

Soft rot in crops is characterized by symptoms such as wilting and yellowing of leaves, and wet stem rot; the disease causes huge economic losses during harvesting and food storage. Soft rot in cabbage, potato, lettuce, or banana is caused by microscopic bacilli that belong to the species *Pectobacterium carotovorum*. Although these microorganisms were included in the list of the top ten bacterial pests of plants, basic knowledge on the plant response to *Pectobacterium* infection is still unclear. Therefore, in this project, we decided to investigate the genetic aspects underlying the response of the model plant thale cress (*Arabidopsis thaliana*) to *Pectobacterium* infection.

Being sessile organisms, plants maintain their adaptation mechanisms through DNA, which makes plant genetics a fascinating field of biological studies. *Arabidopsis* is known for its wide range of habitats in the world, so the plant perfectly adapts to various environmental conditions, including protection against pathogenic stimuli, in particular bacteria, fungi, and viruses. A short life cycle for a plant (about 6 weeks), low breeding requirements, a known genomic sequence and the presence of numerous databases and work tools make *Arabidopsis* an ideal model for studying the plant's response to pathogen infection. At the same time, we can observe the diversity of these responses of plants from different endemic groups (ecotypes). It is this feature of the genetic variability of *Arabidopsis* within one species that we want to use to detect the key factors determining the resistance or sensitivity of plants.

Communication between the plant cell with a pathogen consists of recognizing the pathogenic molecule, activating the emergency state in the cell and involvement of the protective mechanisms. We performed the initial experiment: we infected *Arabidopsis* ecotypes with *Pectobacterium* and then observed how they responded to the infection. We saw that some ecotypes showed no disease symptoms, while the others developed soft rot at the infection sites. For the purposes of this project, we have prepared genomic sequences of selected ecotypes, both resistant and sensitive ones. We plan to compare the sequences of genes encoding proteins involved in pathogen recognition and identify the alleles that contributed to these diverse responses. Next, we intend to sequence the RNA of the studied plants to assess the contribution of each variant to the formation of phenotypic traits. We expect that in the effect of this project we will uncover the genetic mechanisms by which the plants tackle the disease, and consequently these discoveries will contribute to the development of new strategies for increasing the resistance of crop plants and consequently, food safety.