Proposition d'un sujet de stage au M2 ADAM (2017-2018)

Titre	**Host specificity factors of the plant-devouring fungus *Sclerotinia* spp.**
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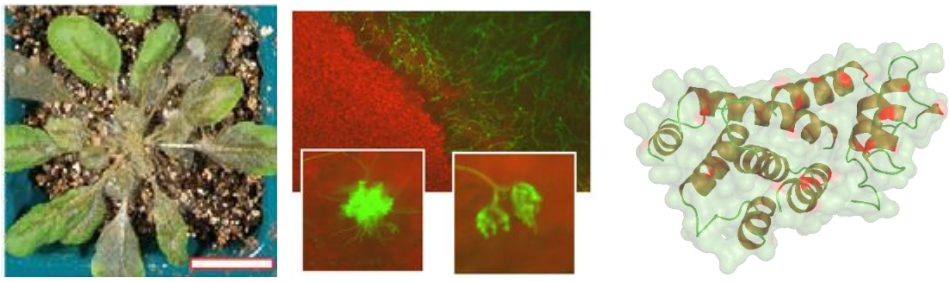
Equipe(s)	Quantitative Immunity in Plants – LIPM (D. Roby – S. Raffaele)
Résumé	The ubiquitous fungus *Sclerotinia* spp. causes the devastating mold disease on many plant species (see **Fig. 1A** and **1B**), including crops like cabbage (*Brassica oleracea*), rapeseed (*Brassica napus*), beans (*Phaseolus* spp.), pea (*Pisum sativum*), and sunflower (*Helianthus annuus*). The range of host plants varies widely in the genus of *Sclerotinia*: *S. sclerotiorum* affects more than 270 plant genera, *S. borealis* can infect plants from 17 genera including barley, while *S. trifoliorum* only infects a few legumes. In this project we address the question what determines the host range of fungal plant pathogens. Plant pathogens secrete so-called effector proteins to subvert plant defense and plant metabolism for their own good. The genome of *S. sclerotiorum* harbours around 70 of such putative effector candidates, such as the cutinase *Ss*Cut1 that degrades plant waxes. Through comparative genome analysis of *S. sclerotiorum* with *S. trifoliorum*, *S. borealis* and other related fungi, we identified two effector candidate genes (*SsEC1* and *SsEC2*) that seem to be present in *S. sclerotiorum* only. *Ss*EC1 is predicted to have sugar- or chitin-binding properties, and localized to undetermined vesicular structures when over-expressed in the plant. *Ss*EC2 has no similarity to any known protein. Another effector, *Ss*EC3, was absent in *S. borealis* and has structural similarity to RNA-binding proteins and oxidoreductases. Three more were found absent in *S. trifoliorum* but present in the other species. *Ss*EC4 and *Ss*EC5 are near-identical, but their function is unknown. The structure of *Ss*EC6 resembles that of a decarboxylase (**Fig. 1C**), which catalyse the removal of carboxyl groups from organic compounds. The project will entail the functional analysis of one or several of these candidate effector proteins. This will include a variety of methodologies: cloning of effector candidates into appropriate expression vectors, transformation of either plant or fungus for over-expression and/or knock-out of the effectors, quantitative plant-pathogen assays to assess the relevance of the effector for infection, and subcellular localization studies in plant and fungus using fluorescent protein tags and confocal laser scanning microscopy. The student should have some experience with molecular biology techniques, and should be able to communicate in English.
Photo	**A** **B** **C**  **Figure 1. A.** *S. sclerotiorum* disease on Arabidopsis (Stolz *et al*., 2011, Plant Journal). **B.** A GFP-expressing *S. sclerotiorum* strain colonizing Arabidopsis leaves. **C.** Predicted protein structure of *Ss*EC6 by Phyre2.