

CURRICULUM VITAE

Luo, Haiwei

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EDUCATION

2008-2010 Ph.D. in Molecular Evolution, University of South Carolina, Columbia, SC, USA

2006-2008 M.S. in Microbial Ecology, University of South Carolina, Columbia, SC, USA

2000-2004 B.S. in Environmental Science, Xiamen University, Xiamen, China

PROFESSIONAL APPOINTMENT

01/2021+, Associate Professor (tenured), School of Life Sciences

The Chinese University of Hong Kong, Hong Kong SAR

01/2015-12/2020, Assistant Professor (tenure-track), School of Life Sciences

The Chinese University of Hong Kong, Hong Kong SAR

09/2015+, Investigator, State Key Laboratory of Agrobiotechnology

The Chinese University of Hong Kong, Hong Kong SAR

05/2010-12/2014, Postdoctoral Research Associate, Department of Marine Sciences

University of Georgia, Athens, GA, USA

RESEARCH INTEREST

We work on microbial genome evolution at different time scales. At the deep time scale, we are interested in developing new genome-enabled clock-based strategies in dating microbial lineages, reconstructing major evolutionary genomic events and linking them to ancient Earth events, using phylogenomics to infer ancestral microbial lineages that may have driven redox changes in early Earth, tracing the evolutionary history of key players in nitrogen and sulfur cycles, and dating co-evolution between symbiotic microbes and their hosts. At the recent and ecological time scale, we integrate well-designed field sampling, high-throughput microbial cultivation, large-scale genomic analyses, and bioinformatics-guided experimental assays to study the ecological and evolutionary mechanisms underlying microbial diversification at the strain and population level.

HONORS AND AWARDS

CUHK Young Researcher Award, 2016-2017

PROFESSIONAL SERVICE AND ACTIVITIES

Editorial Board member, *The ISME Journal*, 05/2020+

Member of "ESF College of Expert Reviewers" for European Science Foundation, 05/2020+

Associate Editor, *Frontiers in Microbiology* (section *Evolutionary and Genomic Microbiology*), 09/2017+

Associate Editor, *Frontiers in Marine Science* (section *Marine Molecular Biology and Ecology*), 08/2017+

Panel member for National Natural Science Foundation of China (NSFC), 2017-2019

Reviewer for research proposals from European Science Foundation (ESF), Swiss National Science

Foundation (SNSF), UK Biotechnology and Biological Sciences Council (BBSRC), U.S. National Science Foundation (NSF)

Reviewer for manuscripts from *Science*, *PNAS*, *Nature Microbiology*, *Science Advances*, *The ISME Journal*, *Molecular Biology and Evolution*, *Genome Biology*, *eLife*, *mBio*, *Environmental Microbiology*

PROFESSIONAL SOCIETIES

American Association for the Advancement of Science (AAAS)

International Society for Microbial Ecology (ISME)

American Society for Microbiology (ASM)

Society for Applied Microbiology (SfAM)

Society for Molecular Biology and Evolution (SMBE)

MANUSCRIPTS SUBMITTED (* corresponding author; ^equal contribution; lab members; visiting student[†])

- S. Wang, **H. Luo**^{*}. 2020. Dating *Alphaproteobacteria* evolution with eukaryotic fossils.
- J. Gu[^], X. Wang[^], X. Ma, Y. Sun, X. Xiao^{*}, **H. Luo**^{*}. 2020. Unexpectedly high mutation rate of a deep-sea hyperthermophilic anaerobic archaeon.
- B-B. Xie[^], J-C. Rong[^], B-L. Tang[^], S. Wang[^], G. Liu, Q-L Qin, X-Y Zhang, W. Zhang, Q. She, Y. Chen, X-L. Chen, **H. Luo**^{*}, Y-Z. Zhang^{*}. 2020. Evolutionary trajectory of the replication mode of bacterial replicons. *mBio* (revision)

RESEARCH PUBLICATIONS (a total of 50 refereed papers, >2,100 GoogleScholar citations, h-index 24)

- Z. Zhang[^], F. Qin[^], F. Chen, X. Chu, **H. Luo**, R. Zhang, S. Du, Z. Tian, Y. Zhao^{*}. 2020. Culturing novel and abundant pelagiphages in the ocean. *Environmental Microbiology* (accepted)
- X. Chu[^], S. Li[^], S. Wang[^], D. Luo, **H. Luo**^{*}. 2020. Gene loss through pseudogenization contributes to the ecological diversification of a generalist *Roseobacter* lineage. *The ISME Journal* (in press)
- X. Wang[^], Y. Zhang[^], M. Ren[^], T. Xia, X. Chu, C. Liu, X. Lin, Y. Huang, Z. Chen, A. Yan, **H. Luo**^{*}. 2020. Cryptic speciation of a pelagic *Roseobacter* population varying at a few thousand nucleotide sites. *The ISME Journal* (in press)
- S. Wang, A. Meade, H-M. Lam, **H. Luo**^{*}. 2020. Evolutionary timeline and genomic plasticity underlying the lifestyle diversity in *Rhizobiales*. *mSystems* 5 (4): e00438-20
- C-X. Xue[†], H. Zhang[^], H-Y. Lin[^], Y. Sun, D. Luo, Y. Huang, X-H. Zhang^{*}, **H. Luo**^{*}. 2020. Ancestral niche separation and evolutionary rate differentiation between sister marine flavobacteria lineages. *Environmental Microbiology* 22 (8):3234–3247
- Z. Zhang, F. Chen, X. Chu, H. Zhang, **H. Luo**, F. Qin, Z. Zhai, M. Yang, J. Sun, Y. Zhao^{*}. 2019. Diverse, abundant and novel viruses infecting the marine abundant *Roseobacter* RCA lineage. *mSystems* 4 (6): e00494-19
- M. Ren[^], X. Feng[^], Y. Huang, H. Wang, Z. Hu, S. Clingenpeel, B.K. Swan, M.M. Fonseca, D. Posada, R. Stepanauskas, J.T. Hollibaugh, P.G. Foster, T. Woyke, **H. Luo**^{*}. 2019. Phylogenomics suggests oxygen availability as a driving force in Thaumarchaeota evolution. *The ISME Journal* 13 (9):2150-2161
- H. Zhang, S. Yoshizawa, Y. Sun, Y. Huang, X. Chu, J.M. González, J. Pinhassi, **H. Luo**^{*}. 2019. Repeated evolutionary transitions of flavobacteria from marine to non-marine habitats. *Environmental Microbiology* 21 (2):648-666
- H. Cao[^], T. Xia[^], Y. Li[^], Z. Xu[^], S. Bougouffa, Y.K. Lo, V.B. Bajic, **H. Luo**, P.C.Y. Woo, A. Yan^{*}. 2019. A multidrug resistant clinical *P. aeruginosa* isolate with a distinctive MLST genotype: uncoupled quorum sensing modulates the interplay of virulence and resistance. *Antimicrobial Agents and Chemotherapy* 63 (4): e01944-18
- G. Yu^{*^}, Y. Jiang[^], J. Wang, H. Zhang, and **H. Luo**^{*}. 2018. BMC3C: Binning Metagenomic Contigs using Codon usage, sequence Composition and read Coverage. *Bioinformatics* 34 (24):4172-4179
- Y. Sun and **H. Luo**^{*}. 2018. Homologous recombination in core genomes facilitates marine bacterial adaptation. *Applied and Environmental Microbiology* 84 (11): e02545-17 (selected as a “Spotlight” article by the journal)
- F.L. Hellweger^{*}, Y. Huang, **H. Luo**^{*}. 2018. Carbon limitation drives GC content evolution of a marine bacterium in an individual-based genome-scale model. *The ISME Journal* 12 (5):1180-1187
- W. Xie^{*}, **H. Luo**, S.K. Murugapiran, J.A. Dodsworth, S. Chen, Y. Sun, B.P. Hedlund, P. Wang, H. Fang, M. Deng, and C. Zhang^{*}. 2018. Localized high abundance of Marine group II archaea in the subtropical Pearl River Estuary: implications for their niche adaptation. *Environmental Microbiology* 20 (2):734-754
- H. Long[^], W. Sung[^], S. Kucukyildirim[^], E. Williams, S. Miller, W. Guo, C. Patterson, C. Gregory, C. Strauss, C. Stone, C. Berne, D. Kysela, W.R. Shoemaker, M. Muscarella, **H. Luo**, J.T. Lennon, Y.V. Brun, and M. Lynch^{*}. 2018. Evolutionary determinants of genome-wide nucleotide composition. *Nature Ecology & Evolution* 2 (2):237-240
- H. Luo**^{*^}, Y. Huang[^], R. Stepanauskas, and J. Tang. 2017. Excess of non-conservative amino acid changes in marine bacterioplankton lineages with reduced genomes. *Nature Microbiology* 2:17091
- H.A. Bullock^{*}, **H. Luo**, and W.B. Whitman. 2017. Evolution of dimethylsulfoniopropionate metabolism in marine phytoplankton and bacteria. *Frontiers in Microbiology* 8:637
- Y. Sun, Y. Zhang, J.T. Hollibaugh, and **H. Luo**^{*}. 2017. Ecotype diversification of an abundant *Roseobacter* lineage. *Environmental Microbiology* 19 (4):1625-1638
- Y. Sun, K.E. Powell, W. Sung, M. Lynch, M.A. Moran, and **H. Luo**^{*}. 2017. Spontaneous mutations of a model heterotrophic marine bacterium. *The ISME Journal* 11 (7):1713-1718

- W. Zhang, W. Ding, B. Yang, R. Tian, S. Gu, **H. Luo**, and P-Y Qian*. 2016. Genomic and transcriptomic evidence for carbohydrate consumption among microorganisms in a cold seep brine pool. *Frontiers in Microbiology* 7:1825
- H. Luo***, Y. Sun, J.T. Hollibaugh, and M.A. Moran. 2016. Low genome content diversity of marine planktonic Thaumarchaeota. *Environmental Microbiology Reports* 8 (4):501-507
- Y. Zhang, Y. Sun, N. Jiao, R. Stepanauskas, and **H. Luo***. 2016. Ecological genomics of the uncultivated marine Roseobacter lineage CHAB-I-5. *Applied and Environmental Microbiology* 82 (7):2100-2111
- H. Luo***, L. Thompson, U. Stingl, and A.L. Hughes. 2015. Selection maintains low genomic GC content in marine SAR11 lineages. *Molecular Biology and Evolution* 32 (10): 2738-2748
- H. Luo***. 2015. Evolutionary origin of a streamlined marine bacterioplankton lineage. *The ISME Journal* 9 (6):1423-1433
- H. Luo***. 2015. The use of evolutionary approaches to understand single cell genomes. *Frontiers in Microbiology* 6: 191
- H. Luo** and M.A. Moran*. 2015. How do divergent ecological strategies emerge among marine bacterioplankton lineages? *Trends in Microbiology* 23 (9):577-584
- J.M. Labonté, B.K. Swan, B. Poulos, **H. Luo**, S. Koren, S.J. Hallam, M.B. Sullivan, T. Woyke, K.E. Wommack, and R. Stepanauskas*. 2015. Single cell genomics-based analysis of virus-host interactions in marine surfacebacterioplankton. *The ISME Journal* 9 (11):2386-2399
- (Before CUHK)
- B.P. Durham, S. Sharma, **H. Luo**, C.B. Smith, S.A. Amin, S.J. Bender, S.P. Dearth, B.A.S. Van Mooy, S.R. Campagna, E.B. Kujawinski, E.V. Armbrust, and M.A. Moran*. 2015. Cryptic carbon and sulfur cycling between surface ocean plankton. *Proc. Natl. Acad. Sci. USA* 112 (2): 453-457
- H. Luo** and M.A. Moran*. 2014. Evolutionary ecology of the marine Roseobacter clade. *Microbiology and Molecular Biology Reviews* 78 (4): 573-587
- M. Lin, M.V. Kitahara, **H. Luo**, D. Tracey, J. Geller, F. Hironobu, D.J. Miller, and C.A. Chen*. 2014. Mitochondrial genome rearrangements in the Scleractinia / Corallimorpharia complex: implications for coral phylogeny. *Genome Biology and Evolution* 6 (5): 1086-1095
- B.P. Durham, J. Grote, K.A. Whittaker, S.J. Bender, **H. Luo**, S.L. Grim, J.M. Brown, J.R. Casey, A. Dron, L. Florez-Leiva, A. Krupke, C.M. Luria, A.H. Mine, S. Pather, A. Talarmin, E.K. Wear, T.S. Weber, J.M. Wilson, M.J. Church, E.F. DeLong, D.M. Karl, G.F. Steward, J.M. Eppley, N.C. Kyrpides, S. Schuster, and M.S. Rappe*. 2014. Draft genome sequence of marine alphaproteobacterial strain HIMB11, the first cultivated representative of a unique lineage within the Roseobacter clade possessing an unusually small genome. *Standards in Genomic Sciences* 9:632-645
- H. Luo**, B.K. Swan, R. Stepanauskas, A.L. Hughes, and M.A. Moran*. 2014. Evolutionary analysis of a streamlined lineage of surface ocean Roseobacters. *The ISME Journal* 8:1428-1439
- H. Luo**, B.K. Swan, R. Stepanauskas, A.L. Hughes, and M.A. Moran*. 2014. Comparing effective population sizes of dominant marine Alphaproteobacteria lineages. *Environmental Microbiology Reports* 6 (2): 167-172
- H. Luo***, B.B. Tolar, B.K. Swan, C.L. Zhang, R. Stepanauskas, M.A. Moran, and J.T. Hollibaugh*. 2014. Single cell genomics shedding light on marine Thaumarchaeota diversification. *The ISME Journal* 8: 732-736
- H. Luo**, M. Csuros, A.L. Hughes, and M.A. Moran*. 2013. Evolution of divergent life history strategies in marine Alphaproteobacteria. *mBio* 4 (4): e00373-13
- B.K. Swan, B. Tupper, A. Sczyrba, F.M. Lauro, M. Martinez-Garcia, J.M. Gonzalez, **H. Luo**, J.J. Wright, Z. C. Landry, N.W. Hanson, B. Thompson, N.J. Poulton, P. Schwientek, S.G. Acinas, S.J. Giovannoni, M.A. Moran, S.J. Hallam, R. Cavicchioli, T. Woyke, and R. Stepanauskas*. 2013. Prevalent genome streamlining and latitudinal divergence of marine bacteria in the surface ocean. *Proc. Natl. Acad. Sci. USA* 110 (28):11463-11468
- H. Luo** and M.A. Moran*. 2013. Assembly-free metagenomic analysis reveals new metabolic capabilities in surface ocean bacterioplankton. *Environmental Microbiology Reports* 5 (5): 686-696
- N. Akram, J. Palovaara, J. Forsberg, M.V. Lindh, D.L. Milton, **H. Luo**, J.M. Gonzalez, and J. Pinhassi*. 2013. Regulation of proteorhodopsin gene expression by nutrient limitation in the marine bacterium *Vibrio* sp. AND4. *Environmental Microbiology* 15 (5): 1400-1415
- M.A. Moran*, B. Satinsky, S.M. Gifford, **H. Luo**, A. Rivers, L. Chan, J. Meng, B.P. Durham, C. Shen, V.A. Varaljay, C.B. Smith, P.L. Yager, and B.M. Hopkinson. 2013. Sizing up metatranscriptomics. *The ISME Journal* 7: 237-243
- H. Luo*** and A.L. Hughes. 2012. d_N/d_S does not show positive selection drives separation of polar-tropical SAR11 populations. *Molecular Systems Biology* 8:625

- H. Luo*. 2012. Predicted protein subcellular localization in dominant surface ocean bacterioplankton. *Applied and Environmental Microbiology* 78 (18): 6550-6557
- H. Luo, W. Arndt, Y. Zhang, G. Shi, M. Alekseyev, J. Tang, A.L. Hughes*, and R. Friedman. 2012. Phylogenetic analysis of genome rearrangements among five mammalian orders. *Molecular Phylogenetics and Evolution* 65 (3): 871-882
- H. Luo, A. Loytynoja, and M.A. Moran*. 2012. Genome content of uncultivated marine *Roseobacters* in the surface ocean. *Environmental Microbiology* 14 (1): 41-51
- H. Luo, R. Friedman, J. Tang, and A.L. Hughes*. 2011. Genome reduction by deletion of paralogs in the marine cyanobacterium *Prochlorococcus*. *Molecular Biology and Evolution* 28 (10): 2751-2760
- H. Luo[^], H. Zhang[^], R.A. Long, and R. Benner. 2011. Depth distributions of alkaline phosphatase and phosphonate utilization genes in the North Pacific Subtropical Gyre. *Aquatic Microbial Ecology* 62: 61-69 (recommended by Faculty of 1000, <http://f1000.com/prime/13445998>)
- H. Luo, J. Tang, R. Friedman, and A.L. Hughes*. 2011. Ongoing purifying selection on the intergenic spacers in the Group A *Streptococcus*. *Infection, Genetics and Evolution* 11 (2): 343-348
- J. Shi, Y. Zhang, H. Luo, and J. Tang*. 2010. Using jackknife to assess the quality of gene order phylogenies. *BMC Bioinformatics* 11:168
- H. Luo*, R. Benner, R. A. Long, and J. Hu. 2009. Subcellular localization of marine bacterial alkaline phosphatases. *Proc. Natl. Acad. Sci. USA* 106 (50): 21219-21223
- H. Luo*, Z. Sun, W. Arndt, J. Shi, R. Friedman, and J. Tang. 2009. Gene order phylogeny and the evolution of methanogens. *PLoS ONE* 4 (6): e6069
- H. Luo, J. Shi, W. Arndt, J. Tang, and R. Friedman*. 2008. Gene order phylogeny of the genus *Prochlorococcus*. *PLoS ONE* 3 (12): e3837
- B. Huang, L. Ou, H. Hong*, H. Luo, and D. Wang. 2005. Bioavailability of dissolved organic phosphorus compounds to typical harmful dinoflagellate *Prorocentrum donghaiense* Lu. *Marine Pollution Bulletin* 51: 838-844

RESEARCH TALKS (selected)

- 09/2019. 23rd Evolutionary Biology Meeting at Marseilles, France (invited talk; invitation turned down due to time conflict with another commitment)
- 07/2018. "Drivers of genome reduction in free-living marine bacteria". Society of Molecular Biology and Evolution annual meeting, Yokohama, Japan (contributed talk)
- 06/2018. "Evolutionary mechanisms driving niche specialization of a marine flavobacterial lineage". First International Conference on Marine Flavobacteria: Ecology, Pathology, Genomics and Integrative Biology, Cargèse (Corsica), France (contributed talk)
- 07/2017. "New evolutionary mechanisms giving rise to marine bacterioplankton lineages with highly reduced genomes". Gordon Research Conference, Marine Molecular Ecology, Hong Kong SAR (invited talk)
- 05/2017. "Environmental genomics of the marine *Roseobacter* group". 9th International Food Safety Symposium: Gut Microbiome of the Infant / Microbes and Environmental Health, The Hong Kong Polytechnic University, Hong Kong SAR (invited talk)
- 06/2016. "Evolutionary genomics of a generalist marine bacterial lineage". 2016 International Symposium on Marine Genomics, Seoul National University, Seoul, South Korea (invited talk)
- 12/2015. "How do bacterial genomes change in the ocean?" Biodiversity Research Center, Academia Sinica, Taipei, Taiwan (invited talk)
- 05/2015. "How do bacterial genomes expand and shrink in the oceans?" Next-Generation Sequencing Data Analysis Workshop 2015. The University of Hong Kong, Hong Kong SAR (invited talk)

RESEARCH GRANTS

- 01/2021-12/2023. Hong Kong Research Grants Council (RGC) General Research Fund (GRF), "Reconstructing the evolutionary history of flavobacteria" (14110820), PI, HK\$1,131,260
- 01/2021-12/2022. the Open Collaborative Research Fund (OCRF), Hong Kong Branch of the Southern Marine Science and Engineering Guangdong Laboratory, "A correlated evolutionary history between the deep sea animals and their associated microbial lineages", PI, HK\$700,000
- 03/2019-09/2022. Shenzhen Science and Technology Committee, "Genomic study of stony coral symbiotic bacteria in Shenzhen coastal waters" (JCYJ20180508161811899), PI, RMB ¥ 3,000,000
- 07/2018-12/2021. National Key R&D Program of China, "Environmental features and biological evolution in hadopelagic waters" (2018YFC0309800), co-I (with Xiang Xiao at Shanghai Jiao Tong University as PI), RMB ¥ 1,453,600 (my allocation)
- 01/2018-12/2020. Hong Kong Research Grants Council (RGC) General Research Fund (GRF),

“Roseobacter genome content diversification in a heterogeneous ocean” (14163917), PI, HK\$848,714
01/2018-12/2021. National Natural Science Foundation of China (NSFC), “Evolution of anaerobic metabolic genes in marine Roseobacters” (41776129), PI, RMB ¥ 680,000
06/2017-05/2025. Hong Kong Research Grants Council (RGC) Area of Excellence Scheme (AoE), “Center for genomic studies on plant-environment interaction for sustainable agriculture and food security”, co-PI (with H-M Lam at CUHK as PI); HK\$1,000,000 (my allocation during the first period 2017-2021)
06/2017-11/2019. Hong Kong Environment and Conservation Fund (ECF), “Genomic analysis of coral associated bacteria in Hong Kong waters” (15/2016), PI, HK\$998,673
01/2016-12/2019. National Natural Science Foundation of China (NSFC), “Genomic diversity of marine planktonic Roseobacters and the underlying ecological and evolutionary mechanisms” (41576141), PI, RMB ¥ 816,000
01/2016-12/2018. Hong Kong Research Grants Council (RGC) Early Career Scheme (ECS), “Metabolism and evolution of uncultivated members of a generalist marine bacterial lineage” (24101015), PI, HK\$1,067,343

TEACHING

Courses Taught or co-Taught at CUHK:

- (1) BIOL4420 Marine Microbial Ecology (Spring, 2020+)
- (2) BIOL3410 General Microbiology (Fall, 2015+)
- (3) BIOL4010 Evolutionary Biology (Fall, 2015+)
- (4) LSCI5011 Advanced Topics in Marine and Environmental Science (Spring, 2015+)
- (5) ENSC2270 Introduction to Environmental Science (Spring, 2015-2017)
- (6) GNB5050 Theories and Algorithms in Bioinformatics (Fall and Spring, 2015-2017)

Postgraduate Students Advised:

Xinyu Zhang, Ph.D student (08/2020+)
Mei Xie, Ph.D student (08/2020+)
Tianhua Liao, Ph.D student (08/2019+)
Jinjin Tao, Ph.D student (08/2019+)
Xiaoyuan Feng, Ph.D student (08/2018+)
Danli Luo, Ph.D student (02/2017+)
Xiao Chu, Ph.D student (08/2017+)
Xiaojun Wang, Ph.D student (08/2016+)
Hao Zhang, Ph.D student (08/2017-12/2020; thesis defence 07/2020)
Siyao Li, MPhil student (08/2015-12/2019; thesis defence 12/2019)
Ying Sun, Ph.D student (08/2015-12/2018; thesis defence 07/2018)

Postdoctoral Assistant/Associate Advised:

Dr. Xingqin Lin (Ph.D from Hong Kong University of Science & Technology, Hong Kong SAR), (01/2019+; based at CUHK-SZRI)
Dr. Sishuo Wang (Ph.D from University of British Columbia, Canada), (11/2017+)
Dr. Zhaoyang Chai (Ph.D from Jinan University, China), (07/2019-08/2020; based at CUHK-SZRI)
Dr. Minglei Ren (Ph.D from Institute of Hydrobiology, CAS, China), (08/2016-12/2018)
Dr. Zhichao Zhou (Ph.D from University of Hong Kong, Hong Kong SAR), (05/2017-11/2018)
Dr. Jesse McNichol (Ph.D from WHOI-MIT joint program, USA), (11/2016-11/2017)
Dr. Yongjie Huang (Ph.D from University of Georgia, USA), (05/2015-06/2017)

Junior Research Assistant Advised:

Yang Qian (07/2020+)
Jinjin Tao (08/2018-07/2019; based at CUHK-SZRI)
Jie Liu (co-advised by Hon-Ming Lam, 08/2018-07/2019)
Rong Zhao (08/2017-01/2019)
Jianjun Xu (09/2018-12/2018; based at CUHK-SZRI)
Hao Zhang (07/2016-07/2017)
Xiao Chu (07/2016-07/2017)