

**Appendix No. 7 to the application for commencement of the procedure for
the conferment of the post-doctoral degree of doctor habilitated to Dr.
Agata Tyczewska**

SUMMARY IN ENGLISH

Abstract

The aim of the research presented in this postdoctoral dissertation was to characterize the molecular basis of plant responses to environmental stress in a temperate climate as exemplified by maize and herbicidal stress, and soybean and cold stress. The well-defined molecular mechanisms activated in plants in response to biotic and abiotic stresses, despite the intense work of scientists around the world, have not yet been fully understood. A stress factor may activate mechanisms which will result in adaptation to the existing conditions and maintaining the normal functioning of the cell and organism. Such adaptive mechanisms can be passed on to daughter organisms and lead to the development of genotypes resistant to a given stress factor.

Maize (*Zea mays*) as a plant grown in a wide row spacing is particularly vulnerable to weed infestation, therefore herbicide spraying is often used in the early stages of seedling growth to reduce competition for light, water and minerals. Herbicidal stress has not been studied extensively so far, despite the fact that maize has shown different phenotypic responses to herbicides used. The details of the structure of the genomes of two maize lines differing in their sensitivity to herbicides, as well as changes in the levels of gene expression, miRNA, and DNA methylation were deciphered using bioinformatics and molecular methods. Based on the obtained results, it was shown that the changes occurring in the studied maize cultivars are multi-level and multi-factorial, as they were identified at each stage of the gene expression regulation, i.e. in genomes, transcriptomes, miRNA pools, and the degradome. As a result of the conducted analyzes, thousands of structural variants were identified, also in protein coding regions, in two maize varieties differing in susceptibility to RoundUp®. The genes and pathways involved in glyphosate metabolism were investigated and a number of changes that could affect gene expression levels were identified. It was also shown that herbicidal stress increased the amount of fully methylated sequences in the genome of the sensitive line by 18.64%. Among the differently methylated sequences were genes encoding transferases, transporter proteins, methyltransferases, hydrolases, transposons, ribosomal proteins, cytochromes and proteins involved in transcription processes and involved in the stress response in maize's response to herbicidal stress.

Soybean is a short-day plant with high thermal requirements, and none of the varieties introduced so far is completely resistant to low temperatures and frosts. In a temperate climate, it is chill that is one of the most important factors negatively affecting the growth and yield of soybeans. The aim of the research was to understand the differences resulting from the effects of cold stress in a pool of small non-coding RNA molecules and the degradome of three soybean varieties (Fiskeby V, Augusta and Toyomusume) and a wild soybean ancestor - *Glycine soja*. Changes in the expression levels of the short regulatory RNA pools and the degradome were studied in 3 tissues of stressed plants at different growth stages. A total of 321 known miRNAs were identified and 348 new miRNAs were predicted. As many as 162 miRNAs, including conserved legume and soybean-specific miRNAs, and 18 new miRNAs, had altered expression profiles under the influence of cold stress. Importantly, several miRNAs, such as miR156, miR169, and miR5770, had similar expression patterns in Augusta, Fiskeby V, and *G. soja*, which was in stark contrast to the cold-sensitive Toyomusume variety. Degradome, GO and KEGG analyzes have assigned potential target genes to miRNA molecules with varying expression levels. Many of these genes have been found to be associated with plant responses to abiotic stress, such as the neutralization of reactive oxygen species, flavonoid biosynthesis, and regulation of the osmotic potential. Phenotypic analyzes of two "resistant" to cold soybean cultivars under controlled stress conditions (phytotron) and under field conditions were also performed. Importantly, Augusta and Fiskeby V plants stressed during the seedling and vegetative growth stage showed an increase of the indexes by ~ 10% compared to the control plants. The reduced seed yield was observed only in the Fiskeby V variety stressed in the R1 phase (reduction by 7.4%) and in the Augusta plants stressed in the VE phase. It was shown that under field conditions the Augusta cultivar is characterized by a higher yield (g of seeds) regardless of the stress occurring, so this cultivar turned out to be better adapted to the Polish cultivation conditions.