

**Monitoring Genetic and Metabolic Potential for In Situ Bioremediation:
Mass Spectrometry**

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Lead Principal Investigator: Michelle V. Buchanan
Oak Ridge National Laboratory
P.O. Box 2008
Oak Ridge TN 37831-6365
(423) 574-4521
buchananmv@ornl.gov

Co-Investigators:

Phillip F. Britt
Mitchel J. Doktycz
Gregory B. Hurst
Yongseong Kim
Oak Ridge National Laboratory

Prof. Mary E. Lidstrom
Anne Auman (graduate student)
Andria Costello (graduate student)
University of Washington
Departments of Chemical Engineering and Microbiology
Box 351750
Seattle WA 98195-1750

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Research Objective: A number of DOE sites are contaminated with dense non-aqueous phase liquids (DNAPLs) such as carbon tetrachloride and trichloroethylene. At many of these sites, microbial bioremediation is an attractive strategy for cleanup, since it has the potential to degrade DNAPLs *in situ*. A rapid screening method to determine the broad range potential of a site's microbial population for contaminant degradation would greatly facilitate assessment for *in situ* bioremediation, as well as for monitoring ongoing bioremediation treatment. Current laboratory-based treatability methods are cumbersome and expensive. In this project, we are developing methods based on matrix-assisted laser desorption/ionization mass spectrometry (MALDI-MS) for rapid and accurate detection of polymerase chain reaction (PCR) products from microbial genes involved in biodegradation of pollutants. PCR primers are being developed to amplify DNA sequences that are amenable to MALDI-MS detection. This work will lay the foundation for development of a field-portable MS-based technique for rapid on site assessment and monitoring of bioremediation processes.

Research Progress and Implications:

This report summarizes work after 2-1/2 years of a 3-year project, during which we have demonstrated MALDI-MS detection of DNA signatures relevant to bacterial bioremediation.

A model system for interfacing PCR amplification with MALDI-MS detection is based on the *pmoA* gene for the active site subunit of particulate methane monooxygenase, a bacterial enzyme that can oxidize trichloroethylene. Andria Costello and Ann Auman, two graduate students in Prof. Lidstrom's laboratory, have developed molecular techniques for analyzing natural populations of methanotrophic bacteria, which are important for *in situ* bioremediation of halogenated solvents such as trichloroethylene, dichloroethylene and vinyl chloride. A DNA sequence database has been developed for methanotrophs in Lake Washington sediment, a habitat studied in detail by the Lidstrom laboratory. This database has been used to design specific PCR primers and hybridization probes that will detect the entire range of these diagnostic genes in known methanotrophs. These molecular tools have been used to analyze the natural populations of methanotrophs in Lake Washington sediments by conventional hybridization techniques. For MALDI-MS detection, PCR primer pairs were designed to amplify relatively short segments (99 bases and 56 bases) of *pmoA* in Type I and Type II methanotrophs. The hybridization analysis is now being compared to the MALDI approach.

A rapid reverse-phase purification of bacterial PCR products allows MALDI-MS detection from a fraction of one 25-microliter reaction. At this level of sensitivity, MALDI-MS is competitive with conventional methods for detecting PCR products in the <100 bp size range, and methodology improvements should allow larger products to be analyzed. Recovery of the purification is 60% to 75% for PCR products of 50 to 200 bases. We have adapted the purification to a microtiter format for parallel treatment of 96 samples in about 10 minutes.

To allow increased throughput, we are exploiting the automated data acquisition features of our PerSeptive Biosystems MALDI-MS instrument. An important aspect of automated, high throughput MALDI analysis is improving the homogeneity of the dried matrix/PCR mixture to allow useful signal to be obtained by aiming the MALDI laser anywhere on the spot. Polymeric substrates are proving useful in this regard. A combination of fluorescence microscopy for visualizing the distribution of DNA in the MALDI sample and MALDI measurements of the same spots guides the optimization of the substrate development work.

To determine the range of conditions over which the combined PCR amplification, purification, and MALDI detection methodology is useable, we have varied amounts and types of bacterial DNA added initially to the PCR. MALDI signal can be detected from a PCR preparation that

uses as little as 10^5 - 10^6 target molecules. The effects of “interfering” DNA from the diverse microbial population found in subsurface environments were explored by performing PCR on mixtures of genomic DNA from the methanotroph *Methylosinus trichosporium* OB3b and *E. coli*. In this initial study, the effect of the “interference” DNA was negligible. Although this simple demonstration does not preclude the possibility of false positives in other cases, the specificity of PCR primer pairs combined with the ability to measure the size of the resulting PCR product greatly diminishes the possibility that our approach would falsely indicate the presence of a targeted gene sequence due to unintended amplification of “interfering” DNA.

Planned Activities:

A manuscript describing 96-well PCR product purification for MALDI is in preparation. Explore MALDI-MS for hybridization detection of targeted methanotroph DNA sequences. Compare conventional hybridization vs. MALDI analysis for Lake Washington samples. Extend MALDI sample homogeneity studies to larger PCR products.

Information Access:

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