the "T" type and also for total restoration (Rf) were identified were 50% (26 populations). In 13.5% of the tested populations (7 populations), the presence of partial maintenance genes was observed. It can be concluded that the local populations tested can constitute sources of germplasm for maintaining "T" type male sterility, but most populations also contain the total restoration genes Rf1 Rf1, Rf2 Rf2.

The reaction of the populations to the source of male sterility "cms ES" is presented in (Table 6). A number of seven populations had all the recessive genes (cms), completely maintaining the male sterility of the "ES" type. Only in one population was the existence of all the genes for total restoration (Rf) of male sterility cms "ES". Most cases (35-66%) were recorded for local populations in which the maintenance and restoration genes were found concomitantly; in most cases the genes for maintaining male sterility were predominant.

For the crosses of local populations with the source "C" of cytoplasmic male sterility, the maintenance of male sterility in a proportion of 100% was observed in a number of 11 populations (21.2 %).

The type of male sterility "M" determined the largest number of local populations that maintain male sterility - 18 (34.6%) and the highest number of local populations that completely restore 5 local populations (9.6%). And in this type of male sterility a high number of the tested populations (18-34.0%) have in their composition the genes for maintaining, but also for completely restoring the male sterility of the "Moldavian" type.

A special remark should be made regarding the local populations "Zagra" and "Răzoare", which maintain all four types of cytoplasmic male sterility.

Specification	Number of populations/percentage of total (52 populations)					
Cms type	cms-T	cms-ES	cms-C	cms-M		
Maintenance of male sterility (cms 100%)	16 (30.8%)	7 (13.5%)	11 (21.2%)	17 (32.7%)		
Restauration of male sterility (Rf 100%)	1 (1.9 %)	1 (1.9%)	-	5 (9.6%)		
% populations in genetic equilibrium of cytoplasmic sterility mechanisms (Nrf) and/or genetic restoration factors	17 (33%)	8 (15%)	11 (21%)	22 (42%)		
Maintenance + partial restoration (cms+pRf)	1 (1.6%)	6 (11.5%)	-	3 (5.8%)		
Maintenance + partial restoration + total restoration (cms+pRf+Rf)	7 (13.5 %)	2 (3.8%)	2 (3.8%)	8 (15.4%)		
Maintenance + total restoration (cms+Rf)	26 (50%)	34 (65.5%)	37 (71.2%)	18 (34.6%)		
Total restoration + partial restoration (Rf+pRf)	-	2 (3.8%)	2 (3.8%)	1 (1.9%)		
Partial restoration (pRf)	-	-	-	-		

Table 6. Evaluation of the heterogeneity of local populations through the interaction with different male sterile cytoplasms: cms-T, cms-C, cms-ES, cms-M

CONCLUSIONS

The collection of local maize populations analised has evidentiated a high degree of variability for all analyzed traits. The genetic diversity of these populations is of particular importance in the breeding process, having an essential role in obtaining new inbred maize lines as well as for their use as gene sources for different traits. Preserving this diversity is also important to avoid genetic erosion and germplasm loss, which is why a large part of the local populations are maintained at ARDS Turda.

The collection of local populations in Turda is particularly important for the early and mid-early maturity groups, the lines obtained from these local populations were used to create hybrids cultivated in Transylvania and Moldavia, areas favorable to early or mid-early maize.

The variability of characters found in the collection of local populations is influenced both by the large number of genotypes. Local and synthetic populations have long been the preferred starting material for the creation of inbred lines, but over time the share of the use of hybrids and crosses has increased. The use of local populations as starting material for inbred work can raise some difficulties. because of the transmission of unfavorable traits, along with those sought. The use of commercial hybrids has been a valuable source of genes for many important characters, such as the number of panicle axes reduced (but rich in pollen), erect or semi-erect leaves, slender plants, resistance to breakage and lodging.

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REFERENCES

- Bernardo, N., Mazzinelli, G., Valoti, P., Laganà, P., Redaelli, R., 2009. Characterization of maize germplasm for the chemical composition of the grain. J. Agric. Food Chem., 57: 2378-2384.
- Brewbaker, J.L., 2015. Diversity and Genetics of Tassel Branch Numbers in Maize. Crop Sci., 55: 65-78, doi:10.2135/cropsci2014.03.0248.
- Cristea, M., 2004. *Originea porumbului*. In: Porumbul studiu monografic, Edit. Acad. Române, I: 363-462.
- Căbulea, I., 1975. Metode statistice pentru analiza componentelor genetice ale variabilității continue, Probl. Genet. Teor. Aplic., VII(6): 391-420.
- Călugăr, R.E., Vana, C.D., Varga, A., Ceclan, L.A., Tritean, N., Ghețe, A.B., 2023. Germplasm collection - valuable resources of variability for plant and ear traits in maize breeding. Notulae Botanicae Horti Agrobotanici Cluj-Napoca, 51(2), 13141. doi:10.15835/nbha51213141
- Duvick, D.E., 2005. Genetic Progress in Yield of United States Maize (Zea mays L.). Maydica, 50: 193-202.
- Flint-Garcia, S.A., Thuillet, A.C., Yu, J., Pressoir, G., Romero, S.M., Mitchell, S.E., Doebley, J., Kresovich, S., Goodman, M.M., Buckler, E.S., 2005. Maize Association Population: A High-Resolution Platform for Quantitative Trait Locus Dissection. Plant J., 44: 1054-1064. doi:10.1111/j.1365-313X.2005.02591.x
- Haş, V., Haş, I., Pamfil, D., Copândean, A., Câmpian, S., 2009. Evaluation of "Turda" maize germplasm for phenotypic variability in grain chemical composition. Maydica, 54: 313-320.
- Reif, J.C., Hamrit, S., Heckenberger, M., Schipprack, W., Maurer, H.P., Bohn, M., Melchinger, A.E., 2005. *Trends in genetic diversity among European maize cultivars and their parental components during the past 50 years*. Theor. Appl. Genet., 111: 838-845.
- Lavergne, V., Lefort-Buson, M., Daudin, J.J., Charcosset, A., Sampoux, J.P., Gallais, A., 1991. Genetic variability among populations of maize germplasm. 1. Comparative analysis of top cross values and per se values of populations. Maydica, 36: 227-236.
- Mickelson, S.M., Stuber, C.S., Senior, L., Kaeppler, S.M., 2002. Quantitative Trait Loci Controlling Leaf and Tassel Traits in a B73 × Mo17 Population of Maize. Crop Sci., 42: 1902-1909. doi:10.2135/cropsci2002.1902
- Murariu, D., Plăcintă, D.D., Simioniuc, D., 2019. Assessing genetic diversity in Romanian maize landraces, using molecular markers. Rom. Agric. Res., 36: 3-9, https://doi.org/10.59665/rar3601.