

Global Gene Expression Profiles of *Phytophthora ramorum* Strain Pr102 in Response to Plant Host and Tissue Differentiation¹

Caroline M. Press² and Niklaus J. Grunwald²

Abstract

The release of the draft genome sequence of *P. ramorum* strain Pr102, enabled the construction of an oligonucleotide microarray of the entire genome of Pr102. The array contains 344,680 features (oligos) that represent the transcriptome of Pr102. *P. ramorum* RNA was extracted from mycelium and sporangia and used to compare gene expression across tissue types and in the presence of the host (*Rhododendron* sp.). The purpose of the experiment was to identify genes whose expression was responsive to tissue types and upon exposure to the host plant for further study. Gene expression studies were performed using a Nimblegen microarray. Genes were determined to be differentially expressed between tissue types if they were statistically significant $P=0.05$ after false discovery rate correction and resulted in a greater than 20-fold change in gene expression selecting only those genes with the greatest response to tissue changes or host influence. In the comparison between mycelia and sporangial tissues, 263 genes demonstrated a greater than 20-fold change in gene expression. Of those genes, 52 genes were significantly downregulated in sporangia as compared to mycelium and 214 genes were significantly upregulated in sporangia as compared to mycelium. Several of the differentially expressed genes appear to be of the same type as those in a similar study in *Phytophthora infestans* by Kim and Judelson (Eukaryotic Cell, 2003, 2:1376–1385) and include genes involved in cell wall restructuring, cell division and signaling functions. Not surprisingly, several genes involved in energy production, electron transport chains and growth are reduced in sporangia. Fifty percent of the genes with differential expression have not yet been classified as to function in the current annotation.

Key words: *Phytophthora ramorum*, gene expression analysis, microarray, sudden oak death.

¹ A version of this paper was presented at the Sudden Oak Death Third Science Symposium, March 5–9, 2007, Santa Rosa, California.

² Horticultural Crops Research Laboratory, Agricultural Research Service, United States Department of Agriculture, Corvallis, OR.