

Plant-Microbe Interfaces: Plant mechanisms shaping poplar root microbiota

Felix Fracchia^{1*} (Felix.Fracchia@inrae.fr), Nancy Engle,² Timothy Tschaplinski,² Francis Martin,¹ Aurélie Deveau,¹ and **Claire Veneault-Fourrey**¹

¹Université de Lorraine, INRAE, IAM, Nancy, France; and ²Biosciences Division, Oak Ridge National Laboratory, Oak Ridge, TN

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Project Goals: The goal of the PMI SFA is to characterize and interpret the physical, molecular, and chemical interfaces between plants and microbes and determine their functional roles in biological and environmental systems. *Populus* and its associated microbial community serve as the experimental system for understanding the dynamic exchange of energy, information, and materials across this interface and its expression as functional properties at diverse spatial and temporal scales. To achieve this goal, we focus on 1) defining the bidirectional progression of molecular and cellular events involved in selecting and maintaining specific, mutualistic *Populus*-microbe interfaces, 2) defining the chemical environment and molecular signals that influence community structure and function, and 3) understanding the dynamic relationship and extrinsic stressors that shape microbiome composition and affect host performance.

Trees interact with complex microbial communities that contribute to their extended phenotype. How early fungal and bacterial root colonization occur and how these interactions take place remain poorly understood. The woody perennial model *Populus* has the ability to interact with distinct trophic guilds, such as endophytes and mycorrhizal fungi, and can help decipher the organization of the early establishment of microbial root communities. We determined that the early establishment of the fungal and bacterial root communities of axenic *Populus tremula x alba* transplanted in environmental soil is dynamic in time and space over 50 days of culture. This microbial colonization involves three successional waves of colonization, for both bacterial and fungal community structures, harboring distinct trophic abilities. Even though bacterial community structures were more stable in time than the fungal community structures, the early colonizers were saprotrophs, fast-growing species that were progressively replaced by endophytes and mycorrhizal fungi. The composition of root exudates and host-based selection through distinct hormonal and metabolic profiles could explain the evolution of these microbial communities. To test these hypothesis, transgenic poplar trees altered in ethylene perception and biosynthesis were grown in sterile condition, transplanted into environmental soil and grown for 30 days in natural soil. We examined fungal root colonization using confocal laser scanning microscopy and combined this analysis with metabarcoding and metabolomics of roots and their exudates. Microbial enzymatic activities associated with rhizospheric soil differed depending on the poplar transgenic and wild type lines. Taken together, these results support the importance of plant genotype in the structuring of microbial communities and their importance in soil functional traits.

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