

TRANSCRIPT PATTERNS OF PHANEROCHETE CHRYSOSPORIUM LIGNIN PEROXIDASE GENES IN ORGANOPOLLUTANT - CONTAMINATED SOILS AND IN WOOD.

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Extracellular peroxidase of the white-rot fungus *Phanerochaete chrysosporium* have been implicated in the degradation of lignin and related aromatic pollutants. In submerged culture, multiple lignin peroxidase isozymes (LiPs) are secreted, and these are encoded by a family of at least 10 structurally related genes designated *lipA* through *lipJ*. Analysis of single basidiospore cultures has shown >97% cosegregation of *lipA*, *lipB*, *lipC*, *lipE*, *lipG*, *lipH*, *lipI*, and *lipJ* and cosmid analysis has generated a detailed map of the region. *LipD* and *lipF* are located on chromosomes separate from all other known peroxidase. Numerous studies have demonstrated differential regulation of LiP genes, particularly in response to nutrient limitation.

Recently, magnetic capture of mRNA and quantitative RT-PCR techniques have permitted analysis of *P. chrysosporium* transcripts in organopollutant-contaminated soil in laboratory studies (AEM 62: 3697-3703). Patterns of LiP transcript levels were markedly different from those previously observed in submerged cultures. Transcript of one gene, *lipF*, were absent from *P. chrysosporium* colonized soil. *LipA*, *lipB*, *lipD*, *lipH*, and *lipI* transcripts peaked within the first week of growth on anthracene amended soil but declined by day 10. In contrast, *lipJ* transcripts appeared only after 10 days incubation and, by day 20, they were the dominant transcript. Transcripts of *lipA* far exceeded *lipC* in anthracene-contaminated soils, while the reverse (i.e. *lipC* >> *lipA*) was observed in pentachlorophenol-contaminated soils. Continuing these investigations, the ability of particular organopollutants to influence gene expression in soil is being examined by suppression subtractive hybridization experiments. Methodology and recent results will be presented.

With minor modifications, the published magnetic capture/RT-PCR techniques have been adapted to transcript analysis in wood. In distinct contrast to defined media and soil cultures, few transcripts were present in appreciable quantities. Specifically, *lipC* and *lipF* transcripts dominated. Currently, we are evaluating transcript patterns of other *P. chrysosporium* strains. Preliminary data shows substantial conservation of gene regulation. Results of transcript analyses and their possible relationships to genomic organization will be discussed.

ABSTRACTS

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