

Deciphering complex tree-microbe interactions using genomics

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Abstract: In this seminar I will provide an overview of different aspects studied in our *Ecogenomics of interactions* team at INRA Nancy (France). After briefly illustrating how comparative fungal genomics analyses can support the study of fungal life traits evolution (Kohler et al. 2015 Nature Genetics), I will more particularly present recently published results. The first one concerns the amazingly large repertoire of resistance genes uncovered in the oak *Quercus robur* genome (Plomion et al. 2018 Nature Plants) and the second one will illustrate how transcriptomics can help progress in dissecting the very complex life cycle of obligate biographic pathogens that are rust fungi (Lorrain et al. 2018 Molecular Plant-Microbe Interactions).

Bio: After an early career on functional genomics of the ectomycorrhizal symbiosis with Francis Martin (INRA Nancy), I moved in 2005 to plant-pathogen interactions, studying the pathosystem established between model trees *Populus* spp. and the fungus responsible for the poplar leaf rust disease *Melampsora larici-populina*. Within our department and in the frame of various collaborations, we have established a project in which we bridge expertise in biochemistry, functional genomics, populational studies and epidemiology to better understand the mechanisms and evolution of the poplar-poplar rust pathosystem. Beyond, I am leading several international genomics projects on rust fungi in collaboration with the US DOE Joint Genome Institute and many teams over the world. I deeply think that collaborations are a necessary support for a better science and I put efforts in the building of an international collaborative effort dedicated to the study of rust fungal biology. I am Deputy Head of the INRA/Lorraine University *Tree-Microbe Interactions* Department (~80 people) and head of the team *Ecogenomics of interactions* (~35 people).

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