

# **Basic microbiology research study unexpectedly uncovers practical findings for growers**

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*Phytobiomes*. Credit: The American Phytopathological Society

Cover cropping, or the practice of growing unharvested crops to protect and enrich the soil during off-season periods, is a promising approach to reducing some of the negative environmental impacts of production agriculture.

Cover cropping also has its risks, especially if dying [cover crops](#) encourage disease pressure that passes on to the next crop. Such is the unexpected lesson behind a recent study published in *Phytobiomes*, a new open-access journal of The American Phytopathological Society.

In this recently-published article, titled "Isolation of Cultivation-Resistant Oomycetes, First Detected as Amplicon Sequences, from Roots of Herbicide-Terminated Winter Rye," Dr. Matthew G. Bakker and several other researchers at the U.S. Department of Agriculture's Agricultural Research Service set out to describe the microbiology of dying rye cover crop roots and how their microbial communities changed over time in a field setting. What they unexpectedly discovered was the potential for elevated disease risk in corn following the use of cereal rye as a cover crop.

In this study, Bakker and colleagues took root samples from a field and brought them back to their lab for DNA analysis. Among the many microorganisms detected, they found that several less-known species of oomycetes, including *Pythium* and *Lagenaria* species, were commonly associated with cereal rye cover [crops](#). These microorganisms are often responsible for plant diseases.

After modifying standard methods to enable collection of these unusual *Pythium* species as pure cultures, researchers continued to study their activity in cover crop roots, including the period after the cover crops died and corn was planted for the regular growing season.

While this research was originally meant to be basic, the study unexpectedly turned out to have some very practical findings. In addition to describing and validating the microbiology of these rye cover crop roots, their work revealed that the *Pythium* species naturally passed on to the corn [plants](#) as they sprouted into seedlings, resulting in seedling disease.

"This study tells a neat story about how new research techniques can lead to unpredictable findings with important and practical applications," said Bakker. "It unexpectedly highlighted a need for more informed management of cover crops in order to minimize disease risk for crops that follow, such as corn."

"Another interesting aspect of this study was that the most abundant species of *Pythium* in the cover crop roots was different on one side of the field than on the other. From the perspective of pathogen biology and ecology, this is very interesting. Is this switch because of competition between the two? Or because of differences in habitat requirements? Or because of limited ability to move across the field?"

Other benefits of this study include...

- An improved understanding of the microbiology of dying plants in natural and managed ecosystems
- The demonstrated importance of using DNA technology to help detect the [microbial communities](#) associated with crops, as microorganisms can be difficult to cultivate in the laboratory
- An improved understanding of the ecology of oomycetes—and of the potential for shared pathogens between cover crops and grain crops

Bakker hopes this and similar work will spark more research in [root](#)-soil dynamics.

"There have been few studies to date that track microbial community dynamics in detail, especially in dying plant roots," said Bakker. "This is surprising, given how important plant roots are to the soil environment and how important below ground plant residues are to the formation of soil organic matter."

**More information:** Matthew G. Bakker et al, Isolation of Cultivation-Resistant Oomycetes, First Detected as Amplicon Sequences, from Roots of Herbicide-Terminated Winter Rye, *Phytobiomes* (2017). [DOI: 10.1094/PBIOMES-10-16-0011-R](https://doi.org/10.1094/PBIOMES-10-16-0011-R)

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