

Researches in Molecular Microbial Ecology

Bongkeun (BK) Song

Assistant Professor, Department of Biological Sciences.



Bongkeun Song
Phone 910-962-2326
Fax 910-962-2410
songb@uncw.edu

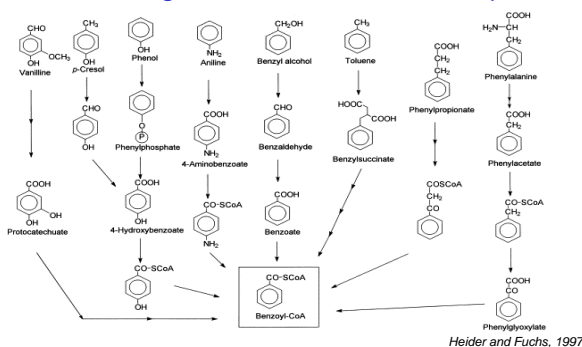
Research Interest

My primary research interests reside in understanding structure and dynamic of microbial communities related to ecological function. In order to determine and monitor microbial activities and community dynamics, molecular techniques such as community fingerprinting, quantitative-PCR and microarray analysis with selected functional genes are used. Furthermore, diverse microorganisms in the environments are accessed using innovative cultivation methods as well as culture independent methods (metagenomes).

Research Area

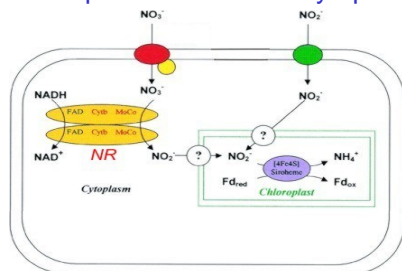
- Anaerobic degradation of aromatic compounds
- Microbial transformation of toxic metals
- Nitrate uptake in marine phytoplankton
- Diversity and dynamics of denitrifying community
- Environmental genomics

Anaerobic Degradation of Aromatic Compounds



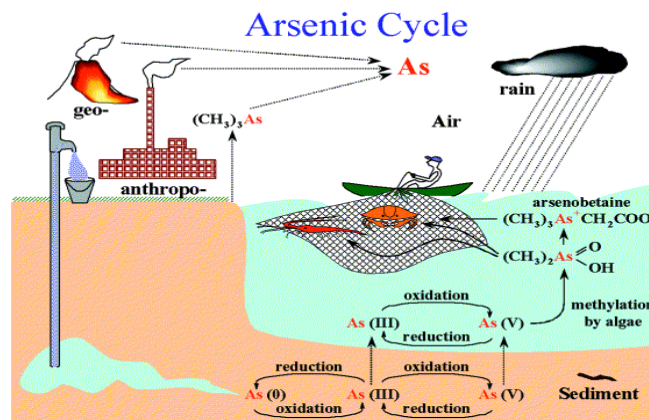
Various aromatic contaminants are transformed to benzoyl-CoA as a central intermediate under anaerobic conditions. The genetic systems involved in benzoyl-CoA degradation can be used as genetic markers to determine and monitor anaerobic bioremediation of aromatic contaminants in subsurface environments.

Nitrate Uptake in Marine Phytoplankton



Moreno-Viván et al., 1999

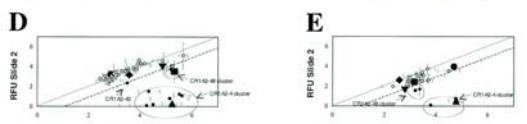
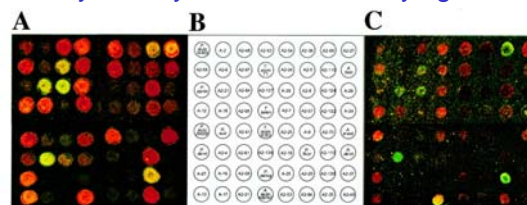
Primary production in the ocean is supported by nutrient inputs. Uptake and assimilation of inorganic nitrogen are essential for phytoplankton growth. Nitrate is major inorganic nitrogen sources for phytoplankton blooms in open ocean. The genes involved in uptake and assimilation are used to monitor phytoplankton community dynamics related to nitrogen inputs in the ocean.



Mukhopadhyay et al., 2002

Arsenic is widely distributed in the environment due to natural weathering of rocks and anthropogenic inputs such as mining and agricultural applications. Contamination of drinking water resources by arsenic caused serious health problems. Microbial activities affects the concentration of arsenic detected in water. The genetic systems involved in arsenic transformation are investigated to monitor microbial activities related to the levels of arsenic found in water.

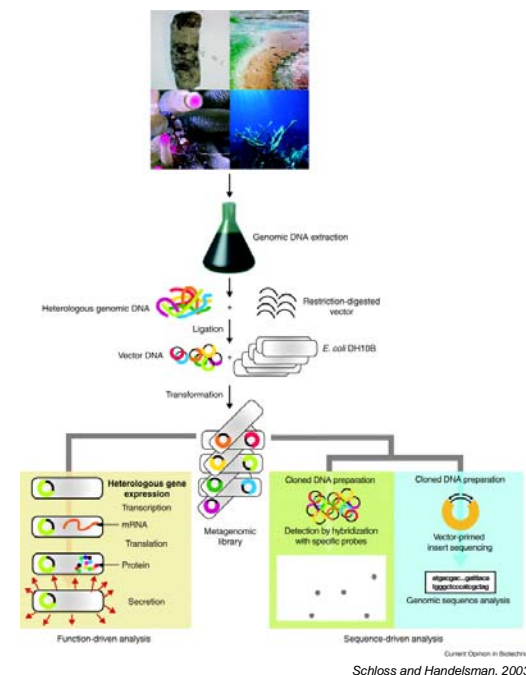
Diversity and Dynamics of Denitrifying Community



Taroncher-Oldenburg et al., 2003

Denitrifying bacteria have essential roles in global nitrogen cycle. Diversity of denitrifying bacteria was examined by detecting central genes (nitrite reductase and nitrous oxide reductase) in various environmental samples without cultivating and isolating bacteria. Furthermore, community dynamics of the detected denitrifiers were examined using microarray analysis.

Environmental Genomics



Schloss and Handelsman, 2003

Molecular studies of microbial diversity in natural habitats has unveiled that less than 1 % of microorganisms are isolated and cultivated because of the bias of cultivation and the nature of microorganisms. The rest of them are not yet cultured or considered to be unculturable. Metagenome is a novel approach to obtain large amounts of genetic materials from uncultured organisms without cultivation efforts. Metagenome is genome shotgun cloning methods to insert large fragments of genomic DNAs (40Kb- 100 Kb) to cosmid, fosmid or BAC vectors. This direct genomic cloning from environmental samples provides the opportunity to catch up whole operon or functional genes involved in biosynthetic and biocatalytic pathways. Thus, metagenomes have various potential for the studies in microbial diversity as well as biotechnological applications.

Research Project

- Diversity and biogeography of anaerobic bacteria capable of degrading aromatic compounds.
- Detection of anaerobic bioremediation of BTEX contaminants in subsurface aquifers.
- Molecular detection of diverse arsenic transforming bacteria in estuarine sediments.
- Denitrifying community dynamics under climate and anthropogenic perturbation.
- Physiological and genomic analysis of microbial respiration on selenium.
- Community dynamics and functional diversity of marine phytoplankton.
- Metagenomic approach to detect novel natural products from marine microbial communities .