CHEMICAL AND PROTEOMIC APPROACHES TO DISSECTING ASH RESISTANCE TO THE EMERALD ASH BORER

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ABSTRACT

The literature contains relatively few studies addressing mechanisms of resistance of deciduous trees to wood-boring beetles. Several studies have hypothesized that both constitutive traits and feeding-induced responses in phloem tissue are key to resistance. Defense traits associated with resistance to herbivory fall into two major categories: 1) the presence of low and high-molecular weight anti-feedant/recalcitrant/deterrent/toxic metabolites, including defense-related proteins; and 2) physical barriers (e.g. lignified tissues) inhibiting spread of the invader. We are using a comparative approach to characterize the biochemical and molecular, constitutive and induced, phloem differences of susceptible and resistant ash species in order to identify key resistance mechanisms. Protein profiles will be compared using differential in-gel electrophoresis (DIGE) and differentially expressed proteins will be sequenced and annotated (where possible). Homologous genes in model plants for which sequenced genomes are available (Arabidopsis, poplar) will be used to design primers to determine gene frequencies and expression levels. Phenolics and other secondary metabolites will be identified using HPLC-mass spectrometry and correlated with resistance. The results of this study may lead to the development of molecular markers in North American ash or North American/Asian ash hybrids that could accelerate selection of resistant individuals for use in ecosystem restoration, urban forestry, and commercial exploitation.