



Potential Applications of Microbial Genomics in Nuclear Non-Proliferation (#18)

Isis Fukai

PhD Student, University of Tennessee, Knoxville

Kurt Ash¹, Heather Macgregor², Adam Arkin², Terry Hazen^{1,3}

1. University of Tennessee Knoxville, 2. University of California Berkeley 3. Oak Ridge National Laboratory



Introduction and Motivation

Existing methods for monitoring the nuclear fuel cycle (NFC) for potential proliferation concerns are largely limited to well controlled, near-source environments and simple sample matrices due to detector and analytical sensitivity. To complement existing approaches, microbiome analysis could provide information about dynamic biological interactions and environmental conditions that control the transformation/distribution of nuclides released from fuel cycle activities.

Previous studies shed light on the diversity of microbial taxa and functional genes at various nuclear facilities and radionuclide contaminated sites. However, the microbial communities reported at different sites vary widely, and characteristic taxa associated with specific stages of the nuclear fuel cycle have yet to be identified.

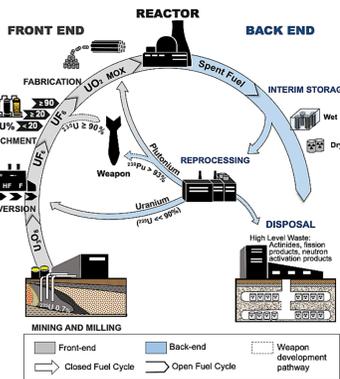


Figure 1. The nuclear fuel cycle.

Mission Relevance

This work presents a systematic review of microbial communities from nuclear facilities across the world to identify prokaryotic taxa commonly associated with each stage of the nuclear fuel cycle (Fig. 1). Findings are further evaluated via analysis of site-specific data from reactor facilities located at Oak Ridge National Laboratory and Savannah River National Laboratory. Identification of characteristic microbial taxa from specific stages of the NFC is intended to provide guidance for development of Wide Area Environmental Sampling programs, in-situ environmental biosensors, and geospatial analysis techniques for monitoring clandestine fuel cycle activities

Technical Approach

In collaboration with partners at UC-Berkeley, previous studies examining prokaryotic communities from engineered and natural environments of 30 different nuclear facilities were reviewed (Table 1). Findings were compared and validated against site-specific analysis of environmental samples collected from areas around R-reactor at the Savannah River Site (SRS) (Fig. 2), the High Flux Isotope Reactor (HFIR) at Oak Ridge National Laboratory (Fig. 3), and associated background locations (undeveloped, non-nuclear) at each site.

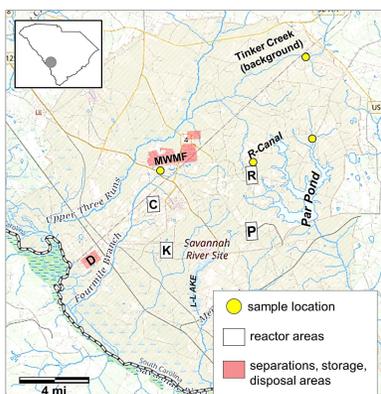


Figure 2. SRS study area and sample locations.

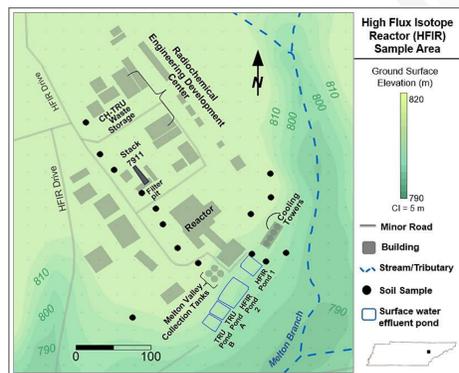


Figure 3. HFIR study area and sample locations.

Results

Table 1. List of the nuclear fuel cycle facilities reviewed.

Table with columns: Fuel Cycle Stage, Country, Facility, Sample Media, Radioactivity (Bq/g or Bq/mL), and References. It lists various facilities like Acatzaco, Cluff Lake, and SRS across different stages of the nuclear fuel cycle.

Pseudomonas, *Bacillus*, and *Sphingomonas* are the most highly reported genera across all stages of the NFC (Fig. 4). *Geobacter*, *Acidovorax*, *Acinetobacter*, and *Arthrobacter* are associated with the front-end facilities reviewed, whereas *Methylobacterium*, *Staphylococcus*, and *Brevibacillus* are reported at more reactor and back-end facilities.

Site-specific analysis shows higher relative abundances of methylotrophic Alphaproteobacteria*, *Bacillus*, *Sphingomonas*, and *Brevibacillus* and/or *Paenibacillus* at HFIR and SRS reactor sites relative to background sites (Fig. 5). A higher percentage of *Staphylococcus* is also observed in SRS samples. In contrast, *Bradyrhizobium* is more abundant in background samples from each site.

Identification of Effluent Sources via Distribution of Key Prokaryotic Taxa: HFIR

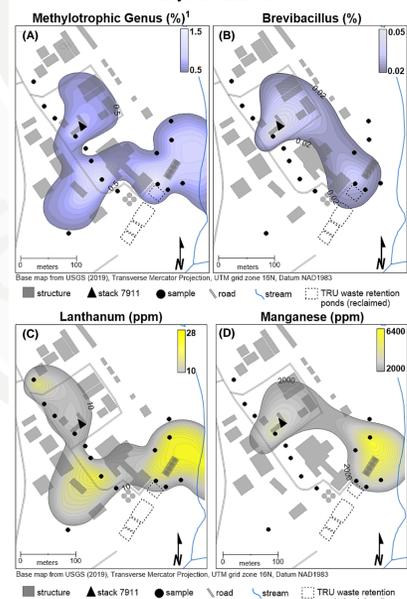


Figure 6. Maps showing higher abundances of (A) an uncultured Methylobacterium genus and (B) Brevibacillus occurring around reactor effluent sources, following similar spatial trends as lanthanum and manganese.

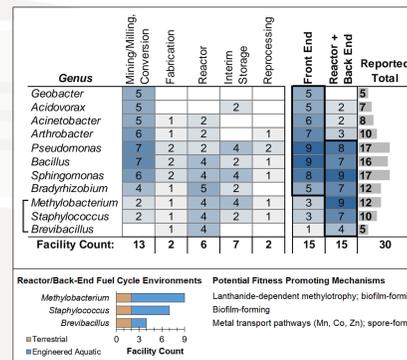


Figure 4. Prokaryotic taxa associated with each stage of the NFC based on the 30 facilities reviewed.

Site-Specific Analysis: High Flux Isotope Reactor and Savannah River Site

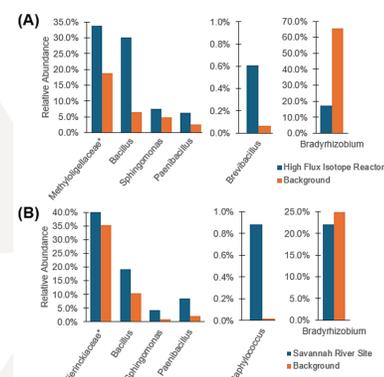


Figure 5. Key taxa associated with reactor and back-end NFC facilities show higher relative abundances in (A) HFIR and (B) SRS samples compared to background samples.

Distributions of an uncultured methylotrophic genus (Methylobacterium) and *Brevibacillus* effectively identify locations of reactor effluent sources, with higher abundances occurring closer to the reactor stack and cooling tower (Fig. 6A,B). Similar spatial trends are observed between the methylotrophic genus and lanthanum concentrations and between *Brevibacillus* and manganese, suggesting lanthanide-dependent methylotrophy and Mn transport systems in each respective genera may promote their fitness in reactor and back-end fuel cycle environments (Fig. 6 C,D; Fig. 7).

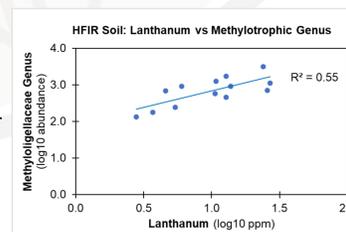


Figure 7. Correlation between lanthanum and the methylotrophic bacterium in HFIR soil.

Expected Impact

Characterization of representative microbial taxa associated with specific stages of the NFC provides important insights on the micro-to-macro-scale processes that govern outcomes of safeguards implementation, monitoring technologies, and contaminant mitigation strategies for the nuclear industry.

Results provide a framework for development of Wide Area Environmental Sampling programs, bio-indicators, and geospatial analysis techniques for monitoring clandestine fuel cycle activities.

In addition, the MTV Consortium has provided extensive support for:

- Interdisciplinary dissertation research, training, workshop participation, and networking opportunities
- Collaboration with ORNL, SRNL on sample collection and laboratory analysis; UC-Berkeley (H. MacGregor, A. Arkin,) on data integration and modeling

Conclusions

Prokaryotic taxa commonly associated with each stage of the nuclear fuel cycle have been identified via review of microbial communities from 30 nuclear facilities in 18 different countries. Site-specific analyses provide further support of findings, including:

- Identification of methylotrophic genera, *Bacillus*, *Sphingomonas*, and *Brevibacillus*/*Paenibacillus* as key taxa associated with reactor and back-end fuel cycle facilities
- Spatial distributions of methylotrophic genera and *Brevibacillus* can be used to effectively identify locations of reactor effluent sources
- Lanthanide-dependent methylotrophy and Mn-transport systems may promote the fitness of methylotrophic genera and *Brevibacillus* in reactor environments

Next Steps

- Evaluate genes and functional potential of microbiomes at each site via shotgun metagenomics
- Integrate data with machine-learning and computational models from UC-Berkeley team Describe plans for ongoing work
- Ongoing collaboration with Consortium members from ORNL, SRNL, and UC-Berkeley on model development, laboratory analysis, and technology transfer.

Acknowledgments

Use of the X-ray fluorescence spectrometer at the Geology and Geophysics Department at Louisiana State University was provided by a generous gift from Chevron.

