

PHENOTYPIC ANALYSIS OF A WHEAT DIVERSITY PANEL FROM THE VEGETAL GENETIC RESOURCES BANK "MIHAI CRISTEA" SUCEAVA

Iulian GABUR¹, Tiberiu Emilian SÂRBU¹, Georgiana Diana GABUR¹, Danela MURARIU², Violeta SIMIONIUC¹, Dănuț Petru SIMIONIUC^{1*}

e-mail: simion@uaiasi.ro

Abstract

Wheat (*Triticum aestivum* L.) is among the first three agro-economic important crop plants, with a high carbohydrate and protein content in grains. In this study, 80 cultivars, from the VGRB germplasm collection, were phenotyped in field experiments. Morphological traits were observed on the harvest spike prior to threshing. Awn roughness will be assessed visually and by sliding one's finger along the central part of the awn in the direction from top to bottom. Flowering dates will be retrieved from digitized records of VGRB propagation cycles. Accessions were evaluated in 2020/2021 field trials under a randomized block experimental design. Among the measured phenotypic records there are traits as germination rate, flowering time, disease resistance and yield. Results indicate that VGRB germplasm contains a wide variety of genotypes that have a high agronomical value. This germplasm could be used in future breeding programs.

Key words: *Triticum aestivum*, phenotypic analysis, randomized block design, plant breeding

Wheat (*Triticum aestivum*) is a cereal grain that is one of the most widely cultivated and consumed crops in the world. It is a grass species belonging to the genus *Triticum*, which includes several subspecies, such as spelt (*Triticum spelta*), emmer (*Triticum dicoccum*), and einkorn (*Triticum monococcum*). Modern wheat (*Triticum aestivum*) is a domesticated grain that was developed from ancestral wild grasses through a process known as domestication (He F. *et al.*, 2019). The exact origins of modern wheat are not well understood, but it is believed, that around 10,000 years ago, wheat have been domesticated from various wild grasses in the Fertile Crescent, a region in the Middle East that includes modern-day Israel, Palestine, Lebanon, and parts of Jordan, Iraq, and Syria (He F. *et al.*, 2019).

Nowadays, wheat is an important food crop that contains carbohydrates, proteins and other nutrients, representing a major crop for many people around the world.

One of the key areas of study in wheat genetics is the identification and characterization of the genes that control important traits in wheat plants. These traits can include things like grain size, grain shape, plant height, resistance to diseases and pests, and the ability to grow in

different climates and soil conditions (Venske 2019).

A major area of research in wheat breeding is the study of genetic diversity within the species. Wheat is a cross-pollinating plant, which means that it can produce offspring with a wide range of genetic combinations. This diversity is important for the long-term health and resilience of the species, as it allows the plant to adapt to changing environmental conditions and resist diseases and pests (Voss-Fels K., Snowdon R.J., 2016). Overall, the study of wheat genetics is a critical field that helps researchers understand the genetic basis of important traits in wheat and develop new strains of the crop that can better meet the needs of farmers and consumers around the world (Voss-Fels K. *et al.*, 2019).

Gene banks are important institutions that play a crucial role in the conservation of plant genetic resources, including those of wheat. Gene banks are collections of living plant material, such as seeds or other reproductive parts, that are stored under specific conditions to ensure their long-term viability. The goal of gene banks is to preserve the genetic diversity of plant species, which is essential for the sustainable production of food and other crops. Wheat gene banks play a vital role in the conservation of the genetic diversity of this

¹ Iasi University of Life Sciences, Romania

² Vegetal Genetic Resources Bank "Mihai Cristea", Suceava, Romania

important crop. Within a gene bank we can find a large variety of wild and domesticated cultivars, that cover the genetic diversity available within the species and help future research and breeding efforts. Wheat gene banks also provide a source of material for researchers studying the genetic basis of important traits in wheat, such as resistance to diseases and pests, and the ability to grow in different climates and soil conditions.

In addition to preserving the genetic diversity of wheat, gene banks also play a key role in the conservation of other plant species that are important to food production, such as rice, maize, and potato. By storing the genetic material of these crops, gene banks help to ensure that they are available for future generations, and that their genetic diversity is maintained (Rajaram S. *et al*, 1996).

Overall, gene banks are a vital part of the global effort to conserve plant genetic resources and ensure the sustainable production of food crops. They are an important resource for researchers, breeders, and policymakers working to address the challenges of food security and environmental sustainability.

Investigation of wheat cultivars, from the Vegetal Genetic Resources Bank "Mihai Cristea" Suceava, Romania (VGRB) germplasm collection, were phenotypes in field experiments. Morphological traits were observed on the harvest spike prior to threshing. Awn roughness will be assessed visually and by sliding one's finger along the central part of the awn in the direction from top to bottom. Flowering dates will be retrieved from digitized records of VGRB propagation cycles. Accessions were evaluated in 2020/2021 field trials under a randomized block experimental design. Among the measured phenotypic records there are traits as germination rate, flowering time, disease resistance and yield. Results indicate that VGRB germplasm contains a wide variety of genotypes that have a high agronomical value. This germplasm could be used in future breeding programs as a source of gene diversity.

MATERIAL AND METHOD

The research material consisted of 150 wheat genotypes, pre-breeding material, breeding varieties and local populations, from a total of 1905 genotypes available in the Vegetal Genetic Resources Bank "Mihai Cristea" Suceava. The researched seed material was divided into bags with 50 seeds for each wheat genotype, labeled with the genus, species, variety and germination percentage.

From each genotype, around approx. 30 seeds (depending on the germination percentage

provided by the VGRB) were sown in the experimental field at the Ezăreni Teaching Farm, Iasi, Romania.

Taxonomic classification of wheat germplasm characterized in the experimental field:

- *Triticum aestivum* ssp. *aestivum* - 127 samples;
- *Triticum aestivum* ssp. *spelta* - 3 samples;
- *Triticum turgidum* - 3 samples.
- *Triticum monoccocum* - 17 samples

At the time of harvesting from samples with a degree of sprouting of more than 70%, 10 plants were taken each for biometrization of plant, ear and seed. The descriptors used for the morpho-physiological characterization of wheat genotypes are given in the table below (Table 1).

Table 1
Phenotypic descriptors used for wheat germplasm analysis

Trait investigated	Phenotypic descriptor analyzed
Type of growth	1. Winter; 2. Optional (intermediate); 3. Spring
Plant height (cm)	Measure the height of the plant, at maturity, from ground level to the tip of the ear, excluding the aristae, per 10 plants per sample. 1. Very lax; 3. Lax; 5. Intermediate; 7. Dense; 9. Very dense (visual observations scale 1 to 9)
Density of ear	0 - no aristae; 1. Short ridges; 7. Obvious ridges
Ridges	1. White; 2. Red to brown; 3. Purple to black
Color of the grooves	0. Absent; 3. Weak; 7. High
Presence of bristles on the glumes	Average number of spikelets per spike per 5 spikes selected from a genotype
Number of spikelet per spike	Average number of seeds per spikelet - obtained from the central area of the spike using 5 ears from each sample
Number of seeds per spikelet	

For the descriptors for which biometrics were performed (plant height, number of spikelet/spike and number of seeds/spike) the arithmetic mean (\bar{x}), range of variation, variance (s^2), standard deviation (\sqrt{s}) and coefficients of variation ($s\%$) were calculated.

RESULTS AND DISCUSSIONS

In autumn 2021, 150 wheat cultivars were sown in the experimental field at the Ezăreni Teaching Farm, Iasi. Field preparation, staking and sowing took place during the week 11-15 October

2021 (Figure 1). Wheat samples were sown in six randomized blocks in a row of 2 m length using approximately 50 seeds for each sample taken in the study. After sowing, the plots were protected with bird netting. Of the 150 genotypes, all samples germinated and entered vegetation in spring 2022. In March 2022, 250 kg/ha ammonium

nitrate was applied and in May hand hoeing was carried out both between rows and between blocks. Harvesting started on 12 July and ended on 16 July 2022. Moisture tests were carried out at the time of harvest, resulting in a sample moisture content of 12-18%.



Figure 1 Soil preparation and sowing at Ezăreni Teaching Farm, Iasi, Romania, Iasi in October 2021

Phenotypic and biometric analysis of selected germplasm was performed for plant height, number of spikelet/spike and number of seeds/spikelets, as the arithmetic mean (\bar{x}), range of variation, variance (s^2), standard deviation (\sqrt{s}) and coefficients of variation ($s\%$) were calculated. The three morphological descriptors for plant,

spicule and seed architecture are presented in Table 2. The interpretation of the results is based on the determination of the coefficient of variation, as an expression of the diversity of the biological material studied, showing a high coefficient of variation, above 20%, for the three descriptors analysed.

Statistical calculations from the phenotypic descriptors carried out on the samples of autumn wheat samples taken in the study, 2021/2022 season

Table 2

Phenotypic descriptor	Mean	Val. max	Val. min	Standard deviation	Variance	Coef. of Variance (%)
Plant height (cm)	69.9	118.7	47.2	15.54	241.504	22.23
Number of spikelet/spike	17.33	36.8	11.2	3.778	14.275	21.80
Number of seeds/spikelets	2.92	5	1	0.685	0.4696	23.45

As for the other descriptors for which FAO scores were given, the results showed the following, using data from the 2021/2022 season:

- Growth type - all wheat samples were autumn.
- Ear density - according to the scores it was observed that the samples showed a high range of variation, between 3 and 9. Thus: one sample had

very lax ear, 7 lax, 76 intermediate ear, 54 dense ear and 17 very dense ear.

- Anthes - from the recorded data it was found that 13 samples were no visible anthes, 49 with short aristae and 88 with obvious aristae.

- Glume colour - in all samples analysed, glumes were white.

- Presence of bristles on glumes - 100 samples had no bristles on glumes, 48 samples had few bristles and 2 samples had many bristles on glumes.

- Seed colour - all samples had white caryopses.

CONCLUSIONS

Wheat is a cereal grain that belongs to the genus *Triticum*, which includes several subspecies, such as spelt, emmer, and einkorn. From a genetic perspective, these subspecies are thought to be the ancestral forms of modern wheat.

Generally, germplasm stored in Gene Banks represents the genetic diversity present in a given crop, as wheat for example. Wheat germplasm is collected, maintained, and distributed by Gene Banks as plant genetic materials for research and breeding purposes.

The importance of wheat germplasm from gene banks is that it provides a valuable resource for plant breeders and researchers to develop new varieties of wheat with improved characteristics. These characteristics may include increased resistance to pests and diseases, improved yield and quality, and better adaptability to different growing conditions.

Gene banks also play an important role in conserving the genetic diversity of wheat. Old genotypes are an important source to maintain a genetic diversity in the depleted wheat genetic pool in order to ensure the long-term sustainability wheat breeding. Gene banks help to preserve the

genetic diversity of wheat by storing a wide range of wheat germplasm from different regions and climates.

In summary, the importance of wheat germplasm from gene banks lies in its potential to be used for plant breeding and research, as well as its role in conserving the genetic diversity of wheat.

ACKNOWLEDGMENTS

This study was supported by a grant from the Romanian Ministry of Education and Research, CNCS—UEFISCDI, project number PN-III-P2-2.1-PED-2019-0175, within PNCDI III.

REFERENCES

- 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.
- Rajaram S et al. 1996** - *CIMMYT's approach to breed for drought tolerance*. Euphytica 92:147-153.
- Venske E., Schreinert dos Santos R., Busanello C., Gustafson P., Costa de Oliveira A., 2019** - *Bread wheat: a role model for plant domestication and breeding*. Hereditas, Volume 156, No. 16 (1-11).
- Voss-Fels, K.P., Stahl, A., Wittkop, B. et al 2019** - *Breeding improves wheat productivity under contrasting agrochemical input levels*. Nat. Plants 5, 706–714. <https://doi.org/10.1038/s41477-019-0445-5>
- Voss-Fels K, Snowdon RJ 2016** - *Understanding and utilizing crop genome diversity via high-resolution genotyping* Plant biotechnology journal 14:1086-1094.