POLOMICS

The Ecological Genomics of Wood Decomposition in Polyporales

Principle investigator: Francis MARTIN et Sundy MAURICE, UMR Interactions Arbres/Micro-organismes (IAM) 1136

LabEx partners: Annie LEBRETON (recrutée sur ce projet) et Annegret KOHLER (UMR IAM)

Collaborations :
Havard KAUSERUD (University of Oslo, Norway)
László NAGY (Hungarian Academy of Sciences, Fungal Genomics and Evolution Group, Hungary)
Marie Nöelle ROSSO (INRAE Marseille)

Thematic actions concerned: WP1 & WP3

Background —
Found in all forest types worldwide on both coniferous and deciduous species and establishing in wood at different successional stages of decay, fungi in the Polyporales (*ca.* 1800 species) play a dominant role as wood decomposers in most forest ecosystems[1,2]. Some polypores, such as *Fomitopsis pinicola,* can decompose wood from both coniferous and deciduous species, whereas others have a narrower range of hosts, such as *F. betulina*, which is only able to decompose birch. Ecological specialization is the process whereby an organism adapts to a narrower range of conditions than a generalist, and this process is central to the distribution and maintenance of global biodiversity.

However, what is the advantage of specialization? We know that the more specialized a species is, the lower the success of colonization, which goes concomitantly with increasing extinction rates. This ecological distribution suggests adaptation in terms of composition or regulation of the repertoire of extracellular enzymes that enable wood decomposition.

Traditionally, wood decay fungi have been categorized as carbohydrate–selective brown rot or lignin–degrading white rot fungi based on wood residues. However, comparative genomics has revealed that the nutritional modes of wood decay saprotrophic fungi are more nuanced [3] and that there is likely a continuum of wood-decomposing species.

Objectives —
In the POLOMICS project, we aimed to identify the molecular patterns underlying functional traits related to wood decomposition through environmental and comparative genomics, focusing on Polyporales species.

Approaches —
To provide an integrated view of the entangled mechanisms involved in wood decomposition, we analyzed a large set of genomes, gene repertoires, and transcriptomes from wood decayers.

Key results —
- Comparison of the gene repertoires of 130 fungal genomes, including 64 polyporoid genomes, was performed.
- The phylogenomic relationships of these species were resolved, and their gene repertoires were grouped into gene families for further analyses.
- Gene families known to be involved in fungal-host interactions and wood decomposition, such as G protein-coupled receptors (GPCR), polyketide synthases (PKS), and nonribosomal peptide synthetases (NRPS), were annotated.
- The repertoires of secreted proteins, called secretome, were characterized, and we focused on genes encoding extracellular enzymes, including those involved in wood decay (e.g., carbohydrate-active enzymes, CAZymes).
- A selection of functional traits (22), hypothesized to be informative for the life history of wood decay fungi, was compiled. These traits, such as niche breadth, hierarchical position in community assembly based on fruiting body appearance, cord formation, type of rot, decay stage, geographic distribution, and fruit body traits, have been measured from previous projects extracted from the literature and European datasets.
Preliminary results of correlations between functional traits and the expansion or contraction of gene families were obtained, such as the enrichment of genes potentially associated with lignin degradation in species found on hardwoods. These analyses also highlighted families with unknown functions that could be candidates for functional characterization.

Main conclusions including key points of discussion —
In this study, we highlighted the core features of Polyporales genomes and identified idiosyncrasies within the families. Polyporales species were segregated into three distinct lineages, one of which underwent a drastic reduction in cellulose- and lignin-degrading enzymes. This lineage is composed of species that produce brown rot disease. These results are therefore consistent with the work published by peers and allow us to refine our knowledge of the enzymes correlated with the brown-white rot transition.
In the first approach, a contrast in terms of enzyme composition was also identified between species found to date only on hardwoods and those found on conifers. However, this result should be taken with caution, as the species in our dataset found on conifers are mainly brown rots, while many of the species found on hardwoods are white rots. The impact of the correlation between these two traits on the results will have to be estimated.

Perspectives —
An ecological shift, for example, from saprotrophy to pathogenicity or from a range of hosts to another, is correlated with the evolution of the repertoire of extracellular enzymes. This project enabled the identification of candidate genes involved in wood decay and fungal-host interactions. Further statistical analyses will allow us to obtain more robust results considering the correlations between traits and to study other ecological traits that have not yet been exploited (e.g., related to the reproductive system such as carpophores and spores). Subsequently, analyses of the transcriptomic approach currently in progress will allow for a better understanding of the regulation of genes associated with wood degradation, identified in the genomic region.

Valorization (publications, presentations, patents, press releases, etc.)
– Poster presented at the conference JOBIM 2022
– Poster presented at the IAM unit (UMR 1136 INRAE/Université de Lorraine) doc and post-doc day
– A manuscript summarizing our results will be submitted in 2024

Leveraging effect of the project—
These research questions have the potential to bring new knowledge, not only to niche characterization and forest ecosystem functioning. From an evolutionary perspective, understanding niche breadth (specialist/generalist) and the mechanisms facilitating its evolution are fundamental to understanding species adaptation to changing environments and the formation of new species. In the long term, understanding the mechanism of wood decomposition will contribute to achieving the sustainable management of forests. In the short-term, the results of POLOMICS can be used in other on-going research projects funded by the LabEx ARBRE, such as those involving Dr. Marc Buée (UMR IaM) and Dr. Delphine Derrien (Biogéochimie des Ecosystèmes Forestiers) focusing on the mechanisms driving soil organic matter and their modelization in forest ecosystems. The POLOMICS project also benefits two early career researchers (ECRs), Dr. Sundy Maurice and Dr. Annie Lebreton, by strengthening their skills and expertise in the developing fields of fungal genomics and phylogenomics in the context of collaboration with experts from different countries.

By liaising researchers in wood decay fungi, both from universities and research institutes, and from different countries such as Norway, Finland, France, the UK, and Hungary, **POLOMICS** will greatly facilitate knowledge transfer across countries and strengthen international collaborations promoting the 2030 Vision of the European Research Area (ERA) on societal and environmental objectives.

References
1. Floudas, D., *et al., Science* 336 (2012).
2. Varga, T*. et al., Nature ecology & evolution* (2019)
3. Riley, R., *et al., Proc Natl Acad Sci U S A* 111, no. 27 (2014).