

S3T4**Characterization of fungal communities associated with soybean cyst nematode infested fields in Ohio using synthetic long-read amplicon sequencing**

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Abstract

Heterodera glycines, the soybean cyst nematode (SCN), is the most economically important pathogen of soybean causing yield losses of over \$1.5 billion in the US alone. Ohio is one of the biggest producers of soybean in the US and SCN has been detected in 82% of its counties. Although the importance of this pathogen is clear, the control measures available are limited to cultural practices and the use of resistant cultivars. Alternative methods, like the use of biological controls, have been studied and fungal groups have shown promising results in addressing SCN infestation. However, the soil microbial communities of soybean fields infested with SCN in the state of Ohio have not been characterized to identify potential biocontrol agents. In this study, we analyzed 170 soil samples with different levels of SCN infestation from 0 to 15,800 SCN eggs per cm³ of soil from 26 counties in Ohio collected in 2019 and 2021. Fungal barcoding ribosomal genes were sequenced using synthetic long-read technology and analyzed to identify the fungal communities present in these soil samples. From our analysis, we found that SCN infestation did not significantly affect the diversity or richness of fungi in the soil. We also learned that SCN infestation was not a primary driver of fungal community composition. While large-scale effects in fungal communities were not seen at different levels of SCN infestation further analysis could uncover fine-scale differences that might point to fungal groups with potential biocontrol activity in the state of Ohio.

