



POLOMICS

The Ecological Genomics of Wood Decomposition in Polyporales

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We propose a conceptual framework to gain insight about ecological and molecular drivers underlying the assembly history in fungal communities during wood decomposition. Recent advances in DNA and RNA sequencing technologies have introduced a new dimension to explore non-model organisms, such as forest fungi, using integrated ‘-omics’ approaches. In addition, development and advancement of genome repositories, such as the U.S. Department of Energy Joint Genome Institute (JGI) MycoCosm database (with >1800 fungal genomes), allow us to explore the underlying genomic basis of fungal ecologies, such as symbiosis or saprotrophy.

To provide an integrated view of the entangled mechanisms involved in wood decomposition, we will analyze a large set of genomes, gene repertoires and transcriptomes from wood decayers in the Polyporales. Transcript profiles of decaying wood(s) will be produced from both *in vitro* experiments, but also collected from *in situ* samples, i.e directly from decayed logs in forests. The chemical and structural evolution of decaying wood samples will be studied to correlate transcript profiles to the physicochemical structure of decaying wood. The main objective of the POLOMICS project is to adopt an ecogenomics approach to reveal patterns underlying functional traits related to a key ecological process: wood decomposition.

We will investigate the content, structure, and evolution of gene families involved in assembly history during wood decay in the Polyporales. The main motivation for conducting ecological-based ‘-omics’ studies in the order Polyporales (ca. 1800 species) is their dominant role as wood decomposers in forest ecosystems, and hence, their importance in the global carbon cycle. In addition, polypores occur worldwide in all forest types, on a wide range of hosts, both conifer and deciduous species. Most importantly, they establish in wood at different successional stages of decay, develop and produce often numerous fruiting bodies in an array of shapes, colors and sizes, allowing to couple ‘-omics’ with trait-based approaches. Such a huge amount of empirical data assembled for a fungal order is very unique; most likely their global distribution together with their conspicuous size have directed such an effort. Finally, the availability of 86 Polyporales genomes at JGI MycoCosm, well-sampled over a fine phylogenetic scale (18 families), will facilitate evolutionary questions of niche breadth (specialist vs. generalist), biotic interactions and pathogenicity.

The research questions have the potential to bring new knowledge, not only limited to niche characterization and forest ecosystem functioning. Because from an evolutionary perspective, understanding niche breadth (specialist vs. generalist) and the mechanisms facilitating its evolution are fundamental knowledge behind species adaptation to changing environments and the formation of new species. Here, we will generate and analyze large multi-omics datasets (genomes, gene repertoires, transcriptomes) and place our findings in the broader context of important ecological process. This combined approach presents a high potential to gain a deeper knowledge in evolutionary mechanisms driving substrate decomposition in the forest biome.

Most importantly, disentangling wood decomposition process to understand the role of fungal community assembly, from different angles: genome footprints, gene expression *in vitro/in situ* and physicochemical dynamics of decaying wood will bring solid baseline information to predict carbon and nutrient dynamics in a changing climate. Decomposers are barely accounted in predictive ecosystem models, despite their significance for maintaining ecosystem resilience to climate change, probably due to the complex nature of decomposition.



In this LabEx ARBRE project, we apply for a postdoctoral position in bioinformatics. The early career researchers (ECRs) involved in POLOMICS, Sundry Maurice and the bioinformatician recruited by ARBRE, will be at the forefront of fungal ecological ‘-omics’. The proposed project is an essential milestone of their career plans. Upon completion of this project, the ECRs will (i) have consolidated their project management abilities, profitable for leadership position, (ii) benefited from research collaborations, essential for their further scientific projects and for mobility of their future students, which will be developed through further multilateral research collaboration frameworks, (iii) consolidated skills in ‘-omics’ approaches, and finally (iv) increased their publication record. The involved ECRs will gain scientific independence and competitiveness for a position in the European research environment.