

**DOE award number: FG02-87ER13712**

**Institution: Board of Regents of the University of Wisconsin System**

**Project title: Extracellular oxidative metabolism of wood decay fungi**

**PI: Daniel Cullen**

**Date of Report: April 21, 2010**

**Period covered: June 1, 1997 to May 31, 2009**

### **Final Technical Report**

Substantial progress has been made toward understanding the fundamental physiology and genetics of wood decay fungi, microbes that are capable of degrading all major components of plant cell walls. Efficient utilization of lignocellulosic biomass has been hampered in part by limitations in our understanding of enzymatic mechanisms of plant cell wall degradation. This is particularly true of woody substrates where accessibility and high lignin content substantially complicate enzymatic 'deconstruction'. The interdisciplinary research has illuminated enzymatic mechanisms essential for the conversion of lignocellulosics to simple carbohydrates and other small molecular weight products. Progress was in large part dependent on substantial collaborations with the Department of Energy's Joint Genome Institute (JGI) in Walnut Creek and Los Alamos, as well as the Catholic University, Santiago, Chile, the Royal Institute of Technology, Stockholm, the University of Minnesota, St. Paul, and colleagues at the University of Wisconsin and the Forest Products Laboratory. Early accomplishments focused on the development of experimental tools (2, 7, 22, 24-26, 32) and characterization of individual genes and enzymes (1, 3-5, 8, 9, 11, 14, 15, 17, 18, 23, 27, 33). In 2004, the genome of the most intensively studied lignin-degrading fungus, *Phanerochaete chrysosporium*, was published (21). This milestone led to additional progress on this important model system (6, 10, 12, 13, 16, 28-31) and was further complemented by genome analysis of other important cellulose-degrading fungi (19, 20). These accomplishments have been highly cited and have paved the way for whole new research areas.

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