

THE *XYLELLA FASTIDIOSA* CELL SURFACE

Project Leader:

Michele M. Igo
Section of Microbiology
Division of Biological Sciences
University of California
Davis, CA 95616

Cooperators:

Bruce Kirkpatrick
Dept of Plant Pathology
University of California
Davis, CA

M. Andrew Walker
Dept of Viticulture and Enology
University of California
Davis, CA

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INTRODUCTION

Pierce's disease is caused by the Gram-negative bacterium *Xylella fastidiosa*, which has been classified as a member of the gamma subgroup of the Proteobacteria and is phylogenically related to the *Xanthomonads*. *X. fastidiosa* is highly specialized and occupies two very different environmental niches. Specifically, the bacteria are capable of multiplying in both the foregut of xylem-feeding insects, such as the glassy-winged sharpshooter and in the xylem system of the host plant. The ability of *X. fastidiosa* to thrive in both the insect foregut and the xylem suggests that the bacterium has evolved regulatory mechanisms that help it to cope with the unique stresses experienced in these two very different ecological niches.

A common response of Gram-negative bacteria to such stresses is to change the composition of their cell surface, particularly the protein composition of their outer membrane. The outer membrane is the outermost continuous structure on the bacterial cell surface and serves as a selective barrier between the cell and the external environment. Changes in the protein composition of the outer membrane are known to have a profound effect on the sensitivity of Gram-negative bacteria to detergents, antibiotics, and bacteriophages. Therefore, in order to develop effective methods for controlling the spread of *X. fastidiosa*, it is important to obtain information concerning the protein composition of the *X. fastidiosa* outer membrane in general and how the composition of this membrane changes in response to environmental signals. The overall goal of this proposal is to identify the major outer membrane proteins of *X. fastidiosa*, to assign the individual proteins to specific genes on *X. fastidiosa* chromosome, and to determine how the relative abundance of these proteins changes in response to environmental signals.

OBJECTIVES

1. Identify the major outer membrane proteins of *Xylella fastidiosa* and assign them to a specific gene on the *Xylella fastidiosa* chromosome.
2. Determine how the protein composition of the *Xylella fastidiosa* outer membrane is influenced by environmental signals and signals from the infected grapevine.

RESULTS AND CONCLUSIONS

We have just received the funding for this project (October 2002).

FUNDING AGENCIES

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