Characterization of Molecular Interactions Between *Geosmithia morbida* and *Juglans nigra* Using Dual RNA-Seq

Aaron Onufrak[1], Grace Pietsch[2], Dawn Klingeman[3], Alyssa Carrell[3], William Klingeman[2], Melissa Cregger[3], Matthew Ginzel[4,5], and Denita Hadziabdic[1]

[1] Entomology and Plant Pathology Department, University of Tennessee, Knoxville, TN, 37996 USA; [2] Department of Plant Sciences, University of Tennessee, Knoxville, TN, 37996 USA; [3] Biosciences Division, Oak Ridge National Laboratory, Oak Ridge, TN, 37830 USA; [4] Department of Forestry and Natural Resources, Purdue University, West Lafayette, IN 47907 USA; [5] Department of Entomology, Purdue University, West Lafayette, IN 47907 USA; *aonufrak@vols.utk.edu

Thousand cankers disease results when the fungus *Geosmithia morbida* is vectored by walnut twig beetles to susceptible *Juglans* host species. At a molecular level, influence of host-pathogen interactions and effects of disease management actions on host-pathogen interactions are not understood. To address these knowledge gaps, dual RNA-seq was used to identify host and pathogen gene expression changes following exposure to chemical (PHOSPHO-jet) and biological (RootShield) management strategy. These treatments were compared to water-only controls using 24 trees per treatment (n=72). One week after treatment, 12 trees per treatment were inoculated with *G. morbida*, and the remaining trees were inoculated with potato dextrose agar (PDA) as a negative control. At 14-, 28-, and 56-days post-treatment application (PTA), RNA was extracted from canker-bordering phloem tissues and sequenced. In *J. nigra*, differentially expressed genes (DEGs) declined across time between *G. morbida* and PDA trees, dropping from 1,897 DEGs (day 14 PTA) to 60 DEGs (day 56 PTA). In *G. morbida*, gene expression also changed with 1,499 DEGs between days 14 and 56 PTA, with reduced expression of putative effectors, including pectate lyase genes. This study provides deeper understanding about interaction mechanisms related to *G. morbida* pathogenicity and provides guidance about how available management strategies influence pathogen virulence at a molecular level.