

Does the microbiome of arable soil influence development of blackleg and soft rot diseases caused by pectinolytic bacteria of the *Dickeya* and *Pectobacterium* genera?

Pathogenic factors causing blackleg and soft rot are pectinolytic bacteria from genera *Dickeya* and *Pectobacterium* classified by phytopathologists among the top ten most important bacterial plant pathogens. They have been included in the above-mentioned list due to the fact that they are responsible for losses reaching ca. 46 million € annually only at European potato market. Other studies indicates that pectinolytic bacteria are responsible for 32% losses in seed potatoes production sector. Study of Prof. Ewa Łojkowska group also confirm the widespread presence of pectinolytic bacteria in Poland, and thus they are responsible for huge economic losses also in our country. Despite significant economic losses there is no effective method protecting plants against those bacteria. Currently preventive measures include only early detection of bacteria and eliminating infected seeds which are often found to be inefficient. Study shows that pectinolytic bacteria of the genera *Dickeya* and *Pectobacterium* are not only spread by infected seeds but also through contaminated soil. Due to this, hypotheses have been made that the occurrence of disease symptoms on cultivated plants may be affected by the microbiological composition of soil meaning so-called soil suppression. That hypothesis indicates the fact that unique composition of microorganisms species in suppressive soils prevent pathogens development and block disease symptoms. On the other hand, non suppressive soils and its microbiological composition may favor cell division of pathogens. Reports from around the world have been made about relation between soil suppressiveness and disease development caused by fungi and bacteria like *Fusarium oxysporum*, *Rhizoctonia solani*, *Streptomyces scabies* and *Ralstonia solanacearum*.

Relation between soil suppressiveness and symptoms intensity caused by bacteria from the genera of *Dickeya* and *Pectobacterium* so far has not been analyzed. Therefore in proposed project a hypothesis has been made that development of disease symptoms of blackleg and soft rot may be linked to microbiome soil composition. Goal of this project is to analyze soil microbiome from cultivated soils with different symptoms intensity of blackleg and soft rot. As a result it should be possible to indicate microorganisms or a composition of microorganisms responsible for preventing disease development caused by bacteria from genera *Dickeya* and *Pectobacterium*.

Initially research will focus on indicating pectinolytic bacterial species causing the biggest threat to potato cultivation in Poland. For this purpose molecular diagnostic (PCR) and spectrometric methods (MALDI-TOF-MS) will be used. Basing on our previous studies we will select potato fields with both suppressive and non-suppressive soils in relation to bacteria causing blackleg and soft rot diseases. In next step a physicochemical soil properties will be determined in order to exclude them as suppressive factors in soil. At the same time microbiological composition of soil will be determined using traditional cultivating methods. In the next step laboratory test will determine the survival of selected pectinolytic bacteria strains in suppressive and non-suppressive soils. Final part of proposed project will include metagenomic analysis of rhizosphere samples collected after potato vegetation in phytotron conditions to identify microorganisms present in soil samples which are not able to grow on cultivated lands and can cause soil to be suppressive or non-suppressive.

Aim of the research planned for this project is to determine whether there is a relationship between microbiome composition of a soil and occurring of potato disease symptoms known as blackleg and soft rot. Achieved results should allow to indicate species/isolates with high potential of practical application which, after greenhouse and /or field tests may be commonly adopted for biocontrol of potato seed plantations.