Curriculum Vitae

Liping Zhao

Eveleigh-Fenton Chair of Applied Microbiology,
Department of Biochemistry and Microbiology,
School of Environmental and Biological Sciences,
Rutgers, The State University of New Jersey,
New Brunswick, NJ 08540, USA

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. *Ad-hoc* 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-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

2015-Pres. Associate editor, Microbiome

Honors & Awards

Outstanding Scientist of Shanghai, 2009.

SJTU Best Teacher of the Year, 2011.

Elected Fellow, American Academy of Microbiology, 2014.

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)

1. Chen, T., W. Long, C. Zhang, S. Liu, **L. Zhao***, and B. R. Hamaker*. 2017. 'Fiber-utilizing capacity varies in Prevotella- versus Bacteroides-dominated gut microbiota', Sci Rep, 7: 2594.

2. 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 Metab, 25: 522-34.

3. 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', Sci China Life Sci.

4. Liu, R., C. Zhang, Y. Shi, F. Zhang, L. Li, X. Wang, Y. Ling, H. Fu, W. Dong, J. Shen, A. Reeves, A. S. Greenberg, **L. Zhao**, Y. Peng, and X. Ding. 2017. 'Dysbiosis of Gut Microbiota Associated with Clinical Parameters in Polycystic Ovary

Syndrome', Front Microbiol, 8: 324.

5. Wang, J. J., J. Wang, X. Y. Pang, **L. P. 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', Sci Rep, 6: 36137.

6. Wang, J., H. Tang, X. Wang, X. Zhang, C. Zhang, M. Zhang, Y. Zhao, **L. Zhao**, and J. Shen. 2016. 'The structural alteration of gut microbiota in low-birth-weight mice undergoing accelerated postnatal growth', Sci Rep, 6: 27780.

7. 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', Front Microbiol, 8: 1242.

8. Wu, G., C. Zhang, H. Wu, R. Wang, J. Shen, L. Wang, Y. Zhao, X. Pang, X. Zhang, **L. Zhao,** and M. Zhang. 2017. 'Genomic Microdiversity of Bifidobacterium pseudocatenulatum Underlying Differential Strain-Level Responses to Dietary Carbohydrate Intervention', MBio, 8.

9. 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.

10. 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.

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

12. 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.

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

14. 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.

15. 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.

16. 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.

17. 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.

18. 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.

19. 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.

20. 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.

21. 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.

22. 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.

23. 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.

24. 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.

25. 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.

26. 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.

27. 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.

28. 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.

29. **Zhao* L.** The gut microbiota and obesity: from correlation to causality. ***Nat Rev Microbiol***, **11**(9): 639-647 (Review)

30. 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.

31. 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.

32. 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.

33. 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.

34. 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.

35. 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): 1848-57.

36. 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.

37. **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)

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

39. 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)

40. 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.

41. 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

42. 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

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

44. 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

45. 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.

46. 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.

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

48. 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.

49. 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.

50. 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.

51. 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.

52. 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-specific16S rRNA gene clone library analysis. ***Syst Appl Microbiol*** 2009, **32**(3): 193-200

53. 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.

54. 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.

55. 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)

56. 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.

57. 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.

58. 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.

59. 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.

60. 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.

61. 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.

62. 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.

63. 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

64. 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

65. 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.

66. 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.

55. 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.

67. 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.

68. 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.

69. 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.

70. 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.

71. 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.

72. 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.

73. 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

74. Bogdanove A. J., Wei Z. M., **Zhao L.** and Beer* S. V. 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)

Seminars & Lectures

Keynote and Plenary Presentations

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 11th 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 4th 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 21th 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 5thSymposium 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, Vanvouver, 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, Microbiotia 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, Novenmber 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.

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

Member of the Nutritional Advisory Board of Barilla Co.

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