师资队伍

教授

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联系方式

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教育背景

2013.09-2017.11，香港大学，生物科学学院，环境微生物，博士

2008.09-2011.06，复旦大学，生命科学学院，微生物，硕士

2004.09-2008.06，淮海工学院（江苏海洋大学），海洋学院，生物技术，学士

研究经历

2017.12-至今，南京师范大学，副教授

2012.09-2013.08，香港大学，研究助理

2011.07-2012.08，复旦大学，研究助理

主要研究方向

1. 新型碳氮转化微生物物质循环

2. 环境微生物基因组学

3. 微生物菌剂应用研究

主讲课程

环境微生物学

获奖情况

江苏省双创博士（世界名校类），2019

香港政府奖学金，2013-2017

复旦大学光华企业奖学金，2009

本科生国家奖学金，2007

承担（参与）主要科研项目

1.国家自然科学基金青年项目（41907202）：典型浅水湖泊沉积物完全氨氧化菌分布特征及环境响应机制研究，2020.01-2022.12，主持；

2.江苏省自然科学基金青年项目（SBK2019043965）：太湖沉积物完全氨氧化菌群动态及生态位形成机制研究，2019.07-2022.06，主持；

3.江苏省高等学校自然科学研究面上项目（19KJB180004）：太湖典型区域沉积物完全氨氧化菌群生态位形成机制研究，2019.07-2022.06，主持；

4.江苏省双创博士人才计划（164080H00631），2019.07-2021.06，主持；

5.南京师范大学优秀高层次人才科研启动基金（164320H133），2019.06-2020.12，主持；

6.国家“水体污染控制与治理”科技重大专项课题（2017ZX07202-004）：太湖运河农业复合污染控制与清洁流域技术集成与应用，2017.01-2020.12，参与；

7.国家重点研发计划重点专项课题（2018YFC1406400-002)：典型生态系统食物产出过程与生态环境效应，2018.01-2021.12，参与；

8.国家重大研究计划（91951112）：根际效应对滨海盐沼甲烷代谢微生物的影响及其地理格局研究，2020.01-2022.12，参与。

近几年发表论文、专利及著作

(1) Han Meng, Xiao-feng Zhang, Yoko Katayama, Qin-ya Ge, Ji-Dong Gu*. Microbial diversity and composition of the Preah Vihear temple in Cambodia by high-throughput sequencing based on genomic DNA and RNA. International Biodeterioration & Biodegradation. 2020, 149: 104936.

(2) Han Meng, Zhi-chao Zhou, Ruo-nan Wu, Yong-feng Wang, Ji-Dong Gu*. Diazotrophic microbial community and abundance in acidic subtropical natural and re-vegetated forest soils revealed by high-throughput sequencing of nifH gene. Applied Microbiology and Biotechnology, 2019, 103(2): 995–1005.

(3) **Han Meng**, Ruo-Nan Wu, Yong-Feng Wang, Ji-Dong Gu*. A comparison of denitrifying bacteria community structures and abundance in acidic soils between natural forest and re-vegerated forest of Nanling Reserve in Southern China. Journal of Environmental Management. 2017, 198(2): 41-49.

(4) **Han Meng**, Yu-Chun Yang, Jih-Gaw Lin, Martin Denecke, and Ji-Dong Gu*. Occurrence of anammox bacteria in a traditional full-scale wastewater treatment plant and successful inoculation for new establishment. International Biodeterioration & Biodegradation. 2017, 120: 224-231.

(5) Ling Luo[#], **Han Meng**[#], Ji-Dong Gu*. Microbial extracellular enzymes in biogeochemical cycling of ecosystems. Journal of Environmental Management. 2017, 197: 539-549.

(6) **Han Meng**, Yong-Feng Wang, Ho-Wang Chan, Ruo-Nan Wu, Ji-Dong Gu*. Co-occurrence of nitrite-dependent anaerobic ammonium and methane oxidation processes in subtropical acidic forest soils. Applied Microbiology and Biotechnology. 2016, 100(17): 7727-7739.

(7) Ling Luo[#], **Han Meng**[#], Ruonan Wu, Ji-Dong Gu*. Impact of nitrogen pollution/deposition on extracellular enzyme activity, microbial abundance and carbon storage in coastal mangrove sediment. Chemosphere, 2017, 177: 275-283.

(8) **Han Meng**, Ho-Wang Chan, Yoko Katayama, and Ji-Dong Gu. More wide occurrence and dominance of ammonia-oxidizing archaea than bacteria at Angkor Sandstone Temples of Bayon, Phnom Krom and Wat Athvea in Cambodia. International Biodeterioration & Biodegradation. 2017, 117: 78-88.

(9) **Han Meng**[#], Ling Luo[#], Ho-Wang Chan, Yoko Katayama, Ji-Dong Gu*. Higher diversity and abundance of ammonia-oxidizing archaea than bacteria detected at the Bayon Temple of Angkor Thom in Cambodia. International Biodeterioration & Biodegradation. 2016, 115: 234-243.

(10) **Han Meng**, Ke Li, Ming Nie*, Jia-Rong Wan, Zhe-Xue Quan, Chang-Ming Fang, Jia-Kuan Chen, Ji-Dong Gu, Bo Li. Responses of bacterial and fungal communities to an elevation gradient in a subtropical montane forest of China. Applied Microbiology and Biotechnology. 2013, 97(5): 2219–2230.

(11) Ruonan Wu, **Han Meng**, Yongfeng Wang, Ji-Dong Gu*. Functional dominance and community compositions of ammonia-oxidizing archaea in extremely acidic soils of natural forests. Applied Microbiology and Biotechnology. 2019, 103(4): 1953–1960.

(12) Zhuoying Wu, **Han Meng**, Xiaowu Huang, Wen Hsing Chen, Ji-Dong Gu, Po-Heng (Henry) Lee*. Salinity-driven heterogeneity toward anammox distribution and growth kinetics. Applied Microbiology and Biotechnology. 2019, 103(13): 1953–1960.

(13) Zhichao Zhou, **Han Meng**, Yang Liu, Ji-Dong Gu*, Meng Li*. Stratified bacterial and archaeal community in mangrove and intertidal wetland mudflats revealed by high throughput 16S rRNA gene sequencing. Frontiers in Microbiology. 2017, 8: 2148.

(14) Ruonan Wu, **Han Meng**, Yongfeng Wang, Wensheng Lan, Ji-Dong Gu*. A more comprehensive community of ammonia-oxidizing archaea (AOA) revealed by genomic DNA and RNA analyses of amoA Gene in Subtropical Acidic Forest Soils. Microbial Ecology. 2017, 74 (4):1-13.

(15) Zi-Ye Hu, **Han Meng**, Jin-Huan Shi, Nai-Shun Bu, Chang-Ming Fang, Zhe-Xue Quan*. Community size and composition of ammonia oxidizers and denitrifiers in an alluvial intertidal wetland ecosystem. Frontiers in Microbiology. 2014, 5: 371.

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