



Role of Poplar defense phytohormones in controlling the root microbiome

Principle investigator: Aurélie Deveau

Partners: UMR1137 SILVA

Collaboration: C. Veneault-Fourrey, F. Fracchia, L. Mangeot-Peter, C. Plain

Context — Microorganisms have a key role in forest ecosystem functioning: bacteria and fungi make available nutrients for trees by degrading dead plant and animal matter and by freeing minerals from rocks. In addition, some fungi and bacteria live in close association with the roots of trees and contribute to the growth of trees and to their resistance to pathogens and climatic stresses. Although it is clear that trees have the ability to shape, at least for a part, the composition of their root associated microbial communities (called root microbiome), the mechanisms involved in this process are not well defined yet.

Objectives — We proposed here to analyse how trees control their microbiome. In particular, we tested whether phytohormones involved in tree defence against pathogens have also a role in shaping the root microbiome using Poplar as a model system.

Approaches — We constructed genetically modified lines of Poplar that are altered in their perceptions or biosynthesis of ethylene, salicylic acid and jasmonic acid. Then we will assess in the laboratory the composition of the root microbiomes of the genetically modified lines and compare it to the ones of wild type roots.

Key results —

- Poplar lines of *Populus tremula alba* 717-1B4 overexpressing or repressed for the expression of genes involved in the perception or synthesis of salicylic acid (*npr1*), jasmonic acid (*jaz6*), ethylene (*ap2*), gibberellic acid (Giberelline oxidase, *della*), terpenes (terpene oxidases) have been generated and the alteration of expression has been validated for at least 3 lines for each construct.
- A miniaturized culture system of seedlings in natural soil has been developed to monitor microbial colonization of roots by confocal microscopy and high throughput sequencing (amplicons, metatranscriptomics).
- The root system of wild seedlings is first massively colonized by saprotrophic and endophytic bacteria and fungi which are then replaced, after about ten days, by several waves of mutualistic fungi (endomycorrhizal and ectomycorrhizal).
- Blocking the perception of jasmonic acid seems to favour the establishment of mutualistic fungi (endo- and ectomycorrhizal fungi) to the detriment of endophytes. However, this would only benefit certain species of mutualistic fungi.

Main conclusions including key points of discussion — Preliminary data obtained suggest that the root microbiome is established in two stages: a first stage in which opportunistic, fast-growing species rapidly and abundantly colonize the roots. After a few days, mechanisms to be defined (interspecific competition? Plant immunity?) are set up and lead to limiting the development of these microorganisms to the benefit of mutualistic microorganisms. The analysis, in progress, of the colonization dynamics of the root systems of the mutant lines generated will make it possible to identify whether defence phytohormones are involved in these selection mechanisms.

Future perspective — A thesis, defended by Lorraine University of Excellence and started in June 2019, aims to analyze the impact of the alteration of the different phytohormonal signalling pathways in the formation and activity of the root microbiome.

Valorisation —

Thesis

L. Mangeot-Peter. Effet des facteurs biotiques et abiotiques influant sur la structuration de la composition du microbiome racinaire du Peuplier. Université de Lorraine. Soutenance prévue le 3 mars 2020.

Poster

Microbial Colonisation Dynamics of Poplar Root Systems. F. Fracchia, L. Mangeot-Peter, C. Veneault-Fourrey, A. Deveau, F. Martin. (Bussang, France, 5-8 novembre 2019).

Article in preparation

Colonization dynamic of *Populus tremula x alba* roots by soil microbial communities. F. Fracchia, L. Mangeot Peter, C. Veneault-Fourrey, F. Martin, A. Deveau.