

THE SEARCH FOR GENETIC DIFFERENCES BETWEEN GRAPE STRAINS OF *XYLELLA FASTIDIOSA*

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Reporting Period: The results reported here are from work conducted January 2009 through July 2009.

ABSTRACT

To create a reliable genetic fingerprint of the Texas Pierce's disease (PD) strains of *Xylella fastidiosa* we have been evaluating both highly variable sequences (small sequence repeats) and genes that are either highly conserved (gyraseB) or moderately conserved (ZOT). To speed the hunt for genes with fingerprinting potential we performed a whole genome comparison (Nimblegen microarray) between the Temecula strain (ATCC) and a Texas strain (Gil Bec 514). Gene regions with potential single nucleotide polymorphisms (SNPs) were further analyzed by individual gene sequencing. We sequenced four genes (pilY, a multi-drug efflux transporter, a phage-related tail protein and a periplasmic protease) for five Texas PD strains in triplicate. On one gene all Texas strains showed one SNP difference from the Temecula strain, two genes showed variable SNPs with only some Texas strains giving a complete match with Temecula. Finally, one gene showed one or more SNP difference between all Texas PD strains and Temecula. These SNP differences will be compared to other genetic analyses to determine the most reliable method for identifying genetic variability within Texas.

Section 4:
Pathogen
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