

A SURVEY OF INSECT VECTORS OF PIERCE'S DISEASE (PD) AND PD-INFECTED PLANTS FOR THE PRESENCE OF BACTERIOPHAGE THAT INFECT *XYLELLA FASTIDIOSA*

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INTRODUCTION

Pierce's disease (PD) is an incurable disease of grapevine caused by strains of *Xylella fastidiosa*. The bacterium gains entrance into the grapevine through the feeding activities of the blue-green sharpshooter, *Graphocephala atropunctata* (Purcell, 1975) and the glassy-winged sharpshooter, *Homalodisca coagulata* (Purcell, 1979). PD is endemic to California, however, with the recent detection of the glassy-winged sharpshooter (GWSS) in California, patterns of PD distribution are likely to change and host plant infection and/or associated plant death rates are likely to soar (Purcell, Personal Communication).

Bacteriophage (phage) therapy is considered an unconventional pathogen countermeasure where viruses are used to kill specific bacteria, primarily pathogens. Recent successful endeavors using phage to control *Lactococcus garvieae* infection in yellowtail (Natai et al., 1999) and the discovery that the natural antibiotic in dog saliva is a bacteriophage (Matzinger, and Arnheiter, 2000) lend momentum toward the exploration and use of novel ways to control many different bacterial infections. Our proposal addresses the possibility that phage exist in nature that infect *X. fastidiosa* and that these phage may be useful for PD control or management.

OBJECTIVES

1. To screen wild *Graphocephala atropunctata*, *Homalodisca coagulata*, and plants with PD for the presence of bacteriophage.
2. To test any/all acquired bacteriophage for its/their ability to infect and destroy *Xylella fastidiosa*.

RESULTS AND CONCLUSIONS

X. fastidiosa isolated from grapevine with PD were found to be infected with what we believe to be two different bacteriophage. One phage type possesses a shape and size resembling phage in the family Microviridae, while the size and shape of the second phage resemble those in the family Podoviridae. Bacteriophage in the Podoviridae are known to infect *Xanthomonas* spp. which are bacterial relatives of *X. fastidiosa*. Currently, we are attempting to isolate these phage. Once isolated, we will attempt to infect a pure culture of *X. fastidiosa* to monitor and describe the destructive nature of the viruses.

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