

# Lawrence Berkeley National Laboratory

## LBL Publications

### Title

Comparative Genome Analysis of Basidiomycete Fungi Reveals the Genetic Signatures of Wood Degraders

### Permalink

<https://escholarship.org/uc/item/9525r9j0>

### Authors

Riley, Robert  
Salamov, Asaf  
Morin, Emmanuelle  
et al.

### Publication Date

2012-03-26

## **Comparative genome analysis of Basidiomycete fungi reveals the genetic signatures of wood degraders**

**Robert Riley**<sup>\*1</sup>, Asaf Salamov<sup>1</sup>, Emmanuelle Morin<sup>2</sup>, Laszlo Nagy<sup>3</sup>, Gerard Manning<sup>4</sup>, Scott Baker<sup>5</sup>, Daren Brown<sup>6</sup>, Bernard Henrissat<sup>7</sup>, Anthony Levasseur<sup>7</sup>, David Hibbett<sup>3</sup>, Francis Martin<sup>2</sup>, Igor Grigoriev<sup>1</sup>

<sup>1</sup>DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598

<sup>2</sup>Institut National de la Recherche Agronomique

<sup>3</sup>Department of Biology, Clark University, 950 Main Street, Worcester, MA 01610

<sup>4</sup>Razavi-Newman Center for Bioinformatics, Salk Institute for Biological Sciences, San Diego, CA 92186

<sup>5</sup>Pacific Northwest National Laboratory, PO Box 999 Richland, WA 99352

<sup>6</sup>USDA, ARS, MWA, NCAUR, BFPM, 1815 N University Street, Peoria, IL, 61604

<sup>7</sup>AFMB UMR 6098 CNRS/UI/UIII, Case 932, 163 Avenue de Luminy, 13288 Marseille cedex 9, France

March 2013

The work conducted by the U.S. Department of Energy Joint Genome Institute is supported by the Office of Science of the U.S. Department of Energy under Contract No. DE-AC02-05CH11231

## **DISCLAIMER**

This document was prepared as an account of work sponsored by the United States Government. While this document is believed to contain correct information, neither the United States Government nor any agency thereof, nor The Regents of the University of California, nor any of their employees, makes any warranty, express or implied, or assumes any legal responsibility for the accuracy, completeness, or usefulness of any information, apparatus, product, or process disclosed, or represents that its use would not infringe privately owned rights. Reference herein to any specific commercial product, process, or service by its trade name, trademark, manufacturer, or otherwise, does not necessarily constitute or imply its endorsement, recommendation, or favoring by the United States Government or any agency thereof, or The Regents of the University of California. The views and opinions of authors expressed herein do not necessarily state or reflect those of the United States Government or any agency thereof or The Regents of the University of California.

## Comparative genome analysis of Basidiomycete fungi reveals the genetic signatures of wood degraders

**Robert Riley**<sup>\*1</sup>, Asaf Salamov<sup>1</sup>, Emmanuelle Morin<sup>2</sup>, Laszlo Nagy<sup>3</sup>, Gerard Manning<sup>4</sup>, Scott Baker<sup>5</sup>, Daren Brown<sup>6</sup>, Bernard Henrissat<sup>7</sup>, Anthony Levasseur<sup>7</sup>, David Hibbett<sup>3</sup>, Francis Martin<sup>2</sup>, Igor Grigoriev<sup>1</sup>

<sup>1</sup>DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598

<sup>2</sup>Institut National de la Recherche Agronomique

<sup>3</sup>Department of Biology, Clark University, 950 Main Street, Worcester, MA 01610

<sup>4</sup>Razavi-Newman Center for Bioinformatics, Salk Institute for Biological Sciences, San Diego, CA 92186

<sup>5</sup>Pacific Northwest National Laboratory, PO Box 999, Richland, WA 99352

<sup>6</sup>USDA, ARS, MWA, NCAUR, BFPM, 1815 N University Street, Peoria, IL, 61604

<sup>7</sup>AFMB UMR 6098 CNRS/UI/UIII, Case 932, 163 Avenue de Luminy, 13288

Marseille cedex 9, France

\*rwiley@lbl.gov

Fungi of the phylum Basidiomycota (basidiomycetes), make up some 37% of the described fungi, and are important in forestry, agriculture, medicine, and bioenergy. This diverse phylum includes the mushrooms, wood rots, symbionts, and plant and animal pathogens. To better understand the diversity of phenotypes in basidiomycetes, we performed a comparative analysis of 35 basidiomycete fungi spanning the diversity of the phylum. Phylogenetic patterns of lignocellulose degrading genes suggest a continuum between the white rot and brown rot modes of wood decay. Patterns of protein kinases, secondary metabolic enzymes, and secreted proteins shed additional light on the broad array of phenotypes found in the basidiomycetes. We suggest that the lignocellulose gene content of an organism can be used to predict its nutritional mode, and predict *Dacryopinax* sp. as a brown rot; *Botryobasidium botryosum* and *Jaapia argillacea* as white rots.