New and novel technologies successfully demonstrated in soilborne disease study

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Sudden Death Syndrome (SDS), a prominent soilborne disease of soybean, can be devastating. Yield losses from SDS can reach 100%, depending on the soybean variety affected and stage of development

when symptoms appear.

Due to increased occurrence, SDS has been studied a lot in recent years, and soil profiling is a major tool for researching this fungal disease. To date, nearly all soil profiling involves identifying the soil's physical and chemical characteristics wherever SDS is present.

In a new *Phytobiomes* journal article, titled "Unraveling Microbial and Edaphic Factors Affecting the Development of Sudden Death Syndrome in Soybean," Srour, et al. show the scientific community a new way of analyzing the soil to determine the incidence and the severity of SDS: by profiling not only the soil's physical and chemical properties, but the soil's microbes.

"The occurrence of SDS in fields is dependent on physical and biological factors, and the suppressiveness of soils to disease is a long-known phenomenon," said Dr. Ahmad Fakhoury, Associate Professor at Southern Illinois University and corresponding author of the article. "Promoting and sustaining the soil's natural suppressiveness to disease can be integral to the effective, sustainable management of soilborne pathogens."

In this study, investigators analyzed soil samples from 45 soybean fields in Illinois, Iowa, and Minnesota. Samples were collected from symptomatic patches in fields, as well as adjacent areas where SDS foliar symptoms did not develop.

Novel tools and techniques were then used in this research to detect microbial populations in "diseased" and "healthy" soils and to correlate their presence with the incidence and severity of SDS.

Through these samples, Srour et al. studied the role of soil microbial communities, as well as the soil samples' physical and chemical

properties in relation to SDS development. They measured multiple soil-related factors and used markers specific to bacteria, fungi, archaea, oomycetes, and nematodes coupled with sequencing, to identify key taxa likely associated with SDS development.

Through these methods, they generated 14,200,000 sequences and mapped them against the National Center for Biotechnology Information's nucleotide database and taxonomically compared them using several bioinformatics tools.

This unique method of analysis found significant differences in the bacterial and fungal community structures between healthy and diseased areas of fields, suggesting the relative abundance of multiple microbial taxa in the soil is a key determinant in the incidence of SDS.

"The work presented in this article, documents the first attempt to assess the importance of biological factors in determining the incidence of Sudden Death Syndrome (SDS) in soybean using metagenomic tools," said Fakhoury. "This is basically a first attempt at resolving the complexity of the biological interactions that affect the occurrence of this disease."

Fakhoury says their novel approach and research techniques are important in several other ways:

- These techniques can be used to indicate the 'health' of the soil and its ability to sustain *Fusarium virguliforme*, the main fungal pathogen that causes SDS.
- Others can build on this research to further characterize the role of species affecting *F. virguliforme* and to study the biology of their interactions.
- Similar techniques can be used to study other soilborne pathogens and diseases in the quest for their efficient and

sustainable management.

"The emerging tools and techniques we used permit the differentiation of complex microbial interactions," said Fakhoury. "This will ultimately allow us to devise and adopt more efficient and sustainable strategies to manage SDS and other diseases that are detrimental to agricultural production."

More information: Ali Y. Srour et al, Unraveling Microbial and Edaphic Factors Affecting the Development of Sudden Death Syndrome in Soybean, *Phytobiomes* (2017). DOI: 10.1094/PBIOMES-02-17-0009-R

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