

## Germplasm collection – valuable resources of variability for plant and ear traits in maize breeding

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### Abstract

Maize is one of the most important crops, both worldwide and in Romania, and preserving the diversity of the biological material used in the breeding of this plant is of particular importance. The Agricultural Research and Development Station (ARDS) Turda, Romania, inbred lines collection includes both its own genotypes and some obtained as a result of germplasm exchanges with other institutions in the country or abroad. In the present study, 575 lines created at Turda were analysed regarding some traits of the plant (plant height, ear height, total number of leaves, number of tassel branches) and the ear (ear length and weight, number of kernel rows and number of kernels/row). The biological material used in this study shows a great diversity: a medium or high variability coefficient was identified for several of the traits analysed (number of tassel branches, ear height, ear height). Frequency histograms were made for the studied lines, for plant and ear traits. A great variability also was observed in the colours of the anther and silk, but also for kernel type and colour and cob colour.

**Keywords:** breeding; germplasm; inbred lines; maize; variability

### Introduction

Biodiversity is essential for sustainable development, adaptation to a changing environment and for human survival itself. Many human activities negatively affect biodiversity, therefore, preserving germplasm as diverse as possible is a necessity (Zedan, 1995). The demographic growth recorded in the last decades determined the periodic inventory of plant genetic resources and the establishment of measures for their preserve and exploit. Mutation, migration, natural selection and genetic drift can cause genetic erosion and implicitly irretrievable losses if the maize germplasm is not properly preserved.

Maize (*Zea mays* L.) is one of the most important crops worldwide, both for human food, animal feed and industry, as well as due to many other uses. According to the Food and Agriculture Organization of the United Nations data (FAOSTAT, 2023), in recent years, worldwide, the crop cultivated in the largest areas is

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wheat, followed by maize and rice. In terms of total production of cereals, maize ranks first, followed by rice and wheat. Also, the same sources indicate a trend of continuous growth of the cultivated areas and implicitly of the total maize production. These aspects make maize occupy an important share in the food security of some continuously growing populations, and preserving the diversity of this crop is essential.

Conservation of maize germplasm can be done *in situ* or *ex-situ*. The one *in situ* refers more to local populations and maize landraces, but in recent years, especially due to the cultivation of hybrids on significant areas, this type of conservation is more difficult to achieve. *Ex-situ* conservation is carried out in gene banks or research centres. The largest gene bank for maize germplasm is CIMMYT, in El Batan, Mexico and includes more than 27,000 samples of maize seeds, the largest collection of maize landraces in the world, as well as samples of wild relatives of maize (teosintes and *Tripsacum*), breeding lines, gene pools, populations and cultivars (Prasanna, 2012). Other important gene banks are the Instituto Nacional de Investigaciones Forestales y Agropecuarias (INIFAP, Mexico), USDA-ARS and the Universidad de Guadalajara (Mexico), the China National Gene Bank in Beijing, the National Gene Bank of the National Bureau of Plant Genetic Resources (NBPGR), New Delhi.

At the level of the European Union, in recent years, Romania occupies the largest areas cultivated with maize (FAOSTAT, 2023), therefore, the conservation of plant resources, breeding and cultivation are important activities. The genetic resources of cultivated plants are conserved at the Suceava Gene Bank, but since the beginning of the breeding activity the conservation of these resources has also been an important objective in the research centres. In recent years, due to the lack of adequate storage facilities, insufficient technical staff, decreased seed germination and the impossibility of regeneration and multiplication due to financial considerations, many sources of germplasm have been lost (Murariu *et al.*, 2012). However, despite the recorded losses, Romania has an important collection of maize germplasm.

The Agricultural Research and Development Station (ARDS) Turda is one of the main agricultural research institutions in Romania, and maize breeding is one of the most important branches of its activity. The 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 1430 inbred lines (including all kernel types; fertile and male sterile cytoplasm inbred lines), 391 local populations, 6 varieties and 72 synthetic populations. It should also be mentioned the 45 registered hybrids, as well as several hundred hybrids currently in testing. Most of the inbred lines were created at ARDS Turda, and some of them were obtained as a result of exchanges of biological materials with research stations in the country or abroad. The population and varieties were mostly collected from Transylvania. The entire inbred line collection is maintained in the field of the ARDS Turda Maize breeding laboratory, by self-pollination and SIB, once every 3-5 years, depending on the germination capacity. A significant number of genotypes are also stored at the Suceava Gene Bank, for long-term conservation, at controlled temperatures.

Maize breeding programs require a genetic base as diverse as possible, so as specific heterosis of maize hybrids can be achieved. The diversity of maize genotypes must also be preserved for future breeding programmes, but it is necessary for the germplasm to be known, taking into account as many traits of agronomic interest as possible. This paper aims to analyse the variability among inbred lines from the ARDS Turda maize germplasm collection for several plant and the ear traits.

## Materials and Methods

The entire inbred line collection of ARDS Turda was studied during 2017-2022 for several traits, but in this paper are presented 575 inbred lines created in the Maize breeding laboratory. Each of these genotypes was sown in two rows, at a density of 70,000 plants/ha, in the field located in the Transylvanian Plateau, in the north-west of Turda, Cluj County, Romania. The plant breeding fields are located on the upper terrace of the Aries River and have a flat appearance, with frequent soil micro-depressions. The dominated soils are of the

vertical clay-illuvial chernozem type. The most important biochemical indices have the following average values: humus content over 3.5%, mobile phosphorus content is 4.5 mg P<sub>2</sub>O<sub>5</sub>/100 g soil and mobile potassium content is over 30 mg K<sub>2</sub>O/100 g sol. The soil reaction is neutral, between 6.2 and 6.8 pH units (Calugar *et al.*, 2022).

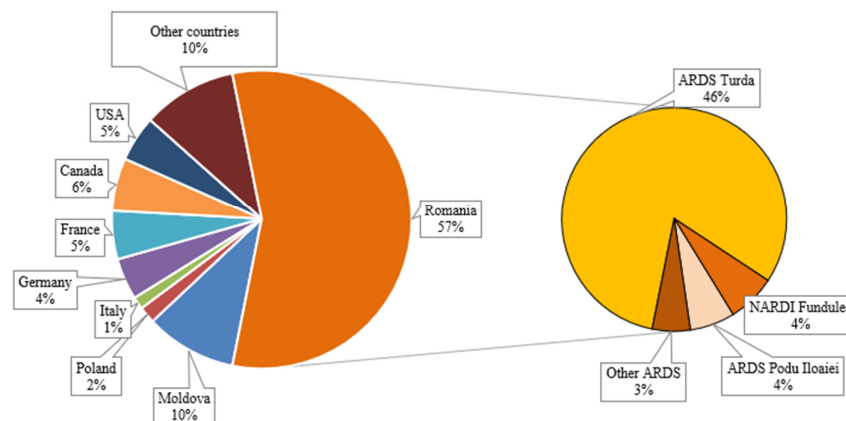
The same technology was used in all experimental years: autumn ploughing; soil fertilization (NPK 27:13.5:0, 400 kg/ha, together with the preparation of the seed bed); sown with the Wintersteiger precision spaced planter; herbicides (pre-emergence with 1.2 l/ha, using dimetanamid-p as the active substance (720 g/l) and post-emergence with 2 l/ha using tembotrione (44 g/l) and isoxadiphen-ethyl (22 g/l) as active substances), mechanical tillage and manual hoeing, manual harvesting. The precursor plant was autumn wheat.

After the flowering period, measurements were made for plant height, ear height, total number of leaves and the number of tassel branches while after harvesting data on ear weight and length, number of kernels/row and kernel row number was obtained. Observations were also made on anthers and silk colours, kernel type, the colour of the kernel and the colour of the cob.

Indices of variability (Lovie, 2005) were calculated within the collection, frequency histograms were drawn for the analysed traits, as well as correlations between different traits.

## Results

The maize germplasm collection of ARDS Turda includes 1430 inbred lines that were obtained through selection at Turda or following exchanges of biological material with other institutes in the country or abroad. The provenance for 805 inbred lines is Romania (57%), most of them (653) were obtained at ARDS Turda, while the rest come from the National Agricultural Research and Development Institute Fundulea and the Agricultural Research and Development Stations from Podu Iloaiei, Suceava, Pitești and Lovrin. The remaining 43% of the inbred lines come from the American continent (USA and Canada) or various countries in Europe (France, Germany, Italy, Poland, Hungary, Austria, Spain etc.) (Figure 1).



**Figure 1.** Provenance of the maize inbred lines from ARDS Turda collection

Among the 653 ARDS Turda inbred lines, 575 have dent kernels, flint or o combination of the two. The rest are sugary, opaque, floury or waxy lines. The previously mentioned 575 inbred lines will be analysed further.

The inbred lines studied can be divided into 4 maturity groups: extra-early, early, semi-early and semi-late, most of the lines belonging to the group of semi-early (44.9%) and early (33.2%) genotypes (Table 1). Early

hybrids were created at the beginning of ARDS Turda maize breeding activity, thus explaining the great number of early lines. In recent decades, especially due to climate changes, breeders' orientations have shifted towards semi-early genotypes, resulting in a significant number of lines belonging to this vegetation group (Haş *et al.*, 2021; Varga *et al.*, 2022).

**Table 1.** Classification of inbred lines according to maturity groups – for 575 inbred lines

Maturity group	Number of inbred lines (no)	Percentage (%)
Extra-early	74	12.9
Early	191	33.2
Semi-early	258	44.9
Semi-late	52	9.0

Plant height and ear height are important traits for mechanized harvesting (both for lines that are used as parental genotypes of the maize hybrids, but also for hybrids). The plant height of the inbred lines is of great importance because it determines the height of the hybrids. Another aspect regarding the plant height is the possibility of being used as silage. In our study, for this trait, the range of values is quite high, between 78 and 236. The coefficient of variation shows a medium variability for plant height (Table 2). The frequency histogram analysis (Figure 2) shows that 56.5% of the inbred lines studied have heights between 158 and 197 cm (325 genotypes), while 35.1% (202 lines) between 118 and 157 cm. The lines with heights over 206 cm belong to the semi-early or semi-late groups.

The ear height has great variability, the coefficient of variation having a value of 22.48, the values ranged between 23 and 102 cm. Regarding the distribution of genotypes on the frequency histogram, it was observed that the majority (59.5%) have the insertion height of the main ear between 42 and 61 cm. Ear height and its uniformity, are important traits to follow in the selection of parental genotypes, due to their readiness to be mechanically harvested. As expected, the highest correlation coefficient for the plant traits was calculated between the plant and ear height, 0.68, indicating a strong relationship between the two ( $p5\%=0.10$ ,  $p1\%=0.13$ ).

The number of leaves is an important determinant of plant architecture in maize. Maize shows a large natural variation for this trait, with total number of leaves ranging from seven to 19 leaves in a panel of different maize inbred lines (Flint-Garcia *et al.*, 2005). The total number of leaves varied between 9 and 17 (Table 2), with most lines having between 11 and 14 leaves (Figure 2). 31 lines with a more developed leaf system were identified, having 15-17 leaves. 13 of these belong to the group of semi-late lines, and 9 to the semi-early ones, while the lines with a reduced number of leaves generally belong to the extra early and early groups. Significant positive correlations with plant height (0.34), as well as with ear height (0.41) were calculated for this trait ( $p5\%=0.10$ ,  $p1\%=0.13$ ).

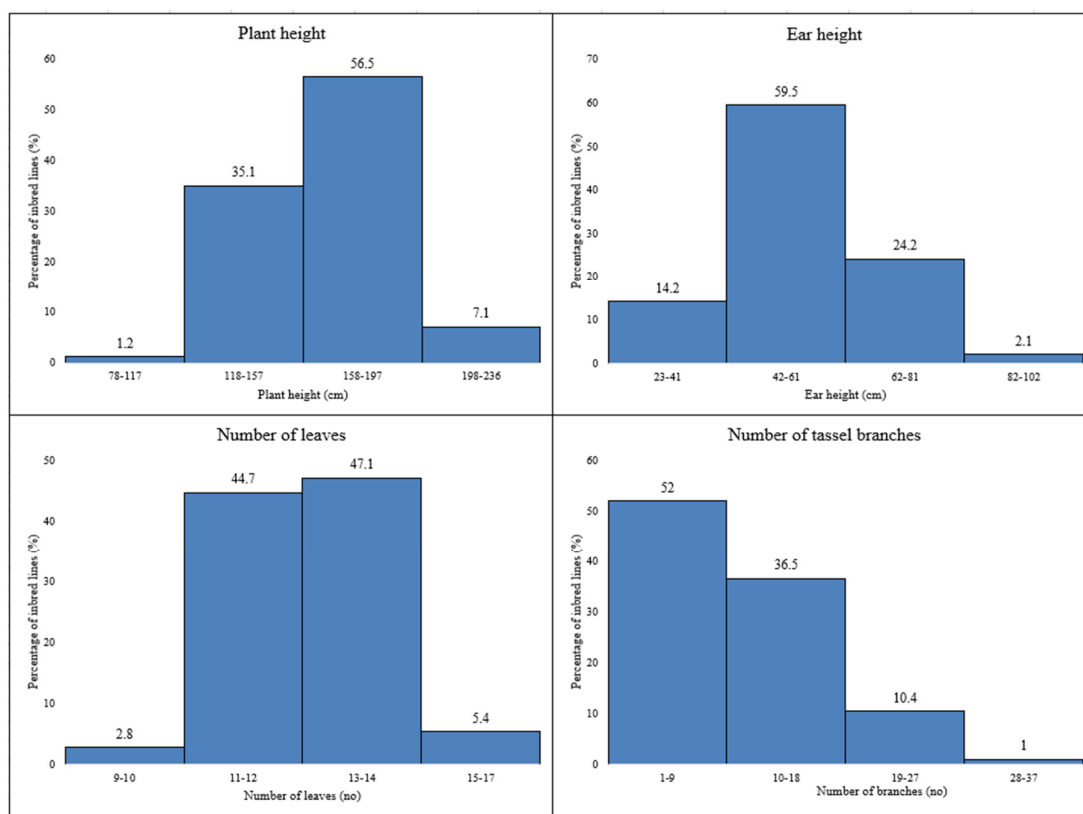


Figure 2. Frequency histogram for plant traits – for 575 inbred lines

Table 2. Range and coefficients of variation (CV) for plant and ear traits – for 575 inbred lines

Parameter	Plant height (cm)	Ear height (cm)	Total number of leaves	Number of tassel branches	Ear length (cm)	Ear weight (g)	No kernels/row	Kernel row number
Mean	165.26	53.96	12.60	10.79	15.09	106.26	26.42	15.49
Median	165.00	53.00	13.00	9.00	15.00	106.00	27.00	16.00
Minimum	78.00	23.00	9.00	1.00	8.00	14.00	11.00	8.00
Maximum	236.00	102.0	17.00	37.00	22.00	191.00	41.00	24.00
Standard Error	0.92	0.51	0.05	0.25	0.09	1.23	0.18	0.10
Standard Deviation	21.79	12.13	1.18	5.94	2.31	29.47	4.34	2.50
Sample variance	474.88	147.17	1.38	35.29	5.32	868.55	18.84	6.25
Confidence level (95%)	1.81	1.00	0.09	0.49	0.19	2.41	0.36	0.20
Coefficient of variation (%)	13.18	22.48	9.36	55.05	15.31	27.73	16.43	16.14

Some lines were distinguished by high plant heights and ear insertion, as well as a large number of leaves: TA 474- 236 cm plant height, 102 cm ear height and 15 leaves; T 433- 217 cm plant height, 91 cm ear height, 15 leaves; TA 452- 212 cm plant height, 92 cm ear height, 15 leaves; TD 364- 208 cm plant height, 86 cm ear height, 15 leaves.

The number of tassel branches has the highest coefficient of variation, 55.05, indicating a very high variability for this trait, the values ranging from 1 to 37. Maize breeding in recent decades has moved towards an ideotype of the plant which in general includes erect leaves, stiff stalks and small tassels, especially by reducing the number of tassel branches (Mickelson *et al.*, 2002; Brewbaker, 2015). 299 genotypes, representing 52% of the analysed lines have tassels with 1-9 branches, while other 210 have between 10 and 18 branches.

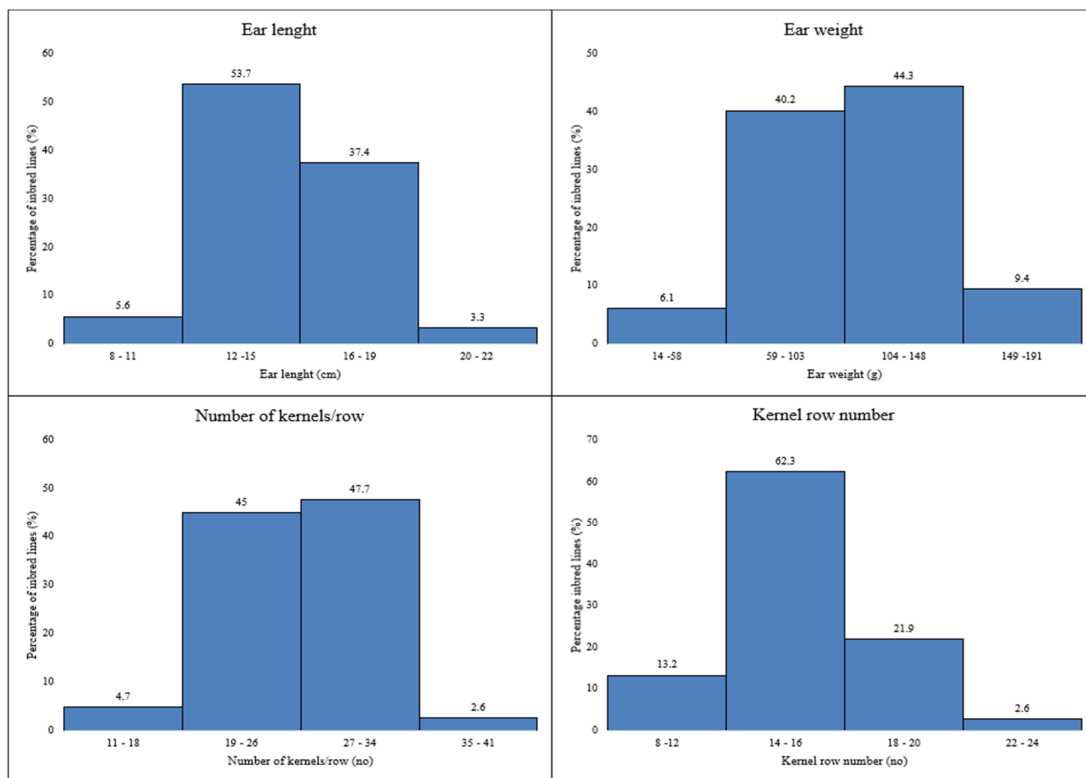
The ear length is a trait whose coefficient of variability indicates an average variation, the values range between 8 and 22 cm (Table 2), the majority having values between 12 and 15 cm (Figure 3). This trait is strongly correlated with the number of kernels/row (0.63) and ear weight (0.51) ( $p_{5\%}=0.10$ ,  $p_{1\%}=0.13$ ).

The ear weight is one of the most important traits that lead to a high yield in maize. The inbred lines have a coefficient of variation of 27.73, indicating a high variability, with values ranging between 14 and 191 grams (Table 2). Frequency histogram analysis (Figure 3) indicates that most lines have ear weights between 104 and 148 grams (255 genotypes). Ear weight has a statistically significant correlation with its length (0.51), the number of kernels/row (0.49) and the number of rows/ear (0.33) ( $p_{5\%}=0.10$ ,  $p_{1\%}=0.13$ ). A relationship between the kernel type and the ear weight was also observed, so the average of all flint lines was 80 grams, flint x dent 101 grams, dent x flint 112 grams, while the average of all dent genotypes was 115 grams.

The number of kernels/row is a trait with an average variability, with values between 11 and 41. The largest group (47.7%) is composed of genotypes with 27-34 kernels/row, followed by the group with 19-26 kernels/row (45%).

The kernel row number shows an average variability, with values ranging from 8 and 24 rows, with most inbred lines having 14-16 rows (358 lines) or 18-20 (126 genotypes). For the lines analysed, a negative correlation (-10) with ear length was determined ( $p_{5\%}=0.10$ ,  $p_{1\%}=0.13$ ).

Some inbred lines were noted for ear traits: TB 363 had the highest ear weight, 191 g, but also a fairly long ear, 19 cm and a high number of kernels/row, 35; TA 481 had the ear weight of 177 g, 16 cm long and 32 kernels/row; TE 203A has a slightly shorter ear (14 cm and 23 kernels/row), but has 20 kernel row and an ear weight of 176 g. Other inbred lines with high ear weight and length are TD 298 (175 g and 18 cm) and TD 357 (174 g and 19 cm).



**Figure 3.** Frequency histogram for ear traits – 575 inbred lines



From the point of view of the anther colour, the distribution of the lines is approximately equal between the two groups, greenish yellow (46.9%) and purple (53.1%). It should be noted that the intensity of the purple colour can vary, from a very light purple to a very intense colour (Figure 4).

Most of the analysed genotypes, 311, have greenish-yellow silk, while the rest have pink or red colour (Figure 4). Regarding the distribution of the (fertile) genotypes according to the colour of the anthers and silk, it can be observed that the genotypes with greenish-yellow silk are equally distributed between the two-colour groups of the anthers. An almost equal distribution is also in the case of the genotypes with pink silk, 73 having greenish yellow anthers and 63 purple ones. In the case of the red silk lines, it is observed that only 33 have greenish-yellow anthers, while a larger number, 75, have purple ones (Table 3).

**Table 3.** Combinations of tassel and silk colour – 540 male fertile inbred lines

Anther colour	Silk colour	Number of inbred lines (no)	Percentage (%)
Greenish yellow	Greenish yellow	147	27.2
	Pink	73	13.5
	Red	33	6.1
Purple	Greenish yellow	149	27.6
	Pink	63	11.7
	Red	75	13.9



**Figure 4.** Tassel and silk colours: a1= greenish-yellow anthers, a2 and a3= purple anthers (different intensities); b1= greenish yellow silk, b2= pink silk, b3= red silk

The lines studied were also classified according to the kernel type into 4 groups: dent, flint and 2 groups representing the combinations between dent and flint, differentiated according to the predominant kernel type. Within the germplasm collection, the lines with the dent kernel or its combinations with flint dominate, but there is also a fairly important number of genotypes with flint kernels (table 4). Most lines have kernels of various intensities of yellow, but dark yellow and normal yellow predominate. Regarding the colour of the cob, it was noticed that most of them are a red (280), but the number of those with white cob is not negligible either (193).

**Table 4.** Classification of the 575 inbred lines based on kernel type and the colour of kernel and cob

Kernel traits	Group	Number of inbred lines (no)	Percentage (%)
Kernel type	Flint	103	17.9
	Flint x dent	58	10.1
	Dent x flint	184	32.0
	Dent	230	40.0
Kernel colour	Light yellow	71	12.3
	Normal yellow	111	19.3
	Dark yellow	307	53.4
	Orange yellow	13	2.3
	Reddish yellow	43	7.5
	Orange	18	3.1
	Reddish	9	1.5
	Red	1	0.2
	Chocolate	1	0.2
	Dark purple	1	0.2
Cob colour	White	193	33.6
	Pink	9	1.5
	Red	280	48.9
	Dark red	93	16.0

Within the lines analysed, 59 groups of possible combinations (Figure 5) were identified between the type of kernel, its colour and the colour of the cob (Table 5). The largest group is represented by the lines with dent x flint, dark yellow kernel and red cob, in which 78 genotypes are included, followed by the group that has the same colours for kernel and cob, but with dent kernel, with 71 genotypes. Other groups with a high number of genotypes are: dent light yellow kernels – white cob (33 lines), dent normal yellow kernels – red cob (29), dent x flint dark yellow kernels – dark red cob (27), dent x flint dark yellow kernels – white cob (23), flint dark yellow kernel – red cob (21), dent normal yellow kernel – white cob (19).

The yellow colour (of normal or dark intensity), as well as reddish yellow were found in all groups, regardless of the type of kernel, but it is noted that all the lines with orange-yellow or orange kernel belong to the flint or flint x dent group. Also, the lines with reddish kernels belong to the flint group or those resulting from the combination of flint and dent, but are missing from the dent lines group. In each of the four kernel type groups, the largest number of genotypes have dark yellow kernels, thus, in the flint group there are 40 lines with this kernel colour, in flint x dent 34, in dent 101, and in dent x flint 132. In all groups, in second place in number of genotypes are those with the normal yellow colour of the kernels.



**Table 5.** The classification of inbred lines into groups, depending on combination of kernel type, kernel colour and cob colour - 575 inbred lines

Kernel type	Cob colour	Kernel colour	Number of lines	Percentage (%)	Kernel type	Cob colour	Kernel colour	Number of lines	Percentage (%)	
Flint	White	Light yellow	4	0.7	Dent	White	Light yellow	33	5.7	
		Normal yellow	14	2.4			Normal yellow	19	3.3	
		Dark yellow	9	1.6			Dark yellow	12	2.1	
		Orange yellow	11	1.9			Reddish yellow	7	1.2	
		Orange	16	2.8			Pink	Light yellow	2	0.3
		Reddish yellow	4	0.7		Red		Light yellow	15	2.6
		Reddish	1	0.2			Normal yellow	29	5.0	
	Pink	Light yellow	1	0.2			Dark yellow	71	12.3	
		Red	Normal yellow	3			0.5	Reddish yellow	14	2.4
			Dark yellow	21			3.7	Dark purple	3	0.5
			Reddish yellow	1		0.2	Dark red	Normal yellow	6	1.0
			Reddish	2		0.3		Dark yellow	18	3.1
	Dark red	Normal yellow	Normal yellow	3		0.5	White	Light yellow	12	2.1
			Dark yellow	10		1.7		Normal yellow	10	1.7
		Reddish yellow	1	0.2	Dark yellow	23		4.0		
		Reddish	1	0.2	Reddish yellow	1		0.2		
		Flint x dent	White	Normal yellow	8	1.4	Pink	Normal yellow	1	0.2
	Dark yellow			5	0.9	Dark yellow		4	0.7	
	Orange yellow			2	0.3	Red	Light yellow	4	0.7	
	Orange			2	0.3		Normal yellow	10	1.7	
Pink	Normal yellow		1	0.2	Dark yellow		78	13.6		
	Red		Normal yellow	3	0.5		Reddish yellow	2	0.3	
			Dark yellow	17	3.0		Reddish	2	0.3	
Reddish yellow			4	0.7	Chocolate		1	0.2		
Dark red	Normal yellow		1	0.2	Dark red		Normal yellow	3	0.5	
	Dark yellow		12	2.1		Dark yellow	27	4.7		
			Reddish yellow	1		0.2	Reddish yellow	5	0.9	
			Reddish	1	0.2	Reddish	1	0.2		

Considering only the colour of the cob and kernels, it can be observed that all the lines with orange or orange-yellow kernels have white cobs, while all the lines with pink cobs have exclusively yellow kernels (light, normal and dark). Most genotypes, 187, have dark yellow kernels and red cob, while 67 have the same kernel colour and dark red cob. In the case of inbred lines with white cobs, 51 genotypes with normal yellow kernels, 49 with light yellow and 49 with dark yellow kernels were identified.



**Figure 5.** Examples of kernel types, kernel colours and cob colours (1-flint, light yellow kernels, white cob; 2- dent x flint, reddish yellow kernels, white cob; 3-dent, normal yellow kernels, pink cob; 4-flint, dark yellow kernels, red cob; 5-dent, dark yellow kernels, red cob; 6- flint, dark yellow, dark red cob)

## Discussion

ARDS Turda has an impressive collection of maize inbred lines, with a high degree of variability for all analysed traits. The genetic diversity of these genotypes is of particular importance in the breeding process, having an essential role both in achieving the specific heterosis of maize hybrids, and for their use as sources of genes for different traits. Preserving this diversity is also important to avoid the loss of germplasm, precisely for this reason, a large part of the genotypes obtained in Turda were also sent to the Suceava Gene Bank to be preserved in the long term.

Among all the Agricultural Research Stations in the country, the one in Turda has in its collection the largest number of maize inbred lines, a similar number of genotypes being maintained at the NARDI Fundulea. At the national level, most genotypes are preserved in the Suceava Gene Bank (Murariu *et al.*, 2012). The ARDS Turda collection is especially important for early and semi-early maturity groups, the lines were created to be used in the creation of hybrids cultivated in Transylvania and Moldavia, areas favourable to early or semi-early maize (Has *et al.*, 2021; Varga *et al.*, 2022).

The variability of the traits found in the collection of inbred lines is influenced both by the large number of genotypes and by the change over time of the sources used as initial material and the objectives pursued. Local and synthetic populations have long been the preferred initial material for the creation of inbred lines (Rotar *et al.*, 2014; Has *et al.*, 2020), but over time the share of the use of hybrids and backcrosses increased.

The use of local populations as initial material for breeding can raise some difficulties, due to the transmission of unfavourable traits, along with those pursued. The use of commercial hybrids has been a valuable source of genes for many traits, such as reduced (but rich in pollen) tassel branches (Gage *et al.*, 2018), erect or semi-erect leaves, thin plants, resistance to lodging and plant-breaking. The introduction of commercial hybrids from America in the selection programs to create new inbred lines has had an effect on kernel type, by increasing the number of dent kernel genotypes. Corn Belt Dent is by far the predominant source of commercial germplasm used in America, especially Reid Yellow Dent and Lancaster Surecrop Varieties (Goodman, 2005; Prasanna, 2012).

The variability of germplasm collections can also be studied with the help of molecular markers, generally preferred are SSRs. Several studies were carried out on CIMMYT germplasm (Xia *et al.*, 2004; Xia *et al.*, 2005; Warburton *et al.*, 2008), but also on germplasm collection from different countries such as: Argentina (Braco *et al.*, 2009; Olmos *et al.*, 2017), China (Qi-Lun *et al.*, 2008), Portugal (Patto *et al.*, 2004), Switzerland (Eschholz *et al.*, 2006) and India (Prasanna *et al.*, 2010). Some of the inbred lines belonging to the ARDS Turda collection were analysed using SSR molecular markers and classified into several germplasm groups (Şuteu *et al.*, 2013), while others were studied for the presence of two alleles for carotenoid content, crtRB1 and lycE (Băcilă *et al.*, 2022). Other genetic studies related to some genotypes from the Turda collection had cytelines as their study object (Miclaus *et al.*, 2016; Ardelean *et al.*, 2023). These studies are of particular importance for the knowledge of the biological material and deserve to be continued, to be able to include the entire germplasm collection, both inbred lines, local populations, synthetic populations and landraces.

A diverse genetic base can be of crucial importance for identifying genes for improving yield, plant architecture, but also tolerance to biotic and abiotic stress factors, nutritional quality (Prasanna, 2012). In addition to old studies, in recent years, various programs have been initiated at ARDS Turda to try to identify some inbred lines that can be used as sources for yield improving (Varga *et al.*, 2017; Calugar *et al.*, 2018; Haş *et al.*, 2021; Varga *et al.*, 2022), adaptability to stress factors (Şoptorean *et al.*, 2018; Bălaş *et al.*, 2019; Vana *et al.*, 2022), biochemical content (Băcilă *et al.*, 2022; Calugar *et al.*, 2022).

## Conclusions

The collection of inbred lines belonging to ARDS Turda presents a high diversity for a great number of traits, the variability within it being particularly important for breeding processes, both for the creation of new hybrids, and for the existence of a broad genetic base that can be used as initial material in selection or as a source of genes for certain traits. Cultivating a relatively small number of genotypes in high areas can lead to the narrowing of the genetic base, which is precisely why it is very important to preserve as many genotypes as possible. The collection of inbred lines from ARDS Turda shows increased variability both for the vegetation period, the plant and ear traits, the highest coefficient of variability being calculated for the number of tassel branches, followed by ear weight. A large variability was also observed for the colours of anthers, silk, kernel and cob, but also for the kernel type.

## Authors' Contributions

Conceptualization: REC; Data curation: REC, CDV; Funding acquisition: NT; Investigation: REC, CDV, AV; Methodology: AV, ABG; Resources: AV, NT; Supervision: Visualization: LAC; Writing - original draft: REC; Writing - review and editing: AV, ABG.

All authors read and approved the final manuscript.

### **Ethical approval** (for researches involving animals or humans)

Not applicable.

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### **Conflict of Interests**

The authors declare that there are no conflicts of interest related to this article.

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