**Fungal biodiversity: a tremendous resource for CAZymes discovery**

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Filamentous fungi are among the most potent degraders of lignocellulosic biomass due to their ability to thrive in lignocellulose-rich environments; they produce a high number and a broad variety of carbohydrate-active enzymes (CAZymes) targeting the different components of biomass. Fungal biodiversity, collected from tree stumps in temperate and tropical regions, was explored using robotic methods to identify fungal strains that deconstruct efficiently recalcitrant polysaccharides. These investigations enabled the unbiased identification of fungal strains issued from biodiversity with high biotechnological potential.

To understand their mechanism of action, some of these fungal strains were further investigated using activity profiling and genomic, transcriptomic and proteomic techniques. The comparative analysis of fungal secretomes using proteomics highlighted the cooperation between fungal enzymes for enhanced degradation of complex lignocellulosic substrates and some discrepancies in CAZymes sets dedicated to different types of biomass.

Over the last ten years, hundreds of fungal secretomes gathering several thousands of lignocellulose-acting enzymes have been analyzed. Bioinformatic exploration of these post-genomic data coupled with functional data is a powerful asset for the discovery of new enzymatic functions. In this lecture, there will be a focus on the discovery of new CAZy families gathering fungal lytic polysaccharide monooxygenases (LPMOs) [1-4].

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