

COMPARISON OF PROTEIN PROFILES OF BEECH BARK DISEASE-RESISTANT OR BEECH BARK DISEASE-SUSCEPTIBLE AMERICAN BEECH

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ABSTRACT

Proteomic analysis of beech bark proteins from trees resistant and susceptible to beech bark disease (BBD) was conducted. Sixteen trees from eight geographically isolated stands, 10 resistant (healthy) and 6 susceptible (diseased/infested) trees, were studied. The genetic complexity of the sample unit, the sampling across a wide geographic area, and the complexity of the BBD “treatment” all contribute to possible protein differences between trees in the study. This complexity required careful study design and more elaborate statistical considerations than many proteomics studies. Identification of up to 101 protein spots unique to an individual tree emphasizes the genetic diversity captured in our study. Despite the experimental complexity, 120 protein spots (22 percent of the matched spots) were identified as BBD significant, so the experiment was effective at finding proteins of interest.

Spots were selected for coring and sequencing based upon the significant BBD effect and the location of the spot in the gel. Sequenced spots have homology to

known stress-, insect-, and pathogen- related proteins in other plants. These proteins can be separated into the following classes: reactive oxygen species-induced genes, pathogenesis-related proteins, proteins that control transcription or translation, genes of unknown function, and genes previously thought to have only a metabolic role but currently identified as stress induced in plants. Taken together, the identification of genes generally identified in stress, insect, and pathogen attack in other plant systems and across several cellular systems indicates that beech trees have an active physiological response to BBD.

We have identified a small number of proteins broadly linked to the BBD disease state of the tree and having a stress-, insect-, or pathogen- related expression in other plant systems. Further study of these proteins should help us understand processes critical to resistance to BBD and to develop biomarkers for selection of BBD-resistant trees before or in early stages of BBD infection in stands.