

# Gene Expression in the Tanoak- *Phytophthora ramorum* Interaction

Katherine J. Hayden,<sup>1</sup> Matteo Garbelotto,<sup>1</sup> Hardeep Rai,<sup>2</sup> Brian Knaus,<sup>3</sup>  
Richard Cronn,<sup>3</sup> and Jessica W. Wright<sup>4</sup>

## Abstract

Disease processes are dynamic, involving a suite of gene expression changes in both the host and the pathogen, all within a single tissue. As such, they lend themselves well to transcriptomic analysis. Here we focus on a generalist invasive pathogen (*Phytophthora ramorum*) and its most susceptible California Floristic Province native host, tanoak (*Notholithocarpus densiflorus* (Hook. & Arn.) Manos, Cannon & S.H. Oh). The advent of new sequencing technologies has made the study of non-model systems possible at a scale never before possible. We argue that this non-model system is ideal for studying the interactions between host and pathogen using massively parallel mRNA sequencing, in part because the *P. ramorum* genome has been fully sequenced. We present early data in a project developed to elucidate the molecular genetic interactions between these two species. We used the Illumina Genetic Analyzer system to sequence all mRNA present in a single tanoak genotype after inoculation with *P. ramorum*, and from a non-inoculated control. We separated sequences from the dataset that originated from the pathogen, or from highly conserved regions, by aligning the reads to the *P. ramorum* genome; this first set includes the genes expressed in vivo by the pathogen. The remaining sequences were used to generate a de novo reference transcriptome for tanoak, and then to subsequently pinpoint gene regions of interest with increased or decreased expression after infection. Each of the three outcomes—the set of expressed *P. ramorum* gene regions, the tanoak gene regions showing changes in expression, and the tanoak transcriptome reference itself—are an important step in understanding the interactions of forest pathogens and their hosts at the molecular level.

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<sup>1</sup> University of California, Berkeley, Environmental Science, Policy, and Management, 137 Mulford Hall, Berkeley, CA 94720.

<sup>2</sup> Utah State University, Logan, UT.

<sup>3</sup> USDA Forest Service, Pacific Northwest Research Station, Corvallis, OR.

<sup>4</sup> USDA Forest Service, Pacific Southwest Research Station, Davis, CA.

Corresponding author: khayden@berkeley.edu.