BIOGRAPHICAL SKETCH

NAME: Minjae Kim

POSITION TITLE: Assistant Professor in Civil Engineering at the University of Kentucky

EDUCATION/TRAINING

INSTITUTION AND LOCATION	DEGREE	Completion Date MM/YYYY	FIELD OF STUDY
Sogang University, Seoul, South Korea	B.S.	02/2010	Chemical and Biomolecular Engineering
Pohang University of Science and Technology, Pohang, South Korea	M.S.	02/2012	Environmental Science and Engineering
Georgia Institute of Technology, Atlanta, GA	Ph.D.	08/2019	Environmental Engineering

A. Personal Statement

I am an emerging Assistant Professor in Civil Engineering, specializing in Environmental Engineering, at the University of Kentucky. My overarching research goal is to pioneer innovative biotechnological solutions that enhance both environmental and human health. My focus has encompassed critical microbial systems, including bioremediation of environmental pollutants like disinfectants, crude oil spills, and wastewater treatment. I have also delved into molecular techniques for tracking antibiotic resistance genes in environmental and clinical contexts, assessing sanitation engineering impacts on the human gut microbiome in developing nations, addressing microbial risks in floodwater, and studying carbon sequestration in soils for climate change mitigation. Employing an interdisciplinary approach, I've seamlessly integrated -omics, molecular biology, and engineering techniques to explore these subjects.

B. Positions, Scientific Appointments, and Honors

Positions and Scientific Appointments

2023 – present   Assistant Professor, Civil Engineering, University of Kentucky, Lexington, KY
2023 – present   Member, Association of Environmental Engineering and Science Professors
2022 – present   Review Editor: Frontiers in Microbiology
2022 – 2023   Research Scientist I, Colorado State University, Fort Collins, CO
2021 – 2022   Postdoctoral Researcher, Colorado State University, Fort Collins, CO
2020 – 2021   Postdoctoral Researcher, Oak Ridge National Laboratory, Oak Ridge, TN
2019 – 2020   ORISE Fellow, National Center for Toxicological Research (U.S. FDA), Jefferson, AR

Honors

2019   The Best Ph.D. Thesis Award by the School of Civil and Environmental Engineering at Georgia Tech

C. Contributions to Science

1. Whether exposure to the widely used benzalkonium chlorides (BAC) disinfectants renders bacteria more resistant to antibiotics remains an unresolved issue, despite its evident practical implications for public health over the past two decades. Throughout my Ph.D. research, I conducted a range of analyses including metagenomic analysis of bioreactors, MinION-based long-read sequence analysis of microbial isolates, adaptive evolution experiments, transcriptomic analysis, and molecular cloning. This comprehensive approach yielded molecular evidence confirming that BAC exposure can indeed co-select for antibiotic-resistant bacteria. Furthermore, my colleagues and I have elucidated the genetic determinants responsible for BAC degradation. Through a combination of time-series metatranscriptomic analysis of the BAC-exposed microbial community,

BAC degradation assays using isolates, and enzymatic assays, we have identified key microorganisms and enzymes that play a pivotal role in this degradation process.

a. **Kim, M.**, Weigand, M.R., Oh, S., Hatt, J.K., Krishnan, R., Tezel, U., Pavlostathis, S.G. and Konstantinidis, K.T., (2018). Widely used benzalkonium chloride disinfectants can promote antibiotic resistance. Applied and environmental microbiology, 84(17), pp.e01201-18. **This article has been selected by the editors of Applied and Environmental Microbiology for inclusion in "Spotlight". Only 4-5 articles from each issue, which typically includes 20-30 articles in total, are chosen for the spotlight based on their scientific merit and potential impact.**
b. **Kim, M.**, Hatt, J.K., Weigand, M.R., Krishnan, R., Pavlostathis, S.G. and Konstantinidis, K.T., (2018). Genomic and transcriptomic insights into how bacteria withstand high concentrations of benzalkonium chloride biocides. Applied and environmental microbiology, 84(12), pp.e00197-18.
c. Oh, S., Kurt, Z., Tsementzi, D., Weigand, M.R., **Kim, M.**, Hatt, J.K., Tandukar, M., Pavlostathis, S.G., Spain, J.C. and Konstantinidis, K.T., (2014). Microbial community degradation of widely used quaternary ammonium disinfectants. Applied and environmental microbiology, 80(19), pp.5892-5900.

2. Monitoring microbial communities in urban floodwater holds significance due to the potential increase in human health risks through pathogen mobilization and virulence gene dissemination. Urban flooding occurrences are on the rise due to climate change and population density growth. Traditional methods for assessing floodwater microbial contamination, such as culture-based approaches (e.g., fecal coliform counts) and molecular techniques (e.g., qPCR for specific pathogens/viruses), are time-intensive and labor-demanding. Additionally, PCR-based methods may yield false positive results due to primer cross-hybridization with non-target genetic material.

In contrast, metagenomic sequencing offers an unbiased approach, theoretically capable of detecting and genotyping all present pathogens, transcending the limitations of coliform-based indicators. My recently published metagenomic study on urban floodwater revealed that flood events occurring after 88 days of drought posed higher potential human health risks compared to post-rain floods. Therefore, monitoring microbial communities, particularly post-drought extreme flooding, can anticipate microbial risks, enabling preparedness for potential engineering solutions such as employing microbial-resistant building materials that hinder biofilm formation.

a. **Kim, M.**†, Kienast Y.†, Hatt, J.K., Kirby, A.E., Konstantinidis, K.T., (2022) Metagenomics indicate that public health risk may be higher from floods following dry relative to rainy periods. Environmental Microbiology Reports, 14(2), p265-273. †Co-first authorship