

## FUNADAPT

Project title: Identification and functional characterization of molecular determinants involved in adaptation of fungal pathogens to different host plants.

Key-words: *Venturia inaequalis*, population, non-host interaction, RNA-seq, molecular evolution

Duration: 24 months. Start date: 18/07/2016 . End date: 17/07/2018

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Summary:

Molecular determinants of co-evolution between fungal pathogens and their host plants have been extensively studied. However, adaptation of pathogens to new host plants is poorly understood and no clear molecular mechanism has been reported. In this project, we aim at identifying and characterizing genes that determine fungal adaptation to different host plants. For this purpose, we will use the tractable apple scab pathogen *Venturia inaequalis*, for which the genome sequences of nearly 90 isolates are already available and are currently being analyzed. This pathosystem is particularly suitable to study two aspects of fungal adaptation because of reported host shift between wild (*Malus sieversii*) and domesticated apple species (*Malus x domestica*) and existence within this species of *formae specialis* that are pathogenic either on apple or firethorn. For each interaction between *V. inaequalis* isolates and their respective hosts, the first objective will be to determine at which stage of the infection process are expressed genes involved in adaptation to different host plants. An indirect method will identify such stage(s) through inoculation of the different isolates tagged with GFP on non-host plants. Confocal microscopy will determine when each isolate is stopped on its respective non-host plant. This knowledge will be used to harvest infected leaves for deep transcriptome sequencing at the adequate time point. Comparison of the transcriptomes of the different isolates on their respective host will identify candidate genes that might be involved in fungal adaptation. This data will complement comparative genomics and evolutionary studies that are currently performed in the laboratory, which are also aiming at identifying candidate genes involved in fungal adaption. Candidate genes will be further characterized using quantitative PCR, deletion mutants and heterologous expression. This project will generate new fundamental knowledge on fungal adaptation associated with host domestication and to different host plant species. Such knowledge might be used to test hypotheses on ecological speciation and circumvention of non-host plant. Importantly, it will also be useful to understand and prevent the emergence of new diseases.

