

Comparison of genomes of plant parasites provides solid clues for response

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As plant scientists unravel the genomes of plant pathogens, comparisons can be made of the different and not-so-different invasion strategies for the organisms that threaten crops. John McDowell, associate professor of plant pathology at Virginia Tech, points out similarities in the strategies of several devastating rusts and mildew.

Based on his own research and the published findings of other scientists, McDowell observes shared traits that different microbes have evolved to survive as absolutely dependent on their hostile hosts – and that can be targeted to turn on crop plant's resistance.

McDowell's comparison of three research articles about the defensive strategies of fungi and oomycetes (fungus-like [microbes](#)) that cause plant disease appears as an invited Commentary in the *Proceedings of the National Academy of Sciences (PNAS)* early edition published online the week of May 16.

Sebastien Duplessis of Nancy University, Champenoux, France, and his colleagues describe the genome of the organisms that cause stem rust of wheat and barley, leaf rust of poplar in an article* in the same issue of PNAS in which McDowell's Commentary appears. McDowell compares this work with two articles that appeared in the journal *Science* in 2010** that looked at adaptations strategies of powdery mildew and downy mildew. One of these articles reports the sequencing of the genome of the pathogen that causes powdery mildew by an international group that included McDowell and other Virginia Tech scientists.

Commonalities between the rust and mildew pathogens include the ability to keep a low profile by reducing the release of toxins that will elicit a response from the host's immune system and secreting molecules called effector proteins that sabotage the immune response in the host.

While questions remain, such as whether effector proteins contribute to alteration of cell structure and metabolism in the host plant, "It's important to know your enemies and the genomes of these devastating parasites have provided some important insights into the strategies that they use to sabotage the plant's immune responses," said McDowell. "It is now possible to translate pathogen [genome](#) data into better tools for diagnosis and disease forecasting. And by comparing the genomes of pathogens that infect different types of crops, we and other [plant pathology](#) researchers are developing and testing new ideas for breeding [crops](#) with stronger disease resistance genes."

More information: * Duplessis S, et al. (2011) Obligate biotrophy features unraveled by the genomic analysis of rust fungi.

[DOI:10.1073/pnas.1019315108](https://doi.org/10.1073/pnas.1019315108)

** Baxter L, et al. (2010) Signatures of adaptation to obligate biotrophy in the *Hyaloperonospora arabidopsidis* genome. *Science* 330:1549-1551

(www.sciencemag.org/content/330/6010/1549.short); and Spanu PD, et

al. (2010) Genome expansion and gene loss in powdery mildew fungi reveal tradeoffs in extreme parasitism. *Science* 330:1543-1546

(www.sciencemag.org/content/330/6010/1543.abstract)

Provided by Virginia Tech

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