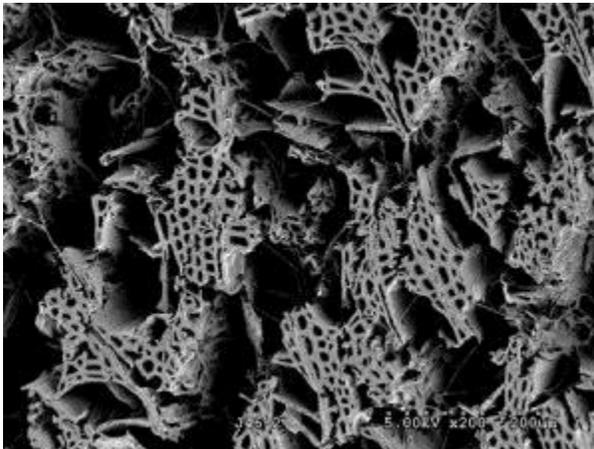


## News Releases

JUNE 28, 2012

# Tracking the Remnants of the Carbon Cycle: How an Ancestral Fungus May Have Influenced Coal Formation

For want of a nail, the nursery rhyme goes, a kingdom was lost. A similar, seemingly innocuous change—the evolution of a lineage of mushrooms—may have had a massive impact on the carbon cycle, bringing an end to the 60-million year period during which coal deposits were formed.



---

Scanning electron micrograph of wood being decayed by the white rot fungus *Punctularia strigoso-zonata* (Robert Blanchette, University of Minnesota)

Coal generated nearly half of the roughly four trillion kilowatt-hours of electricity consumed in the United States in 2010, according to the U.S. Energy Information Administration. This fuel is actually the fossilized remains of plants that lived from around 360 to 300 million years ago. An international team of scientists, including researchers at the U.S. Department of Energy Joint Genome Institute (DOE JGI), has proposed a new factor that may have contributed to the end of the Carboniferous period—named after the large stores of what became coal deposits. The evidence, presented online in the [June 29 edition of the journal \*Science\*](#), suggests that the evolution of fungi capable of breaking down the polymer lignin, which helps keep plant cell walls rigid, may have played a key role in ending the development of coal deposits. With the arrival of the new fungi, dead plant matter could be completely broken down into its basic chemical components. Instead of accumulating as peat, which eventually was transformed into coal, the great bulk of plant biomass decayed and was released into the atmosphere as carbon dioxide.

“We’re hoping this will get into the biology and geology textbooks,” said Clark University biologist David Hibbett, senior author of the comprehensive study comparing the complete

genomes of dozens of species of fungi, most of which were sequenced at the DOE JGI. “When you read about coal formation it’s usually explained in terms of physical processes, and that the rate of coal deposition just crashed at the end of the Permo-Carboniferous. Why was that? There are various explanations. The evolution of white rot fungi could’ve been a factor – perhaps a major factor. Once you have white rot you can break down lignin, the major precursor of coal. So the evolution of white rot is a very important event in the evolution of carbon cycle.”

“The concept of the invention of an enzyme that can break down the ‘unbreakable’ is really great,” said Kenneth Nealson, Wrigley Chair in Environmental Studies and Professor of Earth Sciences and Biological Sciences at the University of Southern California. “The idea that a stable (inedible) form of organic carbon can become edible (and thus more difficult to bury over time), changes our perspective not only on global energy storage in the past, but on what it means for present day carbon sequestration and storage, in that sense this idea will have a big impact on our thinking about the past and the present.”

For their study, Hibbett and his colleagues focused on Basidiomycetes, which include mushroom species with the familiar cap-and-stem look that most people associate with fungi. Basidiomycetes also include brown rot fungi such as the dry rot that can destroy houses by breaking down the cellulose in the construction wood but leave the lignin untouched and white rot fungi of interest to the pulp and paper industries that can break down both types of polymers. Of the 31 brown rot and white rot fungal genomes that were compared for the study, 26 were sequenced at the DOE JGI, including a dozen that were done specifically for the study to flesh out representation of the fungal orders.



---

The “turkey tails” fungus *Trametes versicolor* (Nathan Wilson)

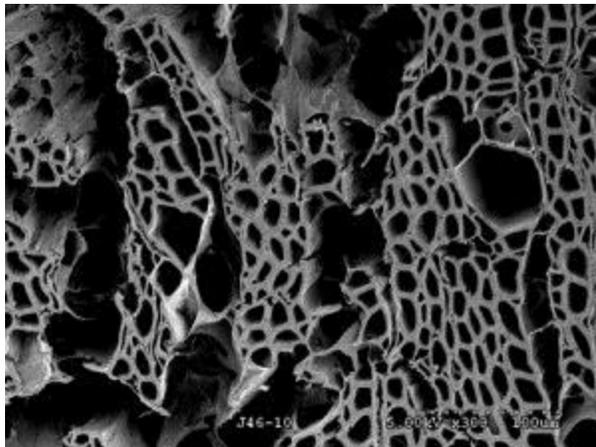
Igor Grigoriev, head of the DOE JGI Fungal Genomics Program noted that the comparative fungal genomics study underscores the abiding interest in support to DOE mission, to harness fungal enzymes for converting biopolymers such as cellulose into simple sugars to optimize biofuels production. In this pursuit, Grigoriev and his colleagues continue to contribute to growing list of firsts. “The first fungus ever sequenced at the DOE JGI was also the first genome of a white rot fungus,” he said. “A few years later, we sequenced the first

brown rot fungus. Less than a decade after that first fungal genome, we're presenting the first large-scale comparison of wood-decaying fungi."

With multiple fungal genomes on hand, the team compared DNA sequences, searching for gene families that encoded enzymes involved in wood decay. They focused particularly on enzymes called class II fungal peroxidases that turned out to be present in the lineages of white rot fungi but not in brown rot fungi, suggesting they played a role in breaking down the lignin in plants.

The researchers then used molecular clock analyses to track the evolution of the enzymes back through the fungal lineages. The idea is that just as the hands of a clock move at a defined rate around the dial, genes accumulate mutations at a roughly constant rate. This rate of change allows researchers to work backwards, estimating when two lineages last shared a common ancestor based on the amount of divergence.

The comparative analyses suggested that around 290 million years ago, right at the end of the Carboniferous period, a white rot fungal ancestor with the capacity to break down lignin appeared. Prior to that ancestor, fungi did not have that ability and thus the lignin in plant matter was not degraded, allowing these lignin-rich residues to build up in soil over time. Because molecular clock analyses have substantial error, fungal "fossils" are needed for calibration. For this study, the molecular clock analyses were calibrated against three fungal fossils. Hibbett said that more fossils would help improve the age estimate. "Unfortunately," he added, "fungal fossils are rare and easily overlooked." He said that his group is interested in trying to reconstruct that ancestral white rot fungal genome. "We're motivated to understand when this metabolic pathway responsible for lignin degradation came into existence. That's why we needed to have that many fungal genomes in this study. Up until fairly recently, it was so much work to just get one genome at a time. Now we have comparative fungal genomics projects as we're transitioning to a cool time with hundreds of fungal genomes."



---

SEM of wood being decayed by the white rot fungus *Fomitiporia mediterranea* (Robert Blanchette, University of Minnesota).

Joseph Spatafora, a professor at Oregon State University and co-author on the study, agrees with Hibbett's assessment that the group's findings could alter biology and geology texts. "When you look at this particular phenomenon of the decrease of coal deposition, by far the majority of explanations have been abiotic and that doesn't seem like that should be the entire story," he said.

Grigoriev said that this paper is the first product of the Genomic Encyclopedia of Fungi, the DOE JGI umbrella project that focuses fungal genome sequencing efforts on DOE-relevant missions in energy and the environment. "This paper is the first chapter in the Encyclopedia," he said, "The data generated has produced the most comprehensive catalog of lignocellulolytic enzymes yet, which is of interest to industry. We've now got the blueprint of all genes across very diverse phylogenies, and we'll get more. This is a huge step forward. The next milestone is the 1000 Fungal Genomes project to complete the entire diversity in Basidiomycetes."

As the head of the 1000 Fungal Genomes project, a part of the DOE JGI's Community Sequencing Program portfolio, Spatafora said that despite the goal of facilitating the sequencing of a thousand fungal genomes, two from each of 500 families, over five years, fungal genomics still has a long way to go. "There's an estimated 1.5 million species of fungi," he said. "We have names for about 100,000 species, and we're looking at 1,000 fungi in this project. This is still the tip of the iceberg in looking at fungal diversity and we're trying to learn even more to gain a better idea of fungal metabolism and the potential to harness fungi for a number of applications, including bioenergy. It's a really exciting time in fungal biology, and part of that is due to the technology today that allows us to address the really longstanding questions."

Video of Hibbett's "Evolutionary Perspectives on Diversity of Lignocellulose Decay Mechanisms in Basidiomycetes" presentation at the DOE Joint Genome Institute's 7th Annual Genomics of Energy & Environment Meeting on March 21, 2012 can be viewed here: <http://bit.ly/JGI7Hibbett>