Plant Pathology Seminar Series

"IDENTIFICATION OF EFFECTOR GENES FOR THE SPINACH FUSARIUM WILT PATHOGEN, *FUSARIUM OXYSPORUM* F. SP. *SPINACIAE*"

Alexander M. Batson

The maritime Pacific Northwest is the only region of the United States suitable for spinach seed production, where mild and dry summers with long day length enable production of high yields of quality seed. Spinach Fusarium wilt, caused by *Fusarium oxysporum* f. sp. *spinaciae*, is the greatest biotic limitation to spinach seed production in this region. Management strategies for Fusarium wilt in spinach seed crops in the maritime Pacific Northwest provide partial or transient suppression of the pathogen. Many parent lines used for hybrid seed production are highly susceptible to the disease. Furthermore, hybrid spinach seed crops are grown on a contract basis because of the proprietary nature of the parent lines, so seed growers usually do not have a choice regarding which inbred lines they are contracted to plant. Recently, host-specificity of other *F. oxysporum* formae speciales (ff. spp.) has been found to be associated with unique combinations of effector genes that are important for pathogenicity. The specific combinations of effector genes have been used to differentiate among *F. oxysporum* ff. spp., and even among races of the same forma specialis. However, almost nothing is known about the profile of effector genes associated with *F. oxysporum* f. sp. *spinaciae*, i.e., what determines host-specificity to spinach genetically.

In this study, *Fusarium* isolates (n = 69) were characterized: i) phenotypically for pathogenicity to spinach using three inbred lines that differ quantitatively in susceptibility to Fusarium wilt; and ii) genotypically for the presence of a family of 14 putative pathogenicity genes, known as the *Secreted in Xylem* (*SIX*) genes, that have been used to differentiate isolates of other *F. oxysporum* ff. spp. Thirty-nine isolates of *F. oxysporum* f. sp. *spinaciae* from diverse geographic regions (AR, CA, OK, OR, TN, WA, Italy, and Japan) and years of spinach production were characterized into two pathogenicity groups based on differential wilt severity ratings for the three spinach inbred lines. Only two of the 14 known *SIX* genes, *SIX8* and/or *SIX14*, were detected in the 39 isolates of *F. oxysporum* f. sp. *spinaciae* - four isolates had only *SIX8*, 18 isolates had only *SIX14*, and 17 isolates had both *SIX8* and *SIX14*. However, these *SIX* gene profiles did not differentiate isolates of this spinach pathogen from other *F. oxysporum* isolates that were not pathogens of spinach. Therefore, full genome sequencing was used to identify other unique putative effector gene profiles associated with isolates of the spinach pathogen. The Illumina platform (for 6 isolates) and the Pacific Biosciences platform (for 1 isolate) were used to sequence the genomes of *F. oxysporum* f. sp. *spinaciae* isolates. In addition, five non-pathogenic isolates of *F. oxysporum* that were found in association with spinach plants, spinach seed, or soil in which spinach plants had been grown, were sequenced using the Illumina platform. In total, 48 putative effector genes were predicted using a software pipeline developed in Dr. Martijn Rep's program at the University of Amsterdam. The presence or absence profile of these 48 effector genes differentiated the seven *F. oxysporum* f. sp. *spinaciae* isolates from the five isolates that were not pathogenic to spinach. Furthermore, two profiles of effector genes were detected for the spinach pathogen that discriminated isolates of the two phenotypic groups of *F. oxysporum* f. sp. *spinaciae* associated with wilt severity on the three spinach inbred lines. Characterization of these predicted effector genes and other regions of the genome of *F. oxysporum* f. sp. *spinaciae* will be carried out to understand mechanisms of pathogenicity, develop molecular tools for rapid detection and quantification of this pathogen, and facilitate breeding spinach cultivars with increased levels of resistance to Fusarium wilt.

9:30 am | Thursday, June 6 | Johnson Hall 343

MS Exit Seminar

College of Agricultural, Human, & Natural Resource Sciences
Washington State University