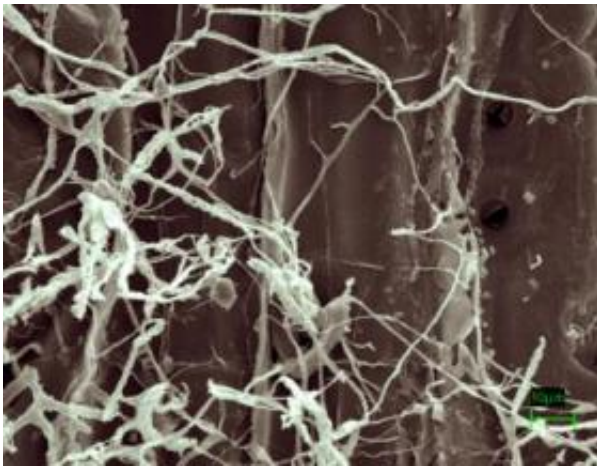


# Rot's unique wood degrading machinery to be harnessed for better biofuels production

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This is the brown-rot fungus *Postia placenta* amongst wood cells. Credit: Thomas Kuster, U.S. Department of Agriculture Forest Service, Forest Products Laboratory

An international team led by scientists from the U.S. Department of Energy Joint Genome Institute and the U.S. Department of Agriculture Forest Service, Forest Products Laboratory have translated the genetic code that explains the complex biochemical machinery making brown-rot fungi uniquely destructive to wood. The same processes that provide easier access to the energy-rich sugar molecules bound up in the plant's tenacious architecture are leading to innovations for the biofuels industry. The research, conducted by more than 50 authors, is reported in the February 4 online edition of the *Proceedings of the National*

*Academy of Sciences (PNAS).*

Among the challenges to more cost-effective production of biofuels from cellulosic biomass—the fibrous material of whole plants—is to find effective means to work around the polymer lignin, the scaffolding that endows the plant's architecture with rigidity and protection from pests. By doing so, the organic compound cellulose—the long chain of glucose (sugar) units can be unbound, broken down, fermented, and distilled into liquid transportation fuel. This is where the destructive capabilities of rot come in.

"The microbial world represents a little explored yet bountiful resource for enzymes that can play a central role in the deconstruction of plant biomass—an early step in biofuel production," said Eddy Rubin, Director of the DOE JGI, where the genome sequencing was conducted. "The brown-rot *Postia placenta*'s genome offers us a detailed inventory of the biomass-degrading enzymes that this and other fungi possess."

Rubin pointed to a complementary strategy that DOE and its Bioenergy Research Centers are pursuing of targeting a new generation of plants—perennial grasses and fast-growing trees such as poplar—bred specifically as biomass for biofuels. Among the desirable characteristics of biofuel "feedstocks" is the ease by which they can be deconstructed. Traditionally, harsh chemicals and expensive high-heat treatments have been employed. In parallel with the development of improved feedstocks is finding just the right mix of enzymes to get the most out of converting biomass into fuel.

"Nature offers some guidance here," said Dan Cullen, FPL scientist and one of the senior authors on the *PNAS* paper. "Postia has, over its evolution, shed the conventional enzymatic machinery for attacking plant material. Instead, the evidence suggests that it utilizes an arsenal of small oxidizing agents that blast through plant cell walls to depolymerize

the cellulose. This biological process opens a door to more effective, less-energy intensive and more environmentally-sound strategies for more lignocellulose deconstruction."

Few organisms in nature can efficiently breakdown lignin into smaller, more manageable chemical units amenable to biofuels production. The exceptions are the basidiomycete fungi, which include white-rot and brown-rot—wood-decayers and essential caretakers of carbon in forest systems. In addition, brown-rot fungi have significant economic impact because their ability to wreak havoc with wooden structures. A significant portion of the U.S. timber harvest is diverted toward replacing such decayed materials.

Unlike white-rot fungi, previously characterized by DOE JGI and FPL, which simultaneously degrades lignin and cellulose, brown-rot rapidly depolymerizes the cellulose in wood without removing the lignin. Up until this study, the underlying genetics and biochemical mechanisms were poorly understood.

DNA sequence is the first step in the central dogma of molecular biology first articulated over 50 years ago by Francis Crick—the transfer of information from DNA to RNA, which in turn, is translated into protein products, such as enzymes. Postia's genome sequence was also the first step in the process that the scientific team employed to home in on the subset of data, the transcriptome, that encodes the specific enzyme activity, and the secretome, the products exported from the cell.

"For the first time we have been able to compare the genetic blue prints of brown-rot, white-rot and soft-rot fungi which play a major role in the carbon cycle of our planet," said Randy Berka, another one of the study's senior authors and Director of Integrative Biology, at Novozymes, Inc., of Davis, Calif. "Such comparisons will increase our understanding of the diverse mechanisms and chemistries involved in lignocellulose

degradation. This type of information may empower industrial biotechnologists to devise new strategies to enhance efficiencies and reduce costs associated with biomass conversion for renewable fuels and chemical intermediates."

Source: DOE/Joint Genome Institute

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