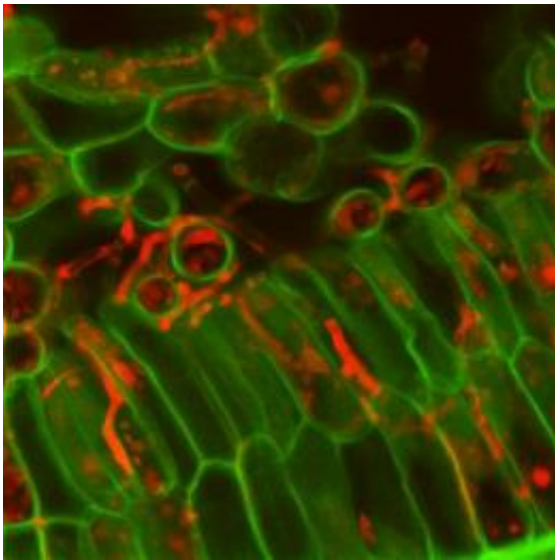


Formidable fungal force counters biofuel plant pathogens

May 3 2011



This is an original confocal microscopy image of infected leaves from poplar cv. Beaupre. Credit: Image by Stéphane Hacquard (INRA Nancy).

Fungi play significant ecological and economic roles. They can break down organic matter, cause devastating agricultural blights, enter into symbiotic relationships to protect and nourish plants, or offer a tasty repast. For industrial applications, fungi provide a source of enzymes to catalyze such processes as generating biofuels from plant biomass. One large fungal group with such enzymes are the rust plant pathogens which cannot survive on their own so they use crops as hosts, leading to reduced yields and potentially hindering efforts to grow biomass for

fuel. Factors that could reduce the growth of plant biomass, thus reducing biofuel production, are a target for investigation of the DOE Joint Genome Institute (JGI).

Published the week of May 2, 2011 in the early edition of the [Proceedings of the National Academy of Sciences](#), the work of an international team of researchers that included Fungal Genome Program head Igor Grigoriev, as well as several members from the DOE JGI, compared the genomes of two rust fungi to identify the characteristics by which these pathogens can invade their plant hosts and to develop methods of controlling the damage they can cause. The team led by co-first author Sebastien Duplessis of the French national agricultural research institute (INRA) worked on the poplar leaf rust fungus while a team led by co-first author Christina Cuomo of the Broad Institute of MIT and Harvard and Les Szabo from Agricultural Research Service USDA and University of Minnesota worked separately on the wheat and Barley stem rust fungus. The two-genome consortia joined their efforts to compare the genomic features of the two rust pathogens to reveal the role they play in infecting the host plant and acquiring nutrients.

Sequenced at the DOE JGI using the Sanger platform under the 2006 Community Sequencing Program, the 101-million base pair genome of *Melampsora larici-populina*, the first tree pathogen sequenced, was made publicly available in 2008. Poplar leaf rust outbreaks weaken poplar trees, a candidate bioenergy feedstock whose genome sequence was published by the DOE JGI in 2007. In this study *Melampsora larici-populina* was compared with the wheat stem rust fungus sequenced by the Broad Institute. This rust fungus causes major epidemics of both barley and wheat worldwide. A strain known as Ug99 has spread across Africa and into Central Asia, and overcome most of the stem rust resistant wheat varieties developed over the past 50 years. This is first joint fungal genomics study for the DOE JGI and the Broad Institute.

Sebastien Duplessis said that unlike wheat and other plants, it is difficult to estimate the economic damage resulting from poplar rust outbreaks though the most common figure indicates as much as 50 percent annual growth loss in poplar plantations following major rust epidemics. Part of the problem lies in the fungal method of attack. "For a perennial species such as poplar attacked by an obligate biotroph, the host is maintained alive and the tree is not killed," he said.

DOE JGI's Grigoriev noted that poplar rust and the wheat rust fungi are distantly related and show genome specific expansions in gene families. NRA's Francis Martin, a senior author on the study and long-time DOE JGI collaborator, said that the work means researchers now have the genomes of two fungi that interact with poplar in very different ways. Martin and his colleagues were part of the group that worked on the symbiont *Laccaria bicolor*, whose genome sequence was published in 2008. "[The *Melampsora* genome] will allow a better understanding on how a 'bioenergy' tree interacts with its cortege of microbial associates," he said. Grigoriev echoed Martin's comments about the benefits of having the genome sequences. "Learning how these all impact each other helps us to grow poplar and other crops for bioenergy production," he said.

Still, one of the goals of the project is to be able to determine how to disrupt the effectors by which the fungus can suppress host defense and recognition. In the paper, the team describes a two-pronged attack where the fungi mask their proximity to the plant and then use enzymes to attach the fungal cell wall to the plant cell wall and then invade the host.

"The precise analysis of these effectors, their localization and their targets in the host plant, and how they evolve to overcome plant resistances will contribute to the selection and management of sustainable resistances of poplar trees to the rust disease," said Duplessis.

He said the researchers plan to sequence more *Melampsora* genomes to better understand the process by which the rust fungus adapts to its host and overcome the plant's resistance. "Our paper demonstrates that the rust fungi genomes contain more than a thousand of such small effectors that likely interfere with plant perception systems and activation of defense reactions. Thus a targeted approach to disrupt the effectors entry and action might be complicated. However, sequencing the [rust fungus](#) genome opens great perspectives to study the evolution of these candidate effectors and further define new resistances through breeding strategies in tree plantations."

"With these blueprints we can then go and analyze at a population biology level the genetic diversity of pathogens as they evolve and adapt to control agents such as fungicides to develop more coordinated management strategies," said Pietro Spanu, a molecular plant biologist at Imperial College London who studies a mildew that is also a fungal pathogen. "The genome sequences are really toolkits," he said. "They give us lots of information on how the organisms evolved, allowing us to make hypotheses on what fungi need to become obligate parasites."

Spanu also said that the paper is part of a recent spate in genome publications on these fungi, and the information allows researchers to see for the first time the "remarkable convergences" in the evolution of these pathogens. "It's like discovering that in order to fly you need wings, and each group has different types of wings."

Provided by DOE/Joint Genome Institute

Citation: Formidable fungal force counters biofuel plant pathogens (2011, May 3) retrieved 13 May 2024 from <https://phys.org/news/2011-05-formidable-fungal-counters-biofuel-pathogens.html>

This document is subject to copyright. Apart from any fair dealing for the purpose of private study or research, no part may be reproduced without the written permission. The content is provided for information purposes only.