

Massive gene loss linked to pathogen's stealthy plant-dependent lifestyle

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These are pathogen-infected *Arabidopsis* plants. Credit: John McDowell, Virginia Tech

An international team of scientists, which includes researchers from Virginia Tech, has cracked the genetic code of a plant pathogen that causes downy mildew disease. Downy mildews are a widespread class of destructive diseases that cause major losses to crops as diverse as maize, grapes, and lettuce. The paper describing the genome sequence of the downy mildew pathogen *Hyaloperonospora arabidopsidis*, which attacks the widely studied model plant *Arabidopsis thaliana*, is the cover story of this week's edition of the journal *Science*.

In the paper, the sequence of *H. arabidopsidis* is compared with other fully sequenced genomes of destructive plant pathogens to shed light on

the differences in the ways microbes interact with their host and how those differences evolve. The payoff could be new ways to investigate how these pathogens wreak havoc and, in the long-term, finding how to prevent billions of dollars of losses for farmers growing crops across the globe.

Downy mildew pathogens are so highly specialized for parasitizing [plants](#) that they can no longer survive away from their hosts. However, they are close cousins of pathogens such as the Sudden Oak Death pathogen *Phytophthora ramorum*, which can attack hundreds of forest species but can also survive away from its hosts by feeding on dead plant matter. Comparisons of the [genetic sequence](#) of *H. arabidopsidis* with other related plant pathogens such as *P. ramorum* have revealed a massive loss of genes related to the microbe's plant-dependent lifestyle.

"Some plant pathogens like *H. arabidopsidis* must keep their host alive throughout the infection cycle in order to survive," said Brett Tyler, professor at the Virginia Bioinformatics Institute (www.vbi.vt.edu) at Virginia Tech and one of the lead authors of the study. "Others, including *Phytophthora* species that destroy soybean and [potato crops](#) as well as oak tree forests, keep plants alive for part of the time before killing and devouring the plant tissue. Now that we have the genome sequence for an obligate parasite member of this family of destructive pathogens, we can use that information to zero in on common genes that could be targeted to create new, widely effective disease control strategies."

Downy mildew and *Phytophthora* pathogens are oomycetes, fungal-like organisms that have evolved from marine algae. The availability of multiple genome sequences for oomycete plant pathogens is an important step in allowing scientists to build a picture of the host-pathogen evolutionary arms race.

"Many plant pathogens contain large families of related genes that serve as powerful weapons but can also trigger equally powerful immune responses in the plant," commented John McDowell (www.ppws.vt.edu/people/faculty/johnmcd/), an associate professor in Virginia Tech's Department of Plant Pathology, Physiology, and Weed Science and one of the project's leaders. "Our comparisons across multiple genomes revealed that many of these gene families have been reduced in size or completely discarded in *H. arabidopsisidis*. This evolution towards stealth helps explain why this mildew and its relatives are widely distributed and cause diseases on many important crops."

The *H. arabidopsisidis* [genome sequence](#) reveals large numbers of effector proteins, the molecules that invade plant cells to suppress plant immunity. It also reveals widespread reduction in the number of genes related to degradative enzymes and other molecules linked to the metabolism of nitrogen and sulfur, which suggests that *H. arabidopsisidis* has dispensed with many genes required for life away from the plant, instead focusing on genes that help it to stealthily take control of host cells. In fact, almost 7000 of the predicted genes in the sequence had no counterpart in the genome sequences of its less-refined *Phytophthora* relatives.

The massive gene loss that is evident in the *H. arabidopsisidis* genome will provide many clues on the evolutionary adaptation necessary for a pathogen to become fully dependent on a plant host. A complete understanding of host-pathogen interactions should lead to the development of novel means of protecting crops from losses in yield caused by disease. It could also help to identify new targets for pathogen control and help in the development of novel disease-resistant varieties.

In addition, several downy mildew pathogens are listed as potential bioterror threats to agriculture in the United States. Understanding how these [pathogens](#) attack crop plants should enable preventative measures

to be put in place.

More information: Baxter L, Tripathy S, Ishaque, N et al (2010) Signatures of adaptation to obligate biotrophy in the *Hyaloperonospora arabidopsidis* genome. *Science* vol. 330: issue 6010.

Read more about the *Hyaloperonospora arabidopsidis* sequence www.vbi.vt.edu/archive/pdf/new...idopsis-sequence.pdf

Provided by Virginia Tech

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