



演題：**Natural decomposition of *Pinus contorta*:
Physiological processes inferred from
metatranscriptome and proteome investigations**

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場所：工学部材料・化学棟講義室（MC208）

主催：工学研究院応用化学部門 バイオ分子工学研究室

要旨：

Wood decay fungi play a pivotal role in forest carbon cycling. Certain basidiomycetes, collectively referred to as white rot fungi, efficiently degrade all the major components of wood, including the recalcitrant lignin. Brown rot fungi are phylogenetically related but unable to remove lignin. The precise mechanisms of lignocellulose conversion by these fungi are uncertain. However, laboratory studies have implicated oxidative systems in lignin and cellulose depolymerization by white rot and brown rot fungi, respectively. Relatively few investigations have examined complex microbial communities in natural environments.

Addressing this issue, metagenome, metatranscriptome and metaproteome analyses of decaying *Pinus contorta* have been being conducted via collaborative efforts of Hokkaido University, Boston University, the US Departments of Energy and Agriculture. For these analyses, genomic DNA, Poly(A)RNA and protein were extracted from extensively decay wood collected in western Montana. Mass spectroscopy-based identification of proteins was initially restrained by the paucity of reference fungal genomes. However, protein databases derived from de novo transcriptome assemblies substantially increased the number of proteins identified. Together with transcript analysis, the data supported the central involvement of white and brown rot fungi in decay and revealed an impressive diversity of enzymes involved in lignocellulose conversions. Systematic studies along these lines contribute to our understanding of microbial communities and physiological processes involved in carbon cycling in forest systems. The investigations also identified novel enzymes of potential value in plant cell wall bioprocessing.

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