DESCRIPTION FOR THE GENERAL PUBLIC (IN ENGLISH)

One of the great challenges for food security in the 21st century is to improve quantity and quality of crops through the development of disease-resistant cultivars. Increasing human populations, climate change, and limited water supply require the greatest reduction of the production losses, caused by pathogen infections. The five major staples produced worldwide, rice, wheat, maize, banana and potato are constantly threatened by devastating microorganisms or insects. A serious problem plaguing food security is potato virus Y (PVY). This virus is one of the most harmful pathogens infecting potato (*Solanum tuberosum* ssp. tuberosum), as well as other plants of the *Solanaceae* family, such as pepper, eggplant and tobacco. The most effective strategy mounted by plants against PVY is referred to as extreme resistance (ER). This phenomenon occurs within the cells adjacent to the infection site and manifests itself in the complete inhibition of the PVY multiplication. Although, ER-type PVY immunity is the most desirable trait used in a breeding practice, its nature remains poorly understood both at molecular and cellular levels.

We have recently cloned potato Ry_{sto} gene conferring the ER phenotype and we have identified its cognate viral component. Thereby we have at our disposal a unique system to characterise the early stages of ER activation at the molecular and cellular level.
Our initial observations indicate, that Ry_{sto} may activate two distinct types of resistance signalling pathways. In contrary to the majority of the resistance genes Ry_{sto} mode of action seems to be salicylic acid independent, which suggests that a different mechanism of ER control operates than described for other pathosystems mounting ER.

The project aims to understand early stages of ER activation. In the proposed project we will test which physiological and molecular markers are associated with the ER activation. Next, using CRISP-Cas9 genome editing technique, we will switch off the function of some known signal components to check which of the are critical for Ry_{sto} function. These results will be supported by profiling of global transcriptome undergoing in the resistant plants after PVY infection. Finally, we will verify our hypothesis that some amino acid residues in the Ry_{sto} structure contribute to temperature insensitive phenotype of the ER.

We have reason to believe that the results obtained will not only contribute to understanding of the molecular basis of potato resistance to PVY infections, but will also facilitate a development of novel breeding programs of edible potato as well as of other plants of the *Solanaceae* family.