

Molecular methods for identification of *Avena* species in collection of National Centre for Plant Genetic Resources, Radzików, Poland

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In collection of *Avena* in National Centre for Plant Genetic Resources in Radzików are more than 2000 accessions. The correct identification of species is essential to the performance of ecological and evolutionary research. Morphological classifications of accessions to specific species are often very difficult because very minor differences between taxa. DNA barcoding is helping to conduct this identification. It is a taxonomic method that uses a short genetic marker in an organism's DNA to identify if it is belonging to a particular species. A desirable locus for DNA barcoding should be standardized, present in most of the taxa of interest and short enough to be easily sequenced. Since last decade as a barcode for plants are used chloroplast genes taken together and adding the nuclear internal transcribed spacer ITS region. This combination proved to provide better resolution between species.

In this study we present results of testing for taxonomic purpose of 5 diagnostic regions: *mat K*, *trnH-psbA*, *trnL-trnF*, *atpF-atpH*, *psbK-psbI*. In addition results of testing of genetic diversity among accessions of *A. strigosa* preserved in National Centre for Plant Genetic Resources in Radzików using SRAP (Sequence-related amplified polymorphism) markers are presented.

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