Abstract

Phylum Actinobacteriota represents one of the major phyla in plant and soil environments. Known for the ability to produce numerous secondary metabolites, Actinobacteriota may affect other bacteria and plants in various ways. The thesis aimed at assessing the connection between the production of secondary metabolites and interactions of actinobacteria in plant and soil environments.

In the first part, we assessed how rare actinobacteria from acid soil affect cultivable soil bacteria. We isolated a collection of actinobacteria from acid soil dominated by previously uncultivable lineage and isolated a representative described as a new family *Treboniaceae* and multiple other potentially novel species of known genera. The genome and metabolome analysis of *Trebonia kvetii, sp.nov. gen.nov.*, demonstrated its ability to produce unusual and potentially novel bioactive metabolites. We designed an experiment where a single strain was co-cultivated with the total soil bacterial community of the same soil in a set up, where a free exchange of diffusible metabolites was allowed between them. Three actinobacteria strains coming from distinct lineages were selected for this interaction. Each strain significantly and specifically affected cultivable bacteria as well as the metabolite pool, part of which was induced by co-cultivation.

In the second part of the thesis, we explored phytopathogenic and biocontrol actinobacteria connected to the common scab of potato. The pathogenicity islands (PAI) bearing virulence genes determining the ability to cause scab disease have been studied in relation to the geographical and phylogenetic origin of the phytopathogenic strains. Both factors influenced PAI type, although in some cases evidence for horizontal gene transfer of similar PAI types between phylogenetically distant species has been observed even across continents. We also observed a vast diversity of species of *Streptomyces* with the detected gene for the phytotoxin thaxtomin, the main determinant of common scab disease. Those strains were previously unknown to be phytopathogenic or even reported as plant beneficial. Finally, we developed and successfully tested an approach for selecting biocontrol actinobacteria based on the ability to inhibit the respective phytopathogen and grow rapidly *in vitro*. We demonstrated that the successful biocontrol strain possesses multiple genes for the production of siderophores and antibiotics and significantly modified soil bacterial community *in situ* towards the plant-beneficial state.