

The main objective of the DivGene project is to widen our knowledge on plant diseases and the factors influencing resistance or susceptibility to pathogens. The research object is potato, the fourth most important cultivated plant in the world, and its economically the most important disease, potato late blight. This is a disease, which attacks potatoes and tomatoes wherever they are grown and which in suitable conditions, at high humidity and moderate temperature, can cause yield losses up to 100%. There is a lack of potato cultivars resistant to late blight that could minimize chemical protection of the plantations. One of the reasons for this lack is the fast evolution of the pathogen causing late blight. It is a fungus-like organism which spread all over the world from America following the potato. Its strong adaptation potential means that soon after the introduction of a new resistant potato variety, new pathogen strains appear and spread, able to overcome the resistance and successfully infect the new cultivar.

Recently, DNA sequences of ca. 20 major resistance genes against potato late blight have been elucidated and ca. 60 of such genes have been identified and mapped in potato and its wild relatives. However, we do not know which of the known resistance genes are present in the currently grown cultivars, especially that the resistance of many of them has been overcome. The first specific objective of the DevGene project is diagnosing of the presence of several late blight resistance genes and analysis of their diversity in potato cultivars grown in Poland and Norway. The products of resistance genes work as alarm switches that recognize pathogen's proteins and start defense reactions that result in resistance. In only 10 cases we know, which late blight proteins are recognized by the potato resistance proteins. They all belong to the family of effectors with a characteristic RxLR motive. A second project objective is diversity analysis of the genes encoding late blight effectors in the populations of the pathogen in Poland and Norway. These two goals will be achieved with use of high throughput next generation sequencing method and a technique allowing for selective sequencing of the genes of interest (AmpSeq). This approach will allow us to obtain data on diversity of the genes crucial for the interaction between potato and late blight in a population scale that was so far not possible. A significant advantage of the Polish-Norwegian cooperation within the project will be that we will obtain data from two different environments, which will be used for stronger verification of the hypothesis that the diversity of plant resistance genes and the genes encoding pathogen's effectors shape the co-evolution of the plant-microbe pathosystem.

Phenotypic validations of the results of the 1) potato and 2) pathogen gene diversity analyses, based on the AmpSeq method, are next two objectives of the DivGene project. In phytopathological tests, using plants differing by their resistance gene contents and pathogen isolates with defined abilities to cause disease, we will confirm both the virulence of the investigated pathogen isolates with different effector variants, and the resistance of potato cultivars with different variants of the resistance genes. We will measure also the expression of the studied genes during the disease development to confirm their actual involvement in the interaction.

The expected effect of the project is new knowledge on plant-pathogen interactions and the most important genes involved in it, illustrated by the model example of the potato-late blight pathosystem. The knowledge will help us to answer the questions: why the plant resistance is not durable, whether the durability of resistance conferred by different genes can also be different, what shapes the late blight pathogen populations and why some strains started to dominate them in Poland and Norway. Better understanding of the interactions between plants and pathogens can in future be exploited in practical plant breeding and in improvement of the disease control methods, which will help to reduce pesticide usage and the negative impact of the agriculture on the natural environment.