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Meta-multi omics analyses of wood decay in nature

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Purpose: Wood decay fungi play a key role in depolymerizing, degrading and mineralizing the major components of woody cell walls, including cellulose, hemicellulose and lignin. Only a fraction of the species has been isolated in pure culture. Moreover, the laboratory conditions employed with model white rot and brown rot fungi for cell wall degrading enzymes (CAZymes) fail to mimic natural decay processes. To identify key enzymes and further understand lignocellulose deconstruction, we have examined the metatranscriptome and metaproteome of extensively decayed lodgepole pine (*Pinus contorta*).

Methods: Three samples of decayed lodgepole pine were collected in the two different locations, U.S. Forest Service's Tenderfoot Creek Experimental Forest (TCEF) and Gibbon's Pass on the Bitterroot National Forest (GP). Poly RNA and proteins were extracted and applied to HiSeq and LC-MS/MS, respectively.

Results and conclusions: This study suggested that lodgepole pine decay mainly involves the combined activities of functionally diverse enzymes from various wood decay fungal species. The known synergistic actions of conventional endo- and exo-cellobiohydrolases in vitro were detected in the environment. More recently, LPMO has been shown to boost the performance of these hydrolases, which worked in the environment as well. We also found genes most closely related to other fungi, slime molds and protists as well as several bacteria many of which have been associated with decomposition. The enzymatic machinery and interactions among these species merit further investigation.