

## **Microbes at the blurred boundary of natural and built environments**

Fangqiong Ling<sup>1\*</sup> ([qiong@mit.edu](mailto:qiong@mit.edu)), Johnathan Friedman<sup>1</sup>, Shijie Zhao<sup>1</sup>, Mark B. Smith<sup>1</sup>, Andrea M. Rocha<sup>2,3</sup>, Charles J. Paradis<sup>2,3</sup>, Jizhong Zhou<sup>4</sup>, Terry C. Hazen<sup>2,3</sup>, **Eric J. Alm**<sup>1</sup>, Adam P. Arkin<sup>5,6</sup> and Paul D. Adams<sup>5,6</sup>

<sup>1</sup>Massachusetts Institute of Technology, Cambridge, MA; <sup>2</sup>University of Tennessee, Knoxville, Knoxville, TN; <sup>3</sup>Oak Ridge National Laboratory, Oak Ridge, TN; <sup>4</sup>University of Oklahoma, Norman, OK; <sup>5</sup>Lawrence Berkeley National Laboratory, Berkeley, CA; <sup>6</sup>University of California, Berkeley, CA

<http://enigma.lbl.gov>

### **Project Goals: This project aims to better understand the assembly of low-diversity communities in a groundwater ecosystem with genomic tools.**

Humans today spend more time working, living, and recreating in the manmade environment than the natural environment. However, the boundary between built and natural environments isn't always clear. The Oak Ridge Field Research Center (FRC) presents a case where past anthropogenic contamination to the natural environment caused by uranium enrichment influences the current built environment through the channel of water supply. Microbes living in this environment have been shown to be useful as quantitative biosensors of contamination. In the present study, we found that microbial communities at the FRC sites exhibited an unusual range of diversity, which correlates to the performance of the microbial sensor. We show that the variation in diversity is poorly explained by chemical gradients or cell count, yet well explained by migration when viewed from a dispersal-limited community assembly perspective. Our ongoing work applies shotgun sequencing to infer strain-level diversity that can provide further insights on the community assembly processes.

#### *Funding statement.*

*This material by ENIGMA- Ecosystems and Networks Integrated with Genes and Molecular Assemblies (<http://enigma.lbl.gov>), a Scientific Focus Area Program at Lawrence Berkeley National Laboratory is based upon work supported by the U.S. Department of Energy, Office of Science, Office of Biological & Environmental Research under contract number DE-AC02-05CH11231.*

*Fangqiong Ling is supported by Alfred P. Sloan Foundation Microbiology of the Built Environment Postdoctoral Fellowship*