New paper published in Phytobiomes may lead to novel methods of Rhizoctonia solani control

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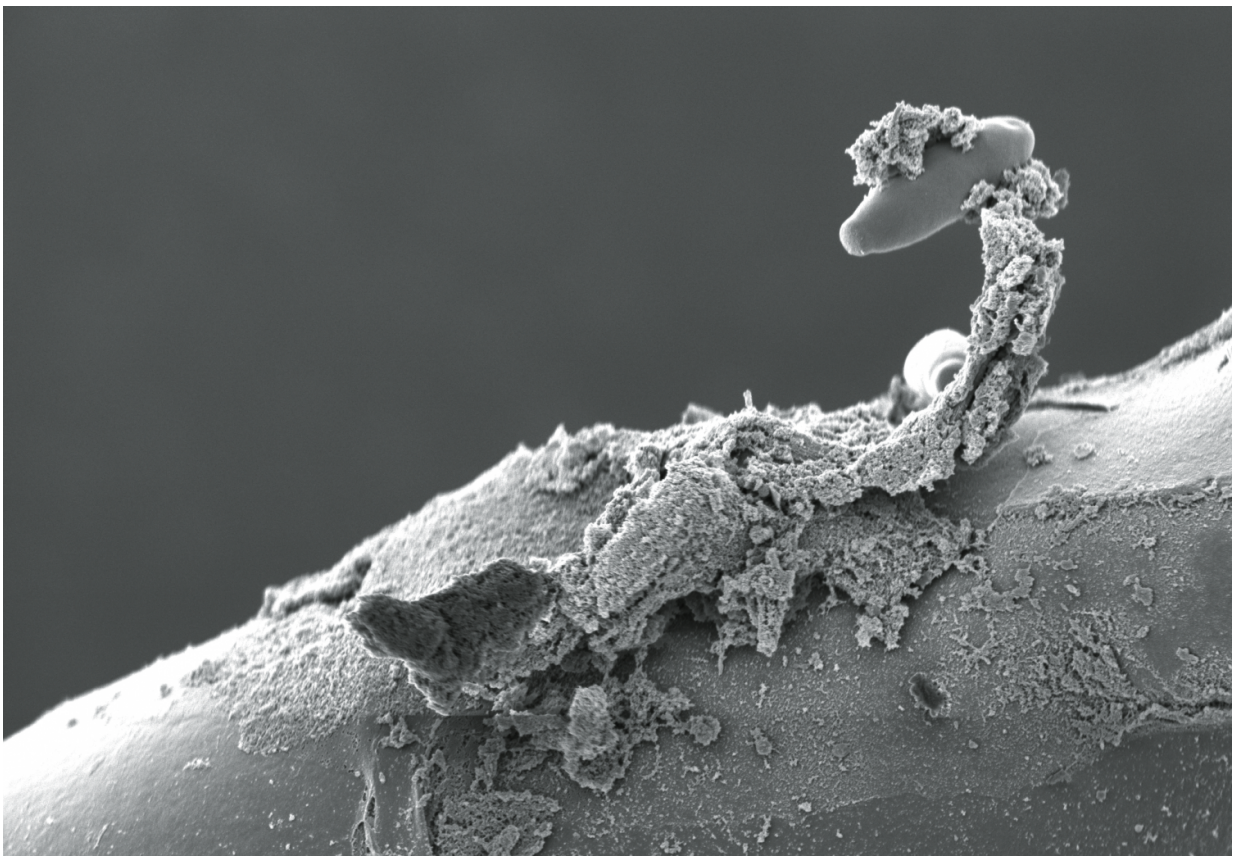

Scanning electron micrograph of the disrupted mycelia of a *Rhizoctonia solani* AG 2-2IIIB isolate showing a bacterium suspended in mid-air by aggregated scorpion-shaped fungal protoplast on a fungal hypha. Sample was prepared by fixation in paraformaldehyde, post-fixed in osmium tetraoxide, dehydrated in an alcohol series, and critical point dried. The dried sample was sputter coated with 5 nm Gold/Palladium and imaged using a Carl Zeiss Field Emission Scanning

Electron Microscope. Credit: The American Phytopathological Society

Rhizoctonia species—and *R. solani* specifically—are a complex group of soil fungi with broad host range and world-wide distribution.

In a research paper just published in *Phytobiomes*, a fully open-access journal of The American Phytopathological Society, University of Florida researcher Ken Obasa and colleagues identified a novel and important biological aspect of *R. solani* while investigating brown patch infected cool-season turfgrasses. The intriguing observation was that *R. solani* isolated from diseased tissue were persistently associated with bacteria during growth on solid media. This led them to uncover the impact of a bacterium on brown patch disease.

The findings of this study suggest that at least some *Rhizoctonia* species in the anastomosis group 2-2IIIB can harbor intracellular bacteria that affect the biology of their fungal host and, in turn, the way the fungus interacts with plants. Ultimately, this research helps raise the prospects for developing alternative *Rhizoctonia* disease management strategies in plants.

The article, titled "A Dimorphic and Virulence-Enhancing Endosymbiont Bacterium Discovered in *Rhizoctonia solani*," offered several interesting findings:

Phytobiomes journal cover image. Credit: The American Phytopathological

- An endosymbiotic bacterium can influence the disease phenotype of the turfgrass brown patch pathogen, as the disease was greater when the bacterium was present.
- The elimination of the bacterium from its fungal host by antibiotic treatment resulted in a significant decrease in the production of the virulence factor phenylacetic acid (PAA).
- Wild-type *R. solani* and *R. solani* cured of the endosymbiontic bacterium appear genetically identical, with no variation seen in cultural characteristics and DNA profile, which suggests that the changes in PAA production and virulence could be attributed to the loss of the bacterium.

This and similar recent discoveries raise important questions about the distribution and significance of fungal microbiomes to our understanding and management of phytopathogenic fungi.

"This research provides novel insights into fungal-bacterial symbioses, and sheds light on the complexity of within-microbiome interactions to enhance fungal virulence and plant disease," said Dr. Carolyn Young, Editor-in-Chief of *Phytobiomes*. "This research represents phytobiomes in action, fungal-bacterial interaction that enhance the virulence of a plant pathogen. We can now utilize this knowledge to identify better management strategies for the disease."

More information: Ken Obasa et al, A Dimorphic and Virulence-Enhancing Endosymbiont Bacterium Discovered in, *Phytobiomes* (2017). DOI: 10.1094/PBIOMES-08-16-0005-R