Improvements to field detection and genomic characterization of *Streptomyces* species

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Common scab on potato is caused by plant pathogenic Streptomyces species, which often contain a pathogenicity island (PAI) that produces a phytotoxin (Thaxtomin A). Real-time polymerase chain reaction (qPCR) can detect Thaxtomin synthetase genes (*txt*) in soils spiked with Streptomyces. However, common scab is not caused by a single Streptomyces species, making field detection assays to accurately assess infection challenging. Additionally, there is tremendous diversity between *Streptomyces* genomes with different species causing varying levels of disease. In this study, we tested the application of a qPCR assay in the greenhouse and the field to amplify *txt*AB and determine if cycle threshold (Ct) values correlated with post-harvest disease scores in soil inoculated for different strains of Streptomyces ranging in concentration from 103 to 107 CFUs/ pot and in potato fields with unknown levels. The assay accurately detected the amount of Streptomyces in greenhouse soils, but the field trials showed greater variability between Ct values and disease scores, indicating that additional factors have a larger impact on disease in the field. To better understand this diversity among pathogenic Streptomyces species, accurate and complete reference genomes are needed. We report the completed or improved genome S3.73 assemblies for 35+ Streptomyces assembled using Illumina short reads with either ONT or PacBio long reads in several hybrid assembly pipelines, as well as a workflow guide for completing these and additional Streptomyces genomes for improved analyses.