

Phosphoproteomics in *Phytophthora infestans* – Differences in life stages and comparative analysis

Phytophthora infestans is a devastating pathogen of tomato and potato. It belongs to oomycetes, a group of plant and animal pathogens with economical as well as ecological impact. The complex life cycle of *P. infestans* consists of both asexual and sexual stages. Of special interest is the period of direct interaction with the host that can be divided into several distinct phases. The transitions between the different stages are tightly regulated on the level of both the expression of stage specific genes as well as the activity of proteins. One of the major mechanisms to regulate the activity of proteins is reversible posttranslational phosphorylation. Phosphoproteomics, the analysis of the set of phosphorylated proteins in the cell, is a 'state of the art' high throughput technology that allows us compare the phosphorylation state of proteins at different stages of the life cycle, especially the infection process. The aim of this project is to analyze and characterize the set of phosphorylated proteins during the different phases of the *P. infestans* life cycle. We want to utilize primary data from experimental collaborators on the phosphoproteome of *P. infestans*, define life-stage specific modifications and identify conserved regulatory targets by comparative studies with closely related species. Finally, integration of posttranslational modification with available microarray data in *P. infestans* might help in developing a comprehensive picture of regulation (at different levels) during different life phases.

We're looking for a motivated and intelligent student with a background in biology, computer sciences or bioinformatics for a period of at least 3 months full time, but preferably 6 months or longer.

We offer the student an opportunity to learn bioinformatic skills and, more importantly, to do bioinformatic research in a stimulating environment. The Theoretical Biology and Bioinformatics group deals with a very wide range of subjects, ranging from modeling of developmental and evolutionary processes, heart modeling, immunological bioinformatics to comparative genomics and evolutionary biology. For further information on this and also other possible research projects within the group please contact Michael Seidl (m.f.seidl@uu.nl).