

Curriculum Vitae

Liping Zhao

Eveleigh-Fenton Chair of Applied Microbiology,
Department of Biochemistry and Microbiology,
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Education

- 1979-1983 B.S., Plant Protection, Shanxi Agricultural University, Taigu, China.
1983-1989 Ph.D., Molecular Plant Pathology, Nanjing Agricultural University, Nanjing, China.

Academic Appointments

- 1989-1993 Associate Director, Institute of Biotechnology, Shanxi Academy of Agricultural Sciences
1993-1995 Visiting Scholar, Department of Plant Pathology, Cornell University
1995-1997 Associate professor, Institute of Biotechnology, Shanxi University
1997-2001 Professor and Director, Institute of Biotechnology, Shanxi University
2000.4-.7 Visiting professor, Department of Civil Engineering, University of Southern Carolina
2001-2014 Professor of microbiology, School of Life Sciences and Biotechnology, SJTU
2003-2012 Associate Dean, School of Life Sciences and Biotechnology, SJTU
2005-2009 Executive Director, Shanghai Center for Systems Biomedicine at SJTU
2012.9-2013.4 Visiting Professor, Brigham Young University, Provo, Utah, USA
2014-2017 Distinguished Professor of Microbiology, School of Life Sciences and Biotechnology, SJTU
2017- Eveleigh-Fenton Chair of Applied Microbiology, Department of Biochemistry and Microbiology, School of Environmental and Biological Sciences, Rutgers, The State University of New Jersey

Other Professional Appointments

- 1999-2001 Member, Committee for Grant Evaluation in Genetics, National Science Foundation (NSF) of China

2001-2003	Member, Committee for Grant Evaluation in Microbiology, NSF of China
2001-Pres.	<i>Ad-hoc</i> reviewer, grants evaluation of NSF of China, China Ministry of Science and Technology and Shanghai Commission of Science and Technology
2001-Pres.	Ad-hoc reviewer, grants evaluation of French ANR, Hong Kong Science Administration, U.S.-Israel Binational Science Foundation, & etc.
2006-2012	Board Member, International Society for Microbial Ecology (ISME)
2008-Pres.	Member, Steering Committee, International Human Microbiome Consortium (IHMC)
2013-2020	Senior Editor, The ISME Journal
2013-Pres.	Member, Editorial Board, FMES Microbiology Ecology
2014-2017	Member, Editorial Board, Scientific Report
2014-2017	Senior Editor, mSystems, American Society for Microbiology
2015-Pres.	Associate editor, Microbiome
2018-pres	Chair of the Big Idea Committee, International Human Microbiome Consortium (IHMC)

Honors & Awards

2009 Outstanding Scientist of Shanghai.

2011 SJTU Best Teacher of the Year, 2011.

2014-Elected Fellow, American Academy of Microbiology.

2016-Senior fellow of Canadian Institute of Advanced Research, CIFAR.

2018- Member of scientific advisory board, Center for Microbiome Research and Education, American Gastroenterological Association (AGA)

Research Interests

- ◇ Developing molecular and genomic tools for systems understanding and predictive manipulation of the complex microbial communities in human and animal guts.
- ◇ Understanding interactions between diet and gut microbiota in onset and progression of chronic diseases such as obesity and diabetes.
- ◇ Formulating interventions integrating traditional Chinese medicine and medicinal foods into modern day diet to modulate the relationship between gut microbiota and humans for achieving preventive health care.

Publications in International Journals (* Corresponding author)

Fei, N., A. Bruneau, X. Zhang, R. Wang, J. Wang, S. Rabot, P. Gérard and **L. Zhao** (2020). "Endotoxin Producers Overgrowing in Human Gut Microbiota as the Causative Agents for Nonalcoholic Fatty Liver Disease." **mBio**

11(1).

Zhai, R., X. Xue, L. Zhang, X. Yang, **L. Zhao** and C. Zhang (2019). "Strain-specific anti-inflammatory properties of two Akkermansia muciniphila strains on chronic colitis in mice." **Frontiers in cellular and infection microbiology** 9: 239.

Zhang, L., X. Xue, R. Zhai, X. Yang, H. Li, **L. Zhao** and C. Zhang (2019). "Timing of Calorie Restriction in Mice Impacts Host Metabolic Phenotype with Correlative Changes in Gut Microbiota." **mSystems** 4(6).

Zhang, M., J. Wang, G. Wu, H. Li and L. Zhao (2019). "Gastrointestinal Microbiology in the Normal Host."

T Liu, Y Wu, L Wang, X Pang, **L Zhao**, H Yuan, C Zhang, 2019, A More Robust Gut Microbiota in Calorie-Restricted Mice Is Associated with Attenuated Intestinal Injury Caused by the Chemotherapy Drug Cyclophosphamide, **MBio** 10 (2), e02903-18

T Chen, AB Liu, S Sun, NJ Ajami, MC Ross, H Wang, L Zhang, K Reuhl, **L Zhao*** et al. 2019, Green Tea Polyphenols Modify the Gut Microbiome in db/db Mice as Co-Abundance Groups Correlating with the Blood Glucose Lowering Effect, **Molecular nutrition & food research** 63 (8), 1801064

R Zhai, X Xue, L Zhang, X Yang, **L Zhao**, C Zhang, 2019, Strain-Specific Anti-inflammatory Properties of Two Akkermansia muciniphila Strains on Chronic Colitis in Mice, **Frontiers in Cellular and Infection Microbiology** 9, 239

L Deng, R Wang, H Li, C Zhang, **L Zhao**, M Zhang, 2019, miRNA-Gene Regulatory Network in Gnotobiotic Mice Stimulated by Dysbiotic Gut Microbiota Transplanted From a Genetically Obese Child, **Frontiers in microbiology** 10

Chen, Q., G. Wu, H. Chen, H. Li, S. Li, C. Zhang, X. Pang, L. Wang, **L. Zhao** and J. Shen (2019). "Quantification of Human Oral and Fecal Streptococcus parasanguinis by Use of Quantitative Real-Time PCR Targeting the groEL Gene." **Frontiers in Microbiology** 10: 2910.

Deng, L., R. Wang, H. Li, C. Zhang, L. Zhao and M. Zhang (2019). "MiRNA-gene regulatory network in gnotobiotic mice stimulated by dysbiotic gut microbiota transplanted from a genetically obese child." *Frontiers in microbiology* 10: 1517.

Liu, S., **L. Zhao**, L. Wang and H. Liu (2019). "Microstructure-modified products from stone-milled wheat bran powder improve glycemic response and sustain colonic fermentation." **International journal of biological macromolecules**.

H Xia, C Liu, CC Li, M Fu, S Takahashi, KQ Hu, K Aizawa, S Hiroyuki, **L. Zhao**, et al. 2018, Dietary Tomato Powder Inhibits High-Fat Diet-Promoted Hepatocellular Carcinoma with Alteration of Gut Microbiota in Mice Lacking Carotenoid Cleavage Enzymes, **Cancer Prevention Research** 11 (12), 797-810

YY Lam, C Zhang, **L Zhao***, 2018, Causality in dietary interventions—Building a case for gut microbiota, **Genome medicine** 10 (1), 62

F Pan, L Zhang, M Li, Y Hu, B Zeng, H Yuan, **L Zhao**, C Zhang, 2018, Predominant gut Lactobacillus murinus strain mediates anti-inflammaging effects in calorie-restricted mice, **Microbiome** 6 (1), 54

R Wang, H Li, X Yang, X Xue, L Deng, J Shen, M Zhang, **L Zhao**, C Zhang, 2018, Genetically obese human gut microbiota induces liver steatosis in germ-free mice fed on normal diet, **Frontiers in microbiology** 9, 1602

X Tong, J Xu, F Lian, X Yu, Y Zhao, L Xu, M Zhang, X Zhao, J Shen, S Wu, **L Zhao***, 2018, Structural alteration of gut microbiota during the amelioration of human type 2 diabetes with hyperlipidemia by metformin and a traditional chinese herbal formula, **MBio** 9 (3), e02392-17

N Qin, X Dong, L Zhao, **2018**, Microbiome: from community metabolism to host diseases, **Science China Life Sciences** 61 (7), 741-743

M Li, Y Wu, Y Hu, L Zhao, C Zhang, 2018, Initial gut microbiota structure affects sensitivity to DSS-induced colitis in a mouse model, **Science China Life Sciences** 61 (7), 762-769

Zhao L.*, Feng Zhang^{1†}, Xiaoying Ding^{2†}, Guojun Wu^{1†}, Yan Y. Lam^{3†}, Xuejiao Wang², Huaqing Fu¹, Xinhe Xue¹, Chunhua Lu⁴, Jilin Ma⁴, Lihua Yu⁴, Chengmei Xu⁴, Zhongying Ren⁴, Ying Xu⁵, Songmei Xu⁵, Hongli Shen⁵, Xiuli Zhu⁵, Yu Shi⁶, Qingyun Shen⁶, Weiping Dong², Rui Liu¹, Yunxia Ling², Yue Zeng⁷, Xingpeng Wang⁷, Qianpeng Zhang¹, Jing Wang¹, Linghua Wang¹, Yanqiu Wu¹, Benhua Zeng⁸, Hong Wei⁸, Menghui Zhang¹, Yongde Peng*, Chenhong Zhang* (2018) Gut bacteria selectively promoted by dietary fibers alleviate type 2 diabetes **Science** 09 Mar 2018: Vol. 359, Issue 6380, pp. 1151-1156 DOI: 10.1126/science.aao5774

Costea, Paul I, Falk Hildebrand, Arumugam Manimozhiyan, Fredrik Bäckhed, Martin J Blaser, Frederic D Bushman, Willem M De Vos, S Dusko Ehrlich, Claire M Fraser, Masahira Hattori, Curtis Huttenhower, Ian B Jeffery, Dan Knights, James D Lewis, Ruth E Ley, Howard Ochman, Paul W O'Toole, Christopher Quince, David A Relman, Fergus Shanahan, Shinichi Sunagawa, Jun Wang, George M Weinstock, Gary D Wu, Georg Zeller, **L. Zhao**, Jeroen Raes, Rob Knight, Peer Bork (2018). "Enterotypes in the landscape of gut microbial community composition." **Nature Microbiology** 3(1): 8.

Costea, Paul I, Georg Zeller, Shinichi Sunagawa, Eric Pelletier, Adriana Alberti, Florence Levenez, Melanie Tramontano, Marja Driessen, Rajna Hercog, Ferris-Elias Jung, Jens Roat Kultima, Matthew R Hayward, Luis Pedro Coelho, Emma Allen-Vercoe, Laurie Bertrand, Michael Blaut, Jillian RM Brown, Thomas Carton, Stéphanie Cools-Portier, Michelle Daigneault, Muriel Derrien, Anne Druesne, Willem M De Vos, B Brett Finlay, Harry J Flint, Francisco Guarner, Masahira Hattori, Hans Heilig, Ruth Ann Luna, Johan van Hylckama Vlieg, Jana Junick, Ingeborg Klymiuk, Philippe Langella, Emmanuelle Le Chatelier, Volker Mai, Chaysavanh Manichanh, Jennifer C Martin, Clémentine Mery, Hidetoshi Morita, Paul W O'Toole, Céline Orvain, Kiran Raosaheb Patil, John Penders, Søren Persson, Nicolas Pons, Milena Popova, Anne Salonen, Delphine Saulnier, Karen P Scott, Bhagirath Singh, Kathleen Slezak, Patrick Veiga, James Versalovic, **L. Zhao**, Erwin G Zoetendal, S Dusko Ehrlich, Joel Dore, Peer Bork (2017). "Towards standards for human fecal sample processing in metagenomic studies." **Nature Biotechnology** 35(11): 1069.

Yao Xiaomin, Chenhong Zhang, Yue Xing, Guang Xue, Qianpeng Zhang, Fengwei Pan, Guojun Wu, Yingxin Hu, Qihong Guo, Ailing Lu, Xiaoming Zhang, Rongbin Zhou, Zhigang Tian, Benhua Zeng, Hong Wei, Warren Strober, **L. Zhao***, Guangxun Meng* (2017). "Remodelling of the gut microbiota by hyperactive NLRP3 induces regulatory T cells to maintain homeostasis." **Nature Communications** 8(1): 1896.

Leulier, F., L. T. MacNeil, W.-j. Lee, J. F. Rawls, P. D. Cani, M. Schwarzer, **L. Zhao** and S. J. Simpson (2017). "Integrative physiology: at the crossroads of nutrition, microbiota, animal physiology, and human health." **Cell Metabolism** 25(3): 522-534.

Zhao*, L. and C. Zhang (2017). "Microbiome: Keeping rhythm with your gut." **Nature Microbiology** 2: 16273.

Zhu, C., M. Miller, S. Marpaka, P. Vaysberg, M. C. Rühlemann, G. Wu, F.-A. Heinsen, M. Tempel, **L. Zhao** and W. Lieb (2017). "Functional sequencing read annotation for high precision microbiome analysis." **Nucleic Acids Research**. gkx1209, <https://doi.org/10.1093/nar/gkx1209>

Wu Guojun, Chenhong Zhang, Huan Wu, Ruirui Wang, Jian Shen, Linghua Wang, Yufeng Zhao, Xiaoyan Pang, Xiaojun Zhang, **L. Zhao**, Menghui Zhang (2017). "Genomic Microdiversity of Bifidobacterium pseudocatenulatum Underlying Differential Strain-Level Responses to Dietary Carbohydrate Intervention." **mBio** 8(1): e02348-02316.

Bridgewater, L. C., C. Zhang, Y. Wu, W. Hu, Q. Zhang, J. Wang, S. Li and **L. Zhao*** (2017). "Gender-based differences in host behavior and gut microbiota composition in response to high fat diet and stress in a mouse model." **Scientific Reports** 7(1): 10776.

Feng, Z., W. Long, B. Hao, D. Ding, X. Ma, **L. Zhao** and X. Pang (2017). "A human stool-derived Bilophila wadsworthia strain caused systemic inflammation in specific-pathogen-free mice." **Gut pathogens** 9(1): 59.

Chen, L., Y. Xu, X. Chen, C. Fang, **L. Zhao** and F. Chen (2017). "The Maturing Development of Gut Microbiota in Commercial Piglets during the Weaning Transition." **Frontiers in Microbiology** 8: 1688.

Liu Rui, Chenhong Zhang, Yu Shi, Feng Zhang, Linxia Li, Xuejiao Wang, Yunxia Ling, Huaqing Fu, Weiping Dong, Jian Shen, Andrew Reeves, Andrew S Greenberg, L. Zhao, Yongde Peng, Xiaoying Ding (2017). "Dysbiosis of Gut Microbiota Associated with Clinical Parameters in Polycystic Ovary Syndrome." **Frontiers in Microbiology** 8: 324.

Wang Jing, Yang Wang, Xu Zhang, Jiaqi Liu, Qianpeng Zhang, Yu Zhao, Jinghua Peng, Qin Feng, Jianye Dai, Shujun Sun, Yufeng Zhao, L. Zhao, Yongyu Zhang, Yiyang Hu, Menghui Zhang (2017). "Gut Microbial Dysbiosis Is Associated with Altered Hepatic Functions and Serum Metabolites in Chronic Hepatitis B Patients." **Frontiers in Microbiology** 8: 2222.

Wang, X., H. Lu, Z. Feng, J. Cao, C. Fang, X. Xu, L. Zhao and J. Shen (2017). "Development of human breast milk microbiota-associated mice as a method to identify breast milk bacteria capable of colonizing gut." **Frontiers in Microbiology** 8: 1242.

Li, M., Y. Wu, Y. Hu, L. Zhao and C. Zhang (2017). "Initial gut microbiota structure affects sensitivity to DSS-induced colitis in a mouse model." **Science China Life Sciences**: 1-8.

Wang, J.-j., J. Wang, X.-y. Pang, **L. Zhao**, L. Tian and X.-p. Wang (2016). "Sex differences in colonization of gut microbiota from a man with short-term vegetarian and inulin-supplemented diet in germ-free mice." **Scientific Reports** 6: 36137.

Wu, G., C. Zhang, J. Wang, F. Zhang, R. Wang, J. Shen, L. Wang, X. Pang, X. Zhang, **L. Zhao**, and M. Zhang. 2016. 'Diminution of the gut resistome after a gut microbiota-targeted dietary intervention in obese children', **Sci Rep**, 6: 24030.

Yan, H., N. Fei, G. Wu, C. Zhang, **L. Zhao**, and M. Zhang. 2016. 'Regulated Inflammation and Lipid Metabolism in Colon mRNA Expressions of Obese Germfree Mice Responding to Enterobacter cloacae B29 Combined with the High Fat Diet', **Front Microbiol**, 7: 1786.

Zhang, C., and **L. Zhao***. 2016. 'Strain-level dissection of the contribution of the gut microbiome to human metabolic disease', **Genome Med**, 8: 41.

Zhang, Q., Y. Wu, J. Wang, G. Wu, W. Long, Z. Xue, L. Wang, X. Zhang, X. Pang, Y. Zhao, **L. Zhao**, and C. Zhang. 2016. 'Accelerated dysbiosis of gut microbiota during aggravation of DSS-induced colitis by a butyrate-producing bacterium', **Sci Rep**, 6: 27572.

Dubilier* N., McFall-Ngai M. and **Zhao L.** Microbiology: Create a global microbiome effort. **Nature** 526(7575): 2015, 631-34.

Zhang C., Yin A., Li H., Wang R., Wu G., Shen J., Zhang M., Wang L., Hou Y., Ouyang H., Zhang Y., Zheng Y., Wang J., Lv X., Wang Y., Zhang F., Zeng B., Li W., Yan F., Zhao Y., Pang X., Zhang X., Fu H., Chen F., Zhao N., Hamaker B. R., Bridgewater L. C., Weinkove D., Clement K., Dore J., Holmes E., Xiao H., Zhao G., Yang S., Bork P., Nicholson J. K., Wei H., Tang* H., Zhang* X. and **Zhao* L.** Dietary modulation of gut microbiota contributes to alleviation of both genetic and simple obesity in children. **EBioMedicine** 2015, 2(8):966-82.

Xu J, Lian F, Zhao L, Zhao Y, Chen X, Zhang X, Guo Y, Zhang C, Zhou Q, Xue Z, Pang X, **Zhao* L.** and Tong* X. Structural modulation of gut microbiota during alleviation of type 2 diabetes with a Chinese herbal formula. **ISME J** 2015, 9(3):552-62.

Wang J., Tang H., Zhang C., Zhao Y., Derrien M., Rocher E., van-Hylckama Vlieg J.E., Strissel K., **Zhao L.**, Obin M., and Shen* J. Modulation of gut microbiota during probiotic-mediated attenuation of metabolic syndrome in high fat diet-fed mice. **ISME J** 2015, 9(1):1-15.

Chen H., Liu Y., Zhang M., Wang G., Qi Z., Bridgewater L., **Zhao L.**, Tang Z. and Pang* X. A Filifactor alocis-centered co-occurrence group associates with periodontitis across different oral habitats. **Sci Rep** 2015, 5:9053.

Karl J. P., Fu X., Wang X., Zhao Y., Shen J., Zhang C., Wolfe B. E., Saltzman E., **Zhao* L.** and Booth* S. L. Fecal menaquinone profiles of overweight adults are associated with gut microbiota composition during a gut microbiota-targeted dietary intervention. **Am J Clin Nutr** 2015, 102(1): 84-93.

Long W., Xue Z., Zhang Q., Feng Z., Bridgewater L., Wang L., **Zhao L.** and Pang* X. Differential responses of gut microbiota to the same prebiotic formula in oligotrophic and eutrophic batch fermentation systems. **Sci Rep** 2015, 5:13469.

- Xue Z., Zhang W., Wang L., Hou R., Zhang M., Fei L., Zhang X., Huang H., Bridgewater L. C., Jiang Y., Jiang C., **Zhao L.**, Pang* X. and Zhang* Z. The bamboo-eating giant panda harbors a carnivore-like gut microbiota, with excessive seasonal variations. *MBio* 2015, **6**(3): e00022-15.
- Zhang J., Guo Z., Xue Z., Sun Z., Zhang M., Wang L., Wang G., Wang F., Xu J., Cao H., Xu H., Lv Q., Zhong Z., Chen Y., Qimuge S., Menghe B., Zheng Y., **Zhao* L.**, Chen* W. and Zhang* H. A phylo-functional core of gut microbiota in healthy young Chinese cohorts across lifestyles, geography and ethnicities. *ISME J* 2015, **9**(9): 1979-90.
- Zhang X., Zhao Y., Xu J., Xue Z., Zhang M., Pang X., Zhang X. and **Zhao* L.** Modulation of gut microbiota by berberine and metformin during the treatment of high-fat diet-induced obesity in rats. *Sci Rep* 2015, **5**:14405.
- Zhang-Sun W., Augusto L. A., **Zhao* L.** and Caroff* M. Desulfovibrio desulfuricans isolates from the gut of a single individual: structural and biological lipid A characterization. *FEBS Lett* 2015, **589**(1): 165-71.
- Ren H., Gao G., Song Z., Wang W., **Zhao L.**, Zhang* X. Bacteria in the injection water differently impacts the bacterial communities of production wells in high-temperature petroleum reservoirs. *Front Microbiol* 2015, **6**:505.
- Xiong S., Li X., Chen J., **Zhao L.**, Zhang H., Zhang* X. Crude oil degradation by bacterial consortia under four different redox and temperature conditions. *Appl Microbiol Biotechnol* 2015, **99**(3): 1451-61.
- Xiao S., Fei N., Pang X., Shen J., Wang L., Zhang B., Zhang M., Zhang X., Zhang C., Li M., Sun, L., Xue Z., Wang J., Feng J., Yan F., Zhao N., Liu J., Long W. and **Zhao* L.** A gut microbiota-targeted dietary intervention for amelioration of chronic inflammation underlying metabolic syndrome. *FEMS Microbiol Ecol* 2014, **87**(2):357-67.
- Xiao S. and **Zhao* L.** Gut microbiota-based translational biomarkers to prevent metabolic syndrome via nutritional modulation. *FEMS Microbiology Ecology*, 2014, **87**(2):303-14.
- Huang F., Ge L., Zhang B., Wang Y., Tian H., **Zhao L.**, He Y. and Zhang* X. A fullerene colloidal suspension stimulates the growth and denitrification ability of wastewater treatment sludge derived bacteria. *Chemosphere* 2014, **108**:411-7.
- Zhao* L.** The gut microbiota and obesity: from correlation to causality. *Nat Rev Microbiol*, **11**(9): 639-647 (Review)
- Zhang C., Li S., Yang L., Huang P., Li W., Wang S., Zhao G., Zhang M., Pang X., Yan Z., Liu Y. and **Zhao* L.** Structural modulation of gut microbiota in life-long calorie-restricted mice. *Nat Commun* 2013, **4**: 2163.
- Fei N. and **Zhao* L.** An opportunistic pathogen from the gut of an obese human causes obesity in germfree mice. *ISME J* 2013, **7**(4): 880-4.
- Zenewicz L.A., Yin X., Wang G., Elinav E., Hao L., **Zhao L.** and Flavell* R.A. IL-22 deficiency alters colonic microbiota to be transmissible and colitogenic. *J Immunol* 2013, **190**(10): 5306-12.
- Yin X., Peng J., **Zhao L.**, Yu Y., Zhang X., Liu P., Feng Q., Hu Y. and Pang* X. Structural changes of gut microbiota in a rat non-alcoholic fatty liver disease model treated with a Chinese herbal formula. *Syst Appl Microbiol* 2013, **36**(3): 188-196.
- Zhang X., Zhao Y., Zhang M., Pang X., Xu J., Kang C., Li M., Zhang C., Zhang Z., Zhang Y., Li X., Ning G. and **Zhao* L.** Structural Changes of Gut Microbiota during Berberine-Mediated Prevention of Obesity and Insulin Resistance in High-Fat Diet-Fed Rats. *PLoS One* 2012, **7**(8): e42529.
- Zhang C., Zhang M., Pang X., Zhao Y., Wang L. and **Zhao* L.** Structural resilience of the gut microbiota in adult mice under high-fat dietary perturbations. *ISME J* 2012, **6**(10): 1848-5
- Wang T., Cai G., Qiu Y., Fei N., Zhang M., Pang X., Jia W., Cai S. and **Zhao* L.** Structural Segregation of Gut Microbiota between Colorectal Cancer Patients and Healthy Volunteers. *ISME J* 2012, **6**(2): 320-9.
- Zhao* L.**, Nicholson J.K., Lu A., Wang Z., Tang H., Holmes E., Shen J., Zhang X., Li J.V., Lindon J.C. Targeting the Human Genome-Microbiome Axis for Drug Discovery: Inspirations from Global Systems Biology and Traditional Chinese Medicine. *J Proteome Res* 2012, **11**(7): 3509-19. (Review)

Shen J., Obin M. and **Zhao* L.** The gut microbiota, obesity and insulin resistance. *Mol Aspects Med* 2012, 34(1): 39-58. (Review)

van Hylckama Vlieg* J.E., Veiga P., Zhang C., Derrien M. and **Zhao L.** Impact of microbial transformation of food on health-from fermented foods to fermentation in the gastro-intestinal tract. *Curr Opin Biotechnol* 2011, 22 (2): 211-9. (Review)

Zhu J., Yin X., Yu H., **Zhao L.**, Sabour P. and Gong J. Involvement of quorum sensing and heat-stable enterotoxin a in cell damage caused by a porcine enterotoxigenic Escherichia coli strain. *Infect Immun* 2011, 79(4): 1688-95.

Wang T., Zhang X., Zhang M., Wang L. and **Zhao* L.** Development of a fluorophore-ribosomal DNA restriction typing method for monitoring structural shifts of microbial communities. *Arch Microbiol* 2011, 193(5): 341-50

Wei H., Dong L., Wang T., Zhang M., Hua W., Zhang C., Pang X., Chen M., Su M., Qiu Y., Zhou M., Yang S., Chen Z., Rantalainen M., Nicholson J.K., Jia W., Wu D. and **Zhao* L.** Structural shifts of gut microbiota as surrogate endpoints for monitoring host health changes induced by carcinogen exposure. *FEMS Microbiol Ecol* 2010, 73(3): 577-86

Zhao* L. and Shen, J. Whole-body systems approaches for gut microbiota-targeted, preventive healthcare. *J Biotech* 2010, 149(3): 183-90 (Review)

Liu Y., Zhang C., **Zhao L.** and C. Nardini*. Adapting functional genomic tools to metagenomic analyses: investigating the role of gut bacteria in relation to obesity. *Brief Funct Genomics* 2011, 9(5-6): 355-61

Zhang* X., Yue S., Zhong H., Hua W., Chen R., Cao Y. and **Zhao L.** A diverse bacterial community in an anoxic quinoline-degrading bioreactor determined by using pyrosequencing and clone library analysis. *Applied Microbial and Biotechnology* 2011, 91(2): 425-34.

Ren H., Zhang* X., Song Z., Rupert W., Gao G., Guo S., **Zhao L.** Comparison of Microbial Community Compositions of Injection and Production Well Samples in a Long-term Water-Flooded Petroleum Reservoir. *PLoS One* 2011, 6(8): e23258.

Zhao* L. Genomics: The tale of our other genome. *Nature* 2010, 465(7300): 879-80.

Zhang C., Zhang M., Wang S., Han R., Cao Y., Hua W., Mao Y., Zhang X., Pang X., Wei C., Zhao G., Chen Y. and **Zhao* L.** Interactions between gut microbiota, host genetics and diet relevant to development of metabolic syndromes in mice. *ISME J* 2010, 4(2): 232-41.

Mao Y., Zhang* X., Xia X., Zhong H., **Zhao L.** Versatile aromatic compound-degrading capacity and microdiversity of *Thauera* strains isolated from a coking wastewater treatment bioreactor. *J Ind Microbiol Biotechnol* 2010, 37(9): 927-34.

Shen J., Zhang B., Wei H., Che C., Ding D., Hua X., Bucheli P., Wang L., Li Y., Pang X. and **Zhao* L.** Assessment of the modulating effects of fructo-oligosaccharides on fecal microbiota using human flora-associated piglets. *Arch Microbiol* 2010, 192(11): 959-68.

Zhang M., Zhang M., Zhang C., Du H., Wei G., Pang X., Zhou H., Liu B. and **Zhao* L.** Pattern extraction of structural responses of gut microbiota to rotavirus infection via multivariate statistical analysis of clone library data. *FEMS Microbiol Ecol* 2009, 70(2): 21-9.

Li M., Zhou H., Hua W., Wang B., Wang S., Zhao G., Li L., **Zhao L.** and Pang* X. Molecular diversity of *Bacteroides* spp. in human fecal microbiota as determined by group-specific 16S rRNA gene clone library analysis. *Syst Appl Microbiol* 2009, 32(3): 193-200

Hong X., Zhang* X., Liu B., Mao Y., Liu Y. and **Zhao L.** Structural differentiation of bacterial communities in indole-degrading bioreactors under denitrifying and sulfate-reducing conditions. *Research in Microbiology* 2010, 161(8): 687-93.

Wei H., Shen J., Pang X., Ding D., Zhang Y., Zhang B., Lu H., Wang T., Zhang C., Hua X., Cui L. and **Zhao* L.** Fatal infection in human flora-associated piglets caused by the opportunistic pathogen *Klebsiella pneumoniae* from an apparently healthy human donor. *J Vet Med Sci* 2008, **70**(7): 715-7.

Jia* W., Li H., **Zhao L.** and Nicholson J.K. Gut microbiota: a potential new territory for drug targeting. *Nat Rev Drug Discov* 2008, **7**(2): 123-9. (Review)

Li M., Wang B., Zhang M., Rantalainen M., Wang S., Zhou H., Zhang Y., Shen J., Pang X., Zhang M., Wei H., Chen Y., Lu H., Zuo J., Su M., Qiu Y., Jia W., Xiao C., Smith L.M., Yang S., Holmes E., Tang H., Zhao G., Nicholson J.K., Li L. and **Zhao* L.** Symbiotic gut microbes modulate human metabolic phenotypes. *Proc Natl Acad Sci USA* 2008, **105**(6):2117-22.

Mao Y., Zhang* X., Yan X., Liu B and **Zhao L.** Development of group-specific PCR-DGGE fingerprinting for monitoring structural changes of *Thauera* spp. in an industrial wastewater treatment plant responding to operational perturbations. *J Microbiol Methods* 2008, **75**(2): 231-6.

Mao Y., Bakken L. R., **Zhao L.**, and Frostegard A. Functional robustness and gene pools of a wastewater nitrification reactor: comparison of dispersed and intact biofilms when stressed by low oxygen and low pH. *FEMS Microbiol Ecol* 2008, **66**: 167-80.

Piao Z., Yang L., **Zhao L.**, and Yin S. Actinobacterial community structure in soils receiving long-term organic and inorganic amendments. *Appl Environ Microbiol* 2008, **74**(2): 526-30.

Yang C., Cao G., Li Y., Zhang X., Ren H., Wang X., Feng J., **Zhao L.** and Xu P. A Constructed Alkaline Consortium and Its Dynamics in Treating Alkaline Black Liquor with Very High Pollution Load. *Plos One* 2008, **3**(11): e3777.

Wang H., Zhang X., **Zhao L.** and Xu Y. Analysis and comparison of the bacterial community in fermented grains during the fermentation for two different styles of Chinese liquor. *J Ind Microbiol Biotechnol* 2008, **35**(6): 603-9.

Pang X., Hua X., Yang Q., Ding D., Che C., Cui L., Jia W., Bucheli P. and **Zhao* L.** Inter-species transplantation of gut microbiota from human to pigs. *ISME J* 2007, **1**(2):156-62.

Zhang M., Liu B., Zhang Y., Wei H., Lei Y. and **Zhao* L.** Structural shifts of mucosa-associated lactobacilli and *Clostridium leptum* subgroup in patients with ulcerative colitis. *J Clin Microbiol* 2007, **45**(2): 496-500

Wei G., Lu H., Zhou Z., Xie H., Wang A., Nelson K. and **Zhao* L.** The microbial community in the feces of the giant panda (*Ailuropoda melanoleuca*) as determined by PCR-TGGE profiling and clone library analysis. *Microb Ecol* 2007, **54**(1):194-202

Yan X., Xu Z., Feng X., Liu Y., Liu B, Zhang X., Zhu C. and **Zhao* L.** Cloning of Environmental Genomic Fragments as Physical Markers for monitoring Microbial populations in Coking Wastewater Treatment System. *Microbial Ecology* 2007, **53**(1): 163-72.

Shen J., Zhang B., Wei G., Pang X., Wei H., Li M., Zhang Y., Jia W. and **Zhao* L.** Molecular profiling of the *Clostridium leptum* subgroup in human fecal microflora by PCR-denaturing gradient gel electrophoresis and clone library analysis. *Appl Environ Microbiol* 2006, **72**(8): 5232-8.

Xiang H., Wei G.F., Jia S., Huang J., Miao X.X., Zhou Z., **Zhao L.** and Huang* Y.P. Microbial communities in the larval midgut of laboratory and field populations of cotton bollworm (*Helicoverpa armigera*). *Can J Microbiol* 2006, **52**(11): 1085-92.

Liu B., Zhang F., Feng X., Liu Y., Yan X., Zhang X., Wang L. and **Zhao L.** *Thauera* and *Azoarcus* as Functionally Important Genera in a Denitrifying Quinoline Removal Bioreactor as Revealed by Microbial Community Structure Comparison. *FEMS Microbiology Ecology* 2006, **55** (2): 274-86.

Cao Y., Wang L., Xu K., Kou C., Zhang Y., Wei G., He J., Wang Y. and **Zhao* L.** Information theory-based algorithm for in silico prediction of PCR products with whole genomic sequences as templates. *BMC Bioinformatics* 2005, **26** (6):190.

Pang X., Ding D., Wei G., Zhang M., Wang L. and **Zhao* L.** Molecular profiling of Bacteroides spp. in human feces by PCR-temperature gradient gel electrophoresis. *J Microbiol Methods* 2005, **61**(3): 413-7.

Zhang X., Yan X., Gao P., Wang L., Zhou Z. and **Zhao* L.** Optimized sequence retrieval from single bands of temperature gradient gel electrophoresis profiles of the amplified 16S rDNA fragments from an activated sludge system. *J Microbiol Methods* 2005, **60**(1): 1-11.

Zhao Y., Li W., Zhou Z., Wang L., Pan Y., **Zhao* L.** Dynamics of Microbial Community Structure and Cellulolytic Activity in Agricultural Soil Amended with two Biofertilizers. *European Journal of Soil Biology* 2005, **41**(1-2):21-9.

Zhang X., Gao P., Chao Q., Wang L., Senior E., and **Zhao* L.** Microdiversity of phenol- hydroxylase genes among phenol-degrading isolates of *Alcaligenes* sp. from an activated sludge system. *FEMS Microbiol Lett* 2004, **237**:369-75.

Wei G., Pan L., Du H., Chen J. and **Zhao* L.** ERIC-PCR fingerprinting-based community DNA hybridization to pinpoint genome-specific fragments as molecular markers to identify and track populations common to healthy human guts. *J Microbiol Methods* 2004, **59**(1): 91-108

Bogdanove A. J., Wei Z. M., **Zhao L.** and Beer* S. V. (1996) *Erwinia amylovora* secretes harpin via a type III pathway and contains a homolog of yopN of *Yersinia* spp. *J Bacteriol* **178**(6): 1720-30.

Publications: Book Chapters & Books

Zhao* L., Shen J. Functional Metagenomics and Systems Biology: understanding the human organismal complexity in disease and health. 2011. *In Metagenomics: Current Innovations and Future Trends*, D. Marco, ed. (Horizon Scientific Press) (Book chapter)

Patents:

- 1, Molecular ecological monitoring method for parallel comparison of microbial community structure, CN1390951
- 2, The application and its production method of a Bacillus preparation, CN1103369C
- 3, Method for analyzing microbial community structure by using fluorescent labeling enzyme restricted gene fragment, CN101565750
- 4, Methods for detecting therapeutic effects of anti-cancer drugs by monitoring changes of gut flora (US patent 8097417 B2)
- 5, The method for constructing gnotobiotic animal model of obesity and its application, CN201210280927.6
- 6, Full nutrient composition and its application for balancing intestinal flora structure and improving metabolic syndrome, CN201210489456.X
- 7, Obesity animal model and methods for making and using thereof, US Patent App. 10/130,080
- 8, Methods and compositions for improving gut microbiota population US Patent App. 10/285,984

9, Determination of microorganism operational taxonomic unit and sequence-assisted separation US Patent App. 16/193,768

10, Bifidobacteria as probiotic foundation species of gut microbiota, US Patent App. 15/738,122

Seminars & Lectures

Keynote and Plenary Presentations

- | | |
|-------|--|
| 2019 | Keystone Symposium Microbiome: Therapeutic Implications, Killarney, Ireland, October 6-10, 2019 |
| 2018. | Keystone Symposium Manipulation of the Gut Microbiota for metabolic Health, Banff, Canada, March 4-8, 2018 |
| 2017 | International Union of Microbiological Societies IUMS Congress 2017, July 17-21, 2017, Singapore. Opening Keynote Speaker |
| 2017 | Animal-Microbe Symbioses, Gordon Research Conference Host-Microbe Associations at the Foundation of the Biosphere, June 11-16, 2017. Mount Snow, West Dover, VT, USA. Closing Keynote Speaker |
| 2015 | Targeting Microbiota 2015, October 22, Paris, The gut microbiota & obesity: from correlation to causality. Keynote speaker. |
| 2014 | Symposium on Model Systems to Understand Microbiota-host Interactions, Biophysical Sciences Institute/BBSRC China-UK Partnership meeting, Durham, UK, April 23-24. Gut microbiota and human obesity: from correlation to causality. Keynote speaker. |
| 2014 | Symposium on The Gut, Its Microbes and Health: New Knowledge and Applications in Asia, Orchard Hotel, Singapore, October 8-9. Basic concepts on the gut microbiota's role in human health. Keynote speaker. |
| 2014 | 11 th Nestlé International Nutrition Symposium Nutrition and the Human Gut Microbiome, Nestlé Research Center, Lausanne, October 22-24. Interactions between gut microbiota, host genetics and diet. Invited speaker. |
| 2013 | IBD11 meeting, November 14-16, Prague, Hungary. The perfect microbiome. Keynote speaker. |
| 2013 | 4 th International Human Microbiome Conference, Hangzhou, China, March. Can we follow Koch's postulates for hunting down human obesity bugs in gut microbiota? Plenary talk. |
| 2012 | 21 th Yakult Symposium intestinal Flora Intestinal Microbiota and Ecology –Diet, Nutrition and Environmental Factors, Tokyo, Japan, November 2. Gut microbiota and metabolic diseases-from correlation to causation. Opening keynote speaker. |

- 2012 4th ASM Conference on Beneficial Microbes, San Antonio, Texas, October 22-23. Microbiome-wide association studies for hunting down the obesity bugs. Opening keynote speaker.
- 2012 14th International Symposium for Microbial Ecology, Copenhagen, Denmark, August. Microbiome-wide association studies for hunting down the obesity bugs. Plenary Talk.
- 2012 5th Symposium on Self-Monitoring of Blood Glucose (SMBG) Applications and Beyond, Dublin, Ireland, May 3-5. Good bugs or bad bugs? The role of the gut microbial ecosystem in obesity and diabetes. Keynote speaker.
- 2011 111th annual meeting of American Society for Microbiology, New Orleans, May. Re-engineering of gut microbiota based on traditional Chinese medicinal foods for early prevention of metabolic diseases. Plenary talk.
- 2011 2nd International Human Microbiome Conference, Vancouver, Canada, March. Health assessment and monitoring with gut microbiota as a primary target. Plenary talk.
- 2010 Diabetes Technology Meeting, Bethesda, Maryland, November. Gut microbiota-based biomarker discovery for prevention of metabolic diseases. Plenary talk.

Invited Presentations

- 2017 Joint ICGEB-ICTP-APCTP Workshop on Systems Biology and Molecular Economy of Microbial Communities 3 - 7 July 2017 Trieste, Italy. Invited speaker
- 2017 Nature Conference on Environmental and Human Microbiomes: Drivers of Future Sustainability 12-15 February 2017, Singapore, Invited presentation
- 2016 2016 World Life Science Conference November 1-3, 2016 in Beijing, China. Chair and Keynote speaker
- 2016 The 13th International Symposium on the Genetics of Industrial Microorganisms (GIM2016), 16–20, October 2016 Wuhan, P. R. China, Keynote presentation
- 2016 Advances in Biotechnology for Food and Medical Applications Workshop". 5-7th, October 2016, Sydney, Invited speaker
- 2016 The Cold Spring Harbor Asia conference on Microbiology and the Environment, September 26-30, 2016 Suzhou, China, Invited speaker
- 2016 2016 International Conference of Physiological Sciences 90th Anniversary of

- CAPS——The Logic of Life September 25-28, 2016, Beijing, China, Invited speaker
- 2016 The 6th U.S.-China Health Summit at the Shaanxi Guesthouse Sept. 2-4, 2016. in Xi'an, China, Invited speaker
- 2016 Distinguished lecture series speaker, National Cheng Kung University, Taiwan, July 15, 2016
- 2016 “The Barcelona Debates on the Human Microbiome. From Microbes to Medicines” to be held on June, 30th and July 1st, 2016, in Barcelona, Spain. Invited speaker
- 2016 Frontiers in Human Microbiota Symbiotic Interactions It will be held in Hong Kong, on May 23rd- 25th, 2016. Invited speaker.
- 2016 The 4th Annual meeting of the Asian Organization for Crohn’s and Colitis, Go on to the next step, from Asia to the world, May 20th, 2016, Invited speaker,
- 2016 Integrative physiology: at the crossroad of nutrition, growth, metabolism and microbiota, April 25-30, Fondation des Treilles
- 2016 The 1st International Meeting on Intestinal Diseases in Conjunction with the Annual Congress of KASID (IMKASID 2016) to be held in Seoul, Korea from April 15-16, 2016. Invited speaker
- 2016 CIFAR Humans & the Microbiome Program Meeting Musée du quai Branly (37 Quai Branly, 75007 Paris) Paris, France, April 10-13, 2016, Invited speaker
- 2016 Better Foods for Better Health Microbiota Health: The challenge of a promising approach to be held from April 6-8th 2016 at “Les Pensières” Conference Center in Veyrier du Lac, France, Invited speaker
- 2016 Gut microbiota in health and disease –from concept to evidence Date; 17th March 2016, Royal Swedish Academy of Science, Stockholm, Sweden. Invited speaker
- 2016 2nd Microbiome R&D and Business Collaboration Congress: Asia. 29 February-1 March 2016 in Kuala Lumpur, Malaysia. Invited speaker

- 2015 Keystone Symposium on Gut Microbiota Modulation of Host Physiology: The Search for Mechanism (C1), Keystone, Colorado, USA, March, 1-6, 2015. Dysbiosis of Gut Microbiota as a Checkpoint for Obesity Development. Invited speaker.
- 2015 International Digestive Disease Forum 2015, Hong Kong, June 5-7, Microbiota in Digestive Health. Invited speaker.
- 2015 EMBL Conference: The Human Microbiome, Heidelberg, Germany, June 10-12, 2015. Gut microbiota-targeted alleviation of genetic obesity. Invited speaker.
- 2015 Gordon Research Conferences-Environmental Microbiology, Mount Holyoke College, July 12-17, 2015. Interactions between gut microbiome and host during diabetes development. Invited Speaker.
- 2015 Human Nutrition, Environment and Health (T1), Beijing, October 14-16, 2015 Dietary Modulation of Gut Microbiota for Obesity Management: From Association to Causation to Translation. Invited Speaker.
- 2015 IBD: East Meets West, Shenzhen, September 11-12, 2015. Microbiota and metabolic health. Invited speaker.
- 2015 International Society for Nutraceuticals and Functional Foods (ISNFF), Wuxi, China, September 20-23, 2015. Modulation of gut microbiome to improve human metabolic health. Invited speaker.
- 2015 Keystone symposium Human Nutrition, Environment and Health (T1), Beijing, October 14-16, 2015. Dietary Modulation of Gut Microbiota for Obesity Management: From Association to Causation to Translation. Invited speaker.
- 2015 6th International Conference on Food Factors (ICoFF 2015), Seoul, November 22-25, 2015. Interactions between nutrition and gut microbiome contribute to human metabolic phenome. Invited speaker.
- 2014 Symposium on The Gut, Its Microbes and Health: New Knowledge and Applications in Asia, Orchard Hotel, Singapore, October 8-9, 2014. Gut microbiota in the development of metabolic diseases. Invited speaker.

- 2014 9th Metabolic Syndrome, Type 2 Diabetes and Atherosclerosis Congress, Kyoto, Japan, September 12-14, 2014. The role of gut microbiota in metabolic diseases-a top-down systems approach. Invited speaker.
- 2014 Keystone Symposium on Exploiting and Understanding Chemical Biotransformations in the Human Microbiome (D1), Big Sky Resort, Big Sky, Montana, April 1-6. 2014. Can We Follow Koch's Postulates for Hunting Down Human Obesity Bugs in Gut Microbiota? Invited speaker.
- 2013 21st Annual Faculty of Medicine Symposium, The Faculty of Medicine, University of Calgary, Calgary, Canada, May 10, 2013. Characterizing the causative role of gut microbiota in human metabolic diseases. Invited Speaker.
- 2011 The 6th International Yakult Symposium on The Gut and Its Role in Health Maintenance, Arcotel Wimberger, Vienna, Austria, May 26th-27th, 2011. Eco-systems biology of gut microbiota for understanding health maintenance. Invited speaker.
- 2010 Symposium on Better Foods for Human Health: Challenges & Solutions (Interfacing Science, Regulation and Industry) Organized by Fondation Mérieux, Veyrier du Lac - France, September 7-9, 2010. Dietary Modulation of Gut Microbiota for Preventive Management of the Metabolic Syndrome. Invited speaker.

Major Research Grants-PI (Current)

Grant title (Grant ID) [Funding Agency Grant Amount]

New Jersey Institute for Food, Nutrition and Health Seed Grant. (PI Lam/Policastro/Zhao)
10/1/2019-9/30/2022

Targeting the foundation guild of gut microbiota for remission of type 2 diabetes

Co-PI

Major Research Grants-PI (Previous)

Grant title (Grant ID) [Funding Agency ¥Grant Amount]

- 2015-2017 Dietary intervention of dysbiotic gut microbiota-induced metabolic syndrome (renewed from 12H100000023) [Perfect China Co. ¥30000k]
- 2014-2018 Ecological interactions between diet and gut microbiota in development of metabolic syndrome (31330005) [National Science Foundation of China ¥3010k]
- 2012-2015 Dietary intervention of dysbiotic gut microbiota-induced metabolic syndrome (12H100000023) [Perfect China Co. ¥30000k]

2012-2015	Translational medicine of zheng-based patient stratification in traditional Chinese medicine (2012ZX10005001) [Ministry of Science and Technology of China ¥120k]
2011-2015	International human microbiome standards (H1009952) [EU IHMS 7 th Framework 60027Euro]
2009-2010	Metagenomics of chronic diseases in Xinjiang autonomous region [Xinjiang Medical University ¥530k]
2010-2012	Probiotic bacteria in inflammation-related metabolic syndrome in mice model [Danon ¥150k]
2012-2013	454 pyrosequencing-based analysis of gut microbiota samples [East China Hospital ¥10k]
2009-2010	Systems understanding of Zheng-based patient stratification in liver viral infection (2009ZX10004-601) [Ministry of Science and Technology of China ¥157.5k]
2009-2011	Dietary impact on gut microbiota and metabolic health in Chinese populations (09XD1402600) [Shanghai Commission of Science and Technology ¥40k]
2009-2010	Colon irrigation with Chinese herbal medicine for inflammatory bowel diseases [Nanjing Hospital of Traditional Chinese Medicine ¥30k]
2009-2010	In vitro fermentation evaluation of functional ingredients on modulating microbiota [Coco-Cola Co ¥1020k]
2008	Metagenomics of giant panda gut microbiota [Chengdu Giant Panda Reserve Base ¥500k]
2008-2011	Structural dynamics and functional dissection of gut microbiota-the diabetes model (30730005) [National Science Foundation of China ¥1650k]
2007—2009	Impact of variations in diet and gut microbiota on human metabolic health (75407001) [Shanghai Commission of Science and Technology ¥1800k]
2007-2009	Impact of Western diet on metabolic health of Chinese people (2007DFC30450) [Ministry of Science and Technology of China ¥2200k]
2007-2010	Internationalization of traditional Chinese medicine via systems biology (2006BAI11B08) [Ministry of Science and Technology of China ¥1100k]
2006-2008	Human flora-associated minipigs as animal model for functional food research [Nestle Company ¥700k]
2006-2007	Metabolomics and metagenomics of human oral microbiota [Liangmianzhen Toothpaste Co. ¥150k]
2006-2007	Metagenomics of oral microbiota in health and disease [P&G Co. ¥150k]
2005-2007	Metabolomics and metagenomics of major cancers in Shanghai (05D)14009) [Shanghai Commission of Science and Technology ¥1000k]

Major Research Grants-co-I (Current)

Grant title (Grant ID) [Funding Agency Grant Amount]

National Institutes of Health (R01AT010242; PI Roopchand) 9/24/2018-8/1/2022
Proanthocyanidin metabolites produced by commensal gut microbes may promote metabolic resilience
Role: Co-Investigator

National Multiple Sclerosis Society (RG-1901-33077; PI Ito) 4/1/2019 – 3/31/2022
Gut dysbiosis-mediated central nervous system (CNS) autoimmunity
Role: Co-Investigator

Rutgers University Busch Biomedical Grant Program. (PI Lam) 9/1/2019-8/31/2021
Characterizing a foundation guild of fiber-utilizing bacteria in the human gut microbiota
Role: Co-Investigator

Major Research Grants-co-PI (Previous)

Grant title (Grant ID) [Funding Agency ¥Grant Amount]

2015-2017 Alleviation of inflammation and calorie restriction-induced modulation of gut microbiota (81401141) [National Science Foundation of China ¥250k]
2014 Mechanistic study on anti-ageing effects of calorie restriction-induced modulation of gut microbiota [Shanghai Jiao Tong University ¥100k]
2012-2014 Catch-up growth of low-birth weight infants on gut microbiota and development of metabolic syndrome (81100632) [National Science Foundation of China ¥230k]
2012 Modulation of gut microbiota by rye-based food products [Shanxi Yuncheng College ¥30k]
2012-2013 The role of gut microbiota in Children's inflammatory bowel diseases (YG2011MS61) [Shanghai Jiao Tong University ¥30k]
2010-2012 Metagenomics of oral microbiota in patients with periodontitis [Shanghai Jiao Tong University ¥80k]
2013-2014 Data-mining of 454 pyrosequencing datasets of healthy Chinese populations [Inner Mongolia Agricultural University ¥100k]
2009-2011 Case-control studies of gut microbiota of diabetes patients (30800155) [National Science Foundation of China ¥190k]
2009-2011 Multi-omics methods for data-mining in newly diagnosed diabetes (20875061) [National Science Foundation of China ¥300k]
2009-2011 Data acquisition and mining for metagenomics based on next generation sequencing (2009AA02Z310) [Ministry of Science and Technology of China ¥1610k]
2008-2009 Microarrays for gut microbiota analysis (75407064) [Shanghai Commission of Science

	and Technology ¥150k]
2007-2010	Computational integration of metagenomics and metabolomics datasets in human metabolic diseases (2008AA02Z315) [Ministry of Science and Technology of China ¥2680k]
2007-2011	Structural diversity and functional genes of human gut microbiota (2007CB513002) Ministry of Science and Technology of China ¥1830k]
2007-2010	Development of monitoring technology for mixed culture fermentation (2007AA02Z203) [Ministry of Science and Technology of China ¥400k]

Mentorship (Ph.D. Students)

Ph.D. graduates: name, dissertation title, current position

2015	Zhengsheng Xue , Diversity profile and phylo-functional core of the mammalian gut microbiota with healthy human and giant panda as models, Product manager, Shanghai Personal Biotechnology Co., Ltd., China
2014	Wu Li , Construction and immunogenicity assessment of a recombinant adenovirus co-expressing immunodominant antigens of CFP10, ESAT6, Ag85A and Ag85B of Mycobacterium tuberculosis, Associated Professor, School of Life Science, Ningxia University, China Jingjing Wang , Studies on effects of various nutrition factors on gut microbiota changes and metabolic syndrome in mouse model, Research Scientist, Shanghai general hospital, China
2013	Na Fei , <i>The role of Enterobacter cloacea in the development of human metabolic syndrome</i> , Postdoctoral Researcher, National Institute for Research in Agriculture (INRA), France. Xu Zhang , <i>Modulating effects of berberine on gut microbiota in rats and their role in berberine mediated prevention and treatment of high fat diet induced metabolic diseases</i> , Postdoctoral Fellow, Ottawa Institute of Systems Biology, University of Ottawa, Canada. Shuiming Xiao , <i>A gut microbiota-targeted dietary intervention for metabolic syndrome: clinical trial and physiological ecological mechanisms</i> , Staff Scientist, Institute of Chinese Medicines, Chinese Academy of Traditional Chinese Medicine, Beijing, China.
2012	Tingting Wang , <i>The interactions between structural shifts of gut microbiota and development of colonrectal cancer</i> , Assistant Professor, Qingdao Institute of Biomass Energy and Bioprocess Technology (QIBEBT), Chinese Academy of Sciences, Qing Dao, China.

- 2011 **Chenhong Zhang**, *Gut microbiota and development of the metabolic syndrome in mouse model*, Assistant Professor, School of Life Sciences and Biotechnology, Shanghai Jiao Tong University, Shanghai, China.
- Jing Zhu**, *Studies on interactions between enterotoxigenic Escherichia coli intestinal epithelial cells and lactic acid bacteria*, Wiley Publishing Shanghai Office, Shanghai, China.
- Hongyan Ren**, *Molecular microbial ecology study of oil reservoir and simulated oil degrading system*, Senior Scientist, Shanghai Major Biotechnology Co., Shanghai, China.
- 2009 **Yuejian Mao**, *Structural and Functional Analysis of Thauera Genus in Wastewater Treatment Plants*, Scientist & Culture Development Group Manager, DuPont Nutrition & Health, Shanghai, China.
- Min Li**, *Co-variation analysis of human gut microbial structure and host global metabolism*, postdoctoral scientist, Johnson & Johnson R&D, U.S.A.
- 2008 **Hua Wei**, *Studies of the structural changes of gut microbiota in response to various perturbations*, Assistant Professor, Medical School of Ningbo University, Ningbo, China.
- Jian Shen**, *Modulating effects of Fructo-oligosaccharides on Gut Microbiota and Host metabolism in Human Flora-Associated Piglet Model*, Associate Professor, Shanghai Center for Systems Biomedicine, Shanghai Jiao Tong University, Shanghai, China.
- 2007 **Meiling Zhang**, *Understanding the relationship between intestinal bacterial community and two kinds of gut diseases*, Associate Professor, School of Life Science, East China Normal University, Shanghai, China.
- Xing Yan**, *System trajectory analysis for spatial community succession and its application in A²/O fixed biofilm process for coking wastewater treatment*, Staff Scientist, Institute of Plant Physiology and Ecology, Chinese Academy of Sciences, Shanghai, China.
- 2006 **Binbin Liu**, *Identification of dominant functional members in efficient wastewater treatment bioreactors*, Research Scientist, Norwegian University of Life Sciences, Ås, Norway.
- 2005 **Xiaoyan Pang**, *Establishment and molecular ecology study of human flora-associated experimental piglet*, Associate Professor at School of Life Sciences and Biotechnology, Shanghai Jiao Tong University, Shanghai, China.
- Guifang Wei**, *Molecular approach based analysis of microbial community structure in gastrointestinal tracts*, Senior Scientist, Shanghai R&D Center of Coco-Cola Co., Shanghai, China.
- Xueli Zhang**, *Microbial ecology of bioreactors for coking wastewater treatment*,

Professor, Tianjin Institute of Industrial Biotechnology, Chinese Academy of Sciences, Tianjin, China.

Mentorship (M.S. Students)

M.S. graduates: name, thesis title

- 2015 **Huan Wu**, *Microdiversity of Lactic Acid Bacteria Enriched by Dietary Intervention in the Gut of a Child with Prader-Willi Syndrome.*
- 2014 **Xinxin He**, *In vitro modulating effects of bitter melon preparations on structure and metabolism of human gut microbiota.*
- 2013 **Huang Tang**, *Association between gut microbiota and metabolic syndrome induced by imbalanced early-life nutrition.*
- 2012 **Lifeng Sun**, *The establishment and application of methods for toxicity detection of human fecal water.*
- 2011 **Jiaqi Liu**, *Understanding the structural shifts of gut microbiota in patients with chronic viral hepatitis B by 454 pyrosequencing.*
- 2010 **Huihui Zhong**, *Microbial community structure and function in a lab-scale denitrifying quinoline-degrading bioreactor.*
- 2009 **Siqing Yue**, *Study on diversity of aromatic compound degrading bacteria and isolation.*
- Jun Yuan**, *Case-control study of the intestinal bacterial community structure between new onset diabetic and healthy people.*
- 2008 **Xuan Hong**, *Study on heterocyclic aromatic hydrocarbon degrading bacteria and method of cloning degrading genes.*
- Liguo Sun**, *Analysis of the Diversity of Lactic Acid Bacteria (LAB) in ICR Mouse Intestine and Preliminary Study of the Relationship Between the LAB Composition with Diabetes.*
- 2007 **Qinli Zhao**, *Structural shifts in gut microbiota of rats in response to bile duct ligation.*
- Jing Zhang**, *Study on molecular ecology of microbe related with cellulose decomposition in straw-amended soil.*
- Lingjun Xu**, *Intestinal Microflora Analysis for Type 1 Diabetic Murine.*
- 2006 **Yulei Zhang**, *Quantitative analysis of the biology sequences based on their frequency profiles.*
- Wu Li**, *The use of DNA fingerprinting methods and clone library analysis in the quality control of microecological preparation.*
- 2005 **Shunzi Xiong**, *The isolation and analysis of the phenol-degrading bacteria in the*

- coking wastewater and pilot study of the phenol hydroxylase gene.*
- Wei Hong**, *Molecular analysis of microbial community in human dental plaque and evaluation the effect of prebiotic on intestinal Bifidobacterium by Quantitative PCR.*
- Haifeng Lu**, *Community DNA Fingerprinting Analysis for Intestinal Microflora of Giant Panda and Effect Evaluation of Prebiotic on Bacteroides population in Piglet gut flora by Real-time PCR.*
- 2004 **Yongyan Sun**, *Research on detection of beer-spoilage microorganisms using RAPD-PCR.*
- Quan Shen**, *Construction of biocontrol agent constitutively expressing happin via type II secretion pathway.*
- Liang Li**, *Comparative analysis of microbial community structure in coking wastewater.*
- 2003 **Meiling Zhang**, *Molecular analysis of the intestinal microflora in rotavirus-infected children.*
- Jinyan Liu**, *The microbiology study of intestinal microflora of middle-distance racers.*
- 2002 **Linghua Wang**, *Study of molecular ecological methods for monitoring novel phenol degrading bacteria Arthrobacter nicotianae P1-7 and Klebsiella sp.P8-14.*
- Guifang Wei**, *Identification and secretion of harpin from Erwinia amylovora by the type III secretion machines of Erwinia carotovora.*
- Lei Sun**, *Study on molecular ecology of gut microbiota of piglet.*
- Li Pan**, *Study on molecular ecology of gut microbiota in diarrhea children.*
- Binbin Liu**, *Dynamic monitoring of oxidizing Bacteria community in coking wastewater using amoA gene as the molecular marker.*

Teaching

Know Your Microbiome, specialty topic course, established and taught the course in 2018, Co-taught this course in 2019 at Rutgers University.
Gave a few guest lectures in various other courses.

2009-2012: Vice dean for teaching, School of Life Sciences and Biotechnology, SJTU.

Courses taught:

Undergraduate courses:

1. Introductory Microbiology (lectures given in English, Brock Biology of Microorganisms as textbook)

2002-03, Fall semester, 2.5 credits, 121 students
 2003-04, Fall semester, 2.5 credits, 110 students
 2004-05, Fall semester, 2.5 credits, 96 students
 2005-06, Spring semester, 2.5 credits, 78 students
 2006-07, Spring semester, 2.5 credits, 68 students
 2007-08, Fall semester, 2.5 credits, 62 students
 2008-09, Fall semester, 2.5 credits, 61 students
 2009-10, Fall semester, 2.5 credits, 59 students
 2010-11, Fall semester, 2.5 credits, 59 students
 2011-12, Spring semester, 2.5 credits, 86 students
 2012-13, Spring semester, 2.5 credits, 58 students
 2013-14, Spring semester, 2.5 credits, 73 students
 2014-15, Spring semester, 2.5 credits, 39 students

2. Computational biology and human health

2010-11, Fall semester, 1 credit, 10 students
 2011-12, Fall semester, 1 credit, 10 students

3. Nutrition, microbiota and health

2012-13, Fall semester, 1 credit, 10 students
 2013-14, Fall semester, 1 credit, 30 students
 2014-15, Fall semester, 1 credit, 30 students
 2015-16, Fall semester, 1 credit, 30 students

4. Drugs and bacteria (lectures given in English)

2014-15, Fall semester, 1 credit, 4 students

Graduate course:

2002-2015, Molecular Microbial Ecology and Ecogenomics, , taught in every Spring semester.

Professional Activities

Editorial Board Memberships & Service as Reviewer

2013-Pres. Senior Editor, The ISME Journal.
 2013-Pres. Member, Editorial Board, FMES Microbiology Ecology.
 2014-Pres. Member, Editorial Board, Scientific Report.
 2014-Pres. Senior Editor, mSystems, American Society for Microbiology.

Ad Hoc Reviewer for the following journals: Nature, Science, Nature Communications, the ISME Journal, FEMS Microbiology Ecology, Applied and Environmental Microbiology, Microbial Ecology.

Advisory Boards

2015-2017, Member of the Nutritional Advisory Board of Barilla Co.

2012-2017, Scientific advisor of the Perfect Co. (Non-paid)

Society Service

Vice chair, Division of Environmental Microbiology, Chinese Society for Microbiology, 2010-Pres.

Vice Chair, Chinese Society for Lactic Acid Bacteria, 2013-Pres.

Chinese Ambassador for International Society for Microbial Ecology (ISME), 2002-2004

Member of International Board, ISME, 2006-2012

Nominated as one of the two candidates for vice president of ISME of the 2016 election

Member of Chinese Society for Microbiology

Member of American Society for Microbiology

Member of ISME