

## Daliang Ning

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### 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, Department of Microbiology and Plant Biology, and Consolidated Core Laboratory, The 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 <i>Frontiers of Environmental Science &amp; Engineering</i> .
2021.3-2022.8	<i>Topic Editor</i> for <i>Frontiers in Microbiology</i> .
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 August 26, 2023: 88 peer-reviewed journal papers, 35 conference presentations, 6 invention patents.  
H-index 37, i10-index 59, cited 6719 times, 7 publications are top 1% highly cited.

- **Representative publications**

- [1] **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)
- [2] **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)
- [3] 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).
- [4] 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)**

- [5] **Ning D**, Wang Y, Fan Y, Wang J, Nostrand JDV, 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. 2023. Microbial Community Assembly Mediated by Environmental Stress in Groundwater. In revision.
- [6] 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. Accepted.
- [7] Cornell CR, Zhang Y, **Ning D**, Xiao N, Wagle P, Xiao X & Zhou J. Land use conversion increases the network complexity and stability of soil microbial communities in a temperate grassland. 2023. Accepted.
- [8] 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. bioRxiv, <https://doi.org/10.1101/2022.04.05.481366>
- [9] Zheng Y, Wang B, Gao P, Yang Y, Su X, **Ning D**, Tao 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. 2023. A novel order-level lineage of ammonia-oxidizing Thaumarchaeota is widespread in marine and terrestrial environments. bioRxiv, <https://doi.org/10.1101/2023.02.17.529030>
- [10] Tao X, Feng J, Jian S, Yang Z, Yang Y, Bates CT, Wang G, Guo X, **Ning D**, Kempfer ML, Liu XA, Ouyang Y, Han S, Wu L, Zeng Y, Kuang J, Zhang Y, Zhou X, Wang J, Firestone MK, Tiedje JM & Zhou J. 2023. In revision.
- [11] Zhou J, Xiao N, **Ning D**, He Q, Leibold MA & Hastings A. 2023. Submitted.
- [12] 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.

- [13] Qin Y, Wu L, Zhang Q, Wen C, Nostrand JDV, **Ning D**, Raskin L, Pinto A & Zhou J. 2023. In prep.
- [14] Michael JP, Putt AD, Yang Y, Adams BG, McBride KR, Fan Y, Lowe KA, **Ning D**, Hazen TC & Zhou J. 2023. In prep.
- [15] 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. 2023. In prep.
- [16] 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. 2023. In prep.

• **Other publications (SCI journals)**

- [17] 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>
- [18] 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>
- [19] Xu T, Tao X, He H, Kempner 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>
- [20] 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>
- [21] 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>.
- [22] Xiao N, Zhou A, Kempner 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>.
- [23] 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>.
- [24] 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>.
- [25] 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>.
- [26] 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>.
- [27] 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>.
- [28] 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>.
- [29] 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>.
- [30] 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>.
- [31] 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>.
- [32] 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>.
- [33] 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>.
- [34] 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>.
- [35] 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>.
- [36] 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>.
- [37] 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)
- [38] 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>.
- [39] 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>.
- [40] 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>.
- [41] 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>.
- [42] 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>.
- [43] 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>.
- [44] 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>.
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- <https://doi.org/10.1186/s40168-020-00825-w>.
- [48] 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>.
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- [50] Wu B, Liu F, Zhou A, Li J, Shu L, Kempfer 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>.
- [51] 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>.
- [52] 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>.
- [53] 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>.
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- **Other publications (other journals)**

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#### • 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]
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- [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 6.400 in 2022). Processed 172 manuscripts since Jun 2021.
- 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.
- **Organizing committee member** of 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. Since Sep 2020, iFAST has held 65 seminars and 4 special symposiums and attracted >200,000 visits from >90 countries.

#### • Bioinformatician

- **Microbiome data analysis**: for >40,700 samples of 136 projects, including results from amplicon sequencing (e.g., 16S, ITS, AMF, 18S, amoA, nosZ, dsrA), GeoChip hybridization, transcriptome sequencing, and shotgun metagenomic sequencing, since Oct. 2012.
- **Developer** of R packages
  - NST: for ecological stochasticity estimation; downloaded 23,368 times since Jun 2019. <https://github.com/DaliangNing/NST>
  - iCAMP: for quantifying community assembly processes; downloaded 19,277 times since Sep 2020. <https://github.com/DaliangNing/icamp1>
  - Built >700 R functions with >120,600 lines of code.
- **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 195 users have run 13,555 jobs since Sep 2019.
  - 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 and USEARCH, and constrained phylogenetic tree construction on galaxy platform. A total of 40 users since Jan 2020.
- **Maintainer** of web-based pipelines

- 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.
- Molecular ecological network analysis pipeline (<http://ieg4.rccc.ou.edu/mena>). A total 7,287 users have uploaded 114,343 datasets and construct to 108,474 networks since Mar 2011.
- Amplicon sequencing data analysis pipeline (<http://zhoulab5.rccc.ou.edu:8080>). A total of 127 users from May 2018 to Jul 2022 (discontinued now).

#### • Teaching

- **Served as a committee member** of 1 PhD student at University of Oklahoma since 2023. **Mentored** 2 graduate students and 5 undergraduate students (5 females) for their graduation thesis work in Tsinghua University, Beijing, China, 2005-2012. Mentored 4 undergraduate exchange students in Institute for Environmental Genomics, University of Oklahoma, Norman, OK, US, 2016.
- **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 graduate course: Advanced Topics in Environmental Genomics (2017 and 2022) at University of Oklahoma, Norman, US.
- **Teach assistant** of undergraduate courses: Environment Microbiology (2004) and Wastewater Treatment Experiment (2005) at Tsinghua University, Beijing, China.

#### • Invited Seminars

- Environmental Microbiome Research and Data Analyses. Invited virtual lectures for China Agricultural University, 2022.
- Beyond the diversity: Microbial Community Assembly Mechanisms. Invited talk 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 of Microbial Chemical Reaction Engineering at the China University of Petroleum, Beijing, China, 2010-2011.

#### • Awards and Honors

- 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.