

Tian Renmao, Ph.D.

Microbial Genomics; Metagenomics; Host-microbe Interaction; Gut Microbiome; Environmental Microbiology; Development of Bioinformatics Tools

Institution: Department of Microbiology and Plant Biology, University of Oklahoma

Position: Postdoctoral Research Associate

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■ Work Experience

➤ **Postdoctoral Research Associate** (05/2016 - present)

Institution: Department of Microbiology and Plant Biology (Joe Jizhong Zhou lab), University of Oklahoma, Norman, USA

Research Fields: Genomics and metagenomics; Host-microbe interaction; Gut microbiome; Eukaryote genome; Environmental Microbiology; Development of bioinformatics tools

Research Projects:

- Genomics of novel bacterial phyla in groundwater microbiome (project funded by DOE)
- Gut microbiome of a mealworm and host genome sequencing using Oxford Nanopore
- Development of automated bioinformatics pipeline for analysis of amplicon, genome and metagenome sequence data

➤ **Postdoctoral Fellow** (08/2015 - 03/2016)

Institution: Division of Life Science (Peiyuan Qian lab), Hong Kong University of Science and Technology (HKUST), Hong Kong

Research Fields: Metagenomics and metatranscriptomics; Host-microbe interaction; Gut microbiome

Research Projects:

- Adaptation and evolution of gut microbiome in deep-sea amphipod

■ Education

➤ **Doctor of Philosophy** (08/2011 - 07/2015)

Institution: Division of Life Science (Peiyuan Qian lab), Hong Kong University of Science and Technology (HKUST), Hong Kong

Major: Microbial Genomics, Metagenomics, Microbial Ecology, Host-microbe Interaction, Bioinformatics

Research Fields: Ecology, function and evolution of marine sponge-associated microbiome

➤ **Master of Science** (09/2008 - 07/2011)

Institution: Beijing Institute of Microbiology and Epidemiology, Beijing, China

Major: Microbial Genomics, Foodborne Pathogen, Bioinformatics

Research Fields: Genomics of foodborne pathogens and the regulatory mechanisms for toxin gene expression

➤ **Bachelor of Science** (9/2004 - 7/2008)

Institution: School of life science, Ludong University, Yantai, Shandong, China

Major: Biological Science

■ Research Skills

➤ **Bioinformatics Skills:**

Next generation sequence (NGS) data analysis

- Amplicon sequence

OTU clustering, exact sequence variant (ESV), taxonomic classification (Naïve Bayes, Scikit-learn), phylogenetic tree, network construction, hypothesis testing etc.

automated pipeline: <http://tianrenmao.net>

- Genome sequence (Eukaryotes and Prokaryotes)

sequence quality control, De Bruijn assembly, BLAST search, HMM search, gene calling, gene annotation, coverage analysis, genome visualization, comparison genomics, metabolic pathway construction

automated pipeline ready locally but not online yet

- Metagenome sequence

sequence quality control, deduplication, DIAMOND search, taxonomic and functional classification, De Bruijn assembly, genome-resolved analysis (genome binning)

automated pipeline: <http://tianrenmao.net>

- Transcriptome / Metatranscriptome sequence

RNA-seq, assembly, mapping, coverage analysis, metabolic pathway, statistical test

Long-read sequence data (Nanopore, PacBio) analysis

- Assembly

OLC-based assembly, hybrid assembly (with Illumina reads), genome finishing

- Epigenetics analysis

methylation analysis: Dam, Dcm, CpG, 5mC, 6mA

Python programming

- Numpy, Pandas, Matplotlib, Seaborn, Biopython etc.

Perl programming, Bioperl

Biostatistics, R

Linux system

- bash script, high performance computer (HPC), cluster supercomputer (SLURM, PBS), big data processing (up to 6 Terabytes), MPI run, software installation, system administration and maintenance

Algorithm and Machine learning (beginner)

- recursion, iteration, brute force algorithms

- learning more

Website-based pipeline development

- frontend HTML, backend PHP, MySQL

- amplicon, genome, metagenome analysis pipeline (e.g. <http://tianrenmao.net>)

➤ **Experimental Skills:**

Molecular biology techniques

- genomic DNA purification, RNA purification, plasmid DNA purification, DNA recombination, transformation (chemical and electroporation), cDNA synthesis, RNA-seq

Microbiology techniques

- bacterial isolation, culture, fermentation, protein expression and purification

Fluorescent in situ hybridization (FISH)

- probe design, tissue slice, probe hybridization, fluorescent microscope

Field trip sampling

Illumina sequencing

- DNA fragmentation, library preparation, size selection

Oxford Nanopore sequencing (MinION)

- DNA fragmentation, library preparation, sequencing, base calling

■ Biography

Dr Tian acquired his bachelor's degree in Biological Science in 2008 and master's degree in Microbial Genomics in 2011 in China. Then he studied in Hong Kong University of Science and Technology and got his PhD degree of Environmental Microbiology in 2015. During this period, Dr Tian published six high-quality papers and won his prize of graduate seminar. After graduation, he worked as a Postdoctoral Research Associate in University of Oklahoma doing research projects (one funded by DOE) in environmental microbiome including soil, groundwater and animal guts. With experience of both experimental biology and computational biology, Dr Tian is good at researches in microbial diversity and function using genomics, metagenomics and metatranscriptomics strategies. He has been doing extensive researches in microbes from environments of food, soil, groundwater, coastal water, deep-sea water, sediment and animal guts. He is good at taking advantage of state-of-the-art technologies in his study, such as genome-resolved metagenomic analysis (genome binning) and third generation sequencing (Nanopore). Upon 2019, he has published eight first-author papers and 39 co-author papers and has >600 citations based on Google Scholar.

■ Research Interest

Research fields: Microbial Genomics; Metagenomics; Host-microbe Interaction; Gut Microbiome; Environmental Microbiology; Development of Bioinformatics Tools

I have been doing extensive studies on the diversity, ecology, function and evolution of microbes in environments of food, soil, groundwater, coastal water, deep-sea water, sediment and animal gut using Next Generation Sequencing (NGS) and long-read sequencing (e.g. Nanopore) technologies. I am also interested in genomics of animal such as insect mealworm which can digest plastics. In terms of bioinformatics, I am interested in algorithm design and implementation, and pipeline development. To automate data analysis, I have developed pipelines for automated process and analysis of NGS sequencing data, including amplicon

sequence (16/18S rRNA and ITS), genomic sequence, and metagenomic sequence.

■ Journal Position

- Advances in Microbiology Research: Editorial Board Member
- Trends in Clinical Microbiology: Editorial Board Member
- Annals of Biotechnology: Editorial Board Member
- SOJ Microbiology & Infectious Diseases: Reviewer Board Member

■ Reviewer Experience

- Bioresource Technology
- BMC Microbiology
- BMC Genomics
- EC Microbiology
- AS Microbiology
- Annals of Biotechnology
- Advances in Microbiology Research
- PLOS ONE
- Scientific Reports

■ Conference presentation

- 15th International Symposium on Microbial Ecology, Seoul, South Korea 2014. Title: *Genomic analysis reveals versatile heterotrophic capacity of a symbiotic sulfur-oxidizing bacterium in sponge*
- Gordon Research Conference (GRC), Hong Kong 2015. Title: *The deep-sea glass sponge *Lophophysema eversa* harbors potential symbionts participating in the carbon, nitrogen and sulfur cycles*
- All-hands ENIGMA (Ecosystems and Networks Integrated with Genes and Molecular Assemblies) Meeting, Berkley, CA, United States 2016. Title: *Functional response of microbial community to environmental stresses in the contaminated groundwater*
- All-hands ENIGMA (Ecosystems and Networks Integrated with Genes and Molecular Assemblies) Meeting, Berkley, CA, United States 2018. Title: *Adaptation of *Patescibacteria* to environments drives the simplicity of genomes*

■ Publications [1-42]

In fields of host-microbe interaction, microbiology, genomics, and bioinformatics. In total 8 first-author papers with average impact factor of 5. Total citation reached 600 until April 2019 in Google Scholar. I also have a first-author manuscript of my recent work under review in Nature Communications.

1. **Tian RM**, Wang Y, Bougouffa S, Gao ZM, Cai L, Bajic V, Qian PY: Genomic analysis reveals versatile heterotrophic capacity of a potentially symbiotic sulfur-oxidizing bacterium in sponge. *Environmental microbiology* 2014, 16(11):3548-3561.
2. **Tian RM**, Sun J, Cai L, Zhang WP, Zhou GW, Qiu JW, Qian PY: The deep-sea glass sponge *Lophophysema eversa* harbours potential symbionts responsible for the nutrient conversions of carbon, nitrogen and sulfur. *Environmental microbiology* 2016, 18(8):2481-2494.
3. **Tian R-M**, Wang Y, Bougouffa S, Gao Z-M, Cai L, Zhang W-P, Bajic V, Qian P-Y: Effect of copper treatment on the composition and function of the bacterial community in the sponge *Haliclona cymaeformis*. *Mbio* 2014, 5(6):e01980-01914.
4. **Tian R-M**, Cai L, Zhang W-P, Cao H-L, Qian P-Y: Rare events of intragenus and intraspecies horizontal transfer of the 16S rRNA gene. *Genome biology and Evolution* 2015, 7(8):2310-2320.
5. **Tian R-M**, Lee OO, Wang Y, Cai L, Bougouffa S, Chiu JMY, Wu RSS, Qian P-Y: Effect of polybrominated diphenyl ether (PBDE) treatment on the composition and function of the bacterial community in the sponge *Haliclona cymaeformis*. *Frontiers in microbiology* 2015, 5:799.
6. Brandon AM, Gao S-H, **Tian R**, Ning D, Yang S, Zhou J, Wu W-M, Criddle CS: Biodegradation of polyethylene and plastic mixtures in mealworms (larvae of *Tenebrio molitor*) and effects on the gut microbiome. *Environmental science & technology* 2018.
7. **Tian R-M**, Zhang W, Cai L, Wong Y-H, Ding W, Qian P-Y: Genome Reduction and Microbe-Host Interactions Drive Adaptation of a Sulfur-Oxidizing Bacterium Associated with a Cold Seep Sponge. *MSystems* 2017, 2(2):e00184-00116.
8. **Tian R-M**, Li T, Hou X-J, Wang Q, Cai K, Liu Y-N, Gao X, Liu H, Xiao L, Tu W: The complete genome sequence of *Clostridium botulinum* F str. 230613, insertion sites, and recombination of BoNT gene clusters. *Genome* 2011, 54(7):546-554.
9. Li T, **Tian R** (co-first author), Cai K, Wang Q, Chen F, Fang H, Luo S, Li Z, Wang D, Hou X: The Effect of pH on growth of *Clostridium botulinum* type A and expression of bontA and botR during different growth Stages. *Foodborne pathogens and disease* 2013, 10(8):692-697.
10. Gao Z-M, Wang Y, **Tian R-M**, Wong YH, Batang ZB, Al-Suwailem AM, Bajic VB, Qian P-Y: Symbiotic adaptation drives genome streamlining of the cyanobacterial sponge symbiont “*Candidatus Synechococcus spongiarum*”. *Mbio* 2014, 5(2):e00079-00014.
11. Zhou G, Cai L, Yuan T, **Tian R**, Tong H, Zhang W, Jiang L, Guo M, Liu S, Qian PY: Microbiome dynamics in early life stages of the scleractinian coral *Acropora gemmifera* in response to elevated pCO₂. *Environmental microbiology* 2017.
12. Zhang W, Wang Y, Bougouffa S, **Tian R**, Cao H, Li Y, Cai L, Wong YH, Zhang G, Zhou

- G: Synchronized dynamics of bacterial niche-specific functions during biofilm development in a cold seep brine pool. *Environmental microbiology* 2015, 17(10):4089-4104.
13. Zhang W, **Tian R-M**, Sun J, Bougouffa S, Ding W, Cai L, Lan Y, Tong H, Li Y, Jamieson AJ: Genome Reduction in Psychromonas Species within the Gut of an Amphipod from the Ocean's Deepest Point. *MSystems* 2018, 3(3):e00009-00018.
 14. Zhang W, **Tian R**, Bo Y, Cao H, Cai L, Chen L, Zhou G, Sun J, Zhang X, Al-Suwailem A: Environmental switching during biofilm development in a cold seep system and functional determinants of species sorting. *Molecular ecology* 2016, 25(9):1958-1971.
 15. Zhang W, Sun J, Cao H, **Tian R**, Cai L, Ding W, Qian P-Y: Post-translational modifications are enriched within protein functional groups important to bacterial adaptation within a deep-sea hydrothermal vent environment. *Microbiome* 2016, 4(1):49.
 16. Lan Y, Sun J, **Tian R**, Bartlett DH, Li R, Wong YH, Zhang W, Qiu JW, Xu T, He LS: Molecular adaptation in the world's deepest-living animal: Insights from transcriptome sequencing of the hadal amphipod Hironellea gigas. *Molecular ecology* 2017.
 17. Zhou G, Yuan T, Cai L, Zhang W, **Tian R**, Tong H, Jiang L, Yuan X, Liu S, Qian P: Changes in microbial communities, photosynthesis and calcification of the coral Acropora gemmifera in response to ocean acidification. *Scientific reports* 2016, 6:35971.
 18. Zhang Y, Li Q, **Tian R**, Lai Q, Xu Y: Pseudovibrio stylochi sp. nov., isolated from a marine flatworm. *International journal of systematic and evolutionary microbiology* 2016, 66(5):2025-2029.
 19. Zhang WP, Wang Y, **Tian RM**, Bougouffa S, Yang B, Cao HL, Zhang G, Wong YH, Xu W, Batang Z: Species sorting during biofilm assembly by artificial substrates deployed in a cold seep system. *Scientific reports* 2014, 4:6647.
 20. Zhang W, Wang Y, Lee OO, **Tian R**, Cao H, Gao Z, Li Y, Yu L, Xu Y, Qian P-Y: Adaptation of intertidal biofilm communities is driven by metal ion and oxidative stresses. *Scientific reports* 2013, 3:3180.
 21. Zhang W, Sun J, Ding W, Lin J, **Tian R**, Lu L, Liu X, Shen X, Qian P-Y: Extracellular matrix-associated proteins form an integral and dynamic system during Pseudomonas aeruginosa biofilm development. *Frontiers in cellular and infection microbiology* 2015, 5:40.
 22. Zhang W, Ding W, Yang B, **Tian R**, Gu S, Luo H, Qian P-Y: Genomic and transcriptomic evidence for carbohydrate consumption among microorganisms in a cold seep brine pool. *Frontiers in microbiology* 2016, 7:1825.
 23. Yang B, Zhang W, **Tian R**, Wang Y, Qian P-Y: Changing composition of microbial communities indicates seepage fluid difference of the Thuwal Seeps in the Red Sea. *Antonie van Leeuwenhoek* 2015, 108(2):461-471.
 24. Xu Y, Li Q, **Tian R**, Lai Q, Zhang Y: Pseudovibrio hongkongensis sp. nov., isolated from a marine flatworm. *Antonie Van Leeuwenhoek* 2015, 108(1):127-132.
 25. Wang Y, Zhang WP, Cao HL, Shek CS, **Tian RM**, Wong YH, Batang Z, Al-Suwailem A, Qian P-Y: Diversity and distribution of eukaryotic microbes in and around a brine pool adjacent to the Thuwal cold seeps in the Red Sea. *Frontiers in microbiology* 2014,

- 5:37.
26. Wang Y, **Tian RM**, Gao ZM, Bougouffa S, Qian P-Y: Optimal eukaryotic 18S and universal 16S/18S ribosomal RNA primers and their application in a study of symbiosis. *PLoS one* 2014, 9(3):e90053.
 27. Wang Y, Gao Z-M, Li J-T, Bougouffa S, **Tian RM**, Bajic VB, Qian P-Y: Draft genome of an Aerophobetes bacterium reveals a facultative lifestyle in deep-sea anaerobic sediments. *Science bulletin* 2016, 61(15):1176-1186.
 28. Wang Q, Hou X-j, Cai K, Li T, Liu Y-n, Tu W, Xiao L, Bao S-z, Shi J, Gao X: Passive protection of purified yolk immunoglobulin administered against Shiga toxin 1 in mouse models. *Canadian journal of microbiology* 2010, 56(12):1003-1010.
 29. Tong H, Cai L, Zhou G, Yuan T, Zhang W, **Tian R**, Huang H, Qian P-Y: Temperature shapes coral-algal symbiosis in the South China Sea. *Scientific reports* 2017, 7:40118.
 30. Luo S, Li T, Wang Q, **Tian R**, Liu H, Fang H, Chen F, Wang H: Development of a fusion protein SNVP as substrate for assaying multi-serotype botulinum neurotoxins. *Analytical biochemistry* 2014, 463:75-81.
 31. Lu L, Wang J, Xu Y, Wang K, Hu Y, **Tian R**, Yang B, Lai Q, Li Y, Zhang W: A high-resolution LC-MS-based secondary metabolite fingerprint database of marine bacteria. *Scientific Reports* 2014, 4:6537.
 32. Lin H-N, Wang K-L, Wu Z-H, **Tian R-M**, Liu G-Z, Xu Y: Biological and Chemical Diversity of Bacteria Associated with a Marine Flatworm. *Marine drugs* 2017, 15(9):281.
 33. Lee OO, Yang J, Bougouffa S, Wang Y, Batang Z, **Tian R**, Al-Suwailem A, Qian P-Y: Pyrosequencing reveals spatial and species variations in bacterial communities associated with corals from the Red Sea. *Appl Environ Microb* 2012:AEM. 01111-01112.
 34. Lee OO, Yang J, Bougouffa S, Wang Y, Batang Z, **Tian R**, Al-Suwailem A, Qian P-Y: Spatial and species variations in bacterial communities associated with corals from the Red Sea as revealed by pyrosequencing. *Appl Environ Microb* 2012, 78(20):7173-7184.
 35. Lee OO, Wang Y, **Tian R**, Zhang W, Shek CS, Bougouffa S, Al-Suwailem A, Batang ZB, Xu W, Wang GC: In situ environment rather than substrate type dictates microbial community structure of biofilms in a cold seep system. *Scientific reports* 2014, 4:srep03587.
 36. Lan Y, Sun J, Xu T, Chen C, **Tian R**, Qiu J-W, Qian P-Y: De novo transcriptome assembly and positive selection analysis of an individual deep-sea fish. *BMC genomics* 2018, 19(1):394.
 37. Gao Z-M, Wang Y, **Tian R-M**, Lee OO, Wong YH, Batang ZB, Al-Suwailem A, Lafi FF, Bajic VB, Qian P-Y: Pyrosequencing revealed shifts of prokaryotic communities between healthy and disease-like tissues of the Red Sea sponge *Crella cyathophora*. *Peerj* 2015, 3:e890.
 38. Gao Z-M, Wang Y, Lee OO, **Tian R-M**, Wong YH, Bougouffa S, Batang Z, Al-Suwailem A, Lafi FF, Bajic VB: Pyrosequencing reveals the microbial communities in the Red Sea sponge *Carteriospongia foliascens* and their impressive shifts in abnormal tissues. *Microbial ecology* 2014, 68(3):621-632.
 39. Gao X, Cai K, Li T, Wang Q, Hou X, **Tian R**, Liu H, Tu W, Xiao L, Fang L: Novel

- fusion protein protects against adherence and toxicity of enterohemorrhagic *Escherichia coli* O157: H7 in mice. *Vaccine* 2011, 29(38):6656-6663.
40. Cai L, Zhou G, Tong H, **Tian R-M**, Zhang W, Ding W, Liu S, Huang H, Qian P-Y: Season structures prokaryotic partners but not algal symbionts in subtropical hard corals. *Applied microbiology and biotechnology* 2018, 102(11):4963-4973.
 41. Cai L, Zhou G, **Tian R-M**, Tong H, Zhang W, Sun J, Ding W, Wong YH, Xie JY, Qiu J-W: Metagenomic analysis reveals a green sulfur bacterium as a potential coral symbiont. *Scientific reports* 2017, 7(1):9320.
 42. Cai L, **Tian R-M**, Zhou G, Tong H, Wong YH, Zhang W, Chui APY, Xie JY, Qiu J-W, Ang PO: Exploring coral microbiome assemblages in the South China Sea. *Scientific reports* 2018, 8(1):2428.