

Abstract

This diploma thesis focused on screening for bacterial pathogens and antagonists suppressing common scab mainly caused by *Streptomyces scabiei*. Common scab affects some agricultural crops causing significant economical losses.

Bacterial strains, mostly streptomycetes, were isolated from potato rhizosphere because they belong to most important producers of secondary metabolites and the causative agents of the disease are also members of this genus. The isolated bacteria were characterised by PCR amplification and sequencing of 16S rRNA gene to reveal their phylogenetic relationships. The ability of isolated strains to suppress growth of *Streptomyces scabiei* was tested by a simple co-cultivation experiment. The strains were tested by PCR for presence of specific genes for biosynthesis of thaxtomin A, a common virulence factor found in all described pathogens causing symptoms of this disease on the surface of affected tubers. Genes for synthesis of thaxtomin belong to pathogenicity island. Standard of phytotoxin thaxtomin A was used to optimize its analysis by mass spectroscopy for further *in vivo* and *in vitro* experiments.

Phylogenetic analysis of strains harboring one of the genes necessary for thaxtomin A biosynthesis supported the hypothesis of sharing the pathogenicity island by horizontal gene transfer with non-pathogenic species. Strains of soil antagonists able to suppress the growth of the main causative agent of common scab *S. scabiei* were isolated as well as strains carrying one of genes necessary for thaxtomin synthesis closely related to the known pathogenic species. Further work on this project will focus on detection of thaxtomin A production by potential new pathogens.