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Developing metagenomic sequencing as a tool for pathogen surveillance and epidemiology

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Abstract

Plant disease diagnostics and genetic epidemiology are critical tools for effective pathogen detection, management, and surveillance. Metagenomics is a high-throughput sequencing tool that can document disease dynamics. We hypothesize that metagenomics can track the genetic changes of the pathogen over time, capture the interaction with the host microbiome and explain limitations with current diagnostic tools. To test this hypothesis, we used bacterial soft rot and blackleg of potato, caused by *Pectobacterium* and *Dickeya* species. These diseases are challenging for current diagnostic tools because of high pathogen genomic variability, identical symptom development, and co-infections. We conducted a diagnostic metagenomics analysis on several samples collected from symptomatic potato tissues in Wisconsin over 2017–2020. We identified *Pectobacterium*- and *Dickeya*-specific sequences from the metagenomic data and assembled partial up to near-complete *Pectobacterium* and *Dickeya* genomes from several samples. Through this analysis, we were able to describe the microbial diversity associated with each sample and document virulence-related genes in the microbial population that could serve as a resource for pathogenicity. In symptomatic tissues where traditional molecular techniques failed, metagenomics revealed *Dickeya* and *Pectobacterium* species. Metagenomics demonstrates the current limitation of some diagnostic tools to detect the causal agent(s). Overall, these results show that metagenomics is an effective method for potato disease diagnosis with the potential, in the future, to impact seed potato certification. We hope this work can be used as a comprehensive reference for molecular epidemiology and diagnostics by utilizing metagenomics as an incorporated tool in disease management strategies.

