

## ASSESSING OF THE GENETIC DIVERSITY OF VARIOUS WHEAT VARIETIES CULTIVATED IN ROMANIA

Maria Camelia GOLEA<sup>1,2\*</sup>, ORCID: 0000-0001-8853-3810

Paula-Maria GALAN<sup>2,3</sup>

Livia-Ioana LEȚI<sup>2,3</sup>

Georgiana Gabriela CODINĂ<sup>1</sup>, ORCID: 0000-0002-6575-0078

<sup>1</sup>Faculty of Food Engineering, Ștefan cel Mare University, Suceava, Romania

<sup>2</sup>Vegetal Genetic Resources Bank "Mihai Cristea, Suceava, Romania

<sup>3</sup>Faculty of Biology, Alexandru Ioan Cuza University, Iasi, Romania

\*Corresponding author: Maria Camelia Golea, [mcgolea78@gmail.com](mailto:mcgolea78@gmail.com)

The genetic diversity of 31 wheat varieties cultivated in Romania was investigated by means of inter simple sequence repeat DNA (ISSR) markers. This molecular biology technique targets microsatellite-directed DNA fingerprinting by polymerase chain reaction (PCR) amplification of the interrepeat region.

The genetic material consisted of different wheat samples of various species such as *Triticum aestivum* L., *Triticum monococcum* L., *Triticum spelta* L. of different biological status: modern variety, local race and breeding line. The wheat varieties were of different origins such as Romania, France, Austria, Germany and Russia.

Eleven ISSR markers were used to analyze and compare genetic diversity among selected wheat varieties. The results from agarose gel electrophoresis showed that only 6 from the total of 11 ISSR primers presented significant patterns of the amplified fragments, with clear and well-defined bands. The number of DNA bands per primer varied between 3 (for UBC 859 and UBC 880) to 8 (for UBC 808), with a mean of 4.83 bands/primer. Most of the primers had a number of polymorphic fragments equal to the number of amplified fragment, excepting UBC 808 which had 7 polymorphic fragments from a total of 8. The migration pattern for each genotype was converted in a binary system where 0 means absence of a certain DNA fragment and 1 means the presence of it.

The obtained data was analyzed in NTSYSpc software using UPGMA method and Jaccard and Dice similarity coefficients were analyzed. The genotypes were divided in 5 clusters (C1-C5). C1 was the most extended cluster and contains 16 genotypes from different countries. C2 contains 6 genotypes, all from Romania, similar to C3 which also includes 6 genotypes from different countries. In C4 was only one genotype from France and in C5 was one genotype from Romania.

**Keywords:** Genetic similarity coefficients, ISSR markers, *Triticum*

**Acknowledgments.** This work was performed within the framework of the “DECIDE - Development through entrepreneurial education and innovative doctoral and postdoctoral research, project code POCU/380/6/13/125031, supported by project co-financed from the European Social Fund through the 2014– 2020 Operational Program Human Capital”.