



## A development of a new plant-microbe pathosystem

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### Abstract

Pectinolytic *Dickeya solani* is a plant pathogenic bacterium causing blackleg and soft rot diseases of agriculturally important crops worldwide including potato (*Solanum tuberosum*). Up till now, a vast majority of the research on understanding the molecular basis of the plant infection have been concentrated on a situation when the pathogenic bacteria have already established the infection in the host. Little is known about the early or symptomless (latent) stages of a colonization, especially on the molecular, gene expression level. The knowledge gap comprises both the primary *D. solani* host – *S. tuberosum*, as well as one of the secondary hosts - *Solanum dulcamara*.

The main objective of the project is to identify, characterize and comparatively analyse genes, up-regulated in primary steps of the plant colonisation by *D. solani*. It is believed that steps of *D. solani* early and late plant infection are tightly governed by specific gene sets, presumably different from each another. In order to capture a picture of the gene set, I have used the random transposon mutagenesis and generated over 10000 Tn5 mutants. The generated mutants possess a promoterless reporter *gusA* gene and constitutively express *gfp* gene, both included in the transposon insertion fragment. Over 1000 mutants which have not revealed the *gusA* activity in neutral (non-inductive) conditions have been chosen for further analyses. The plant-microbe interaction assay is carried out on tissues (stems, leaves and roots) of the primary and the secondary *D. solani* hosts, *S. tuberosum* and *S. dulcamara*, respectively.

Understanding the genetic background of early steps of the plant colonisation by pathogenic, pectinolytic bacteria will help to develop a new pathosystem model of a plant-microbe interaction. Studying the colonisation events both *in plant* and *in vitro* using *D. solani* mutants, which genes expression activation can be visualized *in situ*, will also contribute to the enrichment of the knowledge of the plant-microbe interaction systems, similarly to these well-described for *Agrobacterium* spp. and *Rhizobium* spp.

