

Plant Pathology Seminar Series



“Development of Comprehensive Molecular Detection of Potato Pathogens”

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Abstract

Potato production and quality are affected by a whole variety of infectious diseases caused by viruses, bacteria, fungi, chromists, and nematodes. Early detection and identification of causal pathogens are important to prevent crop loss from diseases. However some diseases are difficult to diagnose due to the absence of characteristic symptoms. For example, soilborne pathogens may elicit above ground symptoms (e.g., wilting, chlorosis, and stunting) that are not unique, not caused by one particular pathogen, and often appear in the late stages of disease. Once disease is visible, it is too late to treat plants due to a lack of curative treatments available. Thus, there is a need for a comprehensive pathogen detection and identification method for plant disease diagnosis. Nucleic acid-based detection methods have shown to be a good choice for plant pathogen detection due to their accuracy and sensitivity, and are, on some occasions, advantageous over conventional methods such as symptom-based or in vitro growth-based disease diagnosis. Quantitative real-time PCR (qPCR) is a reliable tool to detect pathogen genome fragments in specimens and has been used as a versatile, practical application in plant disease diagnostics. High-throughput sequencing (HTS) is an emerging technology as disease diagnostics. Among several HTS methods available, the nanopore-based sequencing MinION is favored for its long-read sequencing capabilities, portability, and relatively inexpensive cost. In this project an on-site sequencing pipeline for comprehensive pathogen detection was developed for potato disease diagnosis using MinION in combination with qPCR. The comprehensive molecular detection developed in this study will be a useful diagnostic tool that contributes to disease risk assessments in the future to assist in decision-making for the application of pesticides, avoiding high-risk fields, matching cultivars to fields according to their respective resistance ratings and disease risk, crop rotation strategies, irrigation regimes, and prioritizing land according to the crop end use. In addition, the sequencing pipeline developed in this study can be adopted for diseases of other crops and even animals.

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Zoom Link: <https://wsu.zoom.us/j/93395333254?pwd=OVlwWk8xcnNadVluVjFYUW5hWWx1dz09>

Meeting ID: 933 9533 3254

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