

**Ran Mei**

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**EDUCATION**

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| 2020 | Ph.D., Environmental Engineering, University of Illinois Urbana-Champaign, USA<br>Dissertation: <i>Investigating the roles of microbial immigration in wastewater treatment processes</i><br>Advisor: Prof. Wen-Tso Liu              |
| 2015 | M.S., Environmental Engineering, University of Illinois Urbana-Champaign, USA<br>Thesis: <i>Microbial community responses of an anaerobic enrichment to temperature shocks</i><br>Advisor: Prof. Wen-Tso Liu                         |
| 2013 | B.S., Energy and Resources Engineering, Peking University, China<br>Thesis: <i>Identification, function evaluation, and genome analysis of a novel bacterial species isolated from Daqing oil field</i><br>Advisor: Prof. Xiaolei Wu |

**PROFESSIONAL EXPERIENCE**

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| 2023-     | Postdoctoral Fellow, Japan Agency for Marine-Earth Science and Technology, Japan             |
| 2021-2023 | Postdoctoral Fellow, National Institute of Advanced Industrial Science and Technology, Japan |
| 2013-2020 | Graduate Research Assistant, University of Illinois Urbana-Champaign, USA                    |
| 2011-2013 | Undergraduate Research Assistant, Peking University, China                                   |

**HONORS AND AWARDS**

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| 2023 | New Investigator Award, Joint Genomic Institute, US Department of Energy  |
| 2022 | Postdoctoral Fellowship for Research in Japan, Japan Society for the Promotion of Science   |
| 2021 | Jacobs Engineering Group/AEESP Outstanding Doctoral Dissertation Award, Association of Environmental Engineering and Science Professors |
| 2020 | Outstanding Self-financed Students Abroad, China Scholarship Council  |
| 2020 | Engelbrecht Fellowship, University of Illinois Urbana-Champaign   |
| 2019 | Warren W. Yee Memorial Fellowship, University of Illinois Urbana-Champaign  |
| 2013 | Civil & Environmental Engineering Department Fellowship, University of Illinois Urbana-Champaign  |
| 2012 | Yihai Kerry Scholarship, Peking University  |
| 2011 | Kwang-Hua Scholarship, Peking University  |

**GRANTS**

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| 2023-2026 | CSP New Investigator Award, Joint Genomic Institute, Department of Energy, USA<br><i>Unraveling the interplay between sediment microorganisms in biomass consumption</i> (library preparation and sequencing of 1 TB genomic data)<br><b>Principal Investigator</b> (co-PI: Masaru K. Nobu; Hiroyuki Imachi) |
| 2022-2024 | Grant-in-Aid for JSPS Fellow, Japan Society for the Promotion of Science<br><i>Global gene cataloging-based reconstruction of the evolutionary transition from simple to complex cells</i> (2.2 mil JPY).<br><b>Foreign Research Fellow</b> (Host researcher in Japan: Masaru K. Nobu)                       |

## RESEARCH INTERESTS

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Microbial ecology in engineered and natural aquatic systems

Biological wastewater treatment

Comparative genomics and microbial evolution

Ecophysiology of anaerobic microorganisms

## PUBLICATIONS

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Peer-reviewed, first/co-first authorship

1. **Mei, R.**, Kaneko, M., Imachi, H., and Nobu, M.K.\*, 2023. The origin and evolution of methanogenesis and *Archaea* are intertwined. *PNAS Nexus*, 2, 1-10.
2. **Mei, R.** and Liu, W.T.\*, 2022. Meta-omics supervised characterization of respiration activities associated with microbial immigration in anaerobic digestion. *Environmental Science & Technology*, 56, 10, 6689-6698.
3. **Mei, R.**, Nobu, M.K. and Liu, W.T.\*, 2020. Identifying anaerobic amino acids degraders through the comparison of short-term and long-term enrichments. *Environmental Microbiology Reports*, 12(2),173-184.
4. **Mei, R.**, Nobu, M.K., Narihiro, T. and Liu, W.T.\*, 2020. Metagenomic and metatranscriptomic analyses revealed uncultured *Bacteroidales* populations as the dominant proteolytic amino acid degraders in anaerobic digesters. *Frontiers in Microbiology*, 11, 2763.
5. Lam, Y.C., **Mei, R.** (co-first author), Wu, Z., Lee, P.K., Liu, W.T.\* and Lee, P.H.\*, 2020. Superior resolution characterization of microbial diversity in anaerobic digesters using full-length 16S rRNA gene amplicon sequencing. *Water Research*, 178, 115175.
6. Kim, J., **Mei, R.** (co-first author), Wilson, F.P., Yuan, H., Bocher, B.T.W. and Liu, W.T.\*, 2020. Ecogenomics-based mass balance model reveals the effects of fermentation conditions on microbial activity. *Frontiers in Microbiology*, 11, 3115.
7. **Mei, R.** and Liu, W.T.\*, 2019. Quantifying the contribution of microbial immigration in engineered water systems. *Microbiome*, 7, 144.
8. **Mei, R.**, Kim, J., Wilson, F.P., Bocher, B.T.W. and Liu, W.T.\*, 2019. Coupling growth kinetics model and machine learning quantifies microbial immigration impacts and identifies key environmental parameters in a biological wastewater treatment process. *Microbiome*, 7, 65.
9. **Mei, R.**, Nobu, M.K., Narihiro, T., Yu, J., Sathyagal, A., Willman, E. and Liu, W.T.\*, 2018. Novel *Geobacter* species and diverse methanogens contribute to enhanced methane production in media-added methanogenic reactors. *Water Research*, 147, 403-412.
10. **Mei, R.**, Nobu, M.K., Narihiro, T., Kuroda, K., Sierra, J., Wu, Z.Y., Ye, L., Lee, P.K.H., Lee, P.H., van Lier, J.B., McInerney, M.J., Kamagata, Y. and Liu, W.T.\*, 2017. Operation-driven heterogeneity and overlooked feed-associated populations in anaerobic digester microbiome. *Water Research*, 124, 77-84.
11. **Mei, R.**, Narihiro, T., Nobu, M.K., Kuroda, K. and Liu, W.T.\*, 2016. Evaluating digestion efficiency in full-scale anaerobic digesters by identifying active microbial populations through the lens of microbial activity. *Scientific Reports*, 6:34090.
12. **Mei, R.**, Narihiro, T., Nobu, M.K. and Liu, W.T.\*, 2016. Effects of heat shocks on microbial community structure and microbial activity of a methanogenic enrichment degrading benzoate. *Letters in Applied Microbiology*, 63(5), 356-362.

Peer-reviewed, contributing authorship

1. Nobu, M.K., Narihiro, T., **Mei, R.**, Kamagata, Y., Lee, P.H., Lee, P.K., McInerney, M.J. and Liu, W.T.\*, 2020. Catabolism and interactions of uncultured organisms shaped by eco-thermodynamics in methanogenic bioprocesses. *Microbiome*, 8, 111.
2. Ye, L.\*, **Mei, R.**, Liu, W.T., Ren H. and Zhang, X.\*, 2020. Machine learning-aided analyses of thousands of draft genomes reveal specific features of activated sludge processes. *Microbiome*, 8, 16.
3. Sun, H., **Mei, R.**, Zhang, X., Ren H., Liu, W.T. and Ye, L.\*, 2020. Bacterial enrichment in highly-selective acetate-fed bioreactors and its application in rapid biofilm formation. *Water Research*, 170.
4. Yuan, H., **Mei, R.**, Liao, J. and Liu, W.T.\*, 2019. Nexus of stochastic and deterministic processes on microbial community assembly in biological systems. *Frontiers in Microbiology*, 10, 1536.
5. Zealand, A. M., **Mei, R.**, Papachristodoulou, P., Roskilly, A. P., Liu, W. T. and Graham, D. W.\*, 2019. Molecular microbial ecology of stable versus failing rice straw anaerobic digesters. *Microbial Biotechnology*, 12(5), 879-891.
6. Narihiro, T., Nobu, M.K., Bocher, B.T.W., **Mei, R.** and Liu, W.T.\*, 2018. Co-occurrence network analysis reveals thermodynamics-driven microbial interactions in methanogenic bioreactors. *Environmental Microbiology Reports*, 10(6), 673-685.
7. Zealand, A. M., **Mei, R.**, Papachristodoulou, P., Roskilly, A. P., Liu, W. T. and Graham, D. W.\*, 2018. Microbial community composition and diversity in rice straw digestion bioreactors with and without dairy manure. *Applied Microbiology and Biotechnology*, 102(19), 8599-8612.
8. Nobu, M.K., Narihiro, T., Liu, M.M., Kuroda, K., **Mei, R.** and Liu, W.T.\*, 2017. Thermodynamically diverse syntrophic aromatic compound catabolism. *Environmental Microbiology*, 19(11), 4576-4586.
9. Kuroda, K., Nobu, M.K., **Mei, R.**, Narihiro, T., Bocher, B.T., Yamaguchi, T. and Liu, W.T.\*, 2016. A Single-Granule-Level Approach Reveals Ecological Heterogeneity in an Upflow Anaerobic Sludge Blanket Reactor. *PloS One*, 11(12), p.e0167788.
10. Nobu, M.K., Narihiro, T., Kuroda, K., **Mei, R.** and Liu, W.T.\*, 2016. Chasing the elusive Euryarchaeota class WSA2: genomes reveal a uniquely fastidious methyl-reducing methanogen. *The ISME Journal*, 10(10), 2478-2487.
11. Pan, X.C., Geng, S., Lv, X.L., **Mei, R.**, Jiangyang, J.H., Wang, Y.N., Xu, L., Liu, X.Y., Tang, Y.Q., Wang, G.J. and Wu, X.L.\*, 2015. *Defluviimonas alba* sp. nov., isolated from an oilfield. *International Journal of Systematic and Evolutionary Microbiology*, 65(6), 1805-1811.
12. Narihiro, T., Kim, N.K., **Mei, R.**, Nobu, M.K. and Liu, W.T.\*, 2015. Microbial community analysis of anaerobic reactors treating soft drink wastewater. *PloS One*, 10(3), p.e0119131.
13. Geng, S., Pan, X.C., **Mei, R.**, Wang, Y.N., Liu, X.Y., Wang, X.B., Tang, Y.Q. and Wu, X.L.\*, 2015. *Glycocalis alkaliphilus* sp. nov., a dimorphic prosthecate bacterium isolated from crude oil. *International Journal of Systematic and Evolutionary Microbiology*, 65(3), 838-844.
14. Geng, S., Pan, X.C., **Mei, R.**, Wang, Y.N., Sun, J.Q., Liu, X.Y., Tang, Y.Q. and Wu, X.L.\*, 2015. *Paradevosia shaoguanensis* gen. nov., sp. nov., Isolated from a Coking Wastewater. *Current Microbiology*, 70(1), 110-118.
15. Pan, X.C., Geng, S., **Mei, R.**, Wang, Y.N., Cai, H., Liu, X.Y., Tang, Y.Q., Nie, Y., Ye, S.Y. and Wu, X.L.\*, 2014. *Nitratireductor shengliensis* sp. nov., isolated from an oil-polluted saline soil. *Current Microbiology*, 69(4), 561-566.

16. Geng, S., Pan, X.C., **Mei, R.**, Wang, Y.N., Sun, J.Q., Liu, X.Y., Tang, Y.Q. and Wu, X.L.\*, 2014. *Ottowia shaoguanensis* sp. nov., isolated from coking wastewater. *Current Microbiology*, 68(3), 324-329.

#### *Book chapter*

1. Narihiro, T., Nobu, M.K., **Mei, R.** and Liu, W.T., 2015. Microbial Community Involved in Anaerobic Purified Terephthalic Acid Treatment Process. *Anaerobic Biotechnology: Environmental Protection and Resource Recovery*. Imperial College Press, London, pp.31-48.

#### ***PRESENTATIONS***

1. The origin and evolution of methanogenesis and Archaea are intertwined. Oral presentation at 2023 AEESP Research & Education Conference, Boston, Massachusetts, USA, 2023
2. The origin and evolution of methanogenesis and Archaea are intertwined. Oral and poster presentation at ASM Microbe, Houston, Texas, USA, 2023
3. Elucidating the diversification Archaea using comparative genomics. Invited talk at Japan Collection of Microorganisms, Tsukuba, Japan, 2023
4. The origin and evolution of methanogenesis and Archaea are intertwined. Invited talk at Japan Agency for Marine-Earth Science & Technology, Yokosuka, Japan, 2022
5. Investigate microbial immigration using eco-genomics. Invited talk at Chinese Academy of Science, Beijing, China, 2022
6. Culture-dependent and independent investigation of anaerobic amino acid degraders. Invited talk at Zhejiang University, Hangzhou, China, 2021
7. Genomics-based investigation of microbial immigration in engineered ecosystems. Invited talk at Nanjing University, Nanjing, China, 2021
8. Culture-dependent and independent investigation of anaerobic amino acid degraders. Invited talk at Sun Yat-sen University, Guangzhou, China, 2021
9. Coupling growth kinetics modeling with machine learning reveals Microbial immigration impacts and identifies key environmental parameters in a biological wastewater treatment process. Oral presentation at IWA MEWE Specialist Conference, Hiroshima, Japan, 2019
10. Identifying anaerobic amino acids degraders through the comparison of short-term and long-term enrichments. Poster presentation at IWA MEWE Specialist Conference, Hiroshima, Japan, 2019
11. Metabolic partitioning among microbial dark matter across anaerobic digesters. Poster presentation at JGI Annual Meeting, Walnut Creek, California, USA, 2018
12. Distribution of populations associated with known syntrophs and methanogens in the global anaerobic digester microbiome. Oral presentation at Anaerobic Microbial Syntrophy Forum, Chengdu, China, 2017
13. Operation-driven heterogeneity and overlooked feed-associated populations in anaerobic digester microbiome. Poster presentation at IWA International Conference on AD, Beijing, China, 2017
14. Operation-driven heterogeneity and overlooked feed-associated populations in anaerobic digesters. Poster presentation at JGI Annual Meeting, Walnut Creek, California, USA, 2017
15. Microbiome of anaerobic digesters in 51 municipal wastewater reclamation plants. Poster presentation at The ISME Symposia, Montreal, Canada, 2016
16. Microbiome of anaerobic digesters in 51 municipal wastewater treatment plants. Poster presentation at JGI Annual Meeting, Walnut Creek, California, USA, 2016
17. Microbial community response of a mesophilic methanogenic enrichment to temperature

perturbations. Poster presentation at ASM Microbe, New Orleans, Louisiana, USA, 2015

## ***TEACHING EXPERIENCES***

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### *Teaching*

- 2018 Full responsibility for course development and instruction. CEE540, *Remediation Design*, University of Illinois Urbana-Champaign  
Topic: Thermodynamics; Phylogeny; Microbial Ecology; Bioinformatics; Reactor Kinetics; Bioremediation.
- 2018 Guest lecture. CEE444, *Biological Principles in Environmental Engineering*, University of Illinois Urbana-Champaign  
Topic: Introduction of Phylogenetic Analysis and Microbial Systematics
- 2017 Guest lecture. CEE538, *Water Quality Control Process II*, University of Illinois Urbana-Champaign  
Topic: Introduction of Nitrogen Cycle in Wastewater Treatment
- 2016 Guest lecture. CEE437, *Water Quality Engineering*, University of Illinois Urbana-Champaign  
Topic: Overview of Microbial Processes in Wastewater Treatment

### *Mentoring*

- 2020 Tzu-Yu Lin, Ph.D. student
- 2019 Gabriella C. Morales, MS student
- 2018 Jinha Kim, MS student
- 2017 Junhui Liao, MS student
- 2016 Qiuye Si, MS student
- 2016 Theodore Chan, undergraduate student
- 2015 Lama Aoudi, undergraduate student
- 2014 Lucas Rocha Melogno, undergraduate student

## ***ACTIVITIES***

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### *Editor*

Letters in Applied Microbiology, Junior Editor, 2023-2025

### *Reviewer*

Environmental Science & Technology, Water Research, Journal of Hazardous Materials, Environment International, Bioresource Technology, Environmental Microbiology Reports, mSphere, Frontiers in Microbiology, Chemical Engineering Journal, PLOS ONE, Science of the Total Environment, Engineering, Bioengineering, iMeta, Biotechnology Reports, BMC Microbiology

### *Professional Memberships*

American Society of Microbiology (ASM)  
Association of Environmental Engineering and Science Professors (AEESP)