Supporting Information

Supporting Information Figure S1. Design of iTRAQ labeling and analysis. All eight iTRAQ tags were used to label the *Pst* and mock inoculated samples. After LC-MS/MS, resulting protein expression was analyzed against its control. This information was then used to examine differences between time points and genotypes.

Supporting Information Figure S2. DAB staining time course. (A) PtoR mock treated and inoculated with *Pst.* (a) PtoR, mock 0hai; (b) PtoR, mock 2hai; (c) PtoR, mock 4hai; (d) PtoR, mock 6hai; (e) PtoR, mock 8hai; (f) PtoR, mock 24hai; (g) PtoR, mock 48hai; (h) PtoR, *Pst* 0hai; (i) PtoR, *Ps*t 2hai; (j) PtoR, *Pst* 4hai; (k) PtoR, *Pst* 6hai; (l) PtoR, *Pst* 8hai; (m) PtoR, *Pst* 24hai; (n) PtoR, *Pst* 48hai. (B) *prf3* mock trated and inoculated with *Pst.* (a) *prf3*, mock 0hai; (b) *prf3*, mock 2hai; (c) *prf3*, mock 4hai; (d) *prf3*, mock 6hai; (e) *prf3*, mock 8hai; (f) *prf3*, mock, 24hai; (g) *prf3*, mock 48hai; (h) *prf3*, *Pst* 0hai; (i) *prf3*, *Ps*t 2hai; (j) *prf3*, *Pst* 4ha; (k) *prf3*, *Pst* 6hai; (l) *prf3*, *Pst* 8hai; (m) *prf3*, *Pst* 24hai; (n) *prf3*, *Pst* 48hai.

Supporting Information Figure S3. Representative peptide sequencing and quantification result showing the levels of pathogenesis-related protein (PR-10) in different samples. (A) Table of b and y ions identified the peptide sequence from PR-10 protein; (B) MS/MS spectrum with b and y ions annotated. The red arrow indicates the cluster of iTRAQ tags; (C) Zoomed in view of the iTRAQ tags indicated in B). The peak intensity correlates to the level of PR-10 protein in each sample shown above the corresponding tag.

Supporting Information Table S1. Confident proteins with an unused score of 1.3 or greater. Significant proteins with a change in expression are highlighted in green for increase (>1.2), red for decrease (<0.8), and yellow for having been identified in different comparisons with an increase and decrease. Accession numbers and protein names are annotated as provided by the Harvaard database. Protein expression values are listed under the relative tag ratios. Tag ratios are composed of the treated sample over the relative control. P-values are listed for statistical significance evaluation.

Supporting Information Table S2. List of Q-RT PCR Primers. Proteins chosen for Q-RT PCR are listed along with the sequence which is observed. Proteins were annotated using Blast2Go annotations.

Supporting Information Table S3. Comparisons between genotypes and time points. Proteins with an increase, decrease, and differential expression were examined between genotype and time point combinations. Comparisons include PtoR4hai and PtoR 24hai, *prf3* 4hai and *prf3* 24hai, PtoR4hai and *prf3* 4hai, and PtoR24hai and *prf3* 24hai. Proteins in this table are significant with an increase or decrease in expression. Expression values and p-values (p-value <0.05) are listed. The biological process the protein was annotated as being involved is listed beside the protein. Proteins were annotated using Blast2Go software.