

### Five significant representative publications

Numerous papers have been published with total citations of >35,000, H-index, **100** based on Web of Science; Google Scholar Citations >48,000, H-index, **117** based on Google Scholar. Recognized as a global influential researcher by all three major complementary metrics: (a) 2018-2020 Global highly cited researcher in Cross-field based on numbers of top 1% highly cited publications by Web of Science. <https://hcr.clarivate.com/>; (b) World's most cited researcher (>99.9% percentile) of ~8 millions scientists across all science and engineering fields (176 subfields of 22 fields) by a composite metric based on the Scopus database from Elsevier (<https://doi.org/10.1371/journal.pbio.3000918>). (c) Most highly cited researcher (H-index > 100) according to Google Scholar Citations.

**148** papers published in **Nature indexed journals**, such as *Science* (4), *Nature Climate Change* (4), *PNAS* (11), *Nature Communication* (7), *Ecology Letters* (2), *The ISME Journal* by Nature Publishing Group (50) (The top one journal in microbial ecology), *Environmental Science & Technology* (23), *Water Research* (11), and *Geochimica et Cosmochimica Acta* (2), and other prestigious journals, e.g., *Nature Ecology and Evolution* (2), *Nature Microbiology* (1), *Nature Review in Microbiology* (2), *Nature Plants* (1), *Microbiology and Molecular Biology Reviews* (1), *mBio* (17), *Ecology* (1), and *Global Change Biology* (9).

1. Wu, L. \*, D. Ning\*, B. Zhang\*, Y. Li, P. Zhang, X. Shan, Q. Zhang, M. Brown, Z. Li, J. D. Van Nostrand, F. Ling, N. Xiao, Y. Zhang, J. Vierheilig, G. F. Wells, Y. Yang, Y. Deng, Q. Tu, A. Wang, Global Water Microbiome Consortium†, Tong Zhang, Z. He, J. Keller, P. H. Nielsen, P. J. J. Alvarez, C. S. Criddle, M. Wagner, J. M. Tiedje, Q. He, T. P. Curtis, D. A. Stahl, L. Alvarez-Cohen, B. E. Rittmann, X. Wen, and **J.-Z. Zhou**. 2019. Global diversity and biogeography of bacterial communities in wastewater treatment plants. *Nature Microbiology*, 4:1183–1195. doi:10.1038/s41564-019-0426-5.

Microorganisms in wastewater treatment plants (WWTPs) are essential for water purification to protect public and environmental health. However, their diversity and the underlying mechanisms are poorly understood. To this end, a global water microbiome consortium (GWMC) was established across more than 70 research groups from 23 countries. Using a systematic global-sampling effort, the 16S rRNA gene sequences from ~1,200 activated sludge samples from 269 WWTPs in 23 countries on 6 continents were analyzed to address theoretical questions, such as species abundance distributions, extent of global microbial diversity, global core bacterial community, latitudinal diversity pattern, scale-dependent distance-decay patterns, structure-functions relationships, and community assembly mechanisms. This is the first comprehensive global scale study to address various theoretical questions in engineered systems. Our results demonstrated extremely high microbiome diversity of global wastewater treatment plants, with a small global core strongly linked to system's performance. Unexpectedly, global microbial turnover is largely driven by stochastic processes. The findings of this study highlight how little we know of the world's microbiome, even in one of the most common and well-controlled systems in the built environment, and have important implications for microbial ecology and wastewater treatment processes. In addition, the relationship between bacterial richness and temperature in WWTPs did not fit predictions from the metabolic theory of ecology. This result is in contrast to our previous studies (**Nature Communication**, 7, Article number:12083), which was the **first demonstration** that temperature plays a primary role in shaping microbial diversity in the forest soils, but it could

operate in different ways between plants and microorganisms, and that MTE is applicable to microbial communities.

2. Xue, K., M. M. Yuan, Z. J. Shi, Y. Qin, Y. Deng, L. Cheng, L. Wu, Z. He, J. D. Van Nostrand, R. Bracho, S. Natali, E. A. G. Schuur, C. Luo, K. T. Konstantinidis, Q. Wang, J.R. Cole, J. M. Tiedje, Y. Luo, and **J.-Z. Zhou**. 2016. Tundra soil carbon is vulnerable to rapid microbial decomposition under climate warming. *Nature Climate Change*, 6: 595-600, doi:10.1038/nclimate2940.

The northern permafrost stores more than 30% of the global soil organic C, which is a wildcard that could alter the future trajectory of climate change. How microorganisms respond to warming (speed, direction, magnitudes) is critical to determine the fates of permafrost C and the feedbacks of the permafrost ecosystems to climate warming. Although a laboratory study indicated that microbial communities can respond to temperature increase rapidly, evidence from **field experiments** remains scarce. Using integrated metagenomic technologies, particularly GeoChip, this study reported a rapid response of the tundra microbial communities to experimental warming after only 1.5 years of warming. This is the **first** comprehensive field study demonstrating the *in situ* **vulnerability** of tundra soil C to climate warming and the importance of microbial communities in mediating such vulnerability. The results presented in this study have important implications for future climate projection. This study was highlighted as a breakthrough in tundra ecosystem studies by *The Washington Post* (<http://wpo.st/O4GE1>), and it was also specifically highlighted by ASM in its *MICROBES* publication, and DOE OBER. This paper is ranked as the top 1% highly cited based on Web of Science.

3. **Zhou, J.-Z.**, Y. Deng, P. Zhang, K. Xue, Y. Liang, J. D. Van Nostrand, Y. Yang, Z. He, L. Wu, D. A. Stahl, T. C. Hazen, J. M Tiedje, and A. P. Arkin. 2014. Stochasticity, Succession and Environmental Perturbations in a Fluidic Ecosystem. *Proc. Nat. Acad. Sci.*, 111: E836-E845

Unraveling the rules that govern assembly and succession of biological communities is a central topic, but poorly understood, in ecology. It is generally believed that both deterministic and stochastic processes play important roles in shaping community composition and structure, but their relative importance remains elusive. To understand their relative importance in mediating microbial community assembly and succession, a novel framework comprised of four theoretical models was proposed and tested with a fluidic groundwater ecosystem after nutrient addition. This study showed that community assembly and succession were driven by a dynamic, time-dependent interaction of stochastic and deterministic processes, with stochastic forces dominating. This is the **first** time to demonstrate that community succession responding to nutrient amendment is primarily controlled by stochastic processes, rather than deterministic processes as traditional ecological succession theory predicted. This is also the **first** demonstration showing that the drivers controlling biodiversity and community succession are dynamic rather than static. By identifying the mechanisms controlling microbial community assembly and succession, this study makes seminal contribution to the mechanistic understanding essential for a predictive microbial ecology of natural and managed ecosystems. The importance of this study is evidenced as Editor's Pick in PNAS and Genomeweb. This study was also highlighted by OBER (<http://genomicscience.energy.gov/program/berhighlights.cfm>) as OBER Research Highlights.

It is listed as a highly cited publication (top 1%) in Web of Science. More recently, based on this study, a general null-model-based framework was further developed (*Proc. Nat. Acad. Sci.*, 116: 16893-16898), which provides an effective and robust tool to ecologists for quantitatively assessing ecological stochasticity.

4. Hazen, T. C., E. Dubinsky, T. DeSantis, G. Andersen, Y. Piceno, N. Singh, J. Jansson, A. Probst, S. Borglin, J. Fortney, W. Stringfellow, M. Bill, M. Conrad, L. Tom, K. Chavarria, T. Alusi, R. Lamendella, D. Joyner, C. Spier, J. Baelum, M. Auer, M. Zemla, R. Chakraborty, E. Sonnenthal, P. D'haeseleer, H.-Y. Holman, S. Osman, Z.M. Lu, J. van Nostrand, Y. Deng, **J.-Z. Zhou**, and O. U. Mason. 2010. Deep-sea oil plume enriches Indigenous oil-degrading bacteria. *Science*, 330: 204-208.

Due to the vast diversity and as-yet uncultivated status, detection, characterization and quantification of microorganisms in natural settings are very challenging, and linking microbial biodiversity to ecosystem processes and functions is even more difficult. To meet these challenges, a revolutionary, high throughput technology (GeoChip) for addressing a central goal in microbial ecology --linking community structure to function. GeoChip was highlighted in the NRC's report on the *New Science of Metagenomics* (2007), and in the roadmap for NSF's National Ecological Observatory Network (NEON, 2009), and won a R&D 100 Award in 2009 as one of 100 most innovative scientific and technological breakthroughs. Several generations of GeoChip (e.g. GeoChip 2.0 in 2007. *ISMZ J.* 1:67-77, Among the 5 top-cited articles in *ISME J* in last 10 years; GeoChip 5.0 in 2019. *mSystems* 4:e00296-19) were developed and used to analyze microbial communities from a variety of environments. As an example, in this study, GeoChip was used as the **primary** tool for assessing the shifts of microbial **functional** composition, structure and activities in response to oil spill of the deep-sea in the Gulf of Mexico --- which was described by President Barack Obama in a prime-time address as "the worst environmental disaster America has ever faced". GeoChip analysis revealed that a variety of hydrocarbon-degrading genes/populations exist in the deep-sea environment, and there were strong linkages between particular hydrocarbon-degrading genes and the hydrocarbon concentrations in the Deep Horizon oil. Primarily based on GeoChip results, along with other integrated analyses, this study convincingly concluded that the potential exists for *intrinsic* bioremediation of the oil plume in the deep-sea, which has been confirmed by many other studies. A subsequent publication with GeoChip data alone in *ISME J* (6: 451-460) was particularly highlighted by *Science for Environment Policy* of European Commission

([http://ec.europa.eu/environment/integration/research/research\\_alert\\_en.htm](http://ec.europa.eu/environment/integration/research/research_alert_en.htm)). This and many other studies clearly demonstrated that GeoChip is an excellent, unique high throughput technology for enabling comprehensive visualization of the functional structure of microbial communities and for establishing the relationships between biodiversity and ecosystem functioning - a central goal in microbial ecology. More importantly, this study provides a shining example on how GeoChip technology is used in an integrated synergistic fashion to address complex emergent environmental problems, which is a cornerstone of basic science.

5. **Zhou, J.-Z.**, M. A. Bruns, and J. M. Tiedje. 1996. DNA recovery from soils of diverse composition. *Appl. Environ. Microbiol.* 62: 316-322.

This pioneering study presented a robust and efficient method to isolate high quality of DNA from a variety of soils. It has been highly influential and widely used by other scientists in molecular ecology as evidenced by citations of ~ **3500** times based on Google Scholar. It is among the **20** most cited papers in Applied and Environmental Microbiology (2008-2019 statistics). Because it recovers high molecular weight pure DNA from soils with high yields and purity, this method laid a **foundation** for the widely used metagenomics (by Jo Handelsman) and other molecular microbial ecology studies.