

## Daliang Ning

Institute for Environmental Genomics  
School of Biological Sciences  
University of Oklahoma  
101 David L Boren Blvd SRTC 2030, Norman, OK 73019, USA  
Website: <https://sites.create.ou.edu/daliang> | Email: [ningdaliang@ou.edu](mailto:ningdaliang@ou.edu)  
Google Scholar: <https://scholar.google.com/citations?user=Y2WdGOkAAAAJ&hl=en>  
GitHub: <https://github.com/DaliangNing>

### A. Education

<b>Postdoc</b>	Institute for Environmental Genomics, Department of Microbiology and Plant Biology, The University of Oklahoma, Norman, USA	2012-2016
<b>Postdoc</b>	School of Environment, Tsinghua University, Beijing, China	2009-2012
<b>PhD</b>	Department of Environmental Science and Engineering, Tsinghua University, China	2009
<b>BE</b>	Department of Environmental Science and Engineering, Tsinghua University, China	2003

### B. Appointment

2022.4-present	<i>Associate Director</i> Institute for Environmental Genomics, University of Oklahoma, Norman, OK, USA
2016.6-present	<i>Research Scientist</i> Institute for Environmental Genomics, School of Biology Sciences (Department of Microbiology and Plant Biology before 2023), University of Oklahoma, Norman, OK, USA
2021.4-present	<i>Affiliate Research Scientist</i> Lawrence Berkeley National Laboratory, Berkeley, CA, USA
2020.6-present	<i>Responsible Editor</i> for Frontiers of Environmental Science & Engineering.
2021.3-2022.8	<i>Topic Editor</i> for Frontiers in Microbiology.
2017.11-2020.12	<i>Adjunct Research Scientist</i> State Key Joint Laboratory of Environment Simulation and Pollution Control, School of Environment, Tsinghua University, Beijing, China

### C. Research interests

- Microbial community assembly mechanisms, e.g., selection, competition, dispersal, ecological drift.
- Microbial ecology in environmental engineering and global changes.
- Global/continental microbiome: biogeography in different dimensions of diversity.
- Development of software/packages/tools for microbial ecology studies.

**D. Publications**

Till January 6, 2025: 97 peer-reviewed journal papers, 37 conference presentations, 6 invention patents.

H-index 43, i10-index 71, cited 11,262 times, 13 publications are top 1% highly cited.

Ranked as [Highly Cited Researcher in cross field](#) by Clarivate in 2024.

- Representative publications**

- [1] **Ning D**, Wang Y, Fan Y, Wang J, Van Nostrand JD, Wu L, Zhang P, Curtis DJ, Tian R, Lui L, Hazen TC, Alm EJ, Fields MW, Poole F, Adams MWW, Chakraborty R, Stahl DA, Adams PD, Arkin AP, He Z & Zhou J. 2024. Environmental stress mediates groundwater microbial community assembly. *Nature Microbiology* 9, 490-501. <https://doi.org/10.1038/s41564-023-01573-x> (top 0.1% highly cited, [Web of Science](#))
- [2] **Ning D**, Yuan M, Wu L, Zhang Y, Guo X, Zhou X, Yang Y, Arkin AP, Firestone MK, and Zhou J. 2020. A quantitative framework reveals ecological drivers of grassland microbial community assembly in response to warming. *Nature Communications* 11, 4717. <https://doi.org/10.1038/s41467-020-18560-z>. (top 1% highly cited, [Web of Science](#))
- [3] **Ning D**, Deng Y, Tiedje JM, Zhou J. 2019. A General Framework for Quantitatively Assessing Ecological Stochasticity. *Proceedings of the National Academy of Sciences of the United States of America* 116:16892-16898. <https://doi.org/10.1073/pnas.1904623116>. (top 1% highly cited, [Web of Science](#))
- [4] Wu L, **Ning D** (co-first author), Zhang B, Li Y, Zhang P, Shan X, Zhang Q, Brown MR, Li Z, Van Nostrand JD, Ling F, Xiao N, Zhang Y, Vierheilig J, Wells GF, Yang Y, Deng Y, Tu Q, Wang A, Global Water Microbiome Consortium, Zhang T, He Z, Keller J, Nielsen PH, Alvarez PJJ, Criddle CS, Wagner M, Tiedje JM, He Q, Curtis TP, Stahl DA, Alvarez-Cohen L, Rittmann BE, Wen X, Zhou J. 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, [Web of Science](#)).
- [5] Zhou J, **Ning D**. 2017. Stochastic Community Assembly: Does It Matter in Microbial Ecology? *Microbiology and Molecular Biology Reviews* 81. <https://doi.org/10.1128/membr.00002-17>. (top 1% highly cited, [Web of Science](#))

- Manuscripts (preprint, in preparation, revision, or accepted)**

- Shi ZJ, Xiao N, **Ning D**, Tian R, Zhang P, Curtis D, Nostrand JDV, Wu L, Hazen TC, Rocha AM, He Z, Arkin AP, Firestone MK & Zhou J. 2022. EcoFun-MAP: An Ecological Function Oriented Metagenomic Analysis Pipeline. In revision. (bioRxiv, <https://doi.org/10.1101/2022.04.05.481366>)
- Su Y, Yang Y, Guo X, Gao Y, Feng J, Wu L, Lei J, Liu S, Gao Q, Qin W, Zeng Y, Liang Z, Yuan M, **Ning D**, Wu L & Zhou J. 2023. Submitted.
- Deng S, Yang Y, Guo X, Wu L, Yuan MM, Zhang Y, Shi W, Zhou X, Cornell CR, Bates CT, Liu S, Liang Z, Lei J, Gao Q, **Ning D**, Wu L, Liu X, Luo Y, Tiedje JM & Zhou J. 2024. Submitted.
- Shi W, Tian R, Guo X, **Ning D**, Zhou X, Yuan M, Feng J, Zhou A, Fu Y, Xu G, Hu N, Mu D, Shi P, Fan X, Teng Y, Zhao X, Li Z, Liu J, Wu L, He Z, Nostrand JDV, Liu X, Luo Y, Tiedje JM, Yang Y & Zhou J. 2024. Submitted.
- Wu L, **Ning D**, Zhu C, Tian R, Gao S, Zhang B, Zhao J, Zhang Y, Xiao N, Wang Y, Brown MR, Tu Q, Global Water Microbiome Consortium, Ju F, Wells GF, Guo J, He Z, Nielsen PH, Wang A, Zhang Y,

- Chen T, He Q, Criddle CS, Wagner M, Tiedje JM, Curtis TP, Wen X, Yang Y, Alvarez-Cohen L, Stahl DA, Alvarez PJJ, Rittmann BE & Zhou J. 2024. Submitted.
- Zhu C, Wu L, **Ning D**, Tian R, Gao S, Zhang B, Zhao J, Zhang Y, Xiao N, Wang Y, Brown MR, Tu Q, Global Water Microbiome Consortium, Ju F, Wells GF, Guo J, He Z, Nielsen PH, Wang A, Zhang Y, Chen T, He Q, Criddle CS, Wagner M, Tiedje JM, Curtis TP, Wen X, Yang Y, Alvarez-Cohen L, Stahl DA, Alvarez PJJ, Rittmann BE & Zhou J. 2024. Submitted.
  - Fan Y, **Ning D**, He Z, Zhang P, Rocha AM, Zhang Y, Nostrand JDV, Wu L, Elias DA, Joyner DC, Adams MWW, Fields MW, Alm EJ, Hazen TC, Adams PD, Arkin AP, Yang Y & Zhou J. 2024. Submitted.
  - Zhou J, Xiao N, **Ning D**, He Q, Leibold MA & Hastings A. 2024. In prep.
  - Han S, **Ning D**, Zhou J, et al. 2024. In prep.
  - Li H, Wang B, Yang Z, Liu X, Ji Y, Zheng Y, Wang D, Han S, Tao X, Zhang Y, Wu L, Lei J, Ouyang Y, Xia L, Zhang P, Gao P, Liu XJA, Jian S, Guo X, Fu Y, Shi Z, Wu L, Zhang Y, Pan C, Yang Y, Martens-Habbena W, Stahl DA, **Ning D**, Zhou J & Qin W. 2024. In prep.

#### • Other publications

- [6] Zhang L, **Ning D**, Mantilla-Calderon D, Xu Y, Liu B, Chen W, Gao J, Hamilton KA, Liu J, Zhou J & Ling F. 2024. Daily sampling reveals household-specific water microbiome signatures and shared antimicrobial resistomes in premise plumbing. *Nature Water* 2, 1178-1194. <https://doi.org/10.1038/s44221-024-00345-z>
- [7] Deng S, Jin R, Liang S, Liu F, Liu J, Lyu L, **Ning D**, Pan B, van Hullebusch E, Wang B, Wen X, Xiao K, Xu EG, Yang H, Ying Q, Zhan X, Zhao D, *Frontiers of Environmental Science & Engineering*. 2024. Publication scope and priorities of FESE in an evolving world: An editorial update and perspective. *Frontiers of Environmental Science & Engineering* 18, 13. <https://doi.org/10.1007/s11783-024-1773-x>
- [8] Lei J, Su Y, Jian S, Guo X, Yuan M, Bates CT, Shi ZJ, Li J, Su Y, **Ning D**, Wu L, Zhou J & Yang Y. 2024. Warming effects on grassland soil microbial communities are amplified in cool months. *The ISME Journal* 18. <https://doi.org/10.1093/ismejo/wrae088>
- [9] Michael JP, Putt AD, Yang Y, Adams BG, McBride KR, Fan Y, Lowe KA, **Ning D**, Jagadamma S, Moon JW, Klingeman DM, Zhang P, Fu Y, Hazen TC & Zhou J. 2024. Reproducible responses of geochemical and microbial successional patterns in the subsurface to carbon source amendment. *Water Research*, 121460. <https://doi.org/10.1016/j.watres.2024.121460>
- [10] Tao X, Yang Z, Feng J, Jian S, Yang Y, Bates CT, Wang G, Guo X, **Ning D**, Kempfer ML, Liu XJA, Ouyang Y, Han S, Wu L, Zeng Y, Kuang J, Zhang Y, Zhou X, Shi Z, Qin W, Wang J, Firestone MK, Tiedje JM & Zhou J. 2024. Experimental warming accelerates positive soil priming in a temperate grassland ecosystem. *Nature Communications* 15, 1178. <https://doi.org/10.1038/s41467-024-45277-0> (top 1% highly cited, Web of Science)
- [11] Zheng Y, Wang B, Gao P, Yang Y, Xu B, Su X, **Ning D**, Tao Q, Li Q, Zhao F, Wang D, Zhang Y, Li M, Winkler M-KH, Ingalls AE, Zhou J, Zhang C, Stahl DA, Jiang J, Martens-Habbena W & Qin W. 2024. Novel order-level lineage of ammonia-oxidizing archaea widespread in marine and terrestrial environments. *The ISME Journal* 18. <https://doi.org/10.1093/ismejo/wrad002>
- [12] Zhang Y, **Ning D**, Wu L, Yuan MM, Zhou X, Guo X, Hu Y, Jian S, Yang Z, Han S, Feng J, Kuang J,

- Cornell CR, Bates CT, Fan Y, Michael JP, Ouyang Y, Guo J, Gao Z, Shi Z, Xiao N, Fu Y, Zhou A, Wu L, Liu X, Yang Y, Tiedje JM & Zhou J. 2023. Experimental warming leads to convergent succession of grassland archaeal community. *Nature Climate Change* 13, 561-569. <https://doi.org/10.1038/s41558-023-01664-x>
- [13] Qin Y, Wu L, Zhang Q, Wen C, Nostrand JDV, **Ning D**, Raskin L, Pinto A & Zhou J. 2023. Effects of error, chimera, bias, and GC content on the accuracy of amplicon sequencing. *mSystems* 8, e01025-01023. <https://doi.org/10.1128/msystems.01025-23>
- [14] Cornell CR, Zhang Y, **Ning D**, Xiao N, Wagle P, Xiao X & Zhou J. 2023. Land use conversion increases network complexity and stability of soil microbial communities in a temperate grassland. *ISME J*. <https://doi.org/10.1038/s41396-023-01521-x>
- [15] Wu L, Yang Y, **Ning D**, Gao Q, Yin H, Xiao N, Zhou BY, Chen S, He Q & Zhou J. 2023. Assessing mechanisms for microbial taxa and community dynamics using process models. *mLife* 2, 239-252. <https://doi.org/10.1002/mlf2.12076>
- [16] Liang Q, Zhang J, **Ning D**, Yu W, Chen G, Tao X, Zhou J, Du Z & Mu D. 2023. Niche Modification by Sulfate-Reducing Bacteria Drives Microbial Community Assembly in Anoxic Marine Sediments. *mBio* 14, e03535-03522. <https://doi.org/doi:10.1128/mbio.03535-22>
- [17] Xu T, Tao X, He H, Kempfer ML, Zhang S, Liu X, Wang J, Wang D, **Ning D**, Pan C, Ge H, Zhang N, He Y-X, and Zhou J. 2023. Functional and structural diversification of incomplete phosphotransferase system in cellulose-degrading clostridia. *The ISME Journal*. <https://doi.org/10.1038/s41396-023-01392-2>
- [18] Shi K, Liang B, Feng K, **Ning D**, Cornell CR, Zhang Y, Xu W, Zhou M, Deng Y, Jiang J, Liu T, Wang A, and Zhou J. 2023. Electrostimulation triggers an increase in cross-niche microbial associations toward enhancing organic nitrogen wastewater treatment. *Journal of Environmental Management* 331, 117301. <https://doi.org/10.1016/j.jenvman.2023.117301>
- [19] Wu L, Zhang Y, Guo X, **Ning D**, Zhou X, Feng J, Yuan MM, Liu S, Guo J, Gao Z, Ma J, Kuang J, Jian S, Han S, Yang Z, Ouyang Y, Fu Y, Xiao N, Liu X, Wu L, Zhou A, Yang Y, Tiedje JM, and Zhou J. 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, Web of Science)
- [20] Xiao N, Zhou A, Kempfer ML, Zhou BY, Shi ZJ, Yuan M, Guo X, Wu L, **Ning D**, Nostrand JV, Firestone MK, and Zhou J. 2022. Disentangling direct from indirect relationships in association networks. *Proceedings of the National Academy of Sciences* 119, e2109995119. <https://doi.org/10.1073/pnas.2109995119>. (top 1% highly cited, Web of Science)
- [21] Kuang J, Deng D, Han S, Bates CT, **Ning D**, Shu W, and Zhou J. 2022. Resistance potential of soil bacterial communities along a biodiversity gradient in forest ecosystems. *mLife* 1, 399-411. <https://doi.org/10.1002/mlf2.12042>.
- [22] Goff JL, Szink EG, Thorgersen MP, Putt AD, Fan Y, Lui LM, Nielsen TN, Hunt KA, Michael JP, Wang Y, **Ning D**, Fu Y, Van Nostrand JD, Poole II FL, Chandonia J-M, Hazen TC, Stahl DA, Zhou J, Arkin AP, and Adams MWW. 2022. Ecophysiological and genomic analyses of a representative isolate of highly abundant *Bacillus cereus* strains in contaminated subsurface sediments. *Environmental Microbiology* <https://doi.org/10.1111/1462-2920.16173>.
- [23] Yang L, **Ning D**, Yang Y, He N, Li X, Cornell CR, Bates CT, Filimonenko E, Kuzyakov Y, Zhou J, Yu

- G, and Tian J. 2022. Precipitation balances deterministic and stochastic processes of bacterial community assembly in grassland soils. *Soil Biology and Biochemistry* 168, 108635. <https://doi.org/10.1016/j.soilbio.2022.108635>. (top 1% highly cited, Web of Science)
- [24] Sun J, Lin Z, **Ning D\***(corresponding), Wang H, Zhang Z, He Z, and Zhou J. 2022. Functional microbial community structures and chemical properties indicated mechanisms and potential risks of urban river eco-remediation. *Science of The Total Environment* 803, 149868. <https://doi.org/10.1016/j.scitotenv.2021.149868>.
- [25] Cornell CR, Zhang Y, Ning D, Wu L, Wagle P, Steiner JL, Xiao X, Zhou J, and Bailey MJ. 2022. Temporal dynamics of bacterial communities along a gradient of disturbance in a U.S. southern plains agroecosystem. *mBio* 13, e03829-03821. <https://doi.org/10.1128/mbio.03829-21>.
- [26] Bates CT, Escalas A, Kuang J, Hale L, Wang Y, Herman D, Nuccio EE, Wan X, Bhattacharyya A, Fu Y, Tian R, Wang G, **Ning D**, Yang Y, Wu L, Pett-Ridge J, Saha M, Craven K, Brodie EL, Firestone M, and Zhou J. 2022. Conversion of marginal land into switchgrass conditionally accrues soil carbon but reduces methane consumption. *The ISME Journal* 16, 10-25. <https://doi.org/10.1038/s41396-021-00916-y>.
- [27] Paradis CJ, Miller JI, Moon JW, Spencer SJ, Lui LM, Van Nostrand JD, Ning D, Steen AD, McKay LD, Arkin AP, Zhou J, Alm EJ, and Hazen TC. 2022. Sustained Ability of a Natural Microbial Community to Remove Nitrate from Groundwater. *Ground Water* 60, 99-111. <https://doi.org/10.1111/gwat.13132>.
- [28] Liu Y, Zeng M, Xie Z, **Ning D**, Zhou J, Yu X, Liu R, Zhang L, and Fang J. 2022. Microbial Community Structure and Ecological Networks during Simulation of Diatom Sinking. *Microorganisms* 10, 639. <https://doi.org/10.3390/microorganisms10030639>.
- [29] Aslani F, Geisen S, **Ning D**, Tedersoo L, and Bahram M. 2022. Towards revealing the global diversity and community assembly of soil eukaryotes. *Ecology Letters* 25, 65-76. <https://doi.org/10.1111/ele.13904>.
- [30] Chen L, Zhang M, **Ning D**, Van Nostrand JD, Yang Y, Zhou J, and Zuo J. 2021. Behaviors of Homologous Antibiotic Resistance Genes in a Cephalosporin WWTP, Subsequent WWTP and the Receiving River. *Frontiers in Environmental Science* 9. <https://doi.org/10.3389/fenvs.2021.783676>.
- [31] Kuang J, Bates CT, Wan X, **Ning D**, Deng D, Shu W, and Zhou J. 2021. High historical variability weakens the effects of current climate differentiation on microbial community dissimilarity and assembly. *Global Change Biology* 27, 5963-5975. <https://doi.org/10.1111/gcb.15848>.
- [32] Wang A, Shi K, **Ning D**, Cheng H, Wang H, Liu W, Gao S, Li Z, Han J, Liang B, and Zhou J. 2021. Electrical selection for planktonic sludge microbial community function and assembly. *Water Research* 206, 117744. <https://doi.org/10.1016/j.watres.2021.117744>.
- [33] Huang Z, Hou D, Zhou R, Zeng S, Xing C, Wei D, Deng X, Yu L, Wang H, Deng Z, Weng S, **Ning D**, Xiao C, Yan Q, Zhou J, He Z, and He J. 2021. Environmental Water and Sediment Microbial Communities Shape Intestine Microbiota for Host Health: The Central Dogma in an Anthropogenic Aquaculture Ecosystem. *Frontiers in Microbiology* 12, 3298. <https://doi.org/10.3389/fmicb.2021.772149>.
- [34] Sun C, Zhang B, **Ning D**, Zhang Y, Dai T, Wu L, Li T, Liu W, Zhou J, and Wen X. 2021. Seasonal dynamics of the microbial community in two full-scale wastewater treatment plants: Diversity, composition, phylogenetic group based assembly and co-occurrence pattern. *Water Research* 200,

117295. <https://doi.org/10.1016/j.watres.2021.117295>.
- [35] Yuan MM, Guo X, Wu L, Zhang Y, Xiao N, **Ning D**, Shi Z, Zhou X, Wu L, Yang Y, Tiedje JM, and Zhou J. 2021. Climate warming enhances microbial network complexity and stability. *Nature Climate Change* 11, 343-348. <https://doi.org/10.1038/s41558-021-00989-9>. (top 0.1% highly cited, Web of Science)
- [36] Ceja-Navarro JA, Wang Y, **Ning D**, Arellano A, Ramanculova L, Yuan MM, Byer A, Craven KD, Saha MC, Brodie EL, Pett-Ridge J, and Firestone MK. 2021. Protist diversity and community complexity in the rhizosphere of switchgrass are dynamic as plants develop. *Microbiome* 9, 96. <https://doi.org/10.1186/s40168-021-01042-9>.
- [37] Shi W, Ma Q, Pan F, Fan Y, Kempfer ML, **Ning D**, Qu Y, Wall JD, Zhou A, Zhou J, and Marshall CW. 2021. Genetic Basis of Chromate Adaptation and the Role of the Pre-existing Genetic Divergence during an Experimental Evolution Study with *Desulfovibrio vulgaris* Populations. *mSystems* 6, e00493-00421. <https://doi.org/10.1128/mSystems.00493-21>.
- [38] Zhang B, **Ning D**, Van Nostrand JD, Sun C, Yang Y, Zhou J, and Wen X. 2021. The call for regional design code from the regional discrepancy of microbial communities in activated sludge. *Environmental Pollution* 273, 116487. <https://doi.org/10.1016/j.envpol.2021.116487>.
- [39] Li L, **Ning D**, Jeon Y, Ryu H, Santo Domingo JW, Kang D-W, Kadudula A, and Seo Y. 2021. Ecological insights into assembly processes and network structures of bacterial biofilms in full-scale biologically active carbon filters under ozone implementation. *Science of The Total Environment* 751, 141409. <https://doi.org/10.1016/j.scitotenv.2020.141409>.
- [40] Gao Q, Gao S, Bates C, Zeng Y, Lei J, Su H, Dong Q, Qin Z, Zhao J, Zhang Q, **Ning D**, Huang Y, Zhou J, and Yang Y. 2021. The microbial network property as a bio-indicator of antibiotic transmission in the environment. *Science of The Total Environment* 758, 143712. <https://doi.org/10.1016/j.scitotenv.2020.143712>.
- [41] Zou Y, **Ning D** (co-first), Huang Y, Liang Y, Wang H, Duan L, Yuan T, He Z, Yang Y, Xue K, Van Nostrand JD, Zhou J. 2020. Functional structures of soil microbial community relate to contrasting N<sub>2</sub>O emission patterns from a highly acidified forest. *Science of The Total Environment* 725:138504. <https://doi.org/10.1016/j.scitotenv.2020.138504>.
- [42] Liang Y, **Ning D**, Lu Z, Zhang N, Hale L, Wu L, Clark IM, McGrath SP, Storkey J, Hirsch PR, Sun B, and Zhou J. 2020. Century long fertilization reduces stochasticity controlling grassland microbial community succession. *Soil Biology and Biochemistry* 151, 108023. <https://doi.org/10.1016/j.soilbio.2020.108023>.
- [43] Zhang B, **Ning D**, Van Nostrand JD, Sun C, Yang Y, Zhou J, and Wen X. 2020. Biogeography and Assembly of Microbial Communities in Wastewater Treatment Plants in China. *Environmental Science & Technology* 54, 5884-5892. <https://doi.org/10.1021/acs.est.9b07950>.
- [44] Zhang B, **Ning D**, Yang Y, Van Nostrand JD, Zhou J, Wen X. 2020. Biodegradability of wastewater determines microbial assembly mechanisms in full-scale wastewater treatment plants. *Water Research* 169:115276. <https://doi.org/10.1016/j.watres.2019.115276>.
- [45] Tian R, **Ning D**, He Z, Zhang P, Spencer SJ, Gao S, Shi W, Wu L, Zhang Y, Yang Y, Adams BG, Rocha AM, Detienne BL, Lowe KA, Joyner DC, Klingeman DM, Arkin AP, Fields MW, Hazen TC, Stahl DA, Alm EJ, Zhou J. 2020. Small and mighty: adaptation of superphylum *Patescibacteria* to groundwater environment drives their genome simplicity. *Microbiome* 8:51.

<https://doi.org/10.1186/s40168-020-00825-w>.

- [46] Guo X, Gao Q, Yuan M, Wang G, Zhou X, Feng J, Shi Z, Hale L, Wu L, Zhou A, Tian R, Liu F, Wu B, Chen L, Jung CG, Niu S, Li D, Xu X, Jiang L, Escalas A, Wu L, He Z, Van Nostrand JD, **Ning D**, Liu X, Yang Y, Schuur EAG, Konstantinidis KT, Cole JR, Penton CR, Luo Y, Tiedje JM, and Zhou J. 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>.
- [47] Gao Q, Wang G, Xue K, Yang Y, Xie J, Yu H, Bai S, Liu F, He Z, **Ning D**, Hobbie SE, Reich PB, and Zhou J. 2020. Stimulation of soil respiration by elevated CO<sub>2</sub> is enhanced under nitrogen limitation in a decade-long grassland study. *Proceedings of the National Academy of Sciences of the United States of America* 117, 33317-33324. <https://doi.org/10.1073/pnas.2002780117>.
- [48] Wu B, Liu F, Zhou A, Li J, Shu L, Kempner ML, Yang X, **Ning D**, Pan F, Zane GM, Wall JD, Van Nostrand JD, Juneau P, Chen S, Yan Q, Zhou J, and He Z. 2020. Experimental evolution reveals nitrate tolerance mechanisms in *Desulfovibrio vulgaris*. *The ISME Journal* 14, 2862-2876. <https://doi.org/10.1038/s41396-020-00753-5>.
- [49] Tao X, Feng J, Yang Y, Wang G, Tian R, Fan F, **Ning D**, Bates CT, Hale L, Yuan MM, Wu L, Gao Q, Lei J, Schuur EAG, Yu J, Bracho R, Luo Y, Konstantinidis KT, Johnston ER, Cole JR, Penton CR, Tiedje JM, and Zhou J. 2020. Winter warming in Alaska accelerates lignin decomposition contributed by Proteobacteria. *Microbiome* 8, 84. <https://doi.org/10.1186/s40168-020-00838-5>.
- [50] Feng J, Wang C, Lei J, Yang Y, Yan Q, Zhou X, Tao X, **Ning D**, Yuan MM, Qin Y, Shi ZJ, Guo X, He Z, Van Nostrand JD, Wu L, Bracho-Garillo RG, Penton CR, Cole JR, Konstantinidis KT, Luo Y, Schuur EAG, Tiedje JM, Zhou J. 2020. Warming-induced permafrost thaw exacerbates tundra soil carbon decomposition mediated by microbial community. *Microbiome* 8:3. <https://doi.org/10.1186/s40168-019-0778-3>.
- [51] Tu Q, Yan Q, Deng Y, Michaletz ST, Buzzard V, Weiser MD, Waide R, **Ning D**, Wu L, He Z, and Zhou J. 2020. Biogeographic patterns of microbial co-occurrence ecological networks in six American forests. *Soil Biology and Biochemistry* 148, 107897. <https://doi.org/10.1016/j.soilbio.2020.107897>.
- [52] Zhao M, Cong J, Cheng J, Qi Q, Sheng Y, **Ning D**, Lu H, Wyckoff K, Deng Y, Li D, Zhou J, Zhang Y. 2020. Soil Microbial Community Assembly and Interactions Are Constrained by Nitrogen and Phosphorus in Broadleaf Forests of Southern China. *Forests* 11:285. <https://doi.org/10.3390/f11030285>.
- [53] Dai T, Zhao Y, **Ning D**, Huang B, Mu Q, Yang Y, Wen D. 2020. Dynamics of coastal bacterial community average ribosomal RNA operon copy number reflect its response and sensitivity to ammonium and phosphate. *Environmental Pollution* 260:113971. <https://doi.org/10.1016/j.envpol.2020.113971>.
- [54] Huang Z, Zeng S, Xiong J, Hou D, Zhou R, Xing C, Wei D, Deng X, Yu L, Wang H, Deng Z, Weng S, Kriengkrai S, **Ning D**, Zhou J, He J. 2020. Microecological Koch's postulates reveal that intestinal microbiota dysbiosis contributes to shrimp white feces syndrome. *Microbiome* 8:32. <https://doi.org/10.1186/s40168-020-00802-3>.
- [55] Miao L, Wang P, Hou J, **Ning D**, Liu Z, Liu S, Li T. 2020. Chronic exposure to CuO nanoparticles induced community structure shift and a delay inhibition of microbial functions in multi-species biofilms. *Journal of Cleaner Production* 262:121353. <https://doi.org/10.1016/j.jclepro.2020.121353>.

- [56] Buzzard V, Michaletz S, Deng Y, He Z, **Ning D**, Shen L, Tu Q, Nostrand JV, Voordeckers J, Wang J, Weiser M, Kaspari M, Waide R, Zhou J, Enquist B. 2019. Continental scale structuring of forest and soil diversity via functional traits. *Nature Ecology & Evolution*, 3:1298–1308. <https://doi.org/10.1038/s41559-019-0954-7>.
- [57] Guo X, Zhou X, Hale L, Yuan M, **Ning D**, Feng J, Shi Z, Li Z, Feng B, Gao Q, Wu L, Shi W, Zhou A, Fu Y, Wu L, He Z, Van Nostrand JD, Qiu G, Liu X, Luo Y, Tiedje JM, Yang Y, Zhou J. 2019. Climate warming accelerates temporal scaling of grassland soil microbial biodiversity. *Nature Ecology & Evolution* 3:612-619. <https://doi.org/10.1038/s41559-019-0848-8>.
- [58] Zhang Z, Deng Y, Feng K, Cai W, Li S, Yin H, Xu M, **Ning D**, Qu Y. 2019. Deterministic Assembly and Diversity Gradient Altered the Biofilm Community Performances of Bioreactors. *Environmental Science & Technology* 53:1315-1324. <https://doi.org/10.1021/acs.est.8b06044>.
- [59] Zelaya AJ, Parker AE, Bailey KL, Zhang P, Van Nostrand J, **Ning D**, Elias DA, Zhou J, Hazen TC, Arkin AP, Fields MW. 2019. High spatiotemporal variability of bacterial diversity over short time scales with unique hydrochemical associations within a shallow aquifer. *Water Research* 164:114917. <https://doi.org/10.1016/j.watres.2019.114917>.
- [60] Shi Z, Yin H, Van Nostrand JD, Voordeckers JW, Tu Q, Deng Y, Yuan M, Zhou A, Zhang P, Xiao N, **Ning D**, He Z, Wu L, Zhou J. 2019. Functional gene array-based ultrasensitive and quantitative detection of microbial populations in complex communities. *mSystems* 4:e00296-00219. <https://doi.org/10.1128/mSystems.00296-19>.
- [61] Hou L, Mulla SI, Niño-Garcia JP, **Ning D**, Rashid A, Hu A, Yu C-P. 2019. Deterministic and stochastic processes driving the shift in the prokaryotic community composition in wastewater treatment plants of a coastal Chinese city. *Applied Microbiology and Biotechnology* 103:9155-9168. <https://doi.org/10.1007/s00253-019-10177-7>.
- [62] Gao Q, Yang Y, Feng J, Tian R, Guo X, **Ning D**, Hale L, Wang M, Cheng J, Wu L, Zhao M, Zhao J, Wu L, Qin Y, Qi Q, Liang Y, Sun B, Chu H, Zhou J. 2019. The spatial scale dependence of diazotrophic and bacterial community assembly in paddy soil. *Global Ecology and Biogeography* 28:1093-1105. <https://doi.org/10.1111/geb.12917>.
- [63] Feng K, Zhang Y, He Z, **Ning D**, Deng Y. 2019. Interdomain ecological networks between plants and microbes. *Molecular Ecology Resources* 19:1565-1577. <https://doi.org/10.1111/1755-0998.13081>.
- [64] Weiser MD, **Ning D**, Buzzard V, Michaletz ST, He Z, Enquist BJ, Waide RB, Zhou J, Kaspari M. 2019. Thermal disruption of soil bacterial assemblages decreases diversity and assemblage similarity. *Ecosphere* 10:e02598. <https://doi.org/10.1002/ecs2.2598>.
- [65] Guo X, Feng J, Shi Z, Zhou X, Yuan M, Tao X, Hale L, Yuan T, Wang J, Qin Y, Zhou A, Fu Y, Wu L, He Z, Van Nostrand JD, **Ning D**, Liu X, Luo Y, Tiedje JM, Yang Y, Zhou J. 2018. Climate warming leads to divergent succession of grassland microbial communities. *Nature Climate Change* 8:813-818. <https://doi.org/10.1038/s41558-018-0254-2>. (top 1% highly cited, Web of Science)
- [66] Chen C, Hemme C, Beleno J, Shi ZJ, **Ning D**, Qin Y, Tu Q, Jorgensen M, He Z, Wu L, Zhou J. 2018. Oral microbiota of periodontal health and disease and their changes after nonsurgical periodontal therapy. *The ISME Journal* 12:1210. <https://doi.org/10.1038/s41396-017-0037-1>.
- [67] He Z, Zhang P, Wu L, Rocha AM, Tu Q, Shi Z, Wu B, Qin Y, Wang J, Yan Q, Curtis D, **Ning D**, Van Nostrand JD, Wu L, Yang Y, Elias DA, Watson DB, Adams MWW, Fields MW, Alm EJ, Hazen TC, Adams PD, Arkin AP, Zhou J. 2018. Microbial functional gene diversity predicts groundwater

- contamination and ecosystem functioning. *mBio* 9:e02435-17. <https://doi.org/10.1128/mBio.02435-17>.
- [68] Deng Y, Ning D, Qin Y, Xue K, Wu L, He Z, Yin H, Liang Y, Buzzard V, Michaletz ST, Zhou J. 2018. Spatial scaling of forest soil microbial communities across a temperature gradient. *Environmental Microbiology* 20:3504-3513. <https://doi.org/10.1111/1462-2920.14303>.
- [69] Whitman T, Neurath R, Perera A, Chu-Jacoby I, Ning D, Zhou J, Nico P, Pett-Ridge J, Firestone M. 2018. Microbial community assembly differs across minerals in a rhizosphere microcosm. *Environmental Microbiology* 20:4444-4460. <https://doi.org/10.1111/1462-2920.14366>.
- [70] Brandon AM, Gao S-H, Tian R, Ning D, Yang S-S, Zhou J, Wu W-M, Criddle CS. 2018. Biodegradation of Polyethylene and Plastic Mixtures in Mealworms (Larvae of *Tenebrio molitor*) and Effects on the Gut Microbiome. *Environmental Science & Technology* 52:6526-6533. <https://doi.org/10.1021/acs.est.8b02301>. (top 1% highly cited, Web of Science)
- [71] Wu B, Liu F, Weiser MD, Ning D, Okie JG, Shen L, Li J, Chai B, Deng Y, Feng K, Wu L, Chen S, Zhou J, He Z. 2018. Temperature determines the diversity and structure of N<sub>2</sub>O-reducing microbial assemblages. *Functional Ecology* 32:1867-1878. <https://doi.org/10.1111/1365-2435.13091>.
- [72] Yang S-S, Brandon AM, Andrew Flanagan JC, Yang J, Ning D, Cai SY, Fan HQ, Wang ZY, Ren J, Benbow E, Ren N-Q, Waymouth RM, Zhou J, Criddle CS, Wu W-M. 2018. Biodegradation of polystyrene wastes in yellow mealworms (larvae of *Tenebrio molitor* Linnaeus): Factors affecting biodegradation rates and the ability of polystyrene-fed larvae to complete their life cycle. *Chemosphere* 191:979-989. <https://doi.org/10.1016/j.chemosphere.2017.10.117>.
- [73] Yang S-S, Wu W-M, Brandon AM, Fan H-Q, Receveur JP, Li Y, Wang Z-Y, Fan R, McClellan RL, Gao S-H, Ning D, Phillips DH, Peng B-Y, Wang H, Cai S-Y, Li P, Cai W-W, Ding L-Y, Yang J, Zheng M, Ren J, Zhang Y-L, Gao J, Xing D, Ren N-Q, Waymouth RM, Zhou J, Tao H-C, Picard CJ, Benbow ME, Criddle CS. 2018. Ubiquity of polystyrene digestion and biodegradation within yellow mealworms, larvae of *Tenebrio molitor* Linnaeus (Coleoptera: Tenebrionidae). *Chemosphere* 212:262-271. <https://doi.org/10.1016/j.chemosphere.2018.08.078>.
- [74] Guo X, Zhou X, Hale L, Yuan M, Feng J, Ning D, Shi Z, Qin Y, Liu F, Wu L, He Z, Van Nostrand JD, Liu X, Luo Y, Tiedje JM, Zhou J. 2018. Taxonomic and Functional Responses of Soil Microbial Communities to Annual Removal of Aboveground Plant Biomass. *Frontiers in Microbiology* 9. <https://doi.org/10.3389/fmicb.2018.00954>.
- [75] Zhou J, Deng Y, Shen L, Wen C, Yan Q, Ning D, Qin Y, Xue K, Wu L, He Z, Voordeckers JW, Van Nostrand JD, Buzzard V, Michaletz ST, Enquist BJ, Weiser MD, Kaspari M, Waide R, Yang Y, Brown JH. 2017. Correspondence: Reply to ‘Analytical flaws in a continental-scale forest soil microbial diversity study’. *Nature Communications* 8:15583. <https://doi.org/10.1038/ncomms15583>.
- [76] Yan Q, Stegen JC, Yu Y, Deng Y, Li X, Wu S, Dai L, Zhang X, Li J, Wang C, Ni J, Li X, Hu H, Xiao F, Feng W, Ning D, He Z, Van Nostrand JD, Wu L, Zhou J. 2017. Nearly a decade-long repeatable seasonal diversity patterns of bacterioplankton communities in the eutrophic Lake Donghu (Wuhan, China). *Molecular Ecology* 26:3839-3850. <https://doi.org/10.1111/mec.14151>.
- [77] Kaspari M, Bujan J, Weiser MD, Ning D, Michaletz ST, He Z, Enquist BJ, Waide RB, Zhou J, Turner BL, Wright SJ. 2017. Biogeochemistry drives diversity in the prokaryotes, fungi, and invertebrates of a Panama forest. *Ecology* 98:2019-2028. <https://doi.org/10.1002/ecy.1895>.
- [78] Liu J, Techtman SM, Woo HL, Ning D, Fortney JL, Hazen TC. 2017. Rapid Response of Eastern Mediterranean Deep Sea Microbial Communities to Oil. *Scientific Reports* 7:5762.

<https://doi.org/10.1038/s41598-017-05958-x>.

- [79] Wen C, Wu L, Qin Y, Van Nostrand JD, **Ning D**, Sun B, Xue K, Liu F, Deng Y, Liang Y, Zhou J. 2017. Evaluation of the reproducibility of amplicon sequencing with Illumina MiSeq platform. *PLoS One* 12:e0176716. <https://doi.org/10.1371/journal.pone.0176716>.
- [80] Zhou M, Zhang X, Yang X, Zhang Y, He H, **Ning D**. 2017. *Flavobacterium ardleyense* sp. nov., isolated from Antarctic soil. *International Journal of Systematic and Evolutionary Microbiology* 67:3996-4001. <https://doi.org/10.1099/ijsem.0.002241>.
- [81] Zhou J, Deng Y, Shen L, Wen C, Yan Q, **Ning D**, Qin Y, Xue K, Wu L, He Z, Voordeckers JW, Nostrand JDV, Buzzard V, Michaletz ST, Enquist BJ, Weiser MD, Kaspari M, Waide R, Yang Y, Brown JH. 2016. Temperature mediates continental-scale diversity of microbes in forest soils. *Nature Communications* 7:12083. <https://doi.org/10.1038/ncomms12083>. (top 1% highly cited, Web of Science)
- [82] **Ning D**, Huang Y, Pan R, Wang F, Wang H. 2014. Effect of eco-remediation using planted floating bed system on nutrients and heavy metals in urban river water and sediment: A field study in China. *Science of The Total Environment* 485:596-603. <https://doi.org/10.1016/j.scitotenv.2014.03.103>.
- [83] **Ning D**, Wang H. 2012. Involvement of Cytochrome P450 in Pentachlorophenol Transformation in a White Rot Fungus *Phanerochaete chrysosporium*. *PLOS ONE* 7:e45887. <https://doi.org/10.1371/journal.pone.0045887>.
- [84] **Ning D**, Wang H, Zhuang Y. 2010. Induction of functional cytochrome P450 and its involvement in degradation of benzoic acid by *Phanerochaete chrysosporium*. *Biodegradation* 21:297-308. <https://doi.org/10.1007/s10532-009-9301-z>.
- [85] **Ning D**, Wang H, Ding C, Lu H. 2010. Novel evidence of cytochrome P450-catalyzed oxidation of phenanthrene in *Phanerochaete chrysosporium* under ligninolytic conditions. *Biodegradation* 21:889-901. <https://doi.org/10.1007/s10532-010-9349-9>.
- [86] **Ning D**, Wang H, Wang L, Ding C. 2009. Induction and function of cytochrome P450 in degradation of refractory organic chemicals by *Phanerochaete chrysosporium*. *China Environmental Science*:407-412.
- [87] **Ning D**, Wang H, Li D. 2009. Induction and measurement of cytochrome P450 in white rot fungi. *Environmental Science-Chinese* 30:2485-2490.
- [88] **Ning D**, Wang H, Zhuang Y, Li D. 2007. Inducement and degradation function of P450 in *Phanerochaete chrysosporium* by in situ spectroscopic analysis. *Chemical Journal of Chinese Universities-Chinese* 28:1469-1474.
- [89] Hou J, Qu Y, **Ning D**, Wang H. 2014. Impact of human exposure factors on health risk assessment for benzene-contaminated site. *Environmental Science & Technology-Chinese* 8.
- [90] Hou J, Qu Y, **Ning D**, Wang H. 2014. Characteristic of human exposure factors in china and their uncertainty analysis in health risk assessment. *Environmental Science & Technology-Chinese* 8.
- [91] He F, Wang L, **Ning D**, Guo G, Wang H. 2012. Phenanthrene biodegradation and dynamic change of expression of naphthalene dioxygenase (ndo) genes in a halophilic bacteria consortium. *China Environmental Science* 32:1662-1669.
- [92] Weng P, **Ning D**, Wang H, Wang F, Jiang D. 2012. Comparison of urban river oxygenation by water transfer and aeration in plain area. *Journal of Changzhou University (Natural Science Edition)* 2:40-44.
- [93] Zeng B, **Ning D**, Wang H. 2008. Preliminary study on biodegradation of pentachlorophenol by white

rot fungus. *Environmental Chemistry* 27:181-185.

- [94] Wei M, Wang H, Liu C, **Ning D**. 2008. Bioaugmentation with immobilized genetically engineered microorganism (GEM)/CAS process for treatment of atrazine wastewater. *Environmental Science-Chinese* 29:1555-1560.
- [95] Jiang J, Wang H, Gao J, Song L, **Ning D**. 2008. Cloning and sequence analysis of 1,2,4-trichlorobenzene dioxygenase and dehydrogenase genes. *Environmental Science-Chinese* 29:1655-1659.
- [96] Wei J, Wang L, **Ning D**, Wei D, Hu H. 2004. Effect of dechlorination on reduction of biotoxication of disinfected wastewater. *China Water & Wastewater* 20:16-19.
- [97] Wei J, Hu H, **Ning D**, Wang L, Wei D. 2004. Study on bio-toxicity of disinfection byproduct after chlorination/dechlorination in wastewater. *China Water & Wastewater* 20:5-8.
- [98] Wei J, Hu H, **Ning D**, Wang L, Wei D. 2004. Effect of wastewater characteristics on acute toxicity incurred by disinfection. *China Water & Wastewater* 20:17-20.

#### • Patents

- [1] Wang H, Zhao BS, **Ning DL**. *Halomonas xianhensis* A-1 which can degrade polycyclic aromatic hydrocarbons and its application. China. (Invention Patent, publication No. CN101838616A).
- [2] Wang H, Zhao BS, **Ning DL**. *Thalassospira xianhensis* P-4 which can degrade polycyclic aromatic hydrocarbons and its application. China. (Invention Patent, publication No. CN101838617A).
- [3] Wang H, Zhao BS, **Ning DL**. Method of screening polycyclic aromatic hydrocarbons degrading bacteria. (Invention Patent, publication No. CN101838629A).
- [4] Wang H, **Ning DL**, Zhou LW, Pan RS, Sun H, Zhang XH. A system for river and scenic water purification. China. (Invention patent, Granted, ZL201210575971.X, 2014-04-09)
- [5] Wang H, Bai XK, **Ning DL**. Preparation and application of a complex that can inhibit release of nitrogen and phosphorus from sediment of river and lake. (Invention Patent, publication No. CN102399045A)
- [6] Wang H, Bai XK, **Ning DL**. Preparation and application of a complex that can inhibit malodorous black in surface water. (Invention Patent, publication No. CN102398936A)

#### • Conference Presentations

- [1] **Ning D**. Reasons and Chance: Quantifying Microbial Community Assembly Mechanisms. in International Forum on Advanced Environmental Sciences and Technology (iFAST) Microbial Ecology - James Tiedje Symposium (Norman, OK, Apr 4-6, 2022). **[Oral]**
- [2] **Ning D**. Delineating Ecological Processes Underpinning Microbial Community Assembly. in World Microbe Forum (the American Society of Microbiology [ASM] and the Federation of Microbiological Societies [FEMS], Online, June 20-24, 2021). **[Oral]**
- [3] **Ning D**, Fan Y, Lui LM, Michael JP, Fu Y, Nostrand JDV, Tian R, Wang Y, Walker KF, Dixon ER, Putt AD, Williams DE, Joyner DC, Lowe KA, Poole FL, Ge X, Thorgersen MP, Adams MWW, Chakraborty R, Wu X, Elias DA, Wilpiseski RL, Fields MW, Hazen TC, Zhou J, Arkin AP, and Adams PD. Physical size matters in groundwater bacterial community assembly. in 2021 Genomic Sciences Program (GSP) Annual Principal Investigator (PI) Meeting (U. S. Department of Energy Office of

- Science, Washington, DC, 2021). [Poster]
- [4] **Ning D** and Zhou J. Temperature regulates continental-scale community assembly processes in forest soils. in The Ecological Society of America Annual Meeting (Virtual, Aug 3-6, 2020). [Oral]
  - [5] **Ning D**. Quantitative understanding of subsurface microbial community assembly mechanisms under a contamination gradient. in 2020 Genomic Sciences Program (GSP) Annual Principal Investigator (PI) Meeting (U. S. Department of Energy Office of Science, Washington, DC, Feb 24-26, 2020) [Oral].
  - [6] **Ning D** and Zhou J. Ecological drivers of grassland soil microbial community assembly in response to climate warming. in American Geophysical Union 2019 Fall Meeting (San Francisco, CA, Dec 9-13, 2019). [Poster]
  - [7] Zhou J, Wen X, Curtis T, He Q, **Ning D**, Yang Y, Wu L, Zhang B, and Ling F. Global Wastewater Microbiome: Diversity and Biogeography. in 255<sup>th</sup> American Chemical Society National Meeting (New Orleans, LA, USA, Mar 18-22, 2018). [Poster]
  - [8] **Ning D**, Deng Y, Tiedje JM, and Zhou J. Ecological stochasticity in groundwater microbial community succession: Application of a general quantitative framework. in The Ecological Society of America Annual Meeting (New Orleans, LA, USA, Aug 5-10, 2018). [Oral]
  - [9] **Ning D**, Deng Y, Nostrand JDV, Wu L, Zhang P, He Z, et al. Ecological stochasticity in subsurface microbial community assembly under stress gradient: application of a general quantitative framework. in 2018 Genomic Sciences Program Annual PI Meeting (U. S. Department of Energy Office of Science, Tysons, VA, Feb 25-28, 2018). [Poster]
  - [10] **Ning D**, Shi Z, Zhang Y, Yang M, and Zhou J. High-throughput antibiotic gene array to profile microbial antibiotic resistance genes and community functional structure in pharmaceutical wastewater treatment system. in 4<sup>th</sup> International Symposium on the Environmental Dimension of Antibiotic Resistance (Lansing, Michigan, USA, Aug 13-17, 2017). [Poster]
  - [11] Gao S, **Ning D**, Yang S, Brandon AM, Luo S, Zhou M, Nostrand JDV, Yang J, Wu W, Criddle CS, and Zhou J. Characterization of gut microbial community structures of mealworms rapidly degrading polystyrene (PS). in American Society for Microbiology Microbe 2017 Meeting (American Society for Microbiology, New Orleans, LA, USA, Jun 1-5, 2017). [Poster]
  - [12] Zhou J, Wen X, Curtis T, He Q, He Z, and **Ning D**. Municipal Wastewater Microbiome Initiative of Global Water Microbiome Consortium. in The 16<sup>th</sup> International Symposium on Microbial Ecology (ISME 16) (The International Society of Microbial Ecology, Montreal, Canada, Aug 21-26, 2016). [Poster]
  - [13] **Ning D**, Xu D, Qin Y, He Z, Wu L, Nostrand JDV, and Zhou J. Microbial community structure, functions and assembly in microbial electrolysis cells. in The 16<sup>th</sup> International Symposium on Microbial Ecology (ISME 16) (The International Society of Microbial Ecology, Montreal, Canada, Aug 21-26, 2016). [Poster]
  - [14] **Ning D**, Wang J, Nostrand JDV, Wu L, Zhang P, He Z, et al. Recognizing the switch of major ecological process and the drivers in subsurface microbial assembly in a nuclear waste site. in The 16<sup>th</sup> International Symposium on Microbial Ecology (ISME 16) (The International Society of Microbial Ecology, Montreal, Canada, Aug 21-26, 2016). [Poster]
  - [15] **Ning D**, Deng Y, Wen C, Yan Q, Shen L, Qin Y, et al. Quantifying ecological processes underlying soil microbial community assembly in North American forests. in The 16<sup>th</sup> International Symposium on Microbial Ecology (ISME 16) (The International Society of Microbial Ecology, Montreal, Canada,

Aug 21-26, 2016). [Poster]

- [16] **Ning D**, Wang J, Nostrand JDV, Wu L, Zhang P, He Z, et al. Disentangling ecological processes and drivers in subsurface microbial community assembly in a nuclear waste site. in American Society for Microbiology Microbe 2016 Meeting (American Society for Microbiology, Boston, Massachusetts, USA, Jun 16-20, 2016). [Poster]
- [17] **Ning D**, He Z, Weiser MD, Kaspari M, and Zhou J. Effects of Temperature on the Phylogenetic and Functional Structures and the Dynamics of Soil Microbial Communities. in American Society for Microbiology 114<sup>th</sup> General Meeting (American Society for Microbiology, Boston, Massachusetts, USA, May 17-20, 2014). [Oral]
- [18] Wang H, **Ning D**, Duan L, He Z, Xue K, Nostrand JDV, and Zhou J. Microbial Communities Driving Significant Nitrous Oxide Emission in a Highly Acidified Forest under Soil Moisture and Nutrient Gradients. in American Society for Microbiology 114<sup>th</sup> General Meeting (American Society for Microbiology, Boston, Massachusetts, USA, May 17-20, 2014). [Poster]
- [19] **Ning D**, Jia Q, Wang H, and Chen J. Metabolism pathway and P450s expression profiling in degradation of polycyclic aromatic hydrocarbons by a white rot fungus. in The 14<sup>th</sup> National Conference on Environmental Microbiology (Chinese Society for Environmental Microbiology, Xiamen, China, Nov 25-28, 2011). [Oral]
- [20] **Ning D**, Huang Y, and Wang H. The phytoplankton community succession during the restoration of an urban river in the Yangtze Plain. in International Conference on Environment Simulation and Pollution Control (Chinese Society for Environmental Sciences, Beijing, China, Nov 24-25, 2011). [Oral]
- [21] **Ning D**, Wang L, and Wang H. Induction and function of cytochrome P450 in white rot fungi. in The 12<sup>th</sup> National Conference on Environmental Microbiology (Chinese Society for Environmental Microbiology, Wuhan, China, Nov 27-30, 2009). [Oral]
- [22] **Ning D**, Zeng B, and Wang H. Induction of cytochrome P450 by refractory organic chemicals in a white rot fungus. in China POPs Forum (Dalian, China, May, 2007). [Oral]

## E. Projects

### • Principal Investigator

- [1] Dimensions US-China: Collaborative Research: Quantifying the Impact of Eutrophication on the World's Grassland Soil Microbial Biodiversity and Functioning. US National Science Foundation (Award No. DEB-2129235), 2021-2026. [Co-PI]
- [2] Collaborative Research: MTM 2: Searching for General Rules Governing Microbiome Dynamics Using Anaerobic Digesters as Model Systems. US National Science Foundation (Award No. EF-2025558), 2020-2025. [Co-PI]
- [3] ENIGMA: From Genomes to Ecosystems: Systems-Level Mechanistic Understanding of Microbial Stress Responses at Chromium Contaminated Sites. US Department of Energy (Award No. DE-AC02-05CH11231), 2019-2024. [Co-PI at OU]
- [4] Expression profiling and regulation of cytochrome P450s in degradation of polycyclic aromatic hydrocarbons by a white rot fungus *Phanerochaete chrysosporium*. National Natural Science Foundation of China (No. 31000066), 2011-2013. [PI]
- [5] Degradation function of cytochrome P450 and enzymic mechanism concerning both extracellular enzymes and P450s in PAHs metabolism by the white rot fungus. China Postdoctoral Science

Foundation (No. 20090460302), 2009-2011. [PI]

#### • Senior Personnel

- [6] Microbes Achieve Resistance to MicroOrganism-influenced Rust ( $\mu$ ARMOR): An Integrated Platform for Defeating Corrosion. US DARPA (Award No. HR00112320006), 2022-2026.
- [7] Risk evaluation and uncertainty analysis of volatile and semi-volatile organic pollutants in the industrial contaminated sites in China. China Environment Protection Public Welfare Program. 2011-2013.
- [8] Technology development and demonstration for water pollution control and water quality improvement in old urban area. The National Key Project on Water Environmental Pollution Control (No. 2008ZX07313-001), 2008-2010.
- [9] P450 inducement by POPs and its involvement in POPs biodegradation in white rot fungus. National Natural Science Foundation of China, 2005-2007.

#### • Participant

- [10] Cross-Kingdom Interactions: the Foundation for Nutrient Cycling in Grassland Soils. US Department of Energy (Award No. DE-SC0020163), 2019-2022.
- [11] Establishment to Senescence: Plant-Microbe and Microbe-Microbe Interactions Mediate Switchgrass Sustainability. US Department of Energy (DE-SC0014079), 2015-2021.
- [12] From Structure to Functions: Metagenomics-Enabled Predictive Understanding of Soil Microbial Feedbacks to Climate Change. U.S. Department of Energy (DE-SC0004601), 2013-2016.
- [13] Experimental Macroecology: Effects of Temperature on Biodiversity. US National Science Foundation (Award No. EF-1065844), 2011-2016.
- [14] Nitrous oxide emission and underlying mechanisms in the subtropical forests with high nitrogen deposition in China. State Key Joint Laboratory of Environment Simulation and Pollution Control Research Foundation. 2010-2012.
- [15] Biological conversion and degradation of typical POPs in environment. The Key project of National Natural Science Foundation of China, 2008-2011.

## F. Service and Synergistic Activities

#### • Journal Editor

- Responsible Editor for *Frontiers of Environmental Science & Engineering*, an international journal published by Springer (impact factor 6.7 in 2022). Processed 194 manuscripts from Jun 2020 to Dec 2024.
- Topic Editor for *Frontiers in Microbiology*. Topic: Community Assembly Mechanisms Shaping Microbiome Spatial or Temporal Dynamics. Processed 8 manuscripts since Apr 2021.  
<https://www.frontiersin.org/research-topics/20916/>

#### • Reviewer

- Review one proposal for US National Science Foundation in Jan. 2020.
- Review five proposals and serve in a review panel for US National Science Foundation in May 2022.
- Review 32 manuscripts for 15 Journals, including Nature Climate Change, Proceedings of the

National Academy of Sciences of the United States of America (PNAS), ISME J, Ecology Letters, mBio, Environmental Microbiology, Applied and Environmental Microbiology, FEMS Microbiology Ecology, Environment International, Applied Microbiology and Biotechnology, Frontiers of Environmental Science & Engineering, Chemosphere, Journal of Hazardous Materials, Microbial Biotechnology, and PLoS One.

#### • Organizer

- **Coordinator** of Global Water Microbiome Consortium (<http://gwmc.ou.edu/>). 2014-Present. Coordinated with over 120 research groups in 30 countries in Africa, Asia, Australasia, Europe, North, and South America, and collected over 3000 samples till now.
- **Principal organizer** of conference sessions
  - An oral session of the Ecological Society of America 2017 annual meeting. Delineating the assembly mechanisms shaping microbial community structure: theoretical and practical perspectives of novel approaches. Portland, Oregon, Aug 6-11, 2017.
  - An inspire session of the Ecological Society of America 2019 annual meeting. Macro-view of microbes: Treasure and challenges in continental- and global-scale microbial ecology researches. Louisville, Kentucky, Aug 11-16, 2019.
  - A symposium session of the Ecological Society of America 2024 annual meeting. Searching for rules governing community dynamics. Long Beach, California, Aug 4-9, 2024.
- **Organizing committee member** of the International Forum on Advanced Environmental Sciences and Technology (iFAST, <https://www.ou.edu/ieg/seminars>), an online forum featured with distinguished seminars from eminent scientists. From Sep 2020 to Dec 2024, iFAST has held 81 seminars and 4 special symposiums and attracted >300,000 visits from >90 countries.

#### • Bioinformatician

- **Microbiome data analysis service**: for >43,900 samples of ~160 projects, including results from amplicon sequencing (e.g., 16S, ITS, AMF, 18S, amoA, nosZ, dsrA), GeoChip hybridization, transcriptome sequencing, and shotgun metagenomic sequencing, from Oct. 2012 to Dec 2024.
- **Developer** of R packages
  - NST: for ecological stochasticity estimation; downloaded 32,409 times from Jun 15 2019 to Jan 5 2025. <https://github.com/DaliangNing/NST>
  - iCAMP: for quantifying community assembly processes; downloaded 31,147 times from Sep 9 2020 to Jan 5 2025. <https://github.com/DaliangNing/icamp1>
  - Built >730 R functions with >127,000 lines of scripts.
- **Developer** of web-based pipelines
  - IEG statistical analysis pipeline (<http://ieg3.rccc.ou.edu:8080>): for various statistical analyses using microbiome data, e.g., biodiversity metrics, dimension reduction, dissimilarity test, dispersion test, null model analysis to infer community assembly mechanisms, etc. A total of 229 users have run 18,893 jobs from Sep 2019 to Sep 2024.
  - IEG data management pipeline (<http://ieg3.rccc.ou.edu:8081>): for GeoChip and MiSeq sequencing data management, including microarray normalization, quality control, implementation of QIIME2, DADA2, and USEARCH, and constrained phylogenetic tree construction on galaxy platform. A total of 49 users from Jan 2020 to Sep 2024.
- **Maintainer** of web-based pipelines

- Molecular ecological network analysis pipeline (<http://ieg4.rccc.ou.edu/mena>). A total of 9,033 users have uploaded 142,413 datasets and construct to 134,154 from Mar 2011 to Jan 2025.
- Microarray data management pipeline (<http://ieg.ou.edu/microarray>). A total of 233 users have analyzed 114,564 sample data from 2007 to Jul 2022 (discontinued).
- Amplicon sequencing data analysis pipeline (<http://zhoulab5.rccc.ou.edu:8080>). A total of 127 users from May 2018 to Jul 2022 (discontinued).

#### • Teaching

- **Served as a committee member** of 1 PhD students at the University of Oklahoma since 2023. **Mentored** 2 graduate students and 5 undergraduate students (5 females) for their graduation thesis work at Tsinghua University, Beijing, China, 2005-2012. Mentored 4 undergraduate exchange students at the Institute for Environmental Genomics, University of Oklahoma, Norman, OK, US, 2016.
- **Teach assistant** of graduate course: Advanced Topics in Environmental Genomics (2017, 2022, and 2024) at the University of Oklahoma, Norman, US.
- **Host and speaker** of workshops: Microbial Community Data Analysis Workshop Series, including 8, 10, and 12 workshops in 2017, 2018, and 2019-2020, respectively, about sequencing/microarray data processing, diversity assessment, statistical analysis, modeling, network analysis, community assembly mechanisms, and basic programming, at University of Oklahoma, Norman, OK, US.
- **Teach assistant** of undergraduate courses: Environment Microbiology (2004) and Wastewater Treatment Experiment (2005) at Tsinghua University, Beijing, China.
- **Mentored** 2 high school students in 2022, 2 high school students and 1 undergraduate in 2024, in the summer research programs; Hosted 11 high school students for lab tours and seminars about microbiome technologies.

#### • Invited Seminars and Lectures

- Is the eternal utterable or measurable: quantifying microbial community assembly mechanisms. Invited talks at Peking University, Beijing; Beijing Forestry University, Beijing; Research Center for Eco-Environmental Sciences, Chinese Academy of Sciences, Beijing; Institute of Urban Environment, Chinese Academy of Sciences, Xiamen, China, June 2024.
- Environmental Microbiome. Invited lecture for an undergraduate course at the University of Oklahoma, Norman, OK, March 2024.
- Environmental Microbiome Research and Data Analyses. Invited virtual lectures for China Agricultural University, Beijing, China, 2022.
- Beyond the diversity: Microbial Community Assembly Mechanisms. Invited talks at School of Environment, Tsinghua University, Beijing; Research Center for Eco-Environmental Science, Chinese Academy of Sciences, Beijing; Institute of Soil Science, Chinese Academy of Sciences, Nanjing; School of Environmental Science and Engineering, Sun Yat-Sen University, Guangzhou, China, 2018.
- Advance in Environmental Microbiology. Invited lecture for a graduate course about Microbial Chemical Reaction Engineering at the China University of Petroleum, Beijing, China, 2010-2011.

#### • Awards and Honors

- Highly Cited Researcher (top 0.1% in the world) in Cross Field in 2024, Clarivate.
- Annual Award for Excellence in Research Grants in 2021, The University of Oklahoma.

- Outstanding Editor in 2021, *Frontiers of Environmental Science & Engineering*.
- Annual Award for Excellence in Research Grants in 2020, The University of Oklahoma.
- Outstanding Editor in 2020, *Frontiers of Environmental Science & Engineering*.
- IEG 2015 Award. Institute for Environmental Genomics, University of Oklahoma.
- IEG 2014 Performance Scholarship. Institute for Environmental Genomics, University of Oklahoma.
- Young Investigator Oral Presentation. American Society for Microbiology 114<sup>th</sup> General Meeting, Boston, Massachusetts, USA. May 2014
- Haoran Jian Award for Excellent Paper on Environmental Microbiology. Chinese Society for Environmental Microbiology, Nov. 2011.