

EVOLUTION OF *XYLELLA FASTIDIOSA* AVIRULENCE

Project Leader:

Rodrigo Almeida
Department of ESPM
University of California
Berkeley, CA 94720
rodrigo@nature.berkeley.edu

Collaborator:

Steven Lindow
Dept. of Plant & Microbial Biology
University of California
Berkeley, CA 94720

Reporting Period: The results reported here are from work conducted July 2007 to September 2007.

ABSTRACT

The main objective is to quantitatively and qualitatively determine how and when *Xylella fastidiosa* (*Xf*) loses pathogenicity and potentially transmissibility, after serial passages *in vitro*. We will replicate *Xf in vitro* for several generations, creating parallel populations that are not pathogenic and maybe not transmissible by insects. We will study host plant colonization by and insect transmission to grape of these populations. Once phenotypes of interest are identified (e.g. reduced pathogenicity or transmissibility), we will compare these *Xf* populations with the original isolate and search for differences. Tools to identify phenotypical differences will include pathogenesis and insect transmission assays, molecular differences will be identified with genomic and proteomic approaches. We will also be able to quantify the rate of genetic change in these populations, providing a molecular calibration data for researchers interested in *Xf* evolution, diversity and ecology.

INTRODUCTION

Much has been learned in the last few years regarding the biology of *Xylella fastidiosa* (*Xf*). In addition, recently reported research has demonstrated, under laboratory conditions, that proof-of-concept approaches to disease control may be successful. Hopkins (2005) tested the capability of weakly virulent and avirulent *Xf* isolates to control infections of pathogenic isolates of the same pathogen. Biological control of plant pathogens with avirulent strains is not a new idea in phytopathology, in fact, it has been successfully used in many occasions. However, it had never been tested for *Xf*. Hopkins' work demonstrated that this approach has great potential to control Pierce's disease (PD) under field conditions.

This project explores the idea developed by Hopkins (2005) that avirulent isolates of *Xf* can control PD symptom progression in grapevines. If such strategy is ever to be used to control PD, understanding how it works will be of paramount importance. To achieve such objective, we propose to conduct research with a pathogenic isolate that has been sequenced, develop avirulent descendent populations of such isolate, and study their ability to reduce disease progression in plants challenged with the original pathogenic isolate. We will also take advantage of the fact that *Xf* can be stored in -80°C to keep samples of the pathogen as it becomes avirulent. This will allow us to retrospectively study when and how an isolate lost pathogenicity, and what is the impact of such change on *Xf*'s biology.

OBJECTIVES

1. Generation of *in vitro* evolved populations
2. Phenotypical and molecular characterization of populations
3. To test avirulent populations as PD biological control agents

RESULTS

This work is ongoing. So far we have sequentially transferred 10 parallel populations of *Xf* on solid media for 50 weeks (estimated 1,150 generations) and have those stored in a -80°C freezer for phenotypical characterization.

CONCLUSIONS

This work is ongoing (objective 1) and the characterization of populations and testing of avirulent isolates as biological control agents will be performed in 2008

REFERENCES

Hopkins, D.L. 2005. Biological control of Pierce's disease in the vineyard with strains of *Xylella fastidiosa* benign to grapevine. Plant Disease 89: 1348-1352.

FUNDING AGENCIES

Funding for this project was provided by the CDFA Pierce's Disease and Glassy-winged Sharpshooter Board.