

# POLOMICS



## The Ecological Genomics of Wood Decomposition in Polyporales

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Actions thématiques concernées : 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<sup>1,2</sup>. Some polypores, such as *Fomitopsis pinicola*, are able to decompose wood from both coniferous and deciduous species while 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.

But what is the advantage of specialization? Because we know that the more specialized a species is, the lower is its success of colonization, which goes concomitantly with increasing extinction rates. This ecological distribution suggests an adaptation in terms of composition or regulation of the repertoire of extracellular enzymes enabling wood decomposition. Traditionally, wood decay fungi have been categorized as carbohydrate-selective brown rot or lignin-degrading white rot fungi on the basis of wood residues. However, comparative genomics revealed that nutritional modes of wood decay saprotrophic fungi is more nuanced<sup>3</sup> and that there is likely a continuum of wood-decomposing species.

### **Objectives —**

In the POLOMICS project, we aim to identify the molecular patterns underlying functional traits related to wood decomposition through environmental and comparative genomics with a focus on Polyporales species.

### **Approaches —**

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

### **Key results —** (presented as separated bullet points)

- Comparison of the gene repertoires of 130 fungal genomes, including 64 polyporoid genomes, has been carried out;
- The phylogenomic relationships of those species was resolved and their genes repertoires were grouped into genes families for further analyses;
- Genes 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, so-called secretome, were characterized and we focused on genes coding for 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, has been compiled. These traits, e.g., 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, has 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 function that could be candidates for functional characterization.

### **Main conclusions including key points of discussion —**

In this study, we highlighted the core features of the Polyporales genomes and identified idiosyncrasies within families. Polyporales species segregated into three distinct lineages, one of them underwent a drastic reduction of cellulose- and lignin-degrading enzymes. This lineage is composed of species producing brown rots. 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.

On a first approach, a contrast in terms of enzyme composition was also identified between species found so far only on hardwoods compared to 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 on the results of the correlation between these two traits will have to be estimated.

### **Perspectives —**

Ecological shift, e.g., from saprotrophy to pathogenicity or from a range of host to another, is corelated with an evolution of the repertoire of extracellular enzymes. This project enabled to pinpoint candidate genes involved in wood decay and fungal-host interactions. Further statistical analyses will allow us to obtain more robust results taking into account 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, the analyses of the transcriptomic approach currently in progress will allow a better understanding of the regulation of genes associated with wood degradation identified in the genomic part.

### **Valorization —** (publications, presentations, patent, press release, ...):

-Poster presented at the conference JOBIM 2022

-Poster presented at the IAM unit (UMR 1136 INRAE/Université de Lorraine) doc and post-doc day

### **Leveraging effect of the project—**

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/generalist) and the mechanisms facilitating its evolution are fundamental knowledge behind species adaptation to changing environments and the formation of new species. In the long-term, understanding the mechanism of wood decomposition will contribute to achieve a 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 modelisation in forest ecosystems. The POLOMICS project also benefits to two early career researchers (ECRs), Dr. Sundry Maurice and Dr. Annie Lebreton, by strengthening their skills and expertise on the developing fields of fungal genomics and phylogenomics in a context of a collaboration with experts from different countries.

By liaising researchers in wood decay fungi, both from universities and research institutes, from different countries like Norway, Finland, France, 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).