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ABSTRACT

The bacterium Xylella fastidiosa (Xf) causes Pierce's disease and a number of other plant diseases of significant economic impact. To date, progress determining mechanisms of host plant susceptibility, tolerance or resistance has been slow, due in large part to the long generation time and limited available genetic resources for grape and other known hosts of Xf. To overcome many of these limitations, Arabidopsis thaliana has been evaluated as a model host for Xf. A pin-prick inoculation method has been developed to infect Arabidopsis with Xf. Following infection, Xf multiplies robustly and can be detected by microscopy, PCR and isolation. Affymetrix ATH1 microarray analysis of inoculated vs. non-inoculated Tsu-1 reveals gene expression changes that differ greatly from changes seen after infection with apoplast colonizing bacteria. Many genes responsive to abiotic stress are differentially regulated while classic pathogenesis-related (PR) genes are not induced by Xfinfection. The Arabidopsis ecotype Tsu-1 was inoculated with the Xf mutants tolC, pglA, and rpfF and their corresponding wild-type parents. The tolC mutant did not grow in Arabidopsis and no live cells were recovered, which is similar to results from tolC infection of grapevine. The rpfF mutant did grow to higher titer, again similar to growth in grape. However, growth of the pglA mutant was indistinguishable from that of the corresponding Fetzer wild type; this contrasts with the situation in grape where pglA is hypervirulent. It may be concluded that Xf growth in Arabidopsis is not enhanced by a functional polygalacturonase protein, perhaps because of differences in xylem and pit membrane structure between grape and Arabidopsis. Because two of the three mutants tested (tolC and rpfF) did behave similarly in Arabidopsis and in grape, it appears that Arabidopsis is an informative model host for the evaluation of at least some Xf mutants.

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