

**Ran Mei, Ph.D.**

Bioproduction Research Institute

National Institute of Advanced Industrial Science and Technology (AIST)

Central 6, Higashi 1-1-1 · Tsukuba · Ibaraki 305-8566 · Japan

+81 80 5970 7199 · r.mei@aist.go.jp

**EMPLOYMENT**

---

*Current*

2021.01 National Institute of Advanced Industrial Science and Technology (AIST), Japan  
Postdoctoral researcher

**EDUCATION**

---

2020.08 Ph.D., University of Illinois at Urbana-Champaign (UIUC), USA

2015.08 MS., University of Illinois at Urbana-Champaign (UIUC), USA

2013.07 B.Eng., Peking University, China

**AWARDS**

---

2021 Jacobs Engineering Group / AEESP Outstanding Doctoral Dissertation Award, 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

**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. Glycocalis alkaliphilus sp. nov., a dimorphic prosthecae 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 review*

1. **Mei, R.**, Kaneko, M., Imachi, H., and Nobu, M.K. Methanogenesis at the fulcrum of Archaea origin and diversification. *Nature Microbiology*, under review.

#### **RESEARCH EXPERIENCE**

- |         |   |                        |
|---------|---|------------------------|
| 2021-   | Postdoctoral researcher, AIST   | PI: Dr. Masaru K. Nobu |
| •       | Deciphering evolutionary history of <i>Archaea</i> and the origin of <i>Eukarya</i> based on large-scale genome analysis. (Funded by the Moore-Simons Foundation)                 |                        |
| 2013-20 | Graduate research assistant, UIUC   | PI: Prof. Wen-Tso Liu  |
| •       | Identifying microbial populations responsible for amino acids degradation in anaerobic digesters using cultivation-dependent and -independent approaches. (Funded by JGI, US DOE) |                        |
| •       | Evaluating co-digestion of waste activated sludge minimization at purified terephthalic acid  |                        |

wastewater treatment processes using an ecogenomics-based growth kinetic model approach. (Funded by EBI & BP America)

- Shedding light on the anaerobic wastewater treatment “black-box” in anthropogenic carbon cycling: exploring the uncharted ecological function of uncultured microbial taxa through next-generation sequencing technology. (Funded by JGI, US DOE)
- Enhancing anaerobic process performance by conductive materials treating soft-drink wastewater. (Project funded by Pepsi Co. America)

2012-13 Undergrad research assistant, Peking University PI: Prof. Xiaolei Wu

- Isolation and characterization of novel microorganisms capable of petrochemicals degradation (with National Laboratory of Wetland Protection and Restoration, Peking University, China)

2011-12 Undergrad research assistant, Peking University PI: Prof. Xidong Wang

- Characterization of nitride-oxide refractory from coal gangue (with Beijing Key Laboratory of Municipal Solid Waste Reclamation and Management, Peking University, China)

### **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 13<sup>th</sup> 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 15<sup>th</sup> IWA International Conference on AD, Beijing, China (poster)
- 2017 “Operation-driven heterogeneity and overlooked feed-associated populations in anaerobic digester microbiome”. The 12<sup>th</sup> 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 11<sup>th</sup> 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 EXPERIENCES**

#### *Teaching*

- 2019 Guest lecture in CEE 444, Biological Principles in Environmental Engineering, UIUC
- 2018 Instructor in CEE 540, Remediation Design, UIUC
- 2017 Guest lecture in CEE 538, Water Quality Control Process II, UIUC
- 2016 Guest lecture in CEE 437, Water Quality Engineering, UIUC

*Mentoring*

- 2016     *Qiuye (Jenny) Si*, master student independent research, UIUC
- 2016     *Theodore Chan*, research experience for undergraduate program, UIUC
- 2015     *Lama Aoudi*, research experience for undergraduate program, UIUC
- 2014     *Lucas Rocha Melogno*, undergraduate student independent research, UIUC