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## **Genome-wide identification and characterization of genes determining cellular polyamine homeostasis in senescing barley leaves**

### **Abstract**

Developmental senescence is an irreversible process that is inevitably followed by cell death. Dark-induced leaf senescence (DILS) is a reversible process to a certain stage. In plants, induced senescence is a highly controlled and active process requiring global metabolic reprogramming aimed at the organized disintegration and remobilization of valuable resources. The efficiency of the regulation of the induced senescence process is a sign of the viability of senescent cells, which at each stage must maintain the ability to maintain homeostasis, manifested, among others, by controlling polyamine (PA) cycle homeostasis. PA homeostasis in the cell is maintained by feedback mechanisms from the levels of biosynthesis, catabolism, import and export. **Polyamines are low molecular weight organic cations belonging to the group of biogenic amines, crucial in many physiological and developmental processes in bacteria, animals and plants. PA metabolism may play an important role in the leaf senescence process.**

Professor Ewa Sobieszczuk-Nowicka's team set themselves the goal to understand the multidirectional connections of polyamine metabolism with the metabolic network organizing the senescence process of barley leaves and to assess whether a change in the direction of senescence-dependent PA metabolism will affect this process. The direction of PA metabolism and transport may control the efficiency of senescence-dependent nitrogen remobilization. An approach based on functional genomics was chosen to achieve the goal.

The lack of information in the literature on the sequence of PA metabolism genes in barley was a major limitation of this approach. **Hence, there was a need to identify PA metabolism genes in barley, which became the goal of my doctoral thesis. I also included the analysis of PA transporters in my research.** PA transporters are little known in plants. PA importers have been described in Arabidopsis, rice and orange. PA exporters have been suggested as potential PA exporters in Arabidopsis and rice.

**As a result of research on the entire barley genome, I identified gene families determining PA homeostasis in the cell, which included 23 PA metabolism genes and 13 transporter genes. I also carried out a detailed characterization of the identified genes and their protein products.** Homology modeling of the studied transporters allowed to predict the three-dimensional structures of proteins with high accuracy, and molecular docking analyzes confirmed the possibility of interactions between transport proteins and PA. **I experimentally confirmed the presence of the genes identified in silico in the genome and examined their organospecific expression.**

**Then, in a dark-induced barley leaf senescence model, expression profiles of PA homeostasis genes. Based on this analysis, I selected candidate genes for functional research.**

**This doctoral dissertation presents the results of the first identification, isolation and comprehensive characterization of barley genes determining cellular PA homeostasis, as well as the assessment of their organospecific and senescence-dependent expression in leaf metabolism.** The results of my research constitute a reference point for functional studies of many teams of scientists explaining the mechanisms of molecular control and regulation by PA of crop development processes and their response to (a)biotic environmental factors. Especially functional studies on the mechanism of action of PA in leaf senescence.

Keywords: genomics, barley, polyamine metabolism, leaf senescence, polyamine transporters