possibly being related to the high metabolic activity in the inflorescences.

Plant-based markers of infection for *Neofusicoccum parvum*. K. BAUMGARTNER[1,*], S. CZEMMEL[2], G.R. CRAMER[2], E.R. GALARNEAU[1], R. TRAVADON[1], D.P. LAWRENCE[1], A.J. MCELRONE[1] and D.A. CANTU[3]. [1]*United States Department of Agriculture, Agricultural Research Service, Crops Pathology and Genetics Research Unit, Davis, CA 95616, USA.* [2]*Department of Biochemistry and Molecular Biology, University of Nevada, Reno, NV 89557, USA.* [3]*Department of Viticulture and Enology, University of California, Davis, CA 95616, USA.* **E-mail: kbaumgartner@ucdavis.edu*

Canopy symptoms of Botryosphaeria dieback do not appear until years after *Neofusicoccum parvum* infects a pruning wound. There are control practices to minimize such infections, but growers tend to wait until symptoms are visible, at which point disease prevention is far less effective. Toward development of an early detection tool that would identify infected plants in nurseries and vineyards, we used RNA-Seq to identify differentially-expressed genes in the leaves of inoculated vs. non-inoculated Cabernet Sauvignon in the greenhouse. Woody stems were examined using light microscopy and high resolution computed tomography (HRCT) to monitor the spread of infection, and its spatial and temporal relationships to wood anatomical changes. The early stage of infection occurred prior to 2 months post-inoculation (MPI), when spread of the pathogen beyond the inoculation site was the farthest. This incubation period was also characterized by the largest stem lesions, the highest levels of fungal colonization and xylem vessels fully-occluded by gels, and the lowest starch content in xylem fibers and rays. Prior to 2 MPI, RNA-Seq and validative qPCR analyses identified eight candidate genes, which were transcriptionally activated by infection, but not by wounding alone. The best candidate genes [a dehydrin, a BURP domain protein, and a peptide similar to abscisic acid-induced wheat plasma membrane polypeptide 19 (AWPM-19)] identified the pathogen's presence with high specificity. Furthermore, expression of the eight candidate genes was not affected by *Planococcus* feeding, powdery or downy mildew infection, or abiotic stresses (heat, UV light), based on screenings of publicly-available, genome-wide expression data.

Variable levels of laccase are secreted by four species of *Ilyonectria* that infect grapevines. B. PATHROSE[1,2], M.O. OUTRAM[2], E.E. JONES[2], M.V. JASPERS[2] and H.J. RIDGWAY[2,*]. [1]*8/38 Cooyong Cres, Toongabbie, NSW, Australia, 2146.* [2]*Faculty of Agriculture and Life Sciences, Lincoln University, PO Box 85084, Lincoln University, Lincoln, New Zealand, 7647.* **E-mail: Hayley.Ridgway@lincoln.ac.nz*

Laccases are a family of enzymes (polyphenol oxidases; PPO-1 and PPO-2) implicated in pathogenesis and degradation of lignin by many phytopathogens, including those that infect grapevines. The aim of this study was to (i) confirm that *Ilyonectria* species pathogenic to grapevines secrete laccase, (ii) to determine whether isolates vary in laccase secretion and (iii) to determine whether the amino acid sequence of laccase (*lcc1*) differs between species. Laccase activity was measured using ABTS (2, 2[1]-azino-bis [3-ethyl-benzthiazoline-6-sulfonic acid]) and DMP (2,6-dimethoxy-phenol). Six isolates of *I. liriodendri* and five isolates of the *I. macrodidyma* complex, including, *I. macrodidyma* (n=3), *I. torrensensis* and *I. novozelandica* were inoculated as agar plugs into minimal liquid media and incubated at 20°C for 7 days. The mycelium free extracellular fluid was assayed for PPO-1 and PPO-2 activity by their oxidation of ABTS and DMP, respectively. The results showed that all isolates produced PPO-1 activity but only seven produced detectable PPO-2 activity. There was isolate variation in both PPO-1 and PPO-2 activity for all species for which >1 isolate was tested ($P<0.000$). Degenerate PCR was used to amplify the *lcc1* gene from *I. macrodidyma, I. novozelandica, I. torrensensis* and *I. liriodendri*. Six amino acid polymorphisms were identified within isolates of *I. liriodendri* and the *I. macrodidyma* complex. Amino acid polymorphism was not found between isolates of the same species. Thus, variable laccase activity is likely to result from variable amount of enzyme secretion rather than isolate differences in enzyme activity.

Evaluating grapevine germplasm for resistance to Eutypa dieback. R. TRAVADON[1,*], J.E. PREECE[2] and K. BAUMGARTNER[1]. [1]*United States Department of Agriculture - Agricultural Research Service, Crops Pathology and Genetics Research Unit, Davis, CA 95616, USA.* [2]*United States Department of Agriculture - Agricultural Research Service, National Clonal Germplasm Repository, Davis, CA 95616, USA.* **E-mail: rtravadon@ucdavis.edu*

Eutypa dieback of grapevine is a trunk disease that impairs vineyard productivity worldwide. In the vineyard, the causal agent *Eutypa lata* infects pruning wounds and forms a canker within months; Eutypa foliar symptoms are observed several years later. Because the wood lesion typically forms first, it is a more common measure of resistance in controlled inoculations. Nonetheless, past research shows a lack of concordance between these two symptoms. We compared three inoculation methods for evaluating resistance among genetically-diverse cultivars originating from the eastern Mediterranean (Black Corinth, Husseine, Thompson Seedless), central Europe (Carignane, Muscat Hamburg, Primi-