

Scientists harvest answers from genome of grain fungus

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Evil forces thrive in an unstable environment. At least, that's the picture being painted in the first waves of data being reaped from the genome sequence of the fungal plant pathogen, *Fusarium graminearum*. The sequencing has provided scientists a road map to someday combat a fungus that infects wheat and barley crops, rendering them unusable.

In the Sept. 7 edition of the journal *Science*, Frances Trail, Michigan State University associate professor of plant biology and of plant pathology, and Jonathan Walton, professor in the MSU-Department of Energy (DOE) Plant Research Laboratory, joined scientists around the world in picking over the inner workings of the fungus. The discovery: The real estate in some parts of the chromosomes, where many switches of disease and toxins reside, is unstable. Other areas of the chromosomes, where basic metabolism and other vital functions dwell, are stable.

“Those unstable areas are places where the organism is ready to evolve,” Trail said. “In those genes there's a lot of mutation. They can change a lot without killing the fungus. The genes that are involved in basic metabolism can't change without killing the fungus.

“We're starting to see this kind of a pattern as genomes have been looked at. It tells us something about what makes a pathogen a pathogen.”

Understanding the layout of the genome is a high-stakes proposition. This fungus is a serious pathogen of wheat and barley in Michigan and

throughout the Midwest. It causes Fusarium head blight, which reduces grain yields, and taints grain with mycotoxins that have been found to be detrimental to human and animal health.

Fusarium begins its blighting ways as pinprick-sized pods that spit spores into the air. The spores float over grain fields, landing on flowering wheat and barley. The spores colonize the wheat flowers. The often cool, wet weather of the Midwest provides an ideal environment for the fungus to take hold.

The result: fields of blight, identified by withered, bleached heads of grain. At harvest, many of the grains are shrunken and white, and harbor the mycotoxins.

The fungal plant pathogen has some 14,000 genes sequenced. Trail said the roles of some of them are understood, including which ones help form the spores or help produce toxins. Trail's team figures that there are 2,000 genes dedicated to making the spores.

“Those spores have to get out to cause the new disease cycle,” she said. “If we can figure out that whole mechanism, it's likely that we can figure out a way to control it.”

Understanding the sequence is the first step in the process. From there, the task is understanding the makeup of the genes – where they're strong and organized, where they're unstable and ready to change strategy. For instance, Trail wonders if that flexibility in the pathogenic-holding parts of the chromosome is the reason this fungus can produce so many different mycotoxins – including zearalenone, which can mimic sex hormones in mammals, including possibly people, and potentially cause developmental and reproductive problems.

The research was funded by a joint program between the U.S.

Department of Agriculture, the National Science Foundation and the DOE as well as supported by the Michigan Agricultural Experiment Station. The sequencing was performed at the Broad Institute at MIT.

Walton's lab helped annotate the completed genome – that is, inspect a subset of the 14,000 gene sequences for accuracy and then compare them to genes in other organisms. In this way, they identified genes that Fusarium has that are lacking in related fungi that aren't pathogenic on plants.

“This gives us additional clues as to what Fusarium needs to be a pathogen, which we hope will lead to new strategies to control the disease”.

Source: Michigan State University

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