

12 representative publications

Summary

- Over 700 peer reviewed publications
- Google Scholar: h-index = **146**, >76,000 citations
- Web of Science: h-index = **128**, >59,000 citations
- **42** publications in *Science*, *Nature*-branded journals, and *Proceedings of the National Academy of Sciences*
- **194** papers published in **Nature indexed journals**, including *Science* (4), *Nature Climate Change* (5), *Nature Geoscience* (1), *PNAS* (11), *Nature Communications* (11), *Ecology Letters* (2), *The ISME Journal* by Nature Publishing Group (54) (The top one journal in microbial ecology), *Environmental Science & Technology* (26), *Water Research* (13), and *Geochimica et Cosmochimica Acta* (2), and other prestigious journals, e.g., *Nature Microbiology* (4), *Nature Ecology and Evolution* (2), *Nature Food* (1), *Nature Plants* (1), *Nature Reviews Microbiology* (2), *Microbiology and Molecular Biology Reviews* (1), *mBio* (25), *Global Change Biology* (17), *Microbiome* (11), and *Ecology* (1).

Impacts

- 2023 *Research.com Best Scientists in the field of Ecology and Evolution*: ranked #40 of nearly 12,000 worldwide and #19 of > 2000 in the United States (<https://research.com/scientists-rankings/ecology-and-evolution>)
- 2021 Among the 2021 Reuters List of World's Top 1000 Climate Scientists (#445)
- 2019-2023 Among world's most highly cited researchers (top 0.1%) across all science & engineering fields among 9.6 million scientists based on Elsevier's *Scopus* (<https://elsevier.digitalcommonsdata.com/datasets/btchxktzyw/6>).
- 2019-present Most highly cited researcher (H-index > 100) according to their Google Scholar Citations, about 6,000 worldwide (<http://www.webometrics.info/en/hlargerthan100>)
- 2018-2023 Top 0.1% global highly cited researcher in **both** fields of Microbiology, and Environment & Ecology based on the numbers of top 1% highly cited publications by Web of Science, < 7,200 in total worldwide. (<https://hcr.clarivate.com/>). Only **6%** of the recognized researchers have the additional distinction of ranking among two categories.

1. Ning, D., Y. Wang, Y. Fan, J. Wang, J.D. van Nostrand, L. Wu, P. Zhang, D.J. Curtis, R. Tian, L. Lui, T.C. Hazen, E.J. Alm, M.W. Field, F. Poole F, M.W.W. Adams, R. Chakraborty, D.A. Stahl, P.D. Adams, A.P. Arkin, Z. He, and **J.-Z. Zhou**. 2024. *Environmental stress mediates groundwater microbial community assembly*. **Nature Microbiology**, 9:490-501. doi.org/10.1038/s41564-023-01573-x.

Community assembly describes how different ecological processes shape biological community composition and structure. How environmental factors impact community assembly remains elusive. A novel framework is first developed to conceptualize the relationships between community assembly processes and environmental stresses, and tested with the experimental data from a former nuclear waste disposal site, one of the most highly heavy-metal contaminated groundwaters worldwide. As predicted, the relative importance of stochastic assembly processes

in shaping community structure decreased as stress increased. In contrast to dispersal limitation and 'drift', heterogeneous selection increased with stresses. These findings highlight the importance of microbial dispersal limitation and environmental heterogeneity in ecosystem restoration and management.

2. Wu, L., Y. Zhang, X. Guo, D. Ning, X. Zhou, J. Feng, M. M. Yuan, S. Liu, J. Guo, Z. Gao, J. Ma, J. Kuang, S. Jian, S. Han, Z. Yang, Y. Ouyang, Y. Fu, N. Xiao, X. Liu, L. Wu, A. Zhou, Y. Yang, J. M. Tiedje, and **J.-Z. Zhou**. 2022. Reduction of microbial diversity in grassland soil is driven by long-term climate warming. *Nature Microbiology*, 7:1054–1062. <https://doi.org/10.1038/s41564-022-01147-3>. (top 1% highly cited)

The rapid loss of biodiversity due to human alteration of the global environment is threatening ecosystem functioning. Soil biodiversity is essential for maintaining the health of terrestrial systems, but how climate change affects soil microbial biodiversity remains elusive. By examining the temporal dynamics of microbial (i.e., bacterial, fungal, and protistan) diversity, this study provides explicit evidences that climate warming decreases microbial diversity via the concomitant reductions in soil moisture, and the enhanced network interactions under warming. Also, microbial biodiversity has strong linkages with various ecosystem functional processes. These results imply that the detrimental effects of biodiversity loss could be more severe in a warmer world, making future ecosystems more vulnerable.

3. Xiao, N., A. Zhou, M. L. Kempher, B. Y. Zhou, Z. Jason Shi, M. Yuan, X. Guo, L. Wu, D. Ning, M. K. Firestone, and **J.-Z. Zhou**. 2022. Disentangling Direct from Indirect Relationships in Association Networks. *Proc. Nat. Acad. Sci.*, 119(2):e2109995119. <https://doi.org/10.1073/pnas.2109995119>. (top 1% highly cited)

Quantitatively disentangling direct and indirect relationships in complex networks remains a formidable task in science and engineering. By tackling several mathematical challenges, this study provides a conceptual framework for disentangling direct and indirect relationships in association networks. The applications of iDIRECT (Inference of Direct and Indirect Relationships with Effective Copula-based Transitivity) to synthetic, gene expression, and microbial community data demonstrate that it is a powerful, robust, and reliable tool for network inference. As a general approach, iDIRECT has great advantages for complex network studies across diverse disciplines in science and engineering, and allows scientists to address research questions that could not be approached previously.

4. Yuan, M., X. Guo, L. Wu, Y. Zhang, N. Xiao, D. Ning, Z. Shi, X. Zhou, L. Wu, Y. Yang, J. M. Tiedje, and **J.-Z. Zhou**. 2021. Climate Warming Enhances Microbial Network Complexity and Stability. *Nature Climate Change*, 11:343-348. <https://doi.org/10.1038/s41558-021-00989-9>. (Highlighted by DOE, <https://www.energy.gov/science/ber/articles/warming-soil-means-stronger-microbe-networks>) (top 1% highly cited)

One fundamental yet controversial question in network ecology is whether and how the complexity of ecological networks influences ecosystem stability, particularly under future climate change scenarios. By examining the temporal changes of grassland soil microbial communities in response to long-term experimental warming, this study provides the **first** evidence that climate warming

enhances network complexity, which begets the stability of the networked microbial communities. The warming-enhanced network complexity and stability is also more tightly associated with microbial community functional structure and ecosystem functional processes. These results imply that preserving microbial interactions could be important to mitigate the detrimental effects of warming-induced biodiversity loss on ecosystem functions.

5. Guo, X., Q. Gao, M. Yuan, G. Wang, X. Zhou, J. Feng, Z. Shi, L. Hale, L. Wu L, A. Zhou, R. Tian R, F. Liu, B. Wu, L. Chen, C. Jung, S. Niu, D. Li, X. Xu, L. Jiang, A. Escalas, L. Wu, Z. He, J.D. Van Nostrand, D. Ning, X. Liu, Y. Yang, E.A.G. Schuur, K.T. Konstantinidis, J. R. Cole, C. R. Penton, Y. Luo, J.M. Tiedje, and **J.-Z. Zhou**. 2020. *Gene-informed decomposition model predicts lower soil carbon loss due to persistent microbial adaptation to warming*. *Nature Communications*, 11:4897. <https://doi.org/10.1038/s41467-020-18706-z>.

One grand challenge in ecology is to integrate microbial omics information into ecosystem models to inform large scale ecosystem sciences. With highly integrated experimental and computational technologies, this is the **first** report demonstrating the feasibility of incorporating microbial functional gene information into soil ecosystem models for improving model predictability. Modeling simulation also revealed persistently warming-induced lower temperature sensitivity of microbial respiration - a critical source of uncertainty in projecting future climate and carbon cycle feedbacks. The results imply that the warming-induced potential positive feedback of soil microbial respiration may be less than previously predicted if such microbially mediated dampening effects occur across different spatial and temporal scales.

6. Ning, D., M. Yuan, L. Wu, Y. Zhang, X. Guo, X. Zhou, Y. Yang, A. P. Arkin, M. K. Firestone, and **J.-Z. Zhou**. 2020. *A quantitative framework reveals ecological drivers of grassland soil microbial community assembly in response to warming*. *Nature Communication*, 11:4717. <https://www.nature.com/articles/s41467-020-18560-z> (Highlighted by DOE, <https://www.energy.gov/science/ber/articles/new-approach-helps-determine-how-much-microbial-community-composition-driven>) (**top 1% highly cited**)

Selection, dispersal, diversification and drift are considered major ecological processes controlling community assembly but quantifying their contribution to the assembly of ecological communities is extremely difficult. The developed framework to quantitatively infer community assembly mechanisms by phylogenetic bin-based null model analysis (iCAMP) has high precision, sensitivity, specificity, and accuracy. Application of iCAMP to grassland soil microbial communities demonstrates that warming increases homogeneous selection, which has important implications for predicting and mitigating the ecological consequences of climate warming. The developed general framework is useful for not only microbial ecology, but also plant and animal ecology.

7. 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 (101 authors)**. 2019. *Global diversity and biogeography of bacterial communities in wastewater treatment plants*. *Nature*

Microbiology, 4:1183–1195. <https://doi.org/10.1038/s41564-019-0426-5>. (top 1% highly cited)

Microorganisms in wastewater treatment plants (WWTPs) are essential for water purification to protect public and environmental health, but their diversity and underlying mechanisms are poorly understood. With ~1200 samples from 269 WWTPs in 23 countries on 6 continents, the global water microbiome consortium (GWMC) revealed various interesting macroecological patterns in worldwide WWTPs. Although global WWTPs have extremely high microbiome diversity (1 billion phylotypes), a small global core, strongly linked to system performance, exists. Unexpectedly, global microbial turnover in these well-controlled engineered ecosystems is largely driven by stochastic, rather than deterministic, processes. These findings have important implications for microbiome manipulation for desired functions and as a model system for microbial ecology in general.

8. **Zhou, J.-Z.**, Y. Deng, L. Shen, C. Wen, Q. Yan, D. Ning, Y. Qin, K. Xue, L. Wu, Z. He, J. W. Voordeckers, J. van Nostrand, V. Buzzard, S. T. Michaletz, B. J. Enquist, M. D. Weiser, M. Kaspari, R. Waide, Y. Yang, and J. H. Brown. 2016. Temperature mediates continental-scale diversity of microbes in forest soils. *Nature Communication*, 7:12083. <https://doi.org/10.1038/ncomms12083>. (Top 1% highly cited)

Metabolic theory of ecology (MTE) predicts that rising temperature would have dramatic effects on biodiversity. Despite intensive studies in macroecology, how temperature rising affects microbial biodiversity remains elusive. This is the **first** demonstration that temperature plays a primary role in shaping the continental biodiversity of bacteria, fungi and nitrogen fixing bacteria in forest soils, but with substantial lower turnover rates than recorded for trees, and that MTE is applicable to microbial communities as a general fundamental ecological theory. These findings have important implications for understanding and predicting the ecological consequences of human-caused changes in climate, land use, and other factors.

9. **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. <https://doi.org/10.1073/pnas.1324044111>. (Top 1% highly cited)

Unraveling the rules that govern assembly and succession of biological communities is a central, but poorly understood, topic in ecology. With a newly developed theoretical framework, this is the **first** time to demonstrate that the succession of groundwater microbial communities is primarily controlled by stochastic rather than deterministic processes as traditional ecological succession theory predicts, and 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 many systems ranging from microbiomes of humans and plants to natural and managed ecosystems.

10. **Zhou, J.-Z.**, K. Xue, J.-P. Xie, Y. Deng, L.Y. Wu, X.L. Cheng, S.F. Fei, S.P. Deng, Z.-H. He, J.D. van Nostrand, and Y.Q. Luo. 2012. Microbial Mediation of Carbon Cycle Feedbacks to

Climate Warming. Nature Climate Change, 2:106-110. <https://doi.org/10.1038/nclimate1331> (Top 1% highly cited)

Feedback between terrestrial carbon and climate warming is one of the major uncertainties in projecting future climate change, primarily owing to the poor understanding of microbial responses to climate warming. Using integrated genomics technologies (mainly GeoChip), this study discovered that microorganisms play crucial roles in regulating soil carbon dynamics through three primary feedback mechanisms: (i) shifting microbial community composition, (ii) differentially stimulating functional genes for degrading labile but not recalcitrant carbon, and (iii) enhancing nutrient-cycling processes. These findings suggested that the microbial community functional structure determines whether microbially mediated feedbacks are positive or negative, which provides a mechanistic basis for future carbon–climate modelling.

11. 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. <https://doi.org/10.1126/science.1195979>. (Top 1% highly cited)

The environmental fate of the vast amount of oil from the Deepwater Horizon blowout - the worst environmental disaster in American history as declared by President Barack Obama, are unknown owing to the depth and magnitude of this event. Primarily with the revolutionary GeoChip-based technology, this study revealed the existence of a variety of hydrocarbon-degrading genes/populations in the deep-sea environment, and strong linkages between particular hydrocarbon-degrading genes and hydrocarbon concentrations, indicating a great potential for *intrinsic* bioremediation of the oil plume, which has been confirmed by many later studies. This study also provides a shining example on how GeoChip technology can be used in an integrated synergistic fashion to address complex emergent environmental problems, which is a cornerstone of basic science.

12. Liu, S., **J.-Z. Zhou**, C.-L. Zhang, D. R. Cole and T. J. Phelps. 1997. Thermophilic Fe(III)-reducing bacteria from the deep subsurface: The evolutionary implications. *Science* 277: 1106-1109. <http://doi.org/10.1126/science.277.5329.1106>.

While thermophilic dissimilatory iron-reducing bacteria are thought to have critical roles in the geochemistry and paleomagnetism of hot primitive planets, non-thermophilic dissimilatory Fe(III)-reducing microorganisms were found in similar environments. This study discovered a unique group of dissimilatory thermophilic metal-reducing and magnetite-producing bacteria in geologically isolated, millions-of-years-old deep subsurface (>860 m), suggesting that thermophily may be an ancestral feature associated with Fe(III)-reduction. Molecular analyses revealed that these bacteria represent an unrecognized phylogenetic group of dissimilatory Fe(III)-reducing bacteria, which are the oldest (up to 200 million years) viable cultivated bacteria available, and should be valuable in studying life on early Earth and Mars.