NEMOFY

Project title: NEw MOlecular factors involved in Fungal pathogenicitY

Project duration: 36 months months – Start date: 2/11/2016 - End date: 31/10/2019

Key-words: fungal necrotroph, eisosome, epigenetic control, signaling pathway

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Total cost of the project: **112 770 k€** (Do not include salaries others than those of the people hired for the project: PhD or post-doc)
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Summary:

Context: Based on the Arabidopsis thaliana/Alternaria brassicicola pathosystem and using genome-wide transcriptomic analyses and functional approaches, we recently identified new fungal molecular determinants that may be involved in pathogenicity. We propose to study them in more detail in this project. The first factor is the associated-membrane structures called eisosomes. These structures would be in particular involved in the fungal adaptive response to severe hydric stress conditions consecutive to the gradual decrease in the water potential in maturing reproductive organs. We showed that the transcriptional control of eisosomal components was mainly mediated by the histidine kinase AbNik1, an upstream component of the high osmolarity glycerol (HOG) pathway, which is also the molecular target of dicarboximide and phenylpyrrole fungicides in A. brassicicola. The second factor is the induction of a chromatin remodeling process during the infection process, as strongly suggested by the over-expression during this step of a pool of genes involved in histone modification, DNA methylation or nucleosome structuration.

Goals: A first part aims to investigate the role of eisosomes in virulence of fungal necrotrophs. We also plan to explore the link between eisosomes and signaling pathways when the fungus is exposed to various environments. A second part of the project aims to evaluate the importance of heterochromatic landscapes for fungal virulence. We plan to identify the key players and the environmental conditions (exposure to defence metabolites, hydric stress…) controlling this process. Then, the impact of this potential epigenetic regulation on gene expression will be evaluated.

Methodology : We plan to use functional genomic approaches by generating mutants that are deficient for eisosomal components or for key players in heterochromatin assembly and maintenance, and compare their behaviour to those of the wild-type strain. Moreover, production and distribution of eisosomes along the membranes and chromatin condensation states will be examined under various stress conditions using confocal and epifluorescence observations of mutants producing fluorescently labelled proteins.