Microbial Biosensors for Detecting Nuclear Fuel Cycle Activities in the Environment

Kurt T Ash[1], Isis Fukai[1], Heather MacGregor[2], Adam Arkin[2], Terry Hazen[1]
[1]University of Tennessee, [2]University of California-Berkeley
Consortium for Monitoring, Technology, and Verification (MTV)

Introduction and Motivation

- The nuclear non-proliferation focus faces a major challenge in detecting nuclear fuel cycle activities that have not been declared.
- Geochemical characteristics of radionuclide-contaminated sites have been identified as signatures of nuclear proliferation activities.
- **This study investigates the potential of biosensors to monitor sensitive fuel cycle activities associated with proliferation by characterizing microbial-geochemical systems in contaminated environments, enabling in-situ monitoring.**

Technical Approach

- Soil and water sample collection from the HFIR (High Flux Isotope Reactor) are at ORNL (Oak Ridge National Lab) and SRNL (Savannah River National Lab).
- 16S rRNA gene sequencing and metagenomic shotgun sequencing.
- Geochemical analysis for trace elements, Radioisotopes, Total C & N, pH, and Biomass.

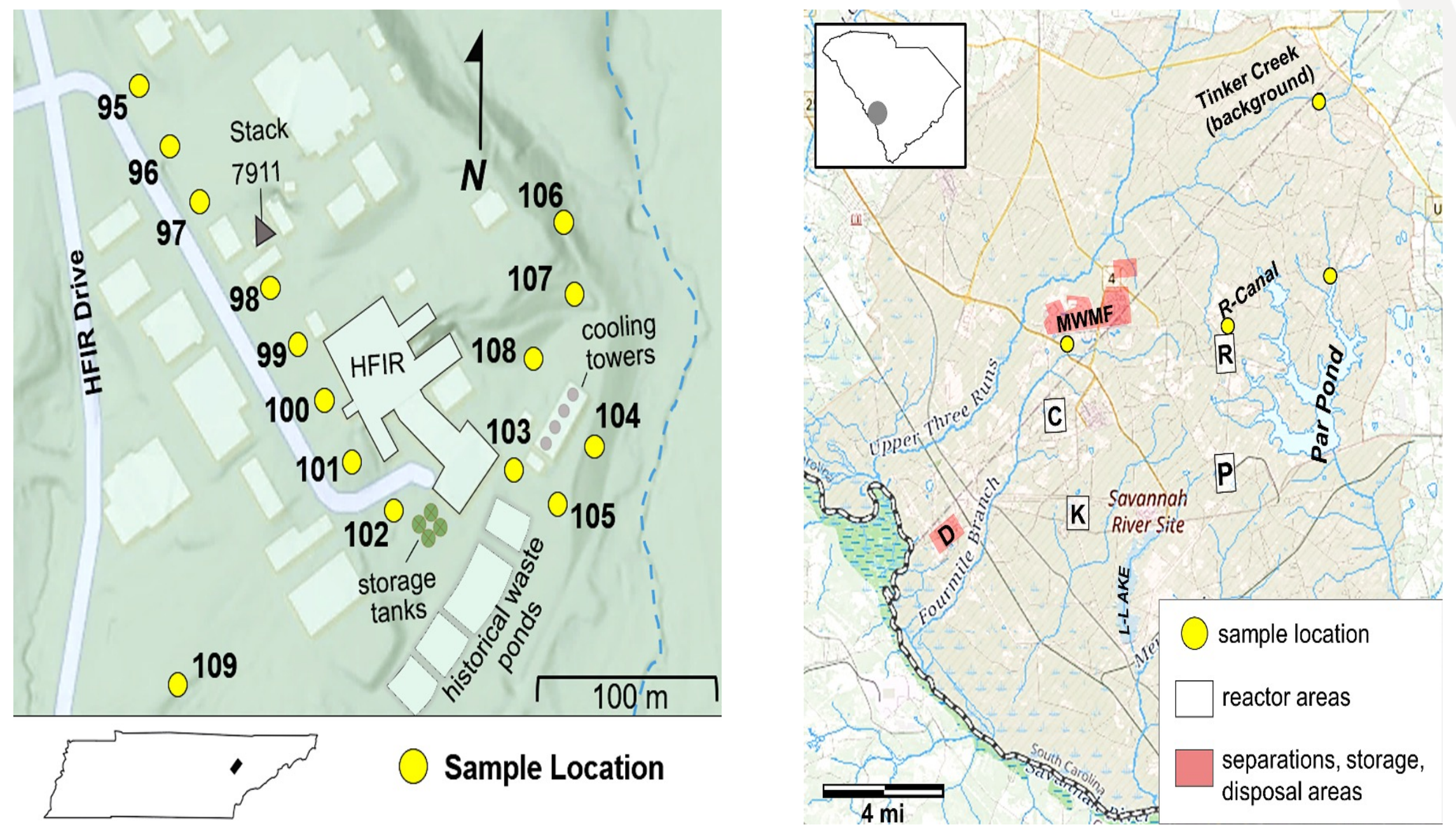

Fig. 1: Maps of sampling locations on the ORNL and SRNL campuses.

Results

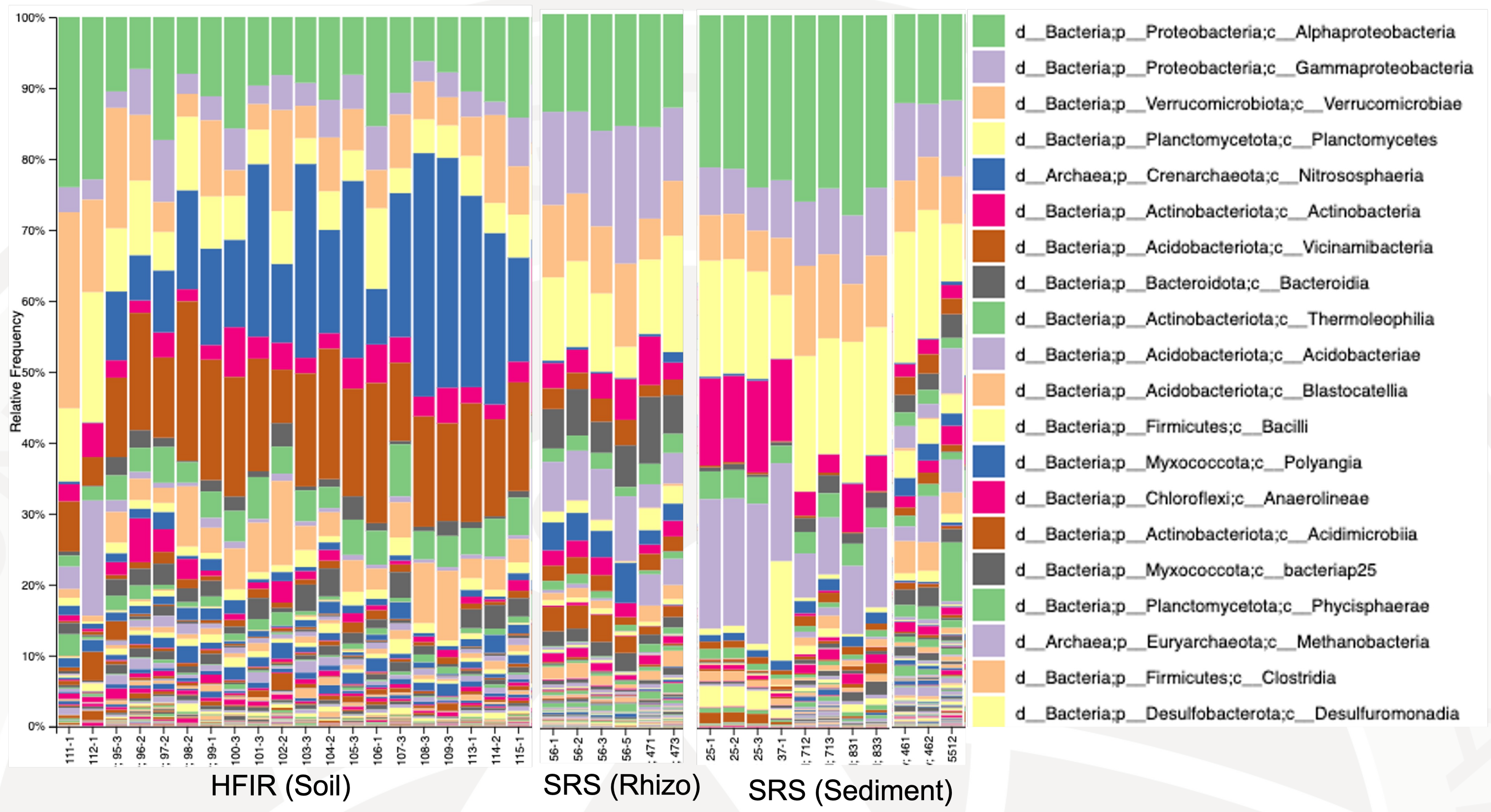

Fig. 2: Bar plot of 16S rRNA community profiles of representative samples

Fig. 3: Krona plot of HFIR sample 99-1 and ORNL background sample 111-1

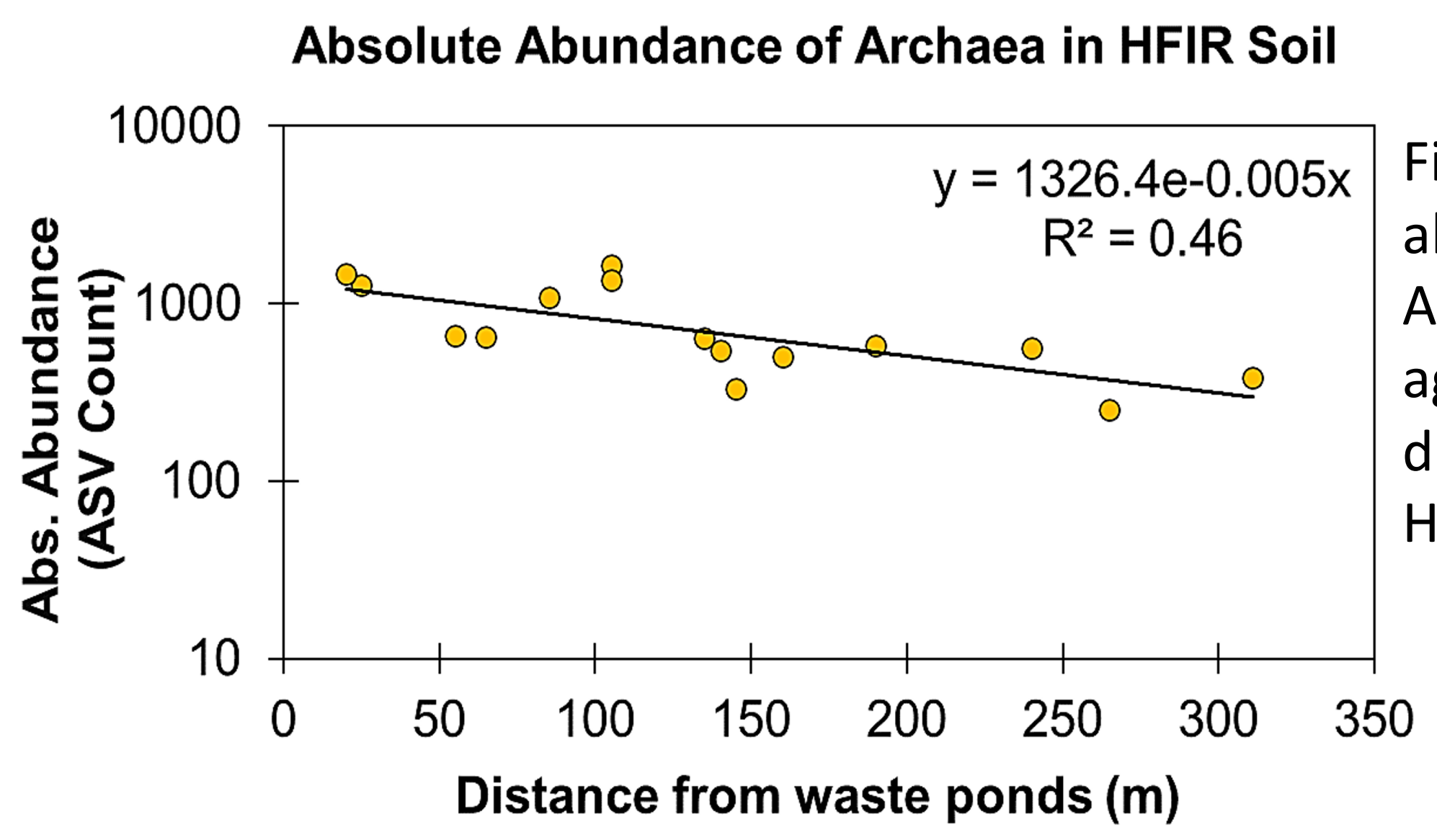

Fig. 4: 16S sample abundance of Archaea plotted against the distance from HFIR

MTV Impact

- Support for graduate student and post-doc training, workshop participation, and interdisciplinary research and networking opportunities.
- Collaborations with ORNL
  - Chris Young, Miguel Rodriguez, Kenneth Lowe, Dawn Klingeman, Jason Nattress
- Collaborations with SRNL
  - Martine Duff, Betsey Pettit, Holly Vermeulen) on sample collection and laboratory analysis.
- Collaborations with UC-Berkeley
  - Adam Arkin, Heather MacGregor, and David Bernstein on data integration and modeling

Conclusion

- Comparison of taxonomic occurrences between the ORNL and SRNL show 320 (out of ~1200) classified genera are unique to the SRS, with at least 20% of these sequences belonging to acidophilic bacteria.
- Out of 808 genera identified in the ORNL samples, 258 are unique to the site and exhibit an abundance of archaeal and bacterial taxa associated with nitrification and radiation tolerance/resistance.
- A comparison of SRS and ORR microbial communities with those from the background sites revealed over 180 genera occurring at both the SRS and ORR sites that are absent from the background sites.

Next Steps

- Completion of metagenomic and trace elemental analysis.
- Integrate data with computational models (Arkin Lab at UC-Berkeley)

This work was funded in-part by the Consortium for Monitoring, Technology, and Verification under DOE-NNSA award number DE-NA0003920