The identification and potential exploitation of xenometabolic genes in *Aspergillus* fungi

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Abstract

The presence of polyciclic aromatic hydrocarbons (PAHs) in soil and water is both toxic and increasingly ubiquitous. While various manual techniques for removal of Persistent Organic Pollutants (POPs) exist, rarely are they time efficient and/or cost effective options. Biodegradation of POPs using microorganisms has been a recent hot topic of study, as modern genetic assays have identified fungal and bacterial life to be present and competitive in even heavily contaminated ecosystem. White-rot fungi, which generally require plant tissue (lignocellulose) for growth, are powerful biocatalysts more commonly considered in fungal microbial degradation experiments. However, the use of white-rot fungi can be limiting in terms of application for bioremediation *in situ*, as contaminated sites may not consistently support plant life. The ascomycetes strain under study in this project are advantageous in that it is a non-ligninolytic fungus, and therefore capable of subsisting in terrain lacking in vegetation.

The fungus used in this study has been observed to degrade anthracene at a considerable rate – eliminating half of the substance in a span of 12 days. Anthracene, a byproduct of coal production, is a simple polycyclic hydrocarbon of three fused benzene rings. The structural simplicity of anthracene makes it an excellent model compound in this controlled study of degradation. The fungus under observation was grown in liquid culture supplemented with anthracene. At various regular intervals during the testing period, samples of the contaminated liquid medium were processed and tested by HPLC for chemical concentrations of anthracene. Additionally, biomass was collected for RNA and DNA extraction to check for levels of genetic expression of enzymes of Phase I and Phase II and of the β-ketoadipate pathway, associated with xenobiotic metabolism. Genetic makeup has been inferred from libraries of the model fungi *Aspergillus niger*, and verified through sequencing.

Understanding the genetic makeup of the xenobiotic metabolism of these species, as well as other microorganisms involved in degradation pathways, can provide a basis for genetic modification and manipulation to improve rates and breadth of microbial bioremediation *in situ*.