The xylem-limited bacterium *Xylella fastidiosa* (*Xf*) causes Pierce’s disease (PD) with the symptoms primarily due to the result of xylem vessel blockage in susceptible grapevines. Grapevine genotypes differ in their susceptibility/tolerance to Pierce’s disease (PD). This may be related to the concentration and presence or absence of chemical compounds in the xylem sap and/or due to anatomical features of the xylem. Experimental as well as anecdotal information indicates that a considerable range in tolerance to PD exists among grapevine genotypes. It appears that a number of *Vitis* as well as *Muscadinia* species have evolved mechanisms that allow them to tolerate infection by *Xf*. However, while it is often thought that many wild genotypes evolved tolerance mechanisms, it is also possible that it is the induction of a deleterious response by *V. vinifera* genotypes that renders them more susceptible than tolerant genotypes which may not respond to a challenge by *Xf*. Therefore, understanding the mechanisms underlying differential sensitivity is critical for the development of PD resistant grapes. The rich diversity of grapevine genotypes tolerant to PD is currently being utilized to serve as a source for PD resistance for breeders. While PD resistant species have been identified (Mortensen et al., 1977; Krivanek and Walker, 2004; Fritschi et al., 2007), the molecular mechanisms of resistance have not been identified. Breeding of resistant genotypes is likely the most sustainable means of combating PD. In order to generate highly PD tolerant grape cultivars, knowledge of the kind and function of resistance mechanisms is paramount. Therefore, our research focuses on:

- Host-pathogen interactions using comparative analyses of *Xf* population dynamics among a group of grapevine genotypes.
- Examination of xylem anatomical factors using microscopic approaches.
- Evaluation of the effects of xylem saps from resistant and susceptible grapevines on planktonic growth, biofilm formation and virulence-related gene expression in *Xf*.
- Microarray global gene expression analysis of PD resistant and susceptible grapes in response to *Xf* infection.

Fourteen *Vitis* genotypes (*V. aestivalis*, *V. arizonica/candicans*, *V. arizonica/girdiana*, *V. candicans*, *V. champinii*, *V. girdiana*, *V. monticola*, *V. nesbittiana*, *V. rufotomentosa*, *V. shuttleworthii*, *V. simpsonii*, *V. smalliana*, *V. tilillifora*, *V. vinifera*), one *M. rotundifolia* cultivar (Cowart) and three hybrids; 8909-15 (*V. rupestris* A. de Serres × *V. arizonica/girdiana* b42-26), 9621-67 and 9621-94 (D8909-15 × F8909-17 (*V. rupestris* A. de Serres × *V. arizonica/candicans* b43-17), were evaluated in this study. Estimated *Xf* concentrations in the stem tissue sampled 113 d post-inoculation varied greatly among the 18 genotypes investigated. The concentration of *Xf* in stem tissue is well suited to measure the level of PD resistance and corresponds well to field resistance (Krivanek and Walker, 2005; Ruel and Walker, 2006; Fritschi et al., 2007). Therefore, screening grape genotypes under greenhouse conditions allows for rapid and efficient evaluation of numerous plants for PD resistance. For *M. rotundifolia*, *G. girdiana*, *V. arizonica/candicans*, *V. candicans*, *V. shuttleworthii*, *V. nesbittiana*, and *V. arizonica/girdiana*, the estimated *Xf* concentration in the stems did not exceed the positive threshold and was less than 2.1 x 10⁶ cells g⁻¹ tissue. In addition, 9621-67, a highly PD-resistant member of a genetic mapping population (Doucleff et al., 2004), had the lowest average *Xf* concentration among stem tissues. *V. simpsonii* also had very low *Xf* concentrations (<2.1 x 10⁶ cells g⁻¹ tissue). Average stem *Xf* concentrations in the remaining genotypes exceeded 5.0 x 10⁶ cells g⁻¹ tissue. PD symptoms are primarily the result of xylem vessel blockage in susceptible grapevines (Goodwin et al., 1988a, 1988b). Stem internode and petiole tissues from infected and uninfected control plants of four grape genotypes differing in PD susceptibility (*Vitis vinifera*, *V. rufotomentosa*, *V. smalliana*, and *V. arizonica/candicans*) were examined using scanning electron microscopy (SEM). Tyloses, fibrillar networks and gum plugs were observed in lumens of tracheary elements in petioles and internodes of both water-inoculated control plants and *Xf*-inoculated plants of all genotypes. Among infected plants, tylose formation in internodes was lowest in *V. arizonica/candicans* and did not differ among the other three genotypes. Infection with *Xf* strongly induced tylose formation in *V. vinifera* and *V. smalliana*.
but not in *V. arizonica/candicans*. Limiting the spread of *Xf* infection by xylem conduit occlusions does not appear to be the mechanism conferring PD resistance or tolerance to *V. arizonica/candicans, V. smal-liana*, or *V. ruftomontosa*. In contrast, the strong induction of tyloses may be detrimental rather than beneficial for *V. vinifera* survival after *Xf* infection (Fritschi et al., 2008).

Because there is direct contact between xylem sap and *Xf*, altering xylem sap composition presents a promising venue to interfere with successful pathogen colonization of the host. A bioassay system was developed to investigate the effects of xylem sap from PD resistant and susceptible grape genotypes on *Xf* growth, biofilm formation and virulence-related gene expression *in vitro*. The results of the *in vitro* study showed that the susceptible xylem sap provided better support for bacterial growth and biofilm formation than resistant xylem sap. A study of pathogenicity and virulence-related gene expression using RT-PCR revealed that glucanase, protease, and a number of virulence genes were differentially expressed in response to the resistant and susceptible xylem sap treatments. These results suggest that differences in xylem cell wall properties and sap chemical composition between PD resistant and susceptible grapes may affect *Xf* pathogenesis.

Plants respond to pathogen attack through a variety of signaling pathways consisting of a large number of regulatory as well as effector genes. Comparison of the PD susceptible *V. vinifera* transcriptional responses to *Xf* infection with those from resistant (9621-67) and susceptible (9621-94) *V. arizonica* hybrids, suggests common as well as distinct responses. Transcript profiling has shown that grape plant response to *Xf* infection is different among species, tissues and between resistant and susceptible siblings, and the stages of infection. While broad spectrum and presumably non-specific plant responses were observed in *V. vinifera* species, including the induction of transcripts such as WRKY transcription factor 30, CBF like transcription factor, NDR-1 like protein, and phi-1 (an AvrPto-Pto, or AP responsive gene), a majority did not overlap with the response of the resistant genotype (Lin et al., 2007).

The goal of this study was to identify and characterize the physiological, anatomical, biochemical and molecular events in the grape/*Xf* interaction between resistant and susceptible genotypes and among different tissue types. Our results have clearly shown differences in response of *Vitis* species to *Xf* infection. In general, tolerant/resistant genotypes tend to have lower *Xf* cell counts in the xylem, even at late stages of disease development, and have fewer tyloses than susceptible genotypes. In fact, an over-induction of responses of the susceptible genotypes such as *V. vinifera* may, at least in part, be the cause their sensitivity to PD. Results of the genome-wide transcriptional studies further support this differential response hypothesis and have helped identify a small group of putative genes involved in signal transduction and defense pathway responses in response to *Xf* infection. Similarly, the xylem sap studies have shown that *in vitro* *Xf* response varies with the nature of xylem sap treatment and that such a response is linked to the differential expression of virulence genes.

**References**


