

Dissecting Intraspecies Diversity in Fungal Wood Decay

Ronald de Vries (PI)¹, Milä Makelä (Co-PI)², Kristina Hildén²

¹CBS-KNAW Fungal Biodiversity Centre, ²Argonne National Laboratory

Abstract: Basidiomycete fungi are essential for degradation of wood in natural eco-systems and therefore a crucial part of the global carbon cycle. Genomic and post-genomic studies into several basidiomycete species have given insight into the process of wood decay, but in most studies only a single isolate was investigated with no real indication whether this isolate is representative of its species. Initial studies in our labs have indicated significant variability between isolates of the same basidiomycete species with respect to their ability to degrade plant biomass components. In this study we aim to dissect the diversity of isolates of the white rot basidiomycete *Dichomitus squalens*. This species is commonly found in North America (known as Western Red Rot that causes significant damage to Ponderosa Pine (*Pinus ponderosa*)) as well as around the globe and is able to colonize both hardwood and softwood. The collections at CBS and UH contain a range of mono- and dikaryotic strains that have already been shown to have different carbon growth profiles.

Rather than comparing specific aspects of the wood decay process in the selected isolates, we aim to analyze their differences in a systems biology fashion. The combination of resources requested from EMSL is essential to achieve this aim.

Samples from different *D. squalens* isolates grown on wood will be taken at two time points and used for extraction of RNA and metabolites, for transcriptomics and metabolomics, respectively. Extracellular and intracellular proteins will be extracted from the cultures and used for proteomics and enzyme assays. In addition, we aim to de novo sequence three isolates that have significantly different carbon source growth profiles and compare this to the reference sequence already generated by JGI to identify the genomic difference between the species.

The combined data will demonstrate at which level(s) the strains differ in their approach to wood degradation and how this will likely affect their contribution to the wood decay process in natural biotopes. In addition, it will demonstrate to which extent a single basidiomycete isolate can be considered a true reflection of the ability of the species with respect to this topic and as such will serve as a reference for studies in other basidiomycetes.