Shi Huang
Ph.D.

Personal Information

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Honors/awards

2020	Second-class Qingdao Science and Technology Progress Award, China (4/5)
2015	First-class Dean Scholarship of Chinese Academy of Sciences for excellent postgraduate
2014	National Graduate Scholarship
2014	BHP Billiton Scholarship

Professional contribution

Reviewer for:

ISMEJ, mSystems, Front Microbiol, Microbiol Spectr, mSphere, Sci Rep, BMC Microbiol, Int J Oral S, Microbiological Res

Education

2012 – 2016	University of Chinese Academy of Sciences, Sino-Danish Center for Research and Education Ph.D., Biochemistry and Molecular Biology
2015 – 2016	Technical University of Denmark Guest Ph.D. student
2008 – 2011	Shanghai Normal University M.S., Hydrobiology
2009 – 2011	Qingdao Institute of Bioenergy and Bioprocess Technology, Chinese Academy of Sciences (CAS-QIBEBT) Guest M.S. student
2003 – 2007	Xinjiang Normal University B.S., Biotechnology

Academic appointments

2022 – now	Assistant Professor in Microbiology Faculty of dentistry, The University of Hong Kong, Hong Kong SAR, China
2017 – 2021	Postdoctoral scholar Department of Pediatrics and Center for Microbiome Innovation, University of California, San Diego, USA
2016 - 2018	Postdoctoral fellow CAS-QIBEBT, China

Funding supports

2014-2017	National Science Foundation of China (31400089; RMB 240K for 3 yrs)
2016-2018	China Postdoctoral Science Foundation-CAS Joint Fellowship for Excellent Postdoctoral Fellows (2016LH00036; RMB 200K for 2 yrs)
2017-2018	International Postdoctoral Exchange Fellowship Program (China Postdoctoral Science Foundation; RMB 300K for 1 yr)

Self-statement

➢ A computational biologist with >10-year experience

➢ Research interests: (1) applying human microbiome, and metabolome data to predict chronic diseases and healthy aging; (2) advanced bioinformatic tool development for metagenomic, and multi-omics analysis; (3) develop novel metagenomics/methylome methods for analyzing microbiomes in the high-host clinical samples (4) adaptive evolutionary strategies of probiotics in the host gut

➢ 18 research publications in prestigious peer-reviewed journals as a (co-)first author or (co-)corresponding author, e.g., *Nature Methods*, *Cell Host Microbe*, *Microbiome*, *Genome Biology*, The *ISME Journal*, *mSystems*, *mBio*; H-index=26 (https://scholar.google.com/citations?user=D6Keal0AAAAJ&hl=en)

➢ Totally involved in 7 patents, including 2 authorized international patents

➢ Research papers highlighted by *Nature*, *The Scientist*, *ScienceDaily*, *ABC Science*

Publications

Research paper ([#]co-first author, *co-corresponding author)

1. Qiyun Zhu[*,#], **Shi Huang**[#], Antonio Gonzalez, Imran McGrath, Daniel McDonald, Niina Haiminen, George Armstrong, Yoshiki Vázquez-Baeza, Julian Yu, Justin Kuczynski, Gregory D. Sepich-Poore, Austin D. Swafford, Promi Das, Justin P. Shaffer, Franck Lejzerowicz, Pedro Belda-Ferre, Aki S. Havulinna, Guillaume Méric, Teemu Niiranen, Leo Lahti, Veikko Salomaa, Ho-Cheol Kim, Mohit Jain, Michael Inouye, Jack A. Gilbert, Rob Knight[*]. Phylogeny-aware analysis of metagenome community ecology based on matched reference genomes while bypassing taxonomy. ***mSystems***, Accepted.
2. Zheng Sun[#], **Shi Huang**[#,*], Pengfei Zhu, Lam Tzehau, Helen Zhao, Jia Lv, Rongchao Zhang, Lisha Zhou, Qianya Niu, Xiuping Wang, Meng Zhang, Gongchao Jing, Zhenmin Bao, Jiquan Liu, Shi Wang[*], Jian Xu[*]. Species-resolved sequencing of low biomass or degraded microbiomes using 2bRAD-M. ***Genome Biology***, 23, 36 (2022).https://doi.org/10.1186/s13059-021-02576-9. (**IF= 13.54**)
3. Chenchen Ma[#], Chengcheng Zhang[#], Denghui Chen[#], Shuaiming Jiang, Siyuan Shen, Dongxue Huo, **Shi Huang**[*], Qixiao Zhai[*], Jiachao Zhang[*]. Probiotic consumption influences universal adaptive mutations in indigenous human and mouse gut microbiota. ***Communications Biology***, 4, 1198 (2021). https://doi.org/10.1038/s42003-021-02724-8. (**IF= 6.268**)
4. Zheng Sun[#], **Shi Huang**[#], Meng Zhang, Qiyun Zhu, Niina Haiminen, Anna-Paola Carrieri, Yoshiki Vázquez-Baeza, Ho-Cheol Kim, Rob Knight*, Yangyu Liu*. Challenges in benchmarking metagenomics profilers. ***Nature Methods***, 2021, 10.1038/s41592-021-01141-3. (**IF= 28.547**)
5. **Shi Huang**[#], Shuaiming Jiang[#], Dongxue Huo[#], Victor Cantu, Pedro Belda-Ferre, Yoshiki Vázquez-Baeza, Qiyun Zhu, Chenchen Ma, Zhengkai You, Haibo Chang, Xin Zhao, Yang-Yu Liu, Rob Knight*, Jiachao Zhang*. Candidate probiotic *Lactiplantibacillus plantarum* HNU082 rapidly and convergently evolves within human, mice, and zebrafish gut but differentially influences the resident microbiome. ***Microbiome***, 9, 151 (2021). https://doi.org/10.1186/s40168-021-01102-0. (**IF= 14.650**)
6. Qiyun Zhu[#], Qiangchuan Hou[#], **Shi Huang**[#], Qianying Ou[#], Dongxue Huo[#], Yoshiki Vázquez-Baeza, Chaoping Cen, Victor Cantu, Mehrbod Estaki, Haibo Chang, Pedro Belda-Ferre, Ho-Cheol Kim, Kaining Chen, Rob Knight*, Jiachao Zhang*. Compositional and genetic alterations in Graves' disease gut microbiome reveal specific diagnostic biomarkers. ***The ISME Journal***, 2021, https://doi.org/10.1038/s41396-021-01016-7. (**IF= 10.302**)
7. **Shi Huang***, Tao He, Feng Yue, Victor Xu, Spring Wang, Pengfei Zhu, Fei Teng, Zheng Sun, Xiaohui Liu, Gongchao Jing, Xiaoquan Su, Lijian Jin, Jiquan Liu, Jian Xu*. Longitudinal multi-omics and microbiome meta-analysis identify an asymptomatic gingival state that links gingivitis, periodontitis and aging. ***mBio***, 2021, 12:e03281-20. (**IF= 7.867**).
8. Ying Zhang[#], **Shi Huang**[#], Songbo Jia, Zheng Sun, Shanshan Li, Fan Li, Lijuan Zhang, Jie Lu, Kaixuan Tan, Fei Teng*, Fang Yang*. The predictive power of saliva electrolytes exceeds

that of saliva microbiomes in diagnosing early childhood caries. *Journal of Oral Microbiology*, 2021, https://doi.org/10.1080/20002297.2021.1921486. (**IF= 5.474**)

9. Armstrong, G., Cantrell, K., **Huang, S.**, McDonald, D., Haiminen, N., Carrieri, A. P., Zhu, Q., Gonzalez, A., McGrath, I., Beck, K. L., Hakim, D., Havulinna, A. S., Méric, G., Niiranen, T., Lahti, L., Salomaa, V., Jain, M., Inouye, M., Swafford, A. D., Kim, H. C., Parida, L., Vázquez-Baeza, Y, Knight, R.[*]. (2021). Efficient computation of Faith's phylogenetic diversity with applications in characterizing microbiomes. *Genome research*, 31(11), 2131–2137. https://doi.org/10.1101/gr.275777.121. (**IF= 9.043**)

10. Clarisse Marotz[#], Pedro Belda-Ferre[#], Farhana Ali, Promi Das, **Shi Huang**, Kalen Cantrell, Lingjing Jiang, Cameron Martino, Rachel E. Diner, Gibraan Rahman, Daniel McDonald, George Armstrong, Sho Kodera, Sonya Donato, Gertrude Ecklu-Mensah, Neil Gottel, Mariana C Salas Garcia, Leslie Y. Chiang, Rodolfo A. Salido, Justin P. Shaffer, MacKenzie Bryant, Karenina Sanders, Greg Humphrey, Gail Ackermann, Niina Haiminen, Kristen L. Beck, Ho-Cheol Kim, Anna Paola Carrieri, Laxmi Parida, Yoshiki Vázquez-Baeza, Francesca J. Torriani, Rob Knight, Jack Gilbert, Daniel A. Sweeney*****, Sarah M Allard[*]. SARS-CoV-2 detection status associates with bacterial community composition in patients and the hospital environment. *Microbiome*, 2021, https://doi.org/10.1186/s40168-021-01083-0. (**IF= 14.650**)

11. Wenjun Liu[#], Zheng Sun[#], Chen Ma[#], Jiachao Zhang, Chenchen Ma, Yinqi Zhao, Hong Wei[*], **Shi Huang**[*], Heping Zhang[*]. Exposure to soil environments during earlier life stages is distinguishable in the gut microbiome of adult mice. *Gut Microbes*, 2020. https://doi.org/10.1080/19490976.2020.1830699. (**IF= 10.245**)

12. Wenyan Ji[#], Ting Jiang[#], Zheng Sun[#], Fei Teng, Chenchen Ma, **Shi Huang***, Suhua Yan*. The enhanced pharmacological effect of modified Traditional Chinese Medicine in attenuation of Atherosclerosis is driven by modulation of gut microbiota. *Frontiers in Pharmacology*, 2020. https://doi.org/10.3389/fphar.2020.546589. (**IF= 5.810**)

13. Chenchen Ma[#], Sanjeev Wasti[#], **Shi Huang**[#], Zeng Zhang, Rajeev Mishra, Shuaiming Jiang, Zhengkai You, Yixuan Wu, Haibo Chang, Yuanyuan Wang, Dongxue Huo, Congfa Li, Zhihong Sun[*], Zheng Sun[*], Jiachao Zhang[*]. Gut microbiome stability is altered by probiotic ingestion and improved with the continuous supplementation of galactooligosaccharide. *Gut Microbes*, 2020;1-13. doi:10.1080/19490976.2020.1785252. (**IF= 10.245**)

14. **Shi Huang**, Niina Haiminen, Anna-Paola Carrieri, Rebecca Hu, Lingjing Jiang, Laxmi Parida, Baylee Russell, Celeste Allaband, Amir Zarrinpar, Yoshiki Vázquez-Baeza, Pedro Belda-Ferre, Hongwei Zhou, Ho-Cheol Kim, Austin D. Swafford, Rob Knight*, Zhenjiang Zech Xu[*]. Human skin, oral, and gut microbiomes predict chronological age. *mSystems*, 2020, 5 (1), 10.1128/mSystems.00630-19 (**IF= 6.496**).

15. Zheng Sun[#], **Shi Huang**[#], Pengfei Zhu, Feng Yue, Helen Zhao, Ming Yang, Yueqing Niu, Gongchao Jing, Xiaoquan Su, Huiying Li, Chris Callewaert, Rob Knight, Jiquan Liu, Ed Smith, Karl Wei, Jian Xu[*]. A Microbiome-Based Index for Assessing Skin Health and Treatment Effects for Atopic Dermatitis in Children. *mSystems*, 2019, 4 (4), e00293-19. (**IF= 6.496**)

16. Fei Teng[#], Fang Yang[#], **Shi Huang**[#], Cunpei Bo, Zhengjiang Zech Xu, Ammon Amir, Rob Knight, Junqi Ling[*], Jian Xu[*]. Prediction of Early Childhood Caries via Spatial-

Temporal Variations of Oral Microbiota. *Cell Host Microbe*. 2015, 18(3): 296-306. (**IF= 21.023**)

This is the first demonstration of temporal prediction of chronic diseases in children via human microbiota.

17. **<u>Shi Huang</u>**[#], Rui Li[#], Xiaowei Zeng, Tao He, Helen Zhao, Alice Chang, Cunpei Bo, Jie Chen, Fang Yang, Rob Knight, Jiquan Liu, Catherine Davis, Jian Xu[*]. Predictive modeling of gingivitis severity and susceptibility via oral microbiota. *The ISME Journal*, 2014. (一区；**IF= 10.302**)

    One of the first quantitative models of chronic diseases via human microbiota.

18. Fang Yang[#], **<u>Shi Huang</u>**[#], Tao He, Carl Catrenich, Fei Teng, Cunpei Bo, Jie Chen, Jiquan Liu, Jiahui Li, Yuli Song, Rui Li and Jian Xu[*]. Microbial basis of oral malodor development in humans, *Journal of Dental Research*, 92(12), 1106-12, 2013. (**IF= 6.116**)

19. **<u>Shi Huang</u>**[#], Zhen Li[#], Tao He, Cunpei Bo, Jinlan Chang, Lin Li, Yanyan He, Jiquan Liu, Duane Charbonneau, Rui Li, Jian Xu[*]. Microbiota-based Signature of Gingivitis Treatments: A Randomized Study. *Scientific Reports*, 2016, doi: 10.1038/srep24705. (**IF= 4.379**)

    Our findings firstly suggest that the outcomes of distinct anti-gingivitis regimens might be predicted by features of the microbiota early in the treatments.

20. **<u>Shi Huang</u>**[#], Fang Yang[#], Xiaowei Zeng, Jie Chen, Rui Li, Ting Wen, Chun Li, Wei Wei, Jiquan Liu, Lan Chen, Catherine Davis and Jian Xu[*]. Preliminary characterization of the oral microbiota of Chinese adults with and without gingivitis, *BMC Oral Health*, 11:33, 2011. (**IF= 2.757；cited by 121 by Jan., 2021**)

21. Qiyun Zhu, Uyen Mai, Wayne Pfeiffer, Stefan Janssen, Francesco Asnicar, Jon Sanders, Pedro Belda-Ferre, Gabriel Al-Ghalith, Evguenia Kopylova, Daniel McDonald, Tomasz Kosciolek, John Yin, **<u>Shi Huang</u>**, Nimaichand Salam, Jian-Yu Jiao, Zijun Wu, Zhenjiang Xu, Kalen Cantrell, Yimeng Yang, Erfan Sayyari, Maryam Rabiee, Jamie Morton, Sheila Podell, Dan Knights, Wen-Jun Li, Curtis Huttenhower, Nicola Segata, Larry Smarr, Siavash Mirarab, and Rob Knight[*]. Phylogenomics of 10,575 bacterial and archaeal genomes updates understanding of domain-level relationships. *Nature Communications*, 2019, 10, 5477, https://doi.org/10.1038/s41467-019-13443-4.

22. Fei Teng[#], Tao He[#], **<u>Shi Huang</u>**, Cunpei Bo, Jie Chen, Zhen Li, Jinlan Chang, Jiquan Liu, Duane Charbonneau, Jian Xu, Rui Li and Junqi Ling[*]. Cetylpyridinium chloride mouth rinse alleviates experimental gingivitis by inhibiting dental plaque maturation. *International Journal of Oral Science*, 2016, 8(3): 182-190.

23. Yifan Tao, Yun Wang, **<u>Shi Huang</u>**, Pengfei Zhu, Wei E Huang, Junqi Ling, Jian Xu[*]. Metabolic-Activity-Based Assessment of Antimicrobial Effects by D2O-Labeled Single-Cell Raman Microspectroscopy. *Analytical Chemistry*, 89 (7), pp 4108–4115, 2017.

24. Xiaoquan Su, Jianqiang Hu, **<u>Shi Huang</u>**, Kang Ning. Rapid comparison and correlation analysis among massive number of microbial community samples based on MDV data model. *Scientific Reports,* 2014.

25. Yuehui He, Peng Zhang, **<u>Shi Huang</u>** and Jian Xu[*]. Label-free, simultaneous quantification of starch, protein and triacylglycerol in single microalgal cells. Biotechnol Biofuels 10, 275 (2017). https://doi.org/10.1186/s13068-017-0967-x

26. Gongchao Jing, Zheng Sun, Honglei Wang, Yanhai Gong, **Shi Huang**, Kang Ning, Jian Xu, Xiaoquan Su. Parallel-META 3: Comprehensive taxonomical and functional analysis platform for efficient comparison of microbial communities. ***Scientific Reports,*** 2017.

27. Jian Xu, Bo Ma, Xiaoquan Su, **Shi Huang**, Xin Xu, Xuedong Zhou, Wei E Huang, Rob Knight. Emerging Trends for Microbiome Analysis: From Single-Cell Functional Imaging to Microbiome Big Data. ***Engineering***, 3: 66-70, 2017.

28. Yun Wang, Yin Chen, Qian Zhou, **Shi Huang**, Kang Ning, Jian Xu, Robert M. Kalin, Stephen Rolfe, Wei E. Huang. A culture-independent approach to unravel uncultured bacteria and functional genes in a complex microbial community, ***PLoS One***, 7(10): e47530, 2012.

29. Qintao Wang, Yandu Lu, Yi Xin, Li Wei, **Shi Huang**, Jian Xu[*]. Genome editing of model oleaginous microalgae Nannochloropsis spp. by CRISPR/Cas9. ***The Plant Journal***. DOI: 10.1111/tpj.13307, 2017.

30. Xiaoxu Li, **Shi Huang**, Jun Yu, Quanxi Wang, Shuangxiu Wu. Improvement of hydrogen production of *Chlamydomonas reinhardtii* by co-cultivation with isolated bacteria, ***International Journal of Hydrogen Energy***, 38(25), 10779–10787, 2013.

31. Jing Li[#], Danxiang Han[#], Dongmei Wang[#], Kang Ning[#], Jing Jia, Li Wei, Xiaoyan Jing, **Shi Huang**, Jie Chen, Yantao Li, Qiang Hu, and Jian Xu[*]. Choreography of transcriptomes and lipidomes of Nannochloropsis reveals the mechanisms of oleaginousness in microalgae, ***Plant Cell***, tpc.113.121418, 2014.

32. Tingting Wang, Yuetong Ji, Yun Wang, Jing Jia, Jing Li, **Shi Huang**, Danxiang Han, Qiang Hu, Wei E Huang, Jian Xu[*]. Quantitative dynamics of triacylglycerol accumulation in microalgae populations at single-cell resolution revealed by Raman microspectroscopy. ***Biotechnology for Biofuels***, 7:58, 2014.

33. Dayi Zhang, James Berry, Di Zhu, Yun Wang, Yin Chen, Bo Jiang, **Shi Huang**, Harry Langford, Guanghe Li, Jian Xu, Eric Aries and Wei E. Huang[*]. Isolation and physiological characterisation of an uncultured degrader in a complex microbial community. ***The ISME Journal,*** 2014.

34. Zhuang Guo[#], Jiachao Zhang[#], Zhanli Wang[#], Kay Ying Ang[#], **Shi Huang**, et al, Jian Xu, Yuan Kun Lee and Heping Zhang[*]. Intestinal Microbiota Distinguish Gout Patients from Healthy Humans. ***Scientific Reports***, 6: 20602, 2016.

To be published (#co-first author, *co-corresponding author)

1. Patrick I. McGrath[#], **Shi Huang**[#], Zhejiang Zech Xu, Rebecca Hu, Manon Morin, Julia M. Gauglitz, Curt Wittenberg, Rachel J Dutton, Yoshiki Vázquez-Baeza, Se Jin Song, Austin D. Swafford, Rob Knight*. Model selection and hyperparameter recommendation improve predictive models for microbiome data. Under review.

2. Fei Teng[#], Fang Yang[#], **Shi Huang**[#], Pengfei Zhu, Jian Xu[*]. Prediction of the early childhood caries (ECC) via oral microbiota from the whole-mouth to single-tooth resolution. In preparation.

Patents

1. Rui Li, **Shi Huang**, Tao He, Jiquan Liu, Jian Xu. METHOD AND SYSTEM FOR IDENTIFYING A BIOMARKER INDICATIVE OF HEALTH CONDITION (**PCT/CN2013/075406**).
2. Rui Li, **Shi Huang**, Tao He, Jiquan Liu, Jian Xu. METHOD AND SYSTEM FOR ASSESSING A HEALTH CONDITION (**PCT/CN2013/075385**).

Media

1. Jyoti Madhusoodanan. Telltale Mouth Microbes. *The Scientist*, Sep 9, 2015. <https://www.the-scientist.com/news-opinion/telltale-mouth-microbes-34852>
2. Niina Haiminen, Anna-Paola Carrieri, and Ho-Cheol Kim. AI Can Predict your Age Based on Your Microbiome. IBM Research Blog, Feb 11, 2020. <https://www.ibm.com/blogs/research/2020/02/ai-predict-age-based-on-microbiome/>
3. Staff reporter. "Human Skin, Oral Microbiomes Can Estimate People's Ages to Within Few Years." genomeweb, Feb 12, 2020. <https://www.genomeweb.com/genetic-research/human-skin-oral-microbiomes-can-estimate-peoples-ages-within-few-years#.XkWlLhNKhZJ>
4. Suzannah Lyons. "Predicting your age from your skin, mouth and gut microbiome." ABC Science, Feb 11, 2020. <https://www.abc.net.au/news/science/2020-02-12/predicting-age-from-bugs-microbiota-mouth-skin-poo/11955090>
5. University of California - San Diego. "More than just a carnival trick: Researchers can guess your age based on your microbes." ScienceDaily. Feb 11, 2020. <www.sciencedaily.com/releases/2020/02/200211134432.htm>.
6. Christopher Wanjek. Skin microbes betray your age. LiveScience, Feb 11, 2020. < https://www.livescience.com/skin-microbes-betray-your-age.html>

Conference papers

1. *The 2017 Annual Conference of Chinese Society of Microbial Ecology*, Beijing, China, Oct 20-23, 2017 (talk)
2. *"Biofilms, Microbiomes and Oral Diseases: Challenges and Future Perspectives" symposium*. Penn Dental Medicine and West China School of Stomatology, Beijing, China, Sept 30, 2017 (Poster)
3. *Cold Spring Harbor Asia: Microbiota, Metagenomics & Health*, Suzhou, China, Sept 4-8, 2017 (talk)
4. *17th Symposium of Chinese Society of Phycology*. Chinese Society of Phycology, Wuhan, China, Oct. 17, 2013 (Poster)
5. *100th FDI World Dental Federation Annual World Dental Congress*. World Dental Federation, Hong Kong, Sept. 10, 2012 (Poster)
6. *International Symposium of Saliva and Oral Health Tentative Program*. Peking University, Beijing, Aug. 24, 2012 (Poster)
7. *ISMB 2014: International Conference on Intelligent Systems for Molecular Biology*. Boston, Massachusetts, USA, July 11, 2014 (Poster)

8. *AI research week—IBM Research.* Boston, USA, Sept 16-18, 2019 (Poster)
9. The 2nd International Virtual Forum on Modern Toxicology, https://meeting.tencent.com/l/tlComYgXFMDm, Feb 11-12, 2021 (Plenary speaker)