

## Molecular Genetics of *Phanerochaete chrysosporium*

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### ABSTRACT

In *Phanerochaete chrysosporium* ME446 lignin degradation is a secondary metabolic event triggered by carbon and nitrogen limitation. It is therefore possible to study lignin degradation at the level of gene expression by comparing mRNA populations produced during primary and secondary growth in both wild-type strains and in strains mutant in lignin degradation.

We have isolated mutants deficient in phenol oxidase activity. These mutants fall into three phenotypic categories with respect to lignin degradation: (1) negative, (2) delayed onset after nitrogen starvation, (3) enhanced.

Polyacrylamide gel electrophoresis of rabbit reticulocyte polypeptide translation products of *Phanerochaete* mRNA shows differences between populations from primary and secondary growth. Differences in the range of polypeptides (and therefore of mRNA) have also been demonstrated between a mutant and its wild-type progenitor under identical conditions.

A gene bank has been prepared from *P. chrysosporium* strain ME446 genomic DNA using a bacteriophage  $\lambda$  vector. This gene bank is being screened with labeled mRNA from secondary growth mycelium in the presence of excess competing cold RNA from primary growth mycelium. Using this method (and/or using labeled cDNA probes), we hope to isolate clones carrying sequences expressed only during lignin degradation.

A gene bank has also been constructed from *Sporotrichum pulverulentum* (Novobranova), which is on morphological criteria considered to be the imperfect form of *P. chrysosporium*. DNA probes from randomly chosen clones of both gene banks have been hybridized to restricted and electrophoresed total DNA of the two "gene bank" strains and of two other isolates of *P. chrysosporium* on Southern blots. We found very strong DNA homology between the two "gene bank" strains, but far less homology between these two strains and the two others. These degrees of relationships were supported by the analysis of mitochondrial DNA from the four strains.

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