

NEWS RELEASE

Media Contacts: Dr. Ralph Dean, 919/513-0020 or ralph_dean@ncsu.edu
Mick Kulikowski, News Services, 919/515-3470 or
mick_kulikowski@ncsu.edu

April 20, 2005

Researchers Uncover Genome Sequence of Major Rice Pathogen

EMBARGOED FOR RELEASE UNTIL 1 P.M. EDT WEDNESDAY, APRIL 20

In a genomics milestone, an international consortium of researchers has for the first time lifted the veil from a fungal plant pathogen by sequencing the genome – or set of all genes – of the most destructive enemy of rice: *Magnaporthe grisea*, the fungus that causes rice blast disease.

Dr. Ralph Dean, professor of plant pathology and director of North Carolina State University's Center for Integrated Fungal Research, is the lead author of a research paper that describes the *M. grisea* genome, published in the April 21 issue of the journal *Nature*.

It is estimated that rice blast, the leading cause of rice loss, is responsible each year for killing enough rice to feed 60 million people worldwide.

In the *Nature* paper, Dean and his co-authors shed some light on the adaptations required by a fungus to cause disease. The researchers identify novel receptors that allow the fungus to recognize its environment; secreted proteins that are likely used as offensive weapons to damage rice plants; and redundant, or duplicate, mechanisms that protect the fungus from efforts to fight against it.

"It's a clever system," Dean says. "If you have important genes, you tend to have a lot of them."

The paper also reports that the *M. grisea* genome contains retro-elements, or remnants of viruses, living in what Dean calls "hot spots" in the genome.

"These virus remnants live in discreet parts of the genome and have high rates of recombination, which may be why the fungus can evolve new strains so quickly," Dean says.

M. grisea undoubtedly produces toxins which may enable it to be a more effective pathogen. However our knowledge is limited to date, Dean says. The genome sequence should

- more -

give researchers “a better idea of what types of genes are involved in making the toxin molecules,” he says.

Some of these genes reside in clusters, Dean says, so one focus will be to take apart the clusters and learn more about toxins and their production.

“The primary mission is to uncover the organism’s weaknesses. You do that by building up an arsenal of information of what genes are involved in plant-pathogen interactions,” Dean says.

In July 2002, Dean and researchers from the Whitehead Institute at MIT, now called the Broad Institute, issued a preliminary genome sequence of *M. grisea*, and made it publicly available so other researchers could work to solve the problems rice blast presents.

“That work decoded the string of letters that comprise the genome,” Dean says. “This paper shows the work of the last two years in bringing this genome to life.”

Bringing the genome to life means capturing the biological meaning of the genome, Dean says. To do this, he and his colleagues used two strategies: comparative genomics and functional genomics.

“In comparative genomics, you compare this genome to that of other organisms, other fungi,” Dean says. “But fungi are very diverse; they’ve evolved tremendously. Fungi within the same family are as dissimilar as man is to a frog.”

In functional genomics, Dean explains, scientists use comparative genomics to get hints about where to concentrate their study efforts.

“*M. grisea* contains about 11,000 genes, so you can’t look at every one,” he says. “The comparative study allows us to look at novel classes of genes and novel proteins and prioritize study efforts.”

- kulikowski -

Editor’s note: An abstract of the *Nature* paper follows.

“The Genome Sequence of the Rice Blast Fungus *Magnaporthe grisea*”

Authors: Ralph Dean, Thomas Mitchell, Resham Kulkarni, Huaqin Pan, Ignazio Carbone, Doug Brown, Yeon Yee, Nicole Donofrio, Robert Nicol, North Carolina State University; et al

Published: April 21, 2005, in *Nature*

Abstract: *Magnaporthe grisea* is the most destructive pathogen of rice worldwide and the principal model organism for elucidating the molecular basis of fungal disease of plants. Here, we report the draft sequence of the *M. grisea* genome. Analysis of the gene set provides an insight into the adaptations required by a fungus to cause disease. The genome encodes a large and diverse set of secreted proteins, including those defined by unusual carbohydrate-binding

- more -

domains. This fungus also possesses an expanded family of G-protein-coupled receptors, several new virulence-associated genes, and large suites of enzymes involved in secondary metabolism. Consistent with a role in fungal pathogenesis, the expression of several of these genes is upregulated during the early stages of infection-related development. The *M. grisea* genome has been subject to invasion and proliferation of active transposable elements, reflecting the clonal nature of this fungus imposed by widespread rice cultivation.