## Ran Mei, Ph.D.

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#### **EDUCATION**

- 2015-2020 Ph.D. · University of Illinois at Urbana-Champaign (UIUC) · USA
- 2013-2015 MS. · University of Illinois at Urbana-Champaign (UIUC) · USA
- 2009-2013 B.Eng. · Peking University · China

## PROFESSIONAL EXPERIENCE

- 2021- Postdoctoral Fellow, AIST | PI: Dr. Masaru K. Nobu
- 2013-2020 Graduate Research Assistant, UIUC | PI: Prof. Wen-Tso Liu
- 2010-2013 Undergraduate Researcher, Peking University | PI: Prof. Xidong Wang; Prof. Xiaolei Wu

#### HONORS AND AWARDS

2022	Postdoctoral Fellowship for Research in Japan, Japan Society for the Promotion of Science (JSPS)
2021	Jacobs Engineering Group/AEESP Outstanding Doctoral Dissertation Award, Association of
	Environmental Engineering and Science Professors (AEESP)
2020	Outstanding Self-financed Students Abroad, China Scholarship Council
2020	Engelbrecht Fellowship, UIUC
2019	Warren W. Yee Memorial Fellowship, UIUC
2013	Environmental Engineering and Science Fellowship, UIUC
2012	Yihai Kerry Scholarship, Peking University
2011	Kwang-Hua Scholarship, Peking University
2011	PKU COE UPOS Fellowship, Peking University

#### **FUNDED RESEARCH**

2022-2024 JSPS

Role: Co-PI | PI: Masaru K. Nobu (AIST).

#### **PUBLICATIONS**

Peer-reviewed, first/co-first authorship

- 1. **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.
- 2. **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.

- 3. **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.
- 4. 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.
- 5. 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.
- 6. **Mei, R.** and Liu, W.T., 2019. Quantifying the contribution of microbial immigration in engineered water systems. *Microbiome*, 7, 144.
- 7. **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.
- 8. **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.
- 9. **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.
- 10. **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.
- 11. **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. *Glycocaulis 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.

# Manuscript under revision

1. **Mei, R.**, Kaneko, M., Imachi, H., and Nobu, M.K. The origin and evolution of methanogenesis and Archaea are intertwined. Under revision in PNAS nexus.

#### **PRESENTATIONS**

2019 "Coupling growth kinetics modeling with machine learning reveals Microbial immigration impacts and identifies key environmental parameters in a biological wastewater treatment process". 8th IWA MEWE Specialist Conference, Hiroshima, Japan (oral)

2019	"Identifying anaerobic amino acids degraders through the comparison of short-term and long-
	term enrichments". 8th IWA MEWE Specialist Conference, Hiroshima, Japan (poster)
2018	"Metabolic partitioning among microbial dark matter across anaerobic digesters". The 13th JGI
	Annual Meeting, Walnut Creek, California (poster)
2017	"Distribution of populations associated with known syntrophs and methanogens in the global
	anaerobic digester microbiome". Anaerobic Microbial Syntrophy Forum, Chengdu, China (oral)
2017	"Operation-driven heterogeneity and overlooked feed-associated populations in anaerobic
	digester microbiome" The 15th IWA International Conference on AD, Beijing, China (poster)
2017	"Operation-driven heterogeneity and overlooked feed-associated populations in anaerobic
	digester microbiome". The 12th JGI Annual Meeting, Walnut Creek, California (poster)
2016	"Microbiome of anaerobic digesters at 51 municipal wastewater reclamation plants". ISME16,
	Montreal, Canada (poster)
2016	"Microbiome of anaerobic digesters at 51 municipal wastewater treatment plants". The 11th JGI
	Annual Meeting, Walnut Creek, California (poster)
2015	"Microbial community response of a mesophilic methanogenic enrichment to temperature
	perturbations". ASM2015, New Orleans, Louisiana (poster)

# TEACHING AND MENTORING

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