

## ***Application of Omics to Field Bioremediation: Current Status, Challenges and Future***

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2:15-5:00pm, Tuesday, April 4, 2006

The availability of entire genome sequences from many organisms and communities marks a new age in biology and has the potential to open innovative and efficient research avenues for studying biological systems at different levels. Recently, the development and application of OMICs approaches for microbial detection and community analysis have received a great deal of attention, and significant progress has been made. It is expected that the rapid advances in OMICs approaches could have great impacts on the efficacy of bioremediation. However, the utility of genome sequence information and associated various OMIC approaches to link microbial genes/populations to community functions in contaminated sites is an immense challenge. The objective of this breakout session is to review some of the most recent advances in OMICs approaches that address fundamental microbial ecology questions with respect to bioremediation, and identify future questions and directions.

Examples of questions include:

- 1. Can sequence-based metagenomics approaches be effective in monitoring microbial diversity and community dynamics at contaminated sites? If so, what are the critical needs to implement metagenomics approaches to bioremediation?*
- 2. Can proteomic approaches be used as a quantitative tool for monitoring in situ microbial activities? What are the technological challenges in applying such tools to field applications?*
- 3. Can functional gene arrays be used as a high throughput, specific, sensitive and quantitative tool for monitoring microbial populations and activities of interest?*
- 4. Can OMICs approaches be used to elucidate relationships between biomarker measurements and in situ functional activities?*
- 5. What is the degree of correlation between the abundance and expression of the functional genes and the rates of contamination degradation or transformation? Can OMICs-based approaches be used to provide insights into rates needed for kinetic models and predictions?*
- 6. How can the data and information be scaled from molecules to populations, to communities, and to subsurface ecosystems for improving our predictive capability of field bioremediation?*

To lead the open discussions, the following five speakers presented brief synopses on different aspects of the above questions (see the attached presentations for details):

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|------------|---|
| T.C. Hazen | What are the challenges and possibilities of OMICs for bioremediation?        |
| A. Konopka | Ecological principles and the practical analysis of functional diversity      |
| M. Lipton  | applications of quantitative proteomics to microbes and microbial communities |

L. Kerkhof     Active bacteria in groundwater at the ERSP-FRC  
J. Zhou        Community genomics and functional gene arrays

Dr. Hazen presented an overview of possible OMICs approaches to field sites, and in particular, discussed the utility of metagenomics. He put forth the idea that sites for metagenomic analyses should be selected based upon biochemical pathway(s) of interest with respect to environmental conditions (e.g., sulfate-reducing, methanogenic, iron-reducing, etc.). Dr. Konopka presented an overview of ecological questions that are inherently intertwined within the bioremediation issues, including diversity, functional redundancy, stability, environmental micro-heterogeneity, genetic micro-diversity, and ecotypes. Dr. Lipton presented recent advances for the use of metaproteomics, and the extent to which peptides can be identified from mixed samples. It seems that the technology is progressing, and the quantitative identification of hundreds if not a thousand proteins is possible. Finally, Dr. Zhou presented recent advances in functional gene arrays, and how functional gene diversity can be related to biochemical processes of interest. The latest version of the functional gene array contains over 23,000 probes involved in major microbial geochemical processes. He also reported the most recent metagenomics analysis of the contaminated groundwater at ERSP Field Research Center.

The main issues discussed and critical needs identified during open discussions were itemized as follows:

### **Issues Discussed**

- Examples of novel insights provided via OMICs approaches
  1. Still in developmental phase.
  2. Need more time for direct demonstration of applicability
- Defining novel functions with OMICs approaches
  1. Differentiate multiple levels of function (genotype/phenotype; active/inactive)
  2. Biochemical functions: Growth and physiology needed
  3. Ecological functions and interactions: *in situ* measurements needed
- Within the context of ecology, evolution and geochemistry
  1. Address specific questions
  2. Hypothesis driven by ecological theory
  3. Need to consider ecotypes and micro-heterogeneity
- Integration with physiology, biochemistry, cultivation
  1. Growth and physiology experiments are crucial
  2. OMICs and wet-bench/field site biochemistry are complementary
- Relating OMICS to the rates of degradation/transformation
  1. Direct measurements of rates of degradation/transformation are always needed
  2. OMICs approaches will increase the confidence of rate measurements (structure/function relationships)
- Sampling and OMICs
  1. Monitoring many desired populations simultaneously over time and space

2. Monitoring competitors and multiple interactions
  3. Adjusting environmental conditions to favor the desired populations
- Functional activity and modeling
    1. Better methods for detecting functional activity: rRNA or mRNA
    2. Better understanding of functional processes
    3. Incorporating functional activity into geochemical models to improve predictive capability

### **Critical Needs**

- Further development to make OMICs approaches mature, convenient and cheaper
- Demonstrated examples of deliverables/proof of concept
- New methods to deal with complex microbial communities
- New or improved biomarkers for detection of populations of interest
- New or improved methods for detecting activities within ecology context
- New strategies for quantitative data comparisons across different laboratories, experiments, and sites
- Bioinformatics tools to facilitate data analysis, comparison and binning
- Integration with genetics, biochemistry, physiology and ecology

During the discussions, one of the main points that emerged from the synopsis was the need for direct proof-of-concepts that demonstrate how OMICs approaches improved predicative capabilities. The techniques and methodology should be used to understand the relationship(s) between community structure/function and desired rates and processes. Ecological questions should also make sure to consider the issues with inherent heterogeneity and micro-diversity. In addition, cultivation of important populations should continue in order to increase our understanding in physiology, biochemistry, and ecology. This increased understanding will both complement and benefit from OMICs approaches. An additional consensus from the group was that metabolomics is not quite a mature method to be applied to mixed communities, but has the potential for great impact once techniques are improved and coordinated with *in situ* activities and metagenomics. In summary, the OMICs approaches should be developed in a fashion to help answer ecological questions within the context of biochemistry, physiology, geochemistry and environments.