

GENOTYPING GRAPE *XYLELLA FASTIDIOSA* ISOLATES IN TEXAS

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ABSTRACT

Pierce's disease (PD) pressure has always been intense along the Texas Gulf Coast, but the disease has been steadily moving north and west. Additionally, PD has been discovered in counties thought to be beyond the ecological range of either the *Xylella fastidiosa* (*Xf*) bacterium or the insect. As part of our genetic analysis we are analyzing conserved genes (such as *gyrB*) to distinguish new isolates as either 'grape,' 'ragweed' or 'oleander.' However, base pair changes within conserved genes are usually too limited to track genetically relatedness within short time periods. To improve discrimination power, we are using multi-locus simple sequence repeat markers for genotyping each individual isolate. Eighteen grape isolates have been fingerprinted so far. The most similar isolates are found in the same county, but some counties have multiple, genetically distinct isolates. Isolates from new infection areas will be run to determine the relationships with other sources. Additionally, *Xf* SSR genotyping profile in Texas will be analyzed and compared with the profile from California isolates.

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Section 4: Pathogen and Disease Management



