

**POLYAMINES - A NEW METABOLIC SWITCH FOR BARLEY LEAF SENESENCE:
DEVELOPING MOLECULAR BASIS OF THE PROCESS NETWORK TO STRATEGIZE FOR
IMPROVING CROP PRODUCTION**

One of the regulators of the senescence process are low-molecular, organic cations belonging to the group of amines - polyamines (PAs). The research carried out by the author of this project allowed to develop a model of PA action on DILS (Dark-Induced Leaf Senescence) program, indicating that the direction of PA metabolism plays a central role in metabolic reprogramming, that introduces or not senescing leaf into the programmed organ death. In this regard, *Arabidopsis* PAO4(bc) mutants, in which PAs catabolism is blocked, by switching off polyamine oxidase activity, have delayed entry into dark-induced senescence.

The conclusion from the research contributed to state the current research hypothesis: **the direction of PA metabolism controls the rate of the senescence process.**

The aim of the project is to learn about the polyamine metabolism crosstalk (multidirectional links) with the metabolic network that organizes the senescence process and to assess whether changes in the direction of the senescence-dependent PA metabolism will affect the initiation of senescence-dependent cell death – senescing leaf will stop to undergo intensive re-mobilization and will enter the death phase.

We will further explore the aim by: **(i)** Using transgenic approach to over-express and silence some of the rate-limiting PA biosynthetic and catabolic genes. **(ii)** Testing specific barley PA transgenics for their adaptability to leaf senescence phenomenon using phenotyping and selecting appropriate phenotype markers of the senescence phases. **(iii)** Profiling of transcriptome of wild type plants vs transformants to establish dependence in metabolic networks between PA metabolism and other pathways involved in senescence and to select molecular markers of the process.

The transformants, which will be characterized by a clear anti- and pro-senescence phenotype, will be crucial for the implementation of the project. Modulating senescence behavior in a versatile species such as barley benefits commercial production in at least two ways: (1) Delaying senescence onset and extending the photosynthetic period in malting grains can increase grain starch content. (2) Accelerating the onset of senescence increases nitrogen content in grains used for animal feed.

Our proposal is to generate new knowledge about the polyamine metabolism as new metabolic switch for barley leaf senescence that controls the rate of the senescence process, so developing a molecular basis to produce resilient crops for the future by developing environmentally friendly BIO-technologies for efficient crop production.

The results of the project will verify the hypothesis, which claims the functioning of a polyamine metabolism direction as metabolic switch in plant senescence biology that controls the rate of the senescence process. This will be an element of novelty in understanding the mechanisms of cell regulation both in relation to plants, that could contribute valuable new information that is useful for breeding practices, and other organisms with distant systematic positions. Regulatory mechanisms of senescence and cell death in plants and animals (including humans) with radically different anatomy and physiology highlight involvement of PAs as universal bioregulators of these processes across kingdoms (Cai et al. 2015). Thus, delineation of the roles of PAs should lead to a better understanding of plant senescence and senescence-related cell death mechanisms, and will also provide new knowledge toward furthering knowledge about senescence and PCD in mammalian systems at cellular and molecular level. In animal systems (cell tumor lines) attempts are made to block cell viability by adding PA inhibitors to the system. This may introduce cancer cells to the path of autophagic death (Madeo et al. 2010). This outcome could also contribute in developing new ways to intervene towards human health wellness. Verification of the hypothesis, on the example of the senescence process, may also let describe a previously unknown metabolic switch - regulatory link of many metabolic and signaling pathways in a cell that may be universal across kingdoms.