Molecular identification of signaling pathways activated by receptor kinase CRK5 during senescence and stress response in *Arabidopsis thaliana*.

The global population growth increases the pressure on new sources of food. On the other hand, the worldwide yield loss due to adverse environmental conditions, such as high/low temperature, drought, flooding, ultraviolet radiation, salt or pathogen attack, is enormous. Therefore, research related to the increase of productivity and stress tolerance in cultivated crops have become one of the major objectives in today's biotechnology.

The analyses of plant genomes revealed the presence of many genes encoding cysteine-rich receptor-like kinases (CRKs). They are anchored in the plasma membrane and contain both kinase and receptor domains. It has been suggested that CRKs might be involved in the perception of signals induced by elevated level of reactive oxygen species (ROS), which is observed e.g. during senescence and stress response. One member of this group, CRK5, appears as an essential component responsible for the maintainance of cellular homeostasis. Physiological characterization of plants with disrupted *CRK5* expression showed their significantly lower biomass production, elevated foliar ROS levels, accelerated aging and increased cell death after exposure to UV radiation. In turn, increased *CRK5* expression correlated with enhanced resistance to pathogens.

Undoubtedly, CRK5 is a promising candidate for detailed studies to improve plant productivity and obtain varieties resistant to adverse environmental conditions. However, research carried out so far was mainly based on the physiological characterization of plants with altered *CRK5* expression at different stages of development. It enabled to assess CRK5-related physiological processes, but its molecular function remains unclear. Nothing is known neither about factors, which activate CRK5, nor about its downstream signaling pathways.

We suggest the following research hypothesis: CRK5 is one of the major sensors of cellular ROS balance, acting as a positive regulator of plant growth and negative regulator of cell death during senescence and stress response.

In order to unravel the molecular mechanisms underlying the molecular function of CRK5, we plan to identify factors regulating CRK5 activity and analyze its downstream signaling pathways, especially participation in ROS-driven hormonal signaling as well as the impact of CRK5 on target genes expression during senescence and stress response. To realize these scientific tasks will use a number of advanced molecular techniques.

Results of this research proposal should lead to the generation of novel knowledge about the molecular function of CRK5 and its signaling networks. This is a necessary and crucial step in terms of practical application in economically important crops in the future, thus reducing reliance on chemical treatments and artificial growth regulators.