

## Multi-omic approach for characterization and detection of the emerging phytopathogenic fungus – *Pilidium lythri*

Global changing of the climate is a leading factor causing spread of fungal pathogens to the temperate climate zones. As the consequence, occurrence of the harmful microorganisms in the regions they are not native, causes agricultural loss in the larger scale. This raises the need for thorough exploration of pathogenic fungi traits to improve understanding of the mechanisms related to their pathogenicity. The pathogenic fungus that have been recently identified by our team as a strawberry pathogen for the first time in Poland is *Pilidium lythri*. This microorganism had been mostly reported as a fungus causing plant diseases in warmer climate zones, but evidently, the dissemination of this fungus to the temperate climate zones takes place and needs to be addressed properly.

We will first select the most harmful fungal strains with the pot experiment, where will artificially infect strawberry plants with *Pilidium lythri*. We will also characterize changes in the abundance of all fungi and bacteria in the soil and the plant as the disease progresses. This will help to emerge microorganisms that can be further use to microbially-enriched biopreparations that will improve the health of agricultural plants.

Next, we will also compare the metabolic activity of different fungal strains that will be grown in different temperatures (~21°C and ~27°C). This experiment will allow to discover how significantly the change of the temperature affects the development of the fungus. Additionally, this stage of the experimentation will allow to elect substances that can be used in the future as growth inhibitors for *Pilidium lythri* to protect crops from its harmful impact.

Then we will find out what genes are used by the pathogen in two temperatures and this will help us to understand how the temperature changes the fungal transcriptome. Also, we will have an answer for the question is there any difference in the action of these genes under different temperature conditions, causing a threat in more countries due to climate warming.

We will also sequence the whole genome of the fungus *P. lythri* and bioinformatically analyze the data, that will allow to discover what known genes responsible for production of toxins and/or allergens are present in the genome of the fungus. This will help us to understand whether this microorganism is a threat only to agriculture, causing economic losses, or if it might be also a danger to the microbiological quality of agricultural products and food, being a hazard to the human health.

Finally, we will develop effective identification method of the pathogen with the application of the molecular biology technique. Having a detection method that allows an unambiguous identification even before manifestation of the disease symptoms of the plant is very important, as the *Pilidium lythri* attacks not only strawberry, but also number of flowers and other plants of agricultural significance. What is more, the disease symptoms are similar to the anthracnose caused by *Colletotrichum* sp., which makes it difficult to correctly identify the pathogen present on a given plantation. Only a correct recognition of the fungus that is present in a given plantation will allow for implementation appropriate protective measures and will limit the damage caused by fungal diseases.

The data obtained in the course of the study will drastically improve the knowledge regarding emerging, so far poorly described phytopathogenic fungus *Pilidium lythri*. The approach proposed in this project will allow to thoroughly portray and understand mechanisms involved in the pathogenicity of the microorganism. Research results obtained during the project will be published in the form of reports, papers and posters during scientific conferences, symposiums and meetings in Poland and abroad. Likewise, the results will be published in international peer-reviewed scientific journals to disseminate acquired knowledge. Additionally, acquired genome of the pathogen will be published in the international bioinformatic database which will allow researchers from all over the world to further analyze the results.