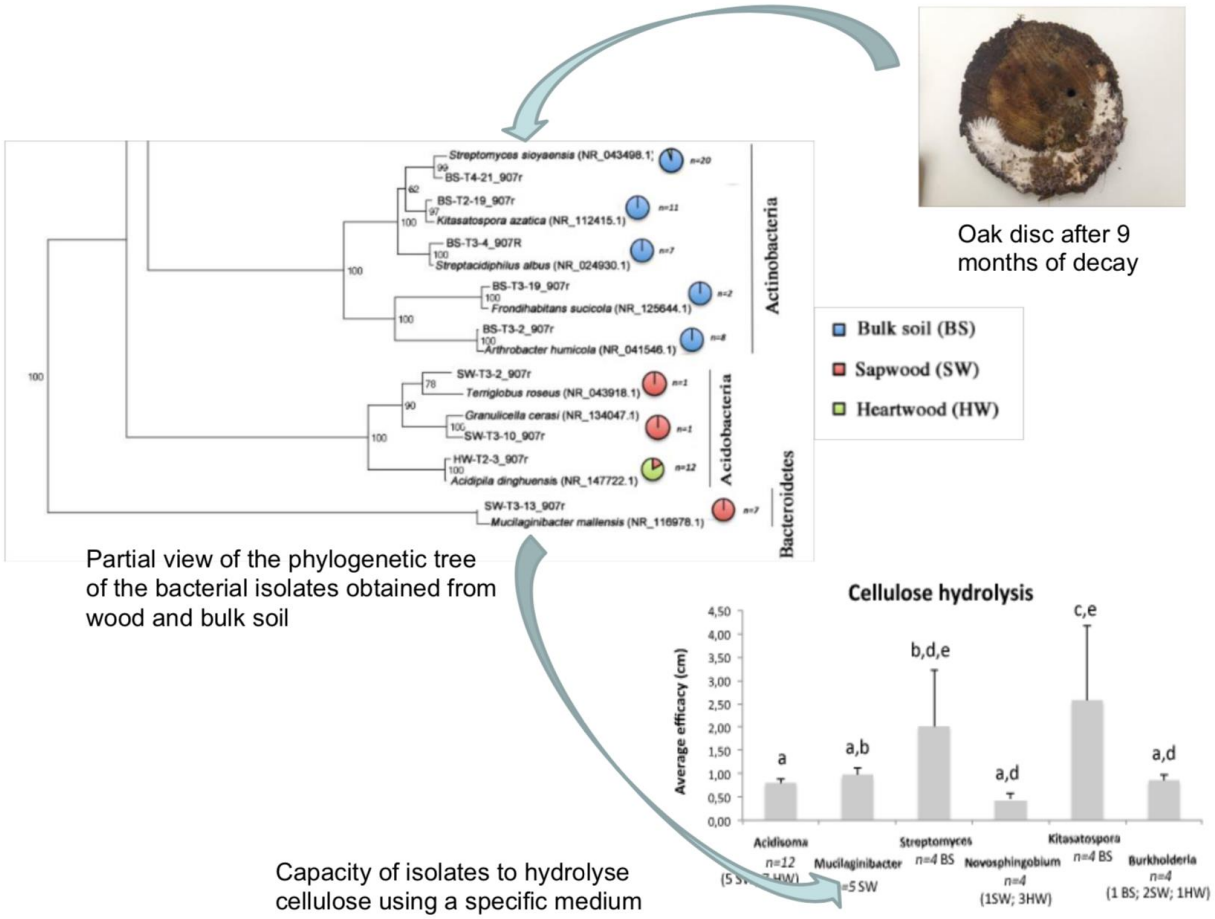
DivBactO



Characterisation of the taxonomic and functional diversity of bacterial communities isolated from heartwood and sapwood of decaying oak

Principle investigator: Sophie Mieszkin

Collaboration: Stéphane DUMARÇAY

Context — Microorganisms are the main wood decomposers in forest ecosystems. Among them, fungi are the most studied and are capable of using various extracellular lignocellulolytic enzymes to degrade complex polymers. While fungi are extensively studied, the role of bacterial communities to degrade carbohydrates was underestimated despite evidences of their involvement in such processes. Recently, a few studies investigated the functional diversity of bacterial communities selected by the wood substrate (Fagus sylvatica and Picea abies) and showed their significant potential to participate to wood decay processes.

Objectives — As bacteria actively participate to wood decay in presence of fungi and in front of the little knowledge we have, it was relevant to investigate how decaying-wood and its different compartments (heartwood versus sapwood) shape both the taxonomic and functional diversity of bacterial communities. These two main compartments of wood are mostly characterized by their content in wood extractives with some molecules potentially toxic toward microorganisms. These two wood bacterial communities are also compared to a bacterial community obtained from bulk soil in direct contact with the decaying oak wood

Approach — A bacterial collection was prepared from 9 months decaying oak heartwood and sapwood and from the soil in direct contact with the decaying oak wood, to characterize its taxonomic diversity using Sanger sequencing. The functional diversity of this collection was assessed using metabolic fingerprints (Biolog GN microplates) and selective media to highlight their cellulolytic, lignolytic, xylanolytic and/or chitinolytic activities but also their capacity to produce siderophores.

Key results —

- 309 bacterial isolates were obtained from the 3 compartments (heartwood, sapwood and bulk soil) and they revealed a total of 4 phyla, 7 classes, 16 families and 32 genera.
- A high proportion of isolates belonged to the Proteobacteria (77.7%), then to the Actinobacteria (15.5%), the Acidobacteria (4.5%) and finally to the Bacteroidetes (2.3%).
- Using Biolog GN microplates, we showed that the bulk soil bacterial community showed a higher metabolic activity than the wood bacterial communities.
- Using selective media to identify bacterial isolates able to degrade complex organic substrates such as cellulose, lignin, xylan and chitin and also to mobilize iron, we found that only a small proportion of bacterial isolates was involved and most of them were isolated from heartwood or bulk soil

Main conclusions including key points of discussion — A bacterial collection using the two main oak decaying wood compartments and bulk soil in direct contact with the wood was obtained for the first time at the laboratory. Taxonomic affiliation of these isolates was clearly linked to their ecological niche (wood versus soil) but some isolates were also commensal to the three niches. Regarding the functional potential of this bacterial collection, bulk soil community was most active to metabolize carbon substrates than the wood bacterial communities notably toward amino acids and carboxylic acids. Bacterial wood communities were more involved in carbohydrate degradation with nevertheless specific features for each community. At the opposite, concerning complex polymers, we identified isolates from heartwood able to hydrolyze cellulose and chitin but also to produce siderophores to capture iron. Overall, these results highlight the importance of the ecological niche (chemical composition as well as microbial community) to structure the bacterial communities and the functional role of the bacteria to participate to the recycling of dead wood.

Future perspectives — An interesting perspective of this work would be to assess the physiological response of the bacterial isolates in presence of toxic oak extractives in order to identified isolates able to degrade these molecules.