Resistant and Susceptible Molecular Host Responses to Hemlock Woolly Adelgid

A.M. Morse[1], A. Mwaniki[2], Y-S. Wang[3], K.E. Smith[4], J. M. Davis[5], C. D. Nelson[6], and G.F. Peter[7]

[1]Research Faculty, [3]Postdoctoral Associate, [5,7]Associate Professor, School of Forest Resources and Conservation; [2]Graduate Student, Plant Molecular and Cellular Biology Program; University of Florida, Gainesville, FL, USA; [4]Biological Sciences Technician, Southern Institute of Forest Genetics, USDA Forest Service, Southern Research Station, Gainesville, FL, USA; [6]Research Geneticist and Project Leader, Southern Institute of Forest Genetics, USDA Forest Service, Southern Research Station, Saucier, MS, USA

Hemlock woolly adelgid (*Adelges tsugae* Annand, HWA) infestations of Carolina (*Tsuga caroliniana* Engelm.) and eastern (*Tsuga canadensis* (L.) Carriere) hemlocks have lead to the decreased vigor and increased mortality of these ecologically important species. Approximately half the native range of hemlocks in the eastern United States is currently infested, with potentially significant consequences for the long-term survival of these species.

Since little is known about potential host tree mechanisms that may impact HWA resistance, we have focused on identifying hemlock genes involved in the host response to this pest. We are using laser capture microdissection followed by EST sequencing to identify genes whose expression levels are altered in response to HWA feeding in infested and non-infested *T. caroliniana* ray parenchyma cells, living cells embedded within the xylem of stems. We focus on these cell types since they are the feeding sites for HWA and are likely to react to the insect on a molecular level. In addition, because HWA is a relatively minor pest of *T. chinensis* and therefore considered resistant to HWA, we are generating EST libraries from needle samples of *T. chinensis* and *T. caroliniana* to compare gene expression patterns between these resistant and susceptible species. Analyses of the EST libraries will provide insights into the molecular mechanisms underlying HWA resistance and provide genetic information for developing molecular markers for breeding.