

There is a constant battle between plants and microorganisms that can invade them and exploit their internal mechanisms in order to hijack their metabolism and consume their nutrients. Since plants cannot move the only way to avoid such scenario was to evolve certain mechanisms preventing the infection or limiting further disease development by restricting the availability of nutrients that can be acquired by the pathogen. Unfortunately pathogens also develop certain ways to bypass plant defence mechanisms, therefore similarly to animals plants suffer numerous diseases. Since this fact has tremendous impact on plant production scientists work intensely to understand plant-pathogen interactions. Such work has direct application for future tolerant and resistant varieties breeding.

Our project aims at understanding of the long distance coordination in plants infected by the biotrophic protist *Plasmodiophora brassicae*. This pathogen infects mainly plants belonging to *brassicaceae* family, including such economically important crop as oilseed rape (OSR). Due to the pathogen driven reprogramming infected plants show very serious disease symptoms like wilting, development of galls on the underground part (hence disease name clubroot). Eventually roots of infected plants disintegrate and resting spores of the pathogen are released to the soil. Deposited this way pathogen particles stay viable in a soil for longer than 20 years and they can infect plants if proper conditions occur. So far we know, that the interaction between *P. brassicae* and infected plant is very complex. As a typical biotrophic organism the pathogen can acquire nutrients and multiply only in living cells, therefore it triggers changes that allows it to exploit the plant but not to kill it instantly. Depending on the severity of the infection plant adjusts its physiology limiting pathogen development or accelerating its life cycle to produce seeds. This acceleration of course leads to limited crop yield including decreased number of produced seeds. The longevity of spores deposited in soil and the biology of the pathogen makes the clubroot disease one of the most serious threat in OSR agriculture. As estimated each year it leads to apr. 15% loss of the OSR crop loss worldwide. In this light it becomes obvious, that winning the battle against the pathogen needs deeper understanding of the biological base of interaction.

The aim of our project is to understand how the *P. brassicae* infection changes long distance coordination within the plant. Due to the fact, that galls are the most characteristic symptoms of the clubroot disease little attention has been payed to the aboveground part of the host. Our knowledge is even more restricted when it comes to understanding the information flow and coordination of host responses between upper and lower part of a plant. Such coordination is necessary for the host but also the pathogen needs to induce serious reprogramming of the physiology and metabolism within the upper part. ***P. brassicae* almost exclusively infects the upper part of the plant, therefore whole reprogramming must be mediated over long distances.** This is particularly important for setting up pathogen-oriented physiological sink. Assimilates produced by plant during the photosynthesis process can be redirected towards the pathogen. So far we have established that vascular tissue structure as well as its role in sugar redirection process are crucial for the successful feeding of the pathogen. Based on current state of knowledge on transport of metabolites, phytohormones, transcription factors or smallRNA molecules we can assume, that long distance coordination has tremendous impact on the whole plant-microorganism interaction. **In this project we will study changes in vascular sap content and functionally characterise the role of identified factors whose concentration alters significantly during the clubroot disease progress.** The first part of the experiment devoted to identification of particular macromolecules will be carried out on oilseed rape plants (OSR). **The role of identified factors will be deeply and functionally characterised** with help of *Arabidopsis thaliana* system that gives as the power to modify the abundance of particular factors or their transport. **We will also use molecular biology and advanced microscopy techniques to visualise changes in signalling networks or distribution patterns within vasculature of infected plants.** During this project we will also study changes in the host vascular system that occurs in infected host. This includes also understanding of the capacity of this tissue to transport particular macromolecules. One of the aspect that we are interested is to characterise the cytokinin transport and signalling role in anatomical changes within vasculature and establishment of the metabolic sink within developing galls. **Integration of our results will help to understand biological bases of the interaction between the *P. brassicae* and the host at the level of system.** Our results will build up our knowledge on how plants can respond do biotic stress and will bring new information regarding plant developmental and physiological plasticity. **Such knowledge can potentially be used for development of tolerant plants or adjusting growth conditions and other agricultural methods related to OSR production to minimise the negative pathogen impact and reduce this way financial losses.**