

IDENTIFICATION AND CHARACTERIZATION OF PROTEOMIC EXPRESSION OF GRAPEVINES IN RESPONSE TO *XYLELLA FASTIDIOSA* INFECTION

Principal Investigator:

Hong Lin
Crop Dis., Pests, & Genet. Res. Unit
USDA ARS
Parlier, CA 93648

Cooperator:

Litao Yang
Agricultural College
Guangxi University
Nanning, Guangxi 530004, China

Cooperator:

M. Andrew Walker
Dept. of Viticulture and Enology
University of California
Davis, CA 95616

ABSTRACT

Xylella fastidiosa (*Xf*) is the bacterial causal agent of Pierce's disease (PD) of grapevines, as well as of other economically important diseases in a number of agronomic, horticultural and ornamental plants. In this study, comparative proteomic analyses were carried out to identify proteins differentially expressed in *Xf*-infected grape stems from a pair of siblings of 9621-67 (highly resistant) and 9621-94 (highly susceptible) grapevines from a cross of *Vitis rupestris* x *V. arizonica* (Yang et al., 2011). The identification of proteins and their expression pattern under given physiological conditions is of fundamental importance for functional analyses of cellular processes associated with PD development and resistance. The proteins were isolated from the stems of healthy and *Xf*-inoculated plants at one, six, and 12 weeks after inoculation. The total proteins were then separated by a 2D-PAGE system and the spots representing differentially expressed proteins were analyzed by an oMALDI-TOF-MS/MS Mass Spectrometry. Protein identification was performed using BLASTp and tBLASTn against NCBI non-redundant protein databases and EST databases. Ten proteins that were differentially expressed at different time points after inoculation were identified. For example, a thaumatin-like protein and the pathogenesis-related protein 10 from both genotypes, and the 40S ribosomal protein S25 from the susceptible genotype were up-regulated in response to *Xf*-infection. Furthermore, the expression of the thaumatin-like protein increased sharply 12 weeks post-inoculation in the PD-resistant genotype only. Three heat shock proteins, 17.9 kDa class II, protein 18 and 21 were highly expressed in healthy tissues compared with those in tissues infected with *Xf*. In addition, a down-regulated putative ripening related protein was found in the *Xf*-inoculated PD-susceptible genotype. Glycoprotein and formate dehydrogenase were identified in the PD-resistant genotype and their expression was constant during plant development. A putative GTP-binding protein was down-regulated in the PD-susceptible genotype. Our results revealed that differential expression of proteins in response to *Xf*-inoculation was genotype and tissue development stage dependent. The specific roles of these candidate proteins in alleviation or aggravation of this disease are under investigation. The information obtained in this study will aid in the understanding of the mechanisms related to the host-pathogen interactions involved in PD.

LITERATURE CITED

Yang, L., H. Lin, Y. Takahashi, F. Chen, M. A. Walker, and E.L. Civerolo. 2011. Proteomic Analysis of Grapevine Tissues in Response to *Xylella fastidiosa* Infection. *Physiological and Molecular Plant Pathology* 75:90-99.

FUNDING AGENCIES

Funding for this project was provided by the USDA-funded University of California Pierce's Disease Research Grants Program. Additional support was provided by the USDA Agricultural Research Service, Appropriated Project 5302-22000-008-00D.