PHENOTYPIC EVALUATION *TRITICUM* SP. GENOTYPES VARIATION

Tiberiu Emilian SÂRBU [1], Violeta SIMIONIUC [1], Iulian GABUR [1*],
Dănuț-Petru SIMIONIUC [1], Danela MURARIU [2]

e-mail: iulian.gabur@iuls.ro

Abstract

The intensity of selection, improvement of different traits and the influence of climate change collectively amplify the frequency of detrimental alleles. This phenomenon causes genetic drift, resulting in an accidental decline in the diversity of plant germplasm sources. Genetic variability is of great importance for the adaptability and tolerance of a species to stress factors. Our investigation centres on Triticum germplasm within the agroclimatic conditions of the Ezareni Farm Iași, encompassing 2021–2022 field trials. Phenotypic characterization was performed for 15 genotypes, which belong to two species of *Triticum* (*T. aestivum* L. and *T. monococcum* L.). The data analysis involved the calculation of amplitude of variation, variance (s2), standard deviation (√s), and coefficients of variation (s%) for three pivotal agronomical traits: plant height, spikelets per spike, and total seeds per spike. The results showed a high coefficient of variation, indicating a significant variability within the analyzed germplasm. The genotypes that stood out with high results of the analyzed parameters can be used in future breeding programs.

Key words: *Triticum* germplasm, genetic variability, phenotypic characterization

INTRODUCTION

Wheat, *Triticum aestivum* L. is responsible for providing an important amount of carbohydrates, proteins and fibers for the diet of the ever growing population (Kumar *et al*, 2021).

Over the past five decades, bread wheat has been one of the most productive crops, and its production has increased due to advances in breeding programs (Rauf K. *et al*, 2020).

Bread wheat is a domesticated plant that originated through the crossing of wild ancestors about 10,000 years ago in the Fertile Crescent, a region in the Middle East, more precisely the territories where Israel, Iraq, Palestine, and Lebanon are located (He F. *et al*, 2019). *T. aestivum* L. (2n = 6x = 42; genome AABBDD), is an allohexaploid species that arose from the crossing of three diploid ancestors with genomes A, B and D. Most of the alleles of common wheat are found in its genome as triple homologous genes, originating from the donor species (Shitsukawa N. *et al*, 2007). Although this plant has 21 pairs of chromosomes, more precisely 3 homologous sets of 7 chromosomes for each of the 3 donor genomes (A, B and D), from a genetic point of view, it behaves like a diploid species (El-Esawi M.A. *et al*, 2022).

The limited genetic variability of wheat compared to other species is due to several reasons, such as the allohexaploid structure resulting from the crossing of three closely related species. Another reason refers to the low initial genetic variability of this species due to the fact that few plants from the ancestral species were involved in the formation of bread wheat. A third reason is the short time interval in which this species evolved (approx. 8000 - 10000 years), insufficient time for the accumulation of mutations or some alleles through interspecific hybridization (Venske E. *et al*, 2019).

The selection methods used in wheat breeding, obtaining semi-dwarf wheat during the Green Revolution, but also the use of highly performing cultivars in breeding programs can result in a decrease in wheat genotypic and phenotypic variability (Trethowan *et al*, 2018).

The identification and characterization of genes that control important traits in wheat is an important step in the breeding work of this species. These traits refer to plant height, spike density, grain weight and shape, resistance to diseases and pests, and tolerance to changing environmental conditions (Gabur I. *et al*, 2022).

Winter wheat genetic resources possess high variability for certain agronomic traits valuable for breeding programs aimed at increasing productivity and improving some agro-morphological traits. Still, the most used method in wheat breeding remains directed hybridization followed by selection works and in some cases backcrossing. The choice of the most valuable

---

[1] “Ion Ionescu de la Brad” Iasi University of Life Sciences, Iasi, Romania
[2] Vegetal Genetic Resources Bank "Mihai Cristea" Suceava, Romania

parents is paramount to the success of the breeding program, and phenotypic variability plays an important role in this activity (Mishra *et al*, 2015).

Germplasm conservation is an increasingly essential activity to overcome the danger of genetic erosion. Wild varieties, local populations and old varieties, have a valuable genetic background for improving some traits, such as mineral, protein, gluten content and of course resistance to biotic and abiotic stress (Yadav I.S. *et al*, 2023).

Genetic diversity is the key to success in wheat breeding programs and beyond. Selection results in high-yielding varieties adapted to diverse climatic conditions and resistant to diseases and pests. At the same time, these works can produce a decrease in phenotypic variability, which is largely determined by genes and their interaction with the environment (Voss-Fels K., Snowdon R., 2016).

In this study, the phenotypic diversity of 15 wheat cultivars was evaluated to identify the most diverse genotypes that can be used as parental forms in future breeding programs.

MATERIAL AND METHOD

The biological material used to determine the phenotypic variability of *Triticum* genotypes consists of the following:

- 10 cultivars of *T. aestivum* ssp. *aestivum*;
- 5 cultivars of *T. monococcum*.

The two species of *Triticum* mentioned above have the biological status of old varieties and local population, as follows:

- *Triticum aestivum*:
  - local population – 5;
  - old varieties – 5.
- *Triticum monococcum*:
  - local population – 5.

The 15 wheat genotypes are part of the strategic national collection of the Suceava Gene Bank, and their choice was made based on the difference between the two species and the biological status.

The local populations, the most valuable genetic resources within the Gene Bank, come from rural areas in Transylvania and Maramureș.

The varieties of *Triticum* sp. were received from agronomic institutes in Romania or other countries.

The 15 wheat cultivars are part of a larger study aimed at the phenotypic evaluation of 380 wheat genotypes. The samples were sown in small blocks in the experimental field of Ezăreni Farm (Figure 1). Each genotype was sown in one row with the length of 2 m and the distance between rows of 50 cm. From each of the 15 genotypes, 10 plants were analyzed to determine the morphological descriptors.

Table 1

International Plant Genetic Resources Institute (IPGRI) descriptors used for the phenotypic evaluation of wheat genotypes

Descriptor	Significance
Growth type (FAO notes)	1. winter; 2. optional; 3. spring.
Plant height (cm)	Measured at maturity of plant height (ground level to tip of the spike), for 10 plants per genotype
Spike density (FAO notes)	Visual scoring using a scale from 1 to 9, ranging from very lax (1) to intermediary (5) to very dense (9)
Awn (FAO notes)	0 – without awn; 1 – short awn; 7 – high awn.
Colour of the glumes (FAO notes)	1 – white; 2 – red to brown; 3 – purple to black.
Presence of hair on the glumes (FAO notes)	0 – absent; 3 – low; 7 – significantly.
Number of spikelets per spike	Average number of spikelets per spike in 5 spikes selected from a genotype
Number of seeds per spikelets	Average number of seeds in a spikelet - sampled from the central area of the spike. 5 spikes from each genotype
Seeds color (FAO notes)	0 – white; 2 – red; 3 – purple (it is tested with NaOH 5%) Seeds were placed in Petri dishes and covered with 5% NaOH solution. Performed with 60–90 seeds. Red seeds – dark brown–orange; white seeds - pale yellow

For the measured parameters such as plant height (cm), number of spikelets/spike and number of seeds/spikelet, average, variance (s^2), standard deviation (√s) and coefficient of variation (s%) were calculated.

RESULTS AND DISCUSSIONS

The wheat genotypes were sown on October 19, 2021 in the experimental field of the Ezăreni Student Research and Practice Station, Iasi (Figure 1). The 380 varieties were grouped into six blocks, each sample being sown in a 2 m long row using approximately 50 seeds, with a row spacing of 50 cm. Due to the drought recorded during the sowing period (5.6 mm of precipitation in October) and low temperatures during the winter, the samples entered vegetation in spring of 2022. The samples were collected from the experimental field between July 12 – 16, 2022, when all genotypes were in the phenophase of full maturity.

Figure 1 **Sowing activity in the Student Research and Practice Station Ezareni, Iasi**

Phenotypic evaluation of selected wheat samples was performed for plant height (cm) (Figure 2), number of spikelets/spike and number of seeds/spikelet by calculating the arithmetic mean (x), variance (s^2), standard deviation (√s) and coefficient of variation (s%).

The results obtained for the three morphological descriptors mentioned above, which refer to the plant and spike architecture, are presented in Table 2. The interpretation of the results is based on the determination of the coefficient of variation (s%), which expresses the variability of the selected germplasm, recording a high coefficient of variation for the three analyzed descriptors (over 20%).

Table 2

The values obtained from statistical calculations for the phenotypic parameters analyzed in *Triticum* cultivars

Coefficients	Plant height (cm)	Number of spikelets/ spike	Number of seeds/ spikelets
Average	78,91	13,01	3,08
Max. value	122	37	5
Cultivar name	***T. monococcum***		***T. aestivum***
Min. value	47	13	1
Cultivar name	***T. aestivum***		***T. monococcum***
Standard deviation	426,67	35,44	2,15
Variance	20,66	5,95	1,47
Coefficients of variance (%)	26,18	45,75	47,66

Regarding the phenotypic descriptors for which FAO scores were given, for the samples harvested in the summer of 2022, the following results were obtained:

- **Growth type** was the same for all cultivars (winter types);
- **Spike density** – the scores given showed that the selected samples have a medium variation, between 5 and 9. Thus 4 genotypes of *T. aestivum* L. had intermediary spike and 6 had dense spike. All 5 einkorn genotypes had very dense spike;
- **Awn –** following the determinations, it was found that 3 genotype 3 genotypes were awnless, 1 genotype presented short awns and 11 had obvious awns; All *T. monococcum* L. samples had obvious awns;
- **Glumes colour** – all 15 *Triticum* genotypes had white glumes;
- **The presence of hair on glumes** - all samples studied were hairless on glumes;

CONCLUSIONS

Wheat is an important plant that belongs to the *Triticum* genus. The hexaploid genetic structure of bread wheat is complex, originating from interspecific crosses that occurred approximately 10,000 years ago between the ancestors of this species.

The results obtained highlight a high genetic variability of the *Triticum* germplasm analyzed. All the morphological traits measured had a coefficient of variation of over 20%.

The highest coefficients of variation were recorded for the number of spikelets/spike (45.75%) and for the number of seeds/spikelet (47.66%).

The samples analyzed were uniform in terms of the type of growth, the awns, the color of glumes, the presence of hair/glumes and the color of the seeds.

Wheat germplasm preserved in gene banks represents a valuable resource of genetic material for researchers and breeders. The conserved genotypes can be used as initial material to obtain new wheat varieties with improved production, quality and stress resistance characteristics.

Due to the high coefficient of variation, analysed genotypes can be introduced into a winter wheat breeding program.

ACKNOWLEDGMENTS

This work was supported by a grant of the Ministry of Research, Innovation and Digitization, CNCS-UEFISCDI, project number PN-IV-P1-PCE2023-0705, within PNCDI IV”.

REFERENCES

El-Esawi M. A., Elashtokhy M. M., Shamseldin S. A., El-Ballat E. M., Zayed E. M., Heikal Y. M. 2022 *– Analysis of genetic diversity and phylogenetic relationships of wheat (Triticum aestivum L.) genotypes using phenological, molecular and DNA barcoding markers.* Genes, 14, 1:34.

Gabur I., Sârbu T. E., Dumitriu Gabur G. D., Murariu D., Simioniuc V., Simioniuc D. P. 2022 - *Phenotypic analysis of a wheat diversity panel from the vegetal genetic resources bank" Mihai Cristea" Suceava*. Lucrări Ştiinţifice seria Agronomie, 65, 2:59-62.

He F, Pasam R, Shi F, et al. 2019 – *Exome sequencing highlights the role of wild-relative introgression in shaping the adaptive landscape of the wheat genome*. Nat Genet. 51, 5:896-904.

Mishra C. N., Tiwari V., Satish-Kumar V. G., Kumar A., Sharma I. 2015 – *Genetic diversity and genotype by trait analysis for agro-morphological and physiological traits of wheat* (*Triticum aestivum* L.). Sabrao J. Breed. Genet, *47*, 1:40-48.

Rauf K., Rahman R., Saeed A., Ali M., Noureen F., Amir R., Gul A., 2020 – *Next-generation sequencing in bread wheat*. Climate Change and Food Security with Emphasis on Wheat, 311-320.