

Researchers sequence genomes of fungi that threaten wheat, poplars

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An international team of researchers co-led by a U.S. Department of Agriculture (USDA) scientist has sequenced the genomes of two fungal pathogens—one that threatens global wheat supplies and another that limits production of a tree crop valued as a future source for biofuel.

The sequencing of the genetic codes of [wheat stem rust](#) pathogen (*Puccinia graminis*) and poplar leaf rust pathogen (*Melampsora larici-populina*) is expected to help researchers develop control strategies to address worldwide threats to wheat fields and tree plantations. The study, published in the [Proceedings of the National Academy of Sciences](#), was a six-year collaborative effort of USDA's Agricultural Research Service (ARS), the U.S. Department of Energy Joint [Genome](#) Institute, the National Science Foundation, the Broad Institute of Harvard and the Massachusetts Institute of Technology, the University of Minnesota and the French National Institute for Agricultural Research.

"The threats these pathogens pose to two essential agricultural products are very real, and that makes it important to learn everything we can about them, from their molecular underpinnings to how they survive and spread infection," said Edward B. Knipling, administrator of ARS, USDA's principal intramural scientific research agency. The research supports the USDA priority of developing new sources of bioenergy and promoting international food security.

Wheat stem rust causes major epidemics of both barley and wheat worldwide. A strain known as Ug99 has spread across Africa and into

Central Asia, and has been able to overcome most of the stem-rust-resistant wheat varieties developed over the past 50 years.

Poplar leaf rust can cause significant losses in [poplar tree](#) plantations. Poplar is an important crop for the wood industry and is becoming increasingly important to the biofuel industry in the United States and Europe because of its rapid and significant production of biomass.

The study represents the first genome-wide characterization of any rust fungus, a diverse group of more than 6,000 species, according to Les Szabo, a lead researcher on this project. Szabo works at the ARS Cereal Disease Laboratory in St. Paul, Minn.

Rust [fungi](#) depend on living tissue of their hosts for survival. The pathogens secrete proteins that enable them to block the host plant's defenses and steal nutrients. The research uncovered evidence that both pathogens have large numbers of such "effector" proteins, an indication that they likely co-evolved with their host plants, according to the study authors.

Because they need a plant host to survive, the pathogens can't be cultured in a laboratory and are notoriously hard to study. But the genetic sequencing opens a window into the never-ending arms race between these pathogens and their hosts, Szabo said.

The team's sequence data has been released in GenBank, a genetic database administered by the National Center for Biotechnology Information at the National Institutes of Health.

Provided by United States Department of Agriculture

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