

## CURRICULUM VITAE

### JIZHONG ZHOU

Presidential Professor, Department of Botany and Microbiology  
Director of the Institute for Environmental Genomics (IEG)  
Editor for Applied and Environmental Microbiology  
University of Oklahoma  
Stephenson Research & Technology Center  
101 David L. Boren Blvd., Norman, OK 73019  
Phone: 405-325-6073 (O)  
Fax: 405-325-3442  
E-mail: [jzhou@ou.edu](mailto:jzhou@ou.edu)  
Web site: <http://ieg.ou.edu>

#### **EDUCATION:**

- |                |           |  |
|----------------|-----------|--|
| BS             | 1978-1981 | <b>Plant Pathology &amp; Entomology</b> , Hunan Agricultural University, Changsha, China   |
| MS             | 1982-1984 | <b>Mathematical Ecology</b> , Hunan Agricultural University, Changsha, China,<br>Advisor: Prof. Changmin Chen<br>Thesis: Mathematical modeling and simulation of predator-prey systems in agro-ecosystems  |
| Ph.D candidate | 1986-1988 | <b>System Ecology</b> , Eco-Environmental Research Center, Chinese Academy of Sciences, Beijing China<br>Advisor: Prof. Shijun Ma (Academician)<br>Thesis: Ecological engineering, simulation and prediction of agroecosystem (Note, not obtaining Ph.D degree for being able to come to US) |
| Ph.D           | 1990-1993 | <b>Molecular Biology</b> , Washington State University, Pullman, WA<br>Advisor: Prof Andris Kleinhofs<br>Thesis: Molecular evolution of plant nitrate reductases   |

#### **PROFESSIONAL EXPERIENCE**

- |              |  |
|--------------|--|
| 2005-present | Director of the Institute for Environmental Genomics (IEG), University of Oklahoma, Norman, OK   |
| 2005-present | <u>Presidential Professor</u> , Department of Botany and Microbiology, University of Oklahoma, Norman, OK  |
| 2006-present | <u>Adjunct Senior Scientist</u> , Lawrence Berkeley National Laboratory (LBL)  |
| 2011-present | <u>Director for Environmental Technology for ENIGMA</u> (Ecosystems and Networks Integrated with Genes and Molecular Assemblies), a large scale Genomics: GTL Foundational Science Program at Lawrence Berkeley National Laboratory. |

2010-present Adjunct Professor, Tsinghua University, Beijing, China  
2003-2005 Distinguished R&D Staff Scientist, Environmental Sciences Division, ORNL  
2004-2005 Member of Science Council, Biological and Environmental Sciences Directorate, ORNL  
2002-2004 Science Leader for Environmental Genomics Program, Biological and Environmental Sciences Directorate, ORNL  
2001-2002 Senior Staff Scientist, Environmental Sciences Division, ORNL  
2000-2001 Science Team Leader for Microbial Genomics and Ecology, Environmental Sciences Division, ORNL  
1997-2000 Staff Scientist, Environmental Sciences Division, ORNL  
1996-1997 Alexander Hollaender Distinguished Postdoctoral Fellow, Environmental Sciences Division, ORNL  
1993-1995 Research Associate, Laboratory of Dr. James M. Tiedje, NSF Center for Microbial Ecology, Michigan State University, East Lansing, MI. Bioreactor Subgroup Leader of the Community Analysis Group  
1990-1993 Graduate Research and Teaching Assistant, Laboratory of Dr. Andris Kleinhofs, Department of Genetics and Cell Biology, Washington State University, Pullman, WA  
1989 Graduate Research and Teaching Assistant, Laboratory of Dr. Alan Berryman, Department of Entomology, Washington State University, Pullman, WA  
1988 Visiting Scientist, Department of Biological Sciences, University of Calgary, Calgary, Alberta, Canada  
1986-1988 Research Associate, Eco-Environmental Research Center, Chinese Academy of Sciences, Beijing, China  
1985-1986 Lecturer in the Department of Plant Pathology and Entomology, Hunan Agricultural University, Changsha, China  
1982-1984 Teaching and Research Assistant, Department of Plant Pathology and Entomology, Hunan Agricultural University, Changsha, China

## TEACHING EXPERIENCE

2005-present Advanced topics on environmental genomics  
2004 A joint course on molecular techniques for microbial ecology for graduate and senior undergraduate students. University of Puerto Rico, Mayaguez, Puerto Rico.  
1993-1995 Trained 8 graduate and undergraduate students on molecular techniques, computer sequence analyses and related software, Michigan State University  
1992 General Genetics for senior undergraduate students, Laboratory Teaching Assistant, Washington State University  
1985-1986 Lecturer, Hunan Agricultural University, Changsha, China  
Courses taught:  
Mathematical Ecology for graduate students  
General Ecology for senior undergraduate students  
Agricultural Pathology and Entomology for junior undergraduate students  
1982-1984 General Biology, Laboratory Teaching Assistant, Hunan Agricultural University  
General Plant Pathology, Laboratory Teaching Assistant

**MAJOR PROFESSIONAL SERVICES**

- 2009 Member of the review Panel, DOE Early Career Research Program on Genomics and Systems Microbiology
- 2009 Member of Advisory Committee, Max-Planck Institute Partner (MPI) Group Between Germany and China
- 2009-present Member, Nominations Committee for the Promega Biotechnology Award, American Academy of Microbiology, American Society of Microbiology
- 2008-present Member of Steering Committee, International Soil Metagenomics Consortium.
- 2008 Member of the review panel for NIEHS program on Development and Application of Nanotechnology-based Tools to Understand Mechanisms of Bioremediation.
- 2008 Member of the review panel for NSF-USDA Microbial Observatories program.
- 2007-present Honorary Director for the Committee of Microbial Ecology, Chinese Society of Ecology
- 2007 Honorary Chair for the 3<sup>rd</sup> Annual Meeting of Microbial Ecology, Chinese Society of Ecology
- 2007-present Member of Academic Committee, Qingdao Institute of Biomass Energy and Bioprocessing Technology (QIBEBT), Chinese Academy of Sciences, Qiangdao, Shandong, China
- 2007-2009 Member of Advisory Committee for the Norman Campus Vice President for Research (AC/VPR), University of Oklahoma
- 2007-present Member of the Oklahoma Bioenergy Center Board appointed by Oklahoma Governor
- 2007 Advisory member of preparing the roadmap for Oklahoma Bioenergy Center
- 2007 Member of VPR Task Forces on Centers, Institutes and Consortia, University of Oklahoma
- 2007 Member of the review panel for Genomics:GTL, New Genomic Strategies and Technologies for Studying Complex Microbial Communities and Validating Genomic Annotations
- 2006-present Member of ASM International Committee - Task Force on China
- 2006-2007 Member of National Key Microbial Program Panel, Chinese National Science Foundation
- 2005 Reviewer for 2005 State Natural Science Award of the People's Republic of China (The highest achievement award for science and technology in China)
- 2004-present US Ambassador for International Society of Microbial Ecology.
- 2004 Member of the review panel for DOE Joint Genome Institute Community Sequencing (CSP) program.
- 2003 Member of the review panel for NSF the Frontiers in Biological Research (FIBR) program.
- 2003-present Specially Invited Oversea Reviewer of Scientific Programs of National Natural Science Foundation of China.
- 2001-present Member of Scientific Advisory Committee on Molecular Environmental studies, Scientific Committee on Problems of the Environment (SCOPE), International Council of Scientific Union (ICSU)
- 2001 Panel member for preparing the roadmap for Genomes to Life program, US

- Department of Energy, in charge of writing Goal 3 on community genomics.
- 2001 Member of the Advisory Committee for Functional Genomics Initiative, Netherlands Institute of Ecology, The Netherlands
- 2000-present Associate Director for the Committee of Microbial Ecology, Chinese Society of Ecology
- 2000-2003 Member of Academic Advisory Committee, Northeastern Forestry University, Harbin, P. R. China
- 1998 Member of the review panel for DOE NABIR Biotransformation and Biodegradation Element
- 1994-1995 Member of seminar committee, NSF Center for Microbial Ecology, Michigan State University
- 1990-present Scientific Advisory Committee for the Department of System Ecology, Eco-Environmental Research Center, Chinese Academy of Sciences
- 1986-1988 Member of Scientific Advisory Committee of the Population Control Program in the Center for National Agricultural Research and Development, State Council, PRC
- 1986-1991 Director of the Ecological Association of Chinese Young Scientists

### **JOURNAL EDITOR**

- 2009-present Editor for mBio®, A new ASM open source integrated Journal.
- 2003-present The American Society for Microbiology journal, Applied and Environmental Microbiology (Gold standard journal in this field).
- 2010-present Associate Editor for Frontiers in Bioremediation
- 2011 Editor, Analytical Biotech 2012 Section in Current Opinion in Biotechnology (COBIOT)
- 2008 Guest Associate Editor for PLoS Computational Biology

### **MEMBER OF EDITORIAL BOARD OF JOURNALS**

- 2008-present Environmental Microbiology and Environmental Microbiology Reports
- 2007-present Chinese Journal of Biotechnology
- 2006-present The ISME Journal
- 2001-2003 The American Society for Microbiology journal, Applied and Environmental Microbiology.
- 2001-2007 Omics: A Journal of Integrative Biology.
- 2001-present Acta Ecologia Sinica.

### **PAPER REVIEW**

- 2011 Genome Biology
- 2009 Global Change Biology
- 2009 Cold Spring Harbor Protocols
- 2009 Applied Energy
- 2008 BMC Genomics
- 2008 BMC Microbiology

2006-present	The ISME Journal
2006-present	Bioinformatics
2006-present	Environmental Microbiology
2001-present	Reviewer for Applied and Environmental Microbiology
2001-present	Reviewer for the Chinese Society of Ecology journal, Ecology
2001-2007	Reviewer for Omics: A Journal of Integrative Biology
2006-present	BMC Bioinformatics
2005	Ad hoc reviewer for Journal of Virological Methods
2005-present	Ad hoc reviewer for FEMS Microbiology Ecology
2005	Ad hoc reviewer for Environmental Monitoring and Assessment
2005	Ad hoc reviewer for Trends in Biotechnology
2004	Ad hoc reviewer for Anaerobe
2004	Ad hoc reviewer for Water Research
2004-2005	Ad hoc reviewer for Analytical Chemistry
2004	Ad hoc reviewer for Soil Biology & Biochemistry
2004	Ad hoc reviewer for Pedosphere
2004	Ad hoc reviewer for Trends in Biotechnology
2004-present	Ad hoc reviewer for Environmental Sciences & Technology
2003-present	Ad hoc reviewer for Biotechniques
2003	Ad hoc reviewer for Plant and Soil
2003	Ad hoc reviewer for Frontiers in Ecology and the Environment
2002	Ad hoc reviewer for Cell Biology International
2002-present	Ad hoc reviewer for Proceedings of the National Academy of Sciences USA
2002-2003	Ad hoc reviewer for Journal of Clinical Microbiology
2002-present	Ad hoc reviewer for Journal of Bacteriology
2001	Ad hoc reviewer for Soil Science Society of America Journal
2001	Ad hoc reviewer for Physiological Genomics
2001	Ad hoc reviewer for Molecular and Cellular Probes
2001-present	Ad hoc reviewer for FEMS Microbiology Letter
2000	Ad hoc reviewer for Biogeochemistry
1998	Ad hoc reviewer for Ecological Engineering

### **AD HOC PROPOSAL REVIEW**

2010	NSF Ecosystem Program
2010	Leaders Opportunity Fund, Canada Foundation for Innovation
2010	Natural Environment Research Council
2009	Member of the Panel for Germany-China program on microbial ecology
2009	Swiss National Science Foundation
2009	Netherlands Organisation for Scientific Research
2009	United States-Israel Binational Science Foundation
2008	Geobiology & Low Temperature Geochemistry Program, National Science Foundation
2008	Instrumentation and Facilities Program, National Science Foundation
2008	Israel Science Foundation (ISF)
2006-2008	Chinese National Science Foundation
2008	NSF-USDA Microbial Observatories Program
2007	Energy Biosciences Institute, University of California, Berkeley

2007 Cellular Systems, National Science Foundation  
 2007 Ecosystem Science Program, National Science Foundation  
 2007 Genomics:GTL program, Department of Energy  
 2007 Environmental Genomics Program, National Science Foundation  
 2007 Frontier in Biological Research, National Science Foundation  
 2007 North Carolina Biotechnology Center  
 2006 The Chilean Research Fund Council  
 2006 The Environment and Water Industry Development Council, Singapore  
 2006 National Research Foundation Board of Singapore  
 2006 Swiss National Science Foundation  
 2005 Austrian Science Fund  
 2005 DOE Biological Investigation – Ocean Margin Program (BI-OMP)  
 2005 NSF Genes and Genome Systems program  
 2005-present Natural Environment Research Council (NERC), United Kingdom  
 2005 Netherlands Organization for Scientific Research  
 2005 Natural Sciences and Engineering Research Council (NSERC) of Canada  
 2004 NSF Microbial Interactions and Processes program  
 2004-present NSF Faculty Early Career Development (CAREER) Program  
 2004 NSF Ocean Sciences Program  
 2004 European Science Foundation  
 2004 NSF Ecology Program  
 2004 Singapore Science & Engineering Research Council  
 2004 NSF Biogeosciences Program  
 2004 Competitive Grant, Utah State University  
 2003-2004 Genome Canada program  
 2003 Idaho Research Center Grant Program  
 2002-2004 NSF Biocomplexity in the Environment (BE): Integrated Research and Education  
 in Environmental Systems  
 2003 US Army Research Office, DOD Young Investigator Program  
 2003 Reviewer for Tamasek Yong Investigator Award, National University of  
 Singapore, Singapore  
 2002-present NSF Microbial Observatories Program  
 2002 NSF Integrated Research Challenges in Environmental Biology Program  
 2002 NSF program for International Opportunities for Scientists and Engineers  
 2002-2005 DOE Small Business Innovation Research and Small Business Technology  
 Transfer Programs  
 2002 National Oceanographic Partnership Program  
 2001-2003 US Department of Energy EPSCoR Program  
 1999 Reviewer for award for Natural Environment Research Council, United Kingdom  
 1995 Reviewer for grants in NSF Young Scientist Program

### **CONFERENCE AND SYMPOSIUM ORGANIZATION**

2010 Member of the Advisory Committee for The 18<sup>th</sup> International Conference on  
 Microbial Genomes, September 12-16, 2010, Lake Arrowhead, CA  
 2010 Member of the organizing committee for the Roundtable Session on  
 TerroGenome at The 13<sup>th</sup> International Symposium on Microbial Ecology,

- Seattle, WA, August 22-27, 2010.
- 2010 Organizer and Chair for the Roundtable Session on High Throughput MetaGenomic Technologies for Complex Microbial Community Analysis at The 13<sup>th</sup> International Symposium on Microbial Ecology, Seattle, WA, August 22-27, 2010.,
- 2009 Member of the Advisory Committee for The 17<sup>th</sup> International Conference on Microbial Genomes, October 11-15, 2009, Rocky Gap State Park, MD
- 2009 Chairperson for the Symposium, High Throughput Genomics Technologies for Complex Microbial Community Analysis, The 109<sup>th</sup> General Meeting of American Society for Microbiology, May 17–21, 2009, Philadelphia, PA.
- 2008 Co-organizer for ASM-CSM (Chinese Society of Microbiology) Joint Workshop on Environmental Microbiology and Bioenergy, November 8, 2008, Haikou, China.
- 2008 Member of the Advisory Committee for The 16<sup>th</sup> International Conference on Microbial Genomes, September 14-18, 2008, Lake Arrowhead, CA
- 2008 Chair and Organizer, The 4<sup>th</sup> SCOPE (The Scientific Committee on Problems of the Environment, International Council of Scientific Union) Workshop on Microbial Environmental Genomics, Changsha, P.R. China, September 20-24, 2008.
- 2008 Oklahoma Bioenergy Center Workshop, April 23, 2008, Norman, OK
- 2007 Member of the Advisory Committee for The 15<sup>th</sup> International Conference on Microbial Genomes, September 16–20, 2007, College Park, MA
- 2006 Member of the Advisory Committee for The 14<sup>th</sup> International Conference on Microbial Genomes, September 24–28, 2006, Lake Arrowhead, CA
- 2006 “Application of OMICS to Field Bioremediation: Current Status, Challenges and Future”. The ERSP Breakout Session 2, Environmental Remediation Science Program, Warrenton, VA, April 3, 2006.
- 2005 Member of the Advisory Committee for The 13<sup>th</sup> International Conference on Microbial Genomes, September 11 – 15, 2005, Madison, WI.
- 2004 Chair for the session Symposium on Microbial Heterogeneity / Bioremediation, American Geophysical Union, San Francisco, CA, December 13–17, 2004.
- 2004 International Convener for the session on “Impacts of Microarrays and Bioinformatics on Microbial Ecology”, The 10<sup>th</sup> International Symposium on Microbial Ecology, August 22-27, 2004, Cancun, Mexico.
- 2004 Chair for the session on “Advanced technologies for microbial ecology”, The 10<sup>th</sup> International Symposium on Microbial Ecology, August 22-27, 2004, Cancun, Mexico.
- 2004 Member of the Advisory Committee for The 12<sup>th</sup> International Conference on Small Genomes, September 26–30, 2004, Lake Arrowhead, CA
- 2003-2008 Member of the SCOPE (The Scientific Committee on Problems of the Environment, International Council of Scientific Union) Workshop on Environmental Genomics.
- 2003 Organizer and Chair, The 11<sup>th</sup> International Conference on Microbial Genomes, September 28 – October 2, 2003, Durham, NC.
- 2002 Member of the Advisory Committee for The 10<sup>th</sup> International Conference on Microbial Genomes, September 8–12, 2002, Lake Arrowhead, CA.
- 2001 Organizer and Chair, The 9<sup>th</sup> International Conference on Microbial Genomes,

- October 27–November 1, 2001, Gatlinburg, TN.
- 2001 Organizer for the session on “Application of Microarray Technology to Environmental Studies”, The 9<sup>th</sup> International Symposium on Microbial Ecology, August 26–31, 2001, Amsterdam, The Netherlands.
- 2001 Chairperson for the Symposium, Microarrays and Microfluidics in Microbial Ecology, The 101<sup>st</sup> General Meeting of American Society for Microbiology, May 20–24, 2001, Orlando, FL.
- 2001 Session Chair, Bioinformatics and functional genomics, TIGR/ASM Conference on Microorganisms, January 28–31, 2001, Monterey, CA.
- 2000 Member of the Advisory Committee for The 8<sup>th</sup> International Conference on Small Genomes, September 24–28, 2000, Lake Arrowhead, CA
- 2000 Chair on the session of Bioremediation, The 8<sup>th</sup> International Conference on Small Genomes, September 24–28, 2000, Lake Arrowhead, CA
- 2000 Co-organizer, The 4<sup>th</sup> Conference on Molecular Ecology, July 15–18, 2000, Harbin, P.R. China
- 1999 Organizer and Chair, The 7<sup>th</sup> Conference on Small Genomes, November 13–17, 1999, Washington, DC.
- 1999 Organizer and Chair, DOE NABIR Workshop in Application of Genomic Technology to Bioremediation, December 5–7, 1999, Washington, DC.
- 1999 Co-organizer, The 3<sup>rd</sup> Conference on Molecular Ecology, August 28–31, 1999, Beijing, P.R. China.
- 1999 Chairperson for the Symposium, Recent Advances in Subsurface Microbial Ecology, The 99<sup>th</sup> General Meeting of American Society for Microbiology, Chicago, IL, May 30 – June 3, 1999.
- 1998 Organizer for the Symposium, Key Issues in Microbial Ecology, the VII International Congress of Ecology, July 19–25, 1998, Florence, Italy.
- 1998 Chairperson on the session of microbial community dynamics, the VII International Congress of Ecology, July 19–25, 1998, Florence, Italy.

### **SPECIALLY INVITED WORKSHOP PARTICIPATION**

- 2009 ISME-IWA Colloquium on The Engineering of Microbial Communities, Singapore, January 18-21, 2009.
- 2008 “Matasted”, Workshop on the Complete Metagenome Sequencing of a Reference Soil, Lyon, France, December 13-14, 2008
- 2008 “Curation of Biological Specimens, Physical Samples and Associated Data”. NMNH (National Museum of Natural History)-NSF NEON Workshop, Smithsonian Institution, Washington, DC, October 19-22, 2008.
- 2008 “Integrating NEON with Microbial Biology”, NSF Workshop, Baton Rouge, Louisiana, February 14-16, 2008
- 2007 “Data-Model Assimilation in Ecology: Techniques and Applications”, NSF Workshop, Norman, Oklahoma, October 22-24, 2007
- 2005 “Molecular Biological Tools Workshop” organized by the Strategic Environmental Research and Development Program (SERDP) and the Environmental Security Technology Certification Program (ESTCP), Charlottesville, Virginia, August 9-10, 2005.

- 2005 “Workshop on Genetic Sensors for Environmental Water Quality”, The Alliance for Coastal Technologies (ACT) and the University of South Florida (USF), St. Petersburg, FL, January 5-7, 2005.
- 2004 “DOE Genomics:GTL Technology Deep-Dive Specification Workshop” Arlington, VA, June 14-16, 2004.
- 2003 “Workshop on Progress and Promise in Systems Microbiology”, The National Academies of Sciences, Washington DC, August 19, 2003.

## **PROFESSIONAL MEMBERSHIPS**

American Society for Microbiology  
 International Society of Microbial Ecology  
 American Association for the Advancement of Sciences  
 Society of Industrial Microbiology

## **AWARDS AND HONORS**

- 2010-present One-Thousand Talent Scholar (Class B), the highest honor awarded by Chinese Government for oversea Chinese Scientists.
- 2010-present Adjunct Professor, Tsinghua University, Beijing, China (One of the best two universities in China)
- 2010-present Guest Professor, Zhongshan University, Guangzhou, China
- 2010 ASM Division N Annual Keynote Speech
- 2010 Innovator of the year, recognizing Oklahoma’s best new products and services by The Journal Record
- 2009 Specially Invited Oversea Chinese American Scientist by the State Government for witnessing the Grand Parade in Tian An Men Square for celebrating 60<sup>th</sup> Anniversary of China. The delegation was received by Chinese President Jindiao Hu and Premier Jiabao Wen.
- 2009 Outstanding Asian American for the Asia Society of Oklahoma
- 2009 R & D 100 Award for GeoChip development by R&D Magazine. (R&D magazine presents awards annually to the 100 most innovative scientific and technical breakthroughs of the year).
- 2009-present Guest Professor, Xiamen University, Xiamen, China
- 2008 Fellow of American Association for the Advancement of Science.
- 2008-present Distinguished Scholar, Qingdao Institute of Biomass Energy and Bioprocessing Technology (QIBEBT), Chinese Academy of Sciences, Qiangdao, Shandong, China.
- 2007-present Guest Professor, Institute of Microbiology, Chinese Academy of Sciences, Beijing, China.
- 2007-present Guest Professor, Shanghai Institute of Plant Physiology, Chinese Academy of Sciences, Shanghai, China.
- 2005-present Shenhua Distinguished Professor, Central South University, Changsha, China (Highest honor in the university, ranked at top 15 in the nation and top 1 in mineral microbiology).
- 2007-present Oversea Changjiang Scholar (One of the greatest awards for Oversea Chinese

- professionals), Chinese Ministry of Education.
- 2006 Presidential professor, University of Oklahoma, Norman, OK
- 2005 Federal Laboratory Consortium (Southeast) award for Excellence in Technology Transfer
- 2005 Fellow of American Academy of Microbiology
- 2004 Member of Interview Panel by Chinese Central TV as the only representative of oversea Chinese Scientists for memorizing Mr. Xiaoping Deng (Chinese Leader) for 100 year of birth for his education reform in China in 1977.
- 2004 Outstanding Oversea Young Scientist (Highest award for oversea young scientist), Chinese National Science Foundation
- 2004 Significant Event Award, Oak Ridge National Laboratory
- 2003 Superior Performance Award, Oak Ridge National Laboratory
- 2002 Superior Performance Award, Oak Ridge National Laboratory
- 2001 Presidential Early Career Award for Scientists and Engineers in 2001 from the President of the United State of America (The highest honor for young scientists and engineers)
- 2001 DOE Office of Science's 2001 Early Career Award for Scientists and Engineers.
- 2001 Significant Event Award, Oak Ridge National Laboratory
- 2001 Research Accomplishment Award, Oak Ridge National Laboratory
- 2001 Superior Performance Award, Oak Ridge National Laboratory
- 2001 Environmental Sciences Division Distinguished Scientific Achievement Award, Oak Ridge National Laboratory
- 2000 Superior Performance Award, Oak Ridge National Laboratory
- 2000-present Guest Professor, Zhejiang University, Hangzhou, China
- 1999 Superior Performance Award, Oak Ridge National Laboratory
- 1999 Most Valuable Player Award, Oak Ridge National Laboratory
- 1998 Superior Performance Award, Oak Ridge National Laboratory
- 1998-present Guest Professor, Eco-Environmental Research Center, Chinese Academy of Sciences, Beijing, China
- 1998 Guest Professor, Northeastern Forestry University, Harbin, China
- 1998 Research Accomplishment Award, Oak Ridge National Laboratory
- 1997-present Guest Professor, Hunan Agricultural University, Changsha, China
- 1996 Alexander Hollaender Distinguished Postdoctoral Fellow
- 1993 First prize from Hunan Science and Technology Committee for the project of integrated pest management of rice, Co-PI
- 1988 Distinguished Young Scientist Fellowship from Chinese Academy of Sciences
- 1987 Excellent scientific paper award from the Science and Technology Association of Hunan Province
- 1979 Excellent Student Award from Hunan Agricultural University

### **INVITED SEMINARS**

- 2011 “GeoChip-Based Metagenomics Insights Of Microbial Communities In Response To BP Oil Spill”. Invited talk at University of Arkansas at Pine Bluff, Pine Bluff, AR, Feburary 22, 2011.
- 2011 “GeoChip-based Metagenomics Technologies for Monitoring Carbon Cycling Processes”. Invited talk at **ASLO (American Society of Liminology and**

Oceanography) Emerging Issues Workshop and The 2nd Meeting of SCOR (Scientific Committee for Oceanic Research, International Council for Science) WG134, San Juan, Puerto Rico, February 18-21, 2011.

- 2011 “Metagenomic Analysis of the Feedback Responses of Soil Microbial Communities to Elevated CO<sub>2</sub>”, Invited talk at Microbial Genome Sequencing and Microbial Observatories Programs Awardee Workshop, Plant & Animal Genome XIX, San Diego, CA, January 15-19, 2011.
- 2010 “High Throughput Metagenomics Technologies for Biogeosciences”, Invited talk at China University of Geosciences, Beijing, China, December 23, 2010.
- 2010 “Systems Microbiology: From Genomes to Ecosystems”, Invited talk at Shandong University, Jinnan, China, December 13, 2010.
- 2010 “From Community Structure to Functions: GeoChip Development and Applications”. Talk at Soils Metagenomics, Braunschweig, Germany, December 8-11, 2010
- 2010 “Metagenomics Insights of The Effects of Long-term Fertilization on Microbial Community Functional Structure”. Invited talk at Argonne Soils Metagenomics Workshop, Argonne, IL, October 7, 2010
- 2010 “Recent Advances in Microbial Metagenomics”, Invited talk at Central South University, Changsha, September 28, 2010.
- 2010 “High Throughput Metagenomics Technologies for Microbial Community Analysis”, Invited plenary talk at Microbial Metagenomics Workshop, Yonsei University, Seoul, South Korea, September 27, 2010.
- 2010 “Applications of Metagenomics Technologies to Environmental Sciences and Engineering”. Invited talk at Academic Salon on Environmental Sciences and Engineering, Tsinghua Univ, Beijing, September 25, 2010.
- 2010 “Microbial Mediation of Carbon Cycle Feedbacks to Climate Change”. Invited plenary talk at China-US 2010 Joint Symposium: “Energy, Ecosystem, and Environmental Change (E3C), Beijing, September 22-24, 2010.
- 2010 “Rapid Genome Evolution and Adaptation to Salt Selection”. The 18<sup>th</sup> International Conference on Microbial Genomes. Lake Arrowhead, CA, September 12-16, 2010.
- 2010 “GeoChip and BP Oil Spill”. Departmental Seminar, Department of Botany and Microbiology, University of Oklahoma, Norman, OK. September 9, 2010.
- 2010 “Systems Microbiology: From Genomes to Ecosystems”, Invited talk at Washington State University, Pullman, WA, August 25, 2010.
- 2010 “Promoting collaboration between American Society of Microbiology and Chinese Society of Microbiology”. Ambassador Meeting for International Symposium on Microbial Ecology, Seattle, WA, August 23, 2010
- 2010 “Linking community structure to functions: Approaches, Problems Challenges, and Strategies”. Roundtable talk at The 13<sup>th</sup> International Symposium on Microbial Ecology, Seattle, WA, August 23, 2010.
- 2010 “Microbial Mediation of Carbon Cycle Feedbacks to Climate Warming”. Invited talk at The 13<sup>th</sup> International Symposium on Microbial Ecology, Seattle, WA, August 23, 2010.
- 2010 “Applications of Metagenomics Technologies to Environmental Sciences and Engineering”. Invited keynote talk at Workshop on Key Issues in Environmental Sciences, Harbin, China, August 16-17, 2010.
- 2010 “Metagenomic Insights of microbial Communities in Response to Climate Change”. Invited keynote talk at 2010 Annual Meeting on Microbial Ecology, Harbin, China,

- August 12-13, 2010.
- 2010 “Systems Microbiology: From Genomes to Ecosystems”. Invited talk at South China Sea Institute of Oceanography (SCSIO), Guangzhou, China, July 8, 2010.
- 2010 “GeoChip: A High Throughput Metagenomics Technology for Characterizing Microbial Functional Community Structure”. Invited talk at Guangdong Institute of Microbiology, Guangzhou, China, July 8, 2010.
- 2010 “Systems Microbiology: From Genomes to Ecosystems”. Invited talk at Zhongshan University, Guangzhou, China, July 7, 2010
- 2010 “Rapid Genome Evolution and Adaptation to Salt Stress”. Invited talk at Halophiles 2010, 9<sup>th</sup> International Conference on Halophilic Microorganisms, Beijing, China, June 29-July 3, 2010
- 2010 “GeoChip: A High Throughput Metagenomics Technology for Characterizing Microbial Functional Community Structure”. Invited talk at Deep Sea Research and Earth Systems Science Symposium, Tongji University, Shanghai, June 29, 2010.
- 2010 “Genomic Insights of Bacterial Stress Responses” Invited talk at Harbin Institute of Technology, Harbin, China, June 4, 2010.
- 2010 “High Throughput Metagenomics Technologies for Microbial Community Analysis”, Invited talk at Harbin Institute of Technology, Harbin, China, June 4, 2010.
- 2010 “Stress Responses: From Genomes to Ecosystems”, Invited talk at The 110<sup>th</sup> General Meeting of American Society for Microbiology, Division N Talk, San Diego, CA, May 24, 2010
- 2010 “GeoChip: High Throughput Metagenomics Technologies for BioGeosciences”, Invited talk at Workshop: US-China Collaborative Research on Geomicrobiological Processes in Extreme Environments, Penn State University, May 18-23, 2010.
- 2010 “High Throughput Metagenomics Technologies for Microbial Community Analysis”, Invited talk at Chinese Academy of Agricultural Sciences, Beijing, China, April 12, 2010.
- 2010 “High Throughput Metagenomics Technologies for Microbial Community Analysis”, Invited talk at Institute of Microbiology, Chinese Academy of Sciences, Beijing, China, April 7, 2010.
- 2010 “High Throughput Metagenomics Technologies for Microbial Community Analysis”, Invited talk at Tsinghua University, Beijing, China, April 8, 2010.
- 2010 “High Throughput Metagenomics Technologies for Microbial Community Analysis”, Invited talk at Institute of Microbiology, Chinese Academy of Sciences, Beijing, China, April 7, 2010.
- 2010 “Systems Microbiology: From Genomes to Ecosystems”, Invited talk at Zhejiang University, Institute of Microbiology, Hangzhou, China, April 6, 2010.
- 2010 “Systems Microbiology: From Genomes to Ecosystems”, Invited talk at Zhejiang University, Medical School, Hangzhou, China, April 6, 2010.
- 2010 “Systems Microbiology: From Genomes to Ecosystems”, Invited talk at Xiamen Institute of Urban Environment, Chinese Academy of Sciences, Xiamen, China, April 2, 2010.
- 2010 “High Throughput Metagenomics Technology for Microbial Community Analysis”, Invited talk at Xiamen University, Xiamen, China, April 2, 2010.
- 2010 “GeoChip-based Analysis of Community Structure in Microbial Electrohydrolysis Cell”, Invited talk at American Chemical Society (ACS) Annual Meeting, San Francisco, CA, March 21, 2010

- 2010 “Systems Microbiology: From Genomes to Ecosystems”, Invited talk at Northwestern University, Evanston, IL, January 22, 2010.
- 2010 “Metagenomic Analysis of the Feedback Responses of Soil Microbial Communities to Elevated CO<sub>2</sub>”, Invited talk at Microbial Genome Sequencing and Microbial Observatories Programs Awardee Workshop, Plant & Animal Genome XVIII, San Diego, CA, January 8-13, 2010.
- 2009 “Metagenomic Analysis of the Feedback Responses of Soil Microbial Communities to Elevated CO<sub>2</sub>”, Invited talk at ASA-CSSA-SSSA, 2009 International Annual Meetings, Pittsburgh, PA, November 1-5, 2009
- 2009 “Spatial Scaling of Microbial Functional Gene Diversity Across Different Soil Ecosystems”, Invited talk at Soil Metagenomics Workshop, Argonne, October 26, 2009
- 2009 “Metagenomic Analysis of the Feedback Responses of Soil Microbial Communities to Elevated CO<sub>2</sub>”, Invited talk at DIVERSITAS, Cape Town, South Africa, October 13-17, 2009
- 2009 “Comparative Genomics of Ethanol-Producing Clostridia”, Invited talk at 17<sup>th</sup> Annual Microbial Genomics Conference, Rocky Gap State Park, Cumberland, MD, October 11-15, 2009
- 2009 “GeoChip: Current Development, Challenges, and Applications”, Invited talk in the Monsoon Asia Agro-Environmental Research Consortium (MARCO): Toward International Research Collaboration, Workshop on Metagenomic approach on the rhizosphere soil microbiome. Tsukuba, Japan, October 4-8, 2009
- 2009 “Systems Microbiology: From Genomes to Ecosystems”, Invited talk at Xiamen University, Xiamen, August 17, 2009.
- 2009 “Random Matrix Theory-based Network Analysis for Microbial Ecology”. Invited talk at European Molecular Biology Organization, World Practical Course, Computational Biology: From (meta)genomes to phenotype and environment, Shanghai Jiaotong University, Shanghai, August 16, 2009
- 2009 “Systems Microbiology: From Genomes to Ecosystems”, Invited talk at Shanghai Institute of Plant Physiology and Ecology, Shanghai, August 14, 2009.
- 2009 “Systems Microbiology: From Genomes to Ecosystems”, Invited talk at Nanjing Agricultural University, Nanjing, August 13, 2009.
- 2009 “Linking Community Structure to Functions: GeoChip Development, Challenges, and Applications”, Invited talk at Nanjing Institute of Soil Science, Nanjing Institute of Geography and Limnology, Chinese Academy of Science, Nanjing, August 12, 2009.
- 2009 “GeoChip: A High Throughput Genomics Technology For Characterizing Microbial Functional Community Structure”, Invited talk at American Phytopathological Society (APS) - Annual Meeting 2009, Portland, OR, August 3, 2009.
- 2009 “Genomics and Bioenergy”. Invited talk at 2009 International Conference for Bioeconomy (BioEco 2009), Tianjin, China, June 25-28, 2009
- 2009 “GeoChip: A High Throughput Genomics Technology for Characterizing Microbial Functional Community Structure”. The 2nd International Symposium on Applied Microbiology and Molecular Biology in Oil Systems (ISMOS-2), Aarhus, Denmark, June 17-19, 2009.
- 2009 “Metagenomic analysis of the feedback responses of soil microbial communities to elevated CO<sub>2</sub>”, The 10th International Symposium on Bacterial Genetics and Ecology (Bageco-10), Uppsala, Sweden, June 15-19, 2009.

- 2009 “Key issues in soil metagenomics”. TerraGenome Workshop, Uppsala, Sweden, June 14-15, 2009.
- 2009 “Key issues in soil metagenomics”. TerraGenome Workshop, Uppsala, Sweden, June 14-15, 2009.
- 2009 “GeoChip as a high throughput tool to analyze microbial communities”. Invited Seminar in International Organization for Biological Control (IOBC) Workshop on Multitrophic Interactions in Soil. Uppsala, Sweden, June 10-13, 2009.
- 2009 “GeoChip: A High Throughput Metagenomics Tool for Functional Microbial Ecology”. Invited Seminar, Eco-Environmental Research Center, Chinese Academy of Sciences, Beijing, May 27, 2009.
- 2009 “GeoChip: A High Throughput Metagenomics Tool for Functional Microbial Ecology”. Invited Seminar, International Ecopolis Forum, Huaibei, China, May 23-26, 2009.
- 2009 “Linking Community Structure to Functions: GeoChip Development and Applications”, The 109<sup>th</sup> General Meeting of American Society for Microbiology, Philadelphia, PA, May 17–21, 2009.
- 2009 “GeoChip: Current Development, Challenges, and Applications”. Invited Seminar, University of Toronto, Toronto, Canada. May 13-14, 2009.
- 2009 “Genomics of Cellulose-Degrading and Ethanol-Producing Bacteria”, Invited talk at Oklahoma NSF EPSCoR Annual State Conference, Oklahoma City, OK, March 31, 2009.
- 2009 “Systems Microbiology: From Genomes to Ecosystems”, Invited Seminar, University of Texas, Arlington, TX, March 12-14, 2009.
- 2009 “Microbial Systems Biology”, Invited Departmental Seminar, Department of Mathematics, University of Oklahoma, Norman, OK, February 17, 2009.
- 2009 “Systems Microbiology: From Genomes to Ecosystems”, Invited Seminar, Louisiana State University, Baton Rouge, LO, February 13, 2009.
- 2009 “Microbial Functional Genomics, Genomic Technologies and Environmental Applications”, Invited talk at National University of Singapore, Singapore, January 22, 2009.
- 2009 “Microbial Functional Genomics, Genomic Technologies and Environmental Applications”, Invited talk at Nanyang Technical University, Singapore, January 21, 2009.
- 2009 “GeoChip: A High Throughput Genomics Technology for Characterizing Microbial Functional Community Structure”, ISME-IWA Colloquium on The Engineering of Microbial Communities, Singapore, January 18-21, 2009.
- 2009 “Genomics of ethanol-producing microorganisms”, NSF EPSCoR Workshop, Oklahoma City, OK, January 12, 2009.
- 2008 “GeoChip: A High Throughput Genomics Technology for Characterizing Microbial Functional Community Structure”, American GeoPhysical Union (AGU) Meeting, San Francisco, December 18, 2008.
- 2008 “Systems Microbiology: From Genomes to Ecosystems”, Invited Departmental Seminar, Michigan State University, East Lansing, MI, November 24-26, 2008.
- 2008 “Target Sequencing Microbial Genes of Interest”, Workshop on the Complete Metagenome Sequencing of a Reference Soil, Lyon, France, December 13-14, 2008
- 2008 “GeoChip: A High Throughput Genomics Technology for Characterizing Microbial Functional Community Structure”. Joint Bioenergy Institute (JBEI), Berkeley, CA, November 14, 2008.

- 2008 “GeoChip: A High Throughput Genomics Technology for Characterizing Microbial Functional Community Structure”. Invited talk at Tsinghua University, Beijing, China, November 13, 2008.
- 2008 “Systems Microbiology: From Genomes to Ecosystems”, Invited talk at China Agricultural University, Beijing, China, November 13, 2008.
- 2008 “Random Matrix Theory-based Network Identification”. Invited talk at Qingdao Institute of Biomass Energy and Bioprocessing Technology (QIBEBT), Chinese Academy of Sciences, Qiangdao, Shandong, China, November 11, 2008
- 2008 “Genomics and Bioenergy”. Invited talk at Annual Meeting on Microbial Ecology, Ecological Society of China, Changsha, China, November 10, 2008.
- 2008 “GeoChip: Recent Development, and its Applications to Global Change Biology”, Invited talk at ASM-CSM (Chinese Society of Microbiology) Joint Workshop on Environmental Microbiology and Bioenergy, Haikou, China, November 8, 2008.
- 2008 “Issues related to Long-Term Microbial Sampling and Analysis”. Invited talk at “Curation of Biological Specimens, Physical Samples and Associated Data”. NMNH (National Museum of Natural History)-NSF NEON Workshop, Smithsonian Institution, Washington, DC, October 19-22, 2008.
- 2008 “GeoChip: Recent Development, and its Applications to Bioenergy and Sustainability”. Invited talk at the joint annual meeting of Geological Society of America (GSA)-Soil Science Society of America (SSSA)-American Society of Agronomy (ASA)-Crop Society of America (CSSA), Houston, TX, October 5-9, 2008.
- 2008 “Systems Microbiology: From Genomes to Ecosystems”, Washington University at St. Louis, St. Louis, MO, October 3, 2008.
- 2008 “Genomics-Enabled Microbial Biogeography”. The 4<sup>th</sup> SCOPE (The Scientific Committee on Problems of the Environment, International Council of Scientific Union) Workshop on Microbial Environmental Genomics, Changsha, P.R. China, September 20-24, 2008.
- 2008 “Random Matrix Theory-based Network Identification”. The 4<sup>th</sup> SCOPE (The Scientific Committee on Problems of the Environment, International Council of Scientific Union) Workshop on Microbial Environmental Genomics, Changsha, P.R. China, September 20-24, 2008.
- 2008 “GeoChip: Recent Advances and Applications”. The 4<sup>th</sup> SCOPE (The Scientific Committee on Problems of the Environment, International Council of Scientific Union) Workshop on Microbial Environmental Genomics, Changsha, P.R. China, September 20-24, 2008.
- 2008 “Metagenomics Insights of the Feedback Responses of a Grassland Ecosystem to Elevated Atmospheric CO<sub>2</sub>”. The 16<sup>th</sup> International Conference on Microbial Genomes. Lake Arrowhead, CA, September 14-18, 2008.
- 2008 “GeoChip: A high throughput genomics technology for linking microbial community structure to functions”, Invited talk at the Roundtable session, Emerging Ecogenomic Methods: Is one better?, The 12<sup>th</sup> International Symposium on Microbial Ecology, Cairns, Australia, August 17-22, 2008.
- 2008 “Microbial Systems Biology”, Invited Talk at The University of Memphis, Memphis, TN, July 3, 2008
- 2008 “GeoChip: Current Development, Challenges, and Applications”, Invited talk at Biocorrosion Workshop, Norman, OK, June 24-25, 2008.
- 2008 “Genomics and Bioenergy”, Invited Talk at National Center for Agricultural Utilization

- Research (NCAUR), Peoria, IL, June 24, 2008
- 2008 “GeoChip: Current Development, Challenges, and Applications”, Invited talk at the US-EC Workshop on Metabolomics and Environmental Biotechnology, Palma de Mallorca, Spain, June 16-17, 2008.
- 2008 “GeoChip: Recent Development, and its Applications to Marine Environments”, Invited talk at the Academy colloquium: "Assessing marine microbial diversity: problems and solutions", the Royal Netherlands Academy of Arts and Sciences, Amsterdam, Netherlands, May 26-30, 2008
- 2008 “Genomics and Bioenergy”, Talk at Oklahoma Bioenergy Center, Norman, Oklahoma, April 23, 2008
- 2008 “Genomics and Bioenergy”, Invited talk at China Summit on Industrial Biotechnology Development • 2008, Tianjin, China, April 18-19, 2008
- 2008 “Microbial Functional Genomics, Genomic Technologies and Environmental Applications”, Invited talk at Tianjin University, Tianjin, China, April 17, 2008
- 2008 “Microbial Functional Genomics, Genomic Technologies and Environmental Applications”, Invited talk at Qingdao Institute of Biomass Energy and Bioprocessing Technology (QIBEBT), Chinese Academy of Sciences, Qiangdao, Shandong, China, April 16, 2008
- 2008 “From Community Structure to Functions: GeoChip Development and Its Applications to Bioremediation”, Invited talk at DOE ERSP Annual PI Meeting, Lansdowne, VA, April 7-9, 2008.
- 2008 “Genomics of Ethanol-Producing Bacteria”, Invited talk at Oklahoma NSF EPSCoR Annual State Conference, March 7, 2008.
- 2008 “Microbial Functional Genomics, Genomic Technologies and Environmental Applications”, Invited talk at University of California, Davis, CA, March 2-4, 2008
- 2008 “GeoChip: Current status, challenges and future perspectives”, Invited talk at NSF Workshop, Integrating NEON with Microbial Biology, Baton Rouge, Louisiana, February 14-16, 2008
- 2007 “Most recent development in metagenomics”, Invited talk at Tsinghua University, Beijing, China, December 19, 2007
- 2007 “Microbial Functional Genomics, Genomic Technologies and Environmental Applications”, Invited talk at Peking University, Beijing, China, December 19, 2007
- 2007 “Microbial ecology in current genome era”, Invited talk at Annual Meeting on Microbial Ecology, Ecological Society of China, Henan, China, December 16-18, 2007.
- 2007 “Metagenomics: Current Status, Challenges, and Future Perspectives”, Invited talk at Central South University, Changsha, China, December 14, 2007
- 2007 “Metagenomics: Current Status, Challenges, and Future Perspectives”, Invited talk at Harbin Institute of Technology, Harbin, China, December 12, 2007
- 2007 “GeoChip: Current Development, Challenges, and Applications”, Invited talk at Harbin Institute of Technology, Harbin, China, December 11, 2007
- 2007 “Systems Genome Biology: Current Status, Challenges and Future Perspectives”, Invited talk at Harbin Institute of Technology, Harbin, China, December 10, 2007
- 2007 “Molecular Microbial Ecology”, Invited talk at Harbin Institute of Technology, Harbin, China, December 9, 2007
- 2007 “Linking Community Structure To Functions: GeoChip-based Analysis Of Microbial Communities In Uranium Bioremediation And Hydrogen Production”, Invited talk

- at The 3rd SCOPE Meeting on Microbial Environmental Genomics, Lyon, France, November 29-December 2, 2007
- 2007 “GeoChips: A comprehensive arrays for studying various biogeochemical, ecological and environmental processes”, University of Minnesota, St Paul, MN November 19-20, 2007
- 2007 “Microbial Functional Genomics, Genomic Technologies and Environmental Applications”, Invited talk at Oklahoma State University, Stillwater, OK, November 12, 2007
- 2007 “Microbial Functional Genomics, Genomic Technologies and Environmental Applications”, Invited talk at Montana State University, Bozeman, MT, November 1-2, 2007
- 2007 “Genomics and Ecology: Challenges and future perspectives”, Invited talk at NSF Workshop: Data-Model Assimilation in Ecology: Techniques and Applications, Norman, Oklahoma, October 22-24, 2007
- 2007 “Microbial Functional Genomics, Genomic Technologies and Environmental Applications”, Invited talk at University of Southern California, Los Angeles, CA, October 17-20, 2007.
- 2007 “Genomics of ethanol-producing bacteria”, The 2<sup>nd</sup> Annual Grow: Oklahoma Biofuels Conference, October 15-17, 2007
- 2007 “GeoChips: A comprehensive arrays for studying various biogeochemical, ecological and environmental processes”, Invited talk, The 15<sup>th</sup> International Conference on Microbial Genomes, College Park, MA, September 16-20, 2007
- 2007 “Recent updates of GeoChips for environmental applications”, Invited talk at Rothamsted Experimental Station, Harpenden, UK, September 7, 2007
- 2007 “GeoChips: A comprehensive arrays for studying various biogeochemical, ecological and environmental processes”, Invited talk, 161<sup>st</sup> Meeting, Society for General Microbiology, University of Edinburgh, Edinburgh, UK, September 3-6, 2007
- 2007 “Applications of Genomics to Ecology and Bioenergy”, Invited talk at Institute of Botany, Chinese Academy of Sciences, Beijing, China, July 30, 2007
- 2007 “Microbial Functional Genomics, Genomic Technologies and Environmental Applications”, Invited talk at The University of Sciences and Technology of China, Anfei, Hefei, China, July 23, 2007
- 2007 “Ecosystem Genomics: Current Status, Challenges and Future Perspectives”, Invited talk at Shanghai Institute of Plant Physiology and Ecology, Shanghai, China, July 19, 2007.
- 2007 “GeoChip development and its applications”, Invited talk at Shanghai Institute of Plant Physiology and Ecology, Shanghai, China, July 19, 2007
- 2007 “Systems Genome Biology: Current Status, Challenges and Future Perspectives”, Invited talk at The Third Institute of Oceanography, Xiamen, China, July 13, 2007
- 2007 “Genomics and Bioenergy”, Invited talk at Hunan Agricultural University, Changsha, China, July 17, 2007
- 2007 “Genomics and Bioenergy”, Invited talk at The Third Institute of Oceanography, Xiamen, China, July 13, 2007
- 2007 “Ecosystem Genomics: Current Status, Challenges and Future Perspectives”, Invited talk at The Third Institute of Oceanography, Xiamen, China, July 13, 2007
- 2007 “Systems Genome Biology: Current Status, Challenges and Future Perspectives”, Invited talk at The Third Institute of Oceanography, Xiamen, China, July 13, 2007

- 2007 “Microbial Functional Genomics, Genomic Technologies and Environmental Applications”, Invited talk at Yunnan University, Kuming, Yunnan, China, July 9, 2007
- 2007 “Community Genomics: Current Status, Challenges and Future Perspectives”, Invited talk at Tsinghua University, Beijing, China, July 5, 2007
- 2007 “Genomics and Bioenergy”, Invited talk at Institute of Microbiology, Chinese Academy of Sciences, Beijing, China, July 4, 2007
- 2007 “Ecosystem Genomics: Current Status, Challenges and Future Perspectives”, Invited talk at Institute of Microbiology, Chinese Academy of Sciences, Beijing, China, July 4, 2007
- 2007 “Systems Genome Biology: Current Status, Challenges and Future Perspectives”, Invited talk at Institute of Microbiology, Chinese Academy of Sciences, Beijing, China, July 4, 2007
- 2007 “Microbial Functional Genomics: Current Status, Challenges and Future Perspectives”, Invited talk at Tsinghua University, Beijing, China, July 3, 2007
- 2007 “Applications of Functional Gene Arrays for Environmental Studies”, Invited talk at Tsinghua University, Beijing, China, July 3, 2007
- 2007 “Development of Functional Gene Arrays for Microbial Community Analysis”, Invited talk at Tsinghua University, Beijing, China, July 2, 2007
- 2007 “Molecular Microbial Ecology”, Invited talk at Tsinghua University, Beijing, China, July 2, 2007
- 2007 “Microbial Functional Genomics, Genomic Technologies and Environmental Applications”, Invited talk at 2007 International Conference for Bioeconomy, Tianjin, China, June 27, 2007
- 2007 “Microbial Functional Genomics, Genomic Technologies and Environmental Applications”, Invited talk at East China Normal University, Shanghai, June 25, 2007
- 2007 “GeoChip: Development and Applications for Microbial Community Analysis”, Conferences Jacques-Monod: Environmental Genomics: from individual genomes to genomes of complex communities, Roscoff, France, June 11, 2007
- 2007 “Genomics-enabled Microbial Ecology: Current Status, Challenges and Future Perspectives”, Central South University, May 29, 2007.
- 2007 “Microbial Ecology at Genome Era: Current Status, Challenges and Future Perspectives” Keynote talk at The 3rd International Ecosummit, Beijing, May 26, 2007
- 2007 “Microbial Functional Genomics, Genomic Technologies and Environmental Applications”, Invited talk at Auburn University, Auburn, AL, May 1, 2007
- 2007 “Genomics of ethanol-producing bacteria”, The 29<sup>th</sup> Symposium on Biotechnology for Fuels and Chemicals, Denver, Co, April 29, 2007
- 2007 “Functional Gene Arrays: Current Status, Challenges and Future”, University of Oklahoma, April 4, 2007
- 2007 “Genomics of ethanol-producing bacteria”, The First Annual Oklahoma Biofuels Symposium, Ponca City, OK, March 10, 2007
- 2007 “Microbial Functional Genomics, Genomic Technologies and Environmental Applications”. Robert M. and Mary Haythornthwaite Distinguished Lecture, College of Engineering, Temple University, Philadelphia, PA, February 23, 2007.
- 2006 “Microbial Functional Genomics, Genomic Technologies and Environmental Applications”. Invited talked, Genomes Division, Los Alamos National Laboratory,

- Los Alamos, November 7, 2006.
- 2006 “Microbial Functional Genomics, Genomic Technologies and Environmental Applications”. Invited talk, Department of Genetics and Biochemistry, Clemson University, Clemson, SC. October 27, 2006.
- 2006 “Microbial Functional Genomics, Genomic Technologies and Environmental Applications”. Lawrence Berkeley National Laboratory, Berkeley, CA. September 29, 2006.
- 2006 “Development and Application of Functional Gene Arrays for Assessing Microbial Community Structure and Functions in Natural Settings”, Department of Environmental Sciences, Policy and Management, University of California, Berkeley, CA. September 28, 2006.
- 2006 “Genomics of ethanol-producing bacteria”. The 14<sup>th</sup> International Conference on Microbial Genomes. Lake Arrowhead, CA, September 24-28, 2006.
- 2006 “Functional Gene Arrays: Current Status, Challenges and Future”. The 4<sup>th</sup> Okazaki Biology Conference, Okazaki, Japan, September 10-15, 2006.
- 2006 “Development and Applications of Functional Gene Arrays to Understanding Microbial Diversity, Distribution and Dynamics in Groundwaters, Soils and Marine Sediments”, Invited talk at Rothamsted Experimental Station, Harpenden, UK, August 25, 2006
- 2006 “Development and Application of Functional Gene Arrays for Assessing Microbial Community Structure and Functions in Natural Settings”, Invited talk at The 11<sup>th</sup> International Symposium on Microbial Ecology, Vienna, Austria, August 20-25, 2006
- 2006 “Functional Gene Arrays: Current Status, Challenges and Future”, Invited talk at Central South University, Changsha, China, August 19, 2006
- 2006 “Microbial Genomics, Genomic Technologies and Environmental Applications”, Keynote speech at The 9<sup>th</sup> National Symposium on Environmental Microbiology, Hangzhou, China, August 15, 2006
- 2006 “Microbial Genomics, Genomic Technologies and Environmental Applications”, Invited talk at Institute of Microbiology, Chinese Academy of Sciences, Beijing, China, August 7, 2006
- 2006 “Functional Gene Arrays: Current Status, Challenges and Future”, Invited talk at Tsinghua University, Beijing, China, August 7, 2006
- 2006 “Microbial Genomics, Genomic Technologies and Environmental Applications”, Invited talk at Zhejiang University, Hangzhou, China, August 4, 2006
- 2006 “Microbial Genomics, Genomic Technologies and Environmental Applications”, Invited talk at Shanghai Jiaotong University, Shanghai, China, August 2, 2006
- 2006 “Challenges and Trends in Contemporary Microbial Ecology”, Keynote speech at 2006 Annual Symposium of Chinese Society of Ecology, August 3, 2006.
- 2006 “GeoChip: A Comprehensive Microarrays for Studying Geochemical, Ecological and Environmental Processes”, Distinguished seminar at the Institute of Applied Ecology, Chinese Academy of Sciences, Shenyang, China, July 31, 2006.
- 2006 “Development and Application for Understanding Spatial Variation in Soil Microbial Communities”, Keynote speech at the 18<sup>th</sup> World Congress of Soil Science, Philadelphia, PA, July 10-14, 2006.
- 2006 “Functional Gene Arrays for Environmental Studies: Current Status, Challenges and Future”, Keynote speech at the International Symposium on Environmental Biotechnology, Leipzig, Germany, July 10-13, 2006.

- 2006 “Challenges in Metagenomics and Microarray-based Functional Analysis of Microbial Communities at Contaminated Sites”. The ERSP PI Meeting, Environmental Remediation Science Program, Warrenton, VA, April 3, 2006.
- 2006 “Development and Use of Integrated Microarray-Based Genomic Technologies for Monitoring Microbial Community Dynamics in groundwaters and marine sediments”, Keynote speech at the 6<sup>th</sup> International Symposium on Global Renaissance by Green Energy Revolution, The 21<sup>st</sup> Century COE (Center of Excellence) Program, Nagaoka, Japan, January 26-28, 2006.
- 2005 “Microbial Genomics, Genomic Technologies and Environmental Applications”, Keynote talk at the 2<sup>nd</sup> International Symposium on Environmental Chemistry and Toxicology, Hong Kong, December 26-29, 2005.
- 2005 “Physiological and Genomic Diversity of Thermophilic Iron-Reducing Bacteria from the Deep Subsurface” The 8th International Thermophiles Conference - *From Evolution to Revolution*, Gold Coast, Queensland, Australia, September 18-22, 2005.
- 2005 “Microbial community diversity at the NABIR Field Research Center, Oak Ridge, TN”, The 13<sup>th</sup> International Conference on Microbial Genomes, Madison, WI, September 11–15, 2005.
- 2005 “Use of Microarray-based Genomic Technologies for Assessing Microbial Community Composition and Dynamics in Contaminated Groundwater” The Joint International Symposia for Subsurface Microbiology (ISSM 2005) and Environmental Biogeochemistry (ISEB XVII), Jackson Hole, Wyoming; August 14-19, 2005.
- 2005 “Application of Microarrays to Microbial Community Analysis”, Eco-Environmental Research Center, Chinese Academy of Sciences, Beijing, China, July 7, 2005.
- 2005 “Genomic Technologies, And Their Applications”, Institute of Zoology, Chinese Academy of Sciences, Beijing, China, July 7, 2005.
- 2005 “Microbial Functional Genomics, Genomic Technologies and Environmental Applications”, China Agricultural University, Beijing, China, July 6, 2005.
- 2005 “Application of Microarrays to Microbial Community Analysis”, Tsinghua University, Beijing, China, July 4, 2005.
- 2005 “Microbial Functional Genomics, Genomic Technologies and Environmental Applications”, Hunan Normal University, Changsha, China, June 30, 2005.
- 2005 “Microbial Functional Genomics, Genomic Technologies and Environmental Applications”, Hunan Agricultural University, Changsha, China, June 29, 2005.
- 2005 “Microbial Functional Genomics, Genomic Technologies and Environmental Applications”, Northwestern University, Xian, China, June 24, 2005.
- 2005 “Microbial Functional Genomics, Genomic Technologies and Environmental Applications”, Chinese Academy of Sciences, Beijing, China. Special keynote talk at Chinese Academy of Sciences under the special seminar series, "Sciences and China", sponsored by Chinese Academy of Sciences, National Academy of Sciences, National Academy of Engineering, Ministry of Science and Technology, Ministry of Education, and Chinese Association of Sciences and Technologies. June 21, 2005.
- 2005 “Microbial Functional Genomics, Genomic Technologies and Environmental Applications”, Central South University, Changsha, China, June 21, 2005.
- 2005 “Microbial Functional Genomics, Genomic Technologies and Environmental Applications”, Medical School, Zhejiang University, Hangzhou, China, June 17, 2005.

- 2005 “Using functional gene arrays to assess microbial community diversity in marine sediments from Gulf of Mexico,” The 2<sup>nd</sup> International Workshop on Microbial Environmental Genomics, Shanghai, China, June 11–16, 2005.
- 2005 “Functional gene arrays: current status, challenges and future,” The 105<sup>th</sup> General Meeting of American Society for Microbiology, Atlanta, GA, June 4 – June 9, 2005.
- 2005 “Microarrays-based functional analysis of stress responses”. The 5<sup>th</sup> Annual Northwestern Gene Expression Conference, University of Washington, Seattle, May 25-27, WA, 2005.
- 2005 “Microarrays-based functional analysis of stress responses”. Departmental Seminar, Plant Science, University of Tennessee at Knoxville, Knoxville, TN, April 28, 2005.
- 2005 “Development and application of integrated genomic technology for microbial community analysis”. The 8<sup>th</sup> Annual PI Meeting, Natural and Accelerated Bioremediation Program (NABIR), Warrenton, VA, April 17–20, 2005.
- 2005 “Microarrays-based Genomic Technologies for Environmental and Microbial Community Analysis”, New England BioLabs, Beverly, MA, March 23-24, 2005.
- 2005 “Microbial Functional Genomics, Genomic Technologies and Environmental Applications”, Medical School, Southern Illinois University, Springfield, IL, March 10-12, 2005.
- 2005 “Novel Random Matrix Theory-Based Approach for Identifying Gene Interaction Network”, Departmental Seminar, Department of Mathematics, University of Tennessee at Knoxville, Knoxville, TN, February 21, 2005.
- 2004 “Microbial Functional Genomics, Genomic Technologies and Environmental Applications”, Departmental Seminar, Environmental and Civil Engineering, Stanford University, Stanford, December 15, 2004.
- 2004 “Microbial Functional Genomics, Genomic Technologies and Environmental Applications”, Departmental Seminar, Environmental and Civil Engineering, University of Tennessee at Knoxville, Knoxville, TN, November 3, 2004.
- 2004 “Application of Functional Gene Arrays for Analyzing Community Structure at NABIR Field Research Center”. DOE Natural and Accelerated Bioremediation Program (NABIR) Workshop, Oak Ridge, TN, October 18-19, 2004.
- 2004 “Microarray-Based Genomic Technologies for Microbial Community Analysis”. Great Lakes and Central States Ecological Observatory (GLACEO) Workshop on Building a Regional Ecological Observatory: Sensors, Tools, and Networking, University of Michigan Biological Station, Pellston, MI, October 15-17, 2004.
- 2004 “Novel random matrix theory-based approach for identifying modular network”, The 12<sup>th</sup> International Conference on Microbial Genomes, Lake Arrowhead, CA, September 26–30, 2004.
- 2004 “Microbial Functional Genomics, Genomic Technologies and Environmental Applications”, Argonne National Lab, September 20, 2004
- 2004 “Microbial Functional Genomics, Genomic Technologies and Environmental Applications”, Brookhaven National Lab, Upton, NY, September 17-18, 2004
- 2004 “Microbial Functional Genomics, Genomic Technologies and Environmental Applications”, Medical School, University of Alabama at Birmingham, Birmingham, AL, September 7-8, 2004
- 2004 “Functional gene arrays for environmental studies”, The 10<sup>th</sup> International Symposium on Microbial Ecology, Cancun, Mexico, August 22-27, 2004
- 2004 “Microarrays-based analysis of stress responses”. The 10<sup>th</sup> International Symposium

- on Microbial Ecology, Cancun, Mexico, August 22-27, 2004
- 2004 “Genomics-based stress responses of meta-reducing bacteria”. Workshop on Stress in Metal-Reducing Bacteria: Ecology, Functional Genomics, Bioinformatics at the Society of Industrial Microbiology Annual Meeting, Anaheim, CA, July 25-29, 2004
- 2004 “Microarrays for bacterial detection and community analysis”, National Institute of Biological Monitoring and Quarantine, Beijing, China, September 15, 2004
- 2004 “Microbial Functional Genomics, Genomic Technologies and Environmental Applications”, Chinese National Sciences Foundation, Beijing, China, September 14, 2004
- 2004 “Microarrays for bacterial detection and microbial community analysis”, Workshop, Nucleic Acids-based Technologies, Amplifications Amplified. Cambridge Health Tech Institute, McLean, VA, June 21-23, 2004.
- 2004 “Functional Genomics of Environmentally Important Model Microorganisms”, The South East Structural Genomics Workshop on Frontier in Biology, The University of Georgia, Athens, GA, May 20-21, 2004.
- 2004 “Microarray-Based Genomic Technologies for Environmental Studies”. The 2<sup>nd</sup> International Workshop in Biochips and Environmental Biosensors, Gwangju, Korea, May 1-2, 2004.
- 2004 “Integrated Functional Analysis Of Environmentally Important Microorganisms”. The 5<sup>th</sup> International Symposium on Advanced Environmental Monitoring, Seoul, Korea, April 29-30, 2004.
- 2004 “Microarray-Based Functional Analysis of the Radiation-Resistant Bacterium, *Deinococcus radiodurans*”. 2004 European Symposium on Environmental Biotechnology, Oostende, Belgium, April 27-29, 2004.
- 2004 “DOE genomics programs”. The 1<sup>st</sup> International Workshop on Microbial Environmental Genomics, Wageningen, The Netherlands, April 18–20, 2004.
- 2004 “Microarray-Based Genomic Technologies for Environmental Studies”. The 1<sup>st</sup> International Workshop on Microbial Environmental Genomics, Wageningen, The Netherlands, April 18–20, 2004.
- 2004 “Functional Gene Arrays for Studying Microbial Community Structure”. The 7<sup>th</sup> Annual PI Meeting, Natural and Accelerated Bioremediation Program (NABIR), Warrenton, VA, March 14–16, 2004.
- 2004 “Microbial functional genomics, genomic technology and environmental applications”, The University of Georgia, Athens, GA, February 10, 2004.
- 2004 “Molecular Microbial Ecology And Community Genomics”, Savannah River Ecology Laboratory, Aiken, SC, February 12, 2004.
- 2004 “Functional genomic analysis of *Shewanella oneidensis* MR-1”, The University of Georgia, Athens, GA, February 11, 2004.
- 2004 “Microbial functional genomics, genomic technology and environmental applications”, The University of Georgia, Athens, GA, February 10, 2004.
- 2004 “Microbial functional genomics, genomic technology and environmental applications”, Zhongshan University, Guangzhou, China, January 1, 2004.
- 2003 “Microbial functional genomics, genomic technology and environmental applications”, Central South University, Changsha, China, December 25, 2003.
- 2003 “Microbial functional genomics, genomic technology and environmental applications”, Hunan Agricultural University, Changsha, China, December 24, 2003.
- 2003 “Future Perspectives of Microbial Ecology: Ecological Genomics Beyond Single

- Cells”, Eco-Environmental Research Center, Chinese Academy of Sciences, Beijing, China, December 24, 2003.
- 2003 “Microarray-based functional analysis of environmentally important microorganisms and communities”, Tsinghua University, Beijing, China, December 23, 2003.
- 2003 “Microarray-based functional analysis of environmentally important microorganisms and communities”, Chinese Academy of Forestry Sciences, Beijing, China, December 23, 2003.
- 2003 “Microbial functional genomics, genomic technology and environmental applications”, Keynote speaker, The 5<sup>th</sup> National Symposium on Microbial Ecology, Beijing, China, December 22, 2003.
- 2003 “Extremophilic metal-reducing bacteria”, NASA Astrobiology Workshop: Looking into the Extremes of Life, American Society for Gravitational and Space Biology (ASGSB), Huntsville, AL, November 12-15, 2003.
- 2003 “Application microarray-based genomic technology to environmental studies”, Savannah River Ecology Laboratory, Aiken, SC, October 22-23, 2003.
- 2003 “Soil microbial diversity, controlling mechanisms and detection”. International Symposium on Structure and Function of Soil Microbiota, Marburg, Germany, September 18-20, 2003.
- 2003 “Microbial genomics, genomic technology and environmental applications”, Lawrence Berkeley National Laboratory, Berkeley, CA, July 30-31, 2003.
- 2003 “Microbial genomics, genomic technology and environmental applications”, DOE Joint Genome Institute, Walnut Creek, CA, May 6-8, 2003.
- 2003 “Microarray-based functional analysis of the radiation-resistant bacterium, *Deinococcus radiodurans*”. The 10<sup>th</sup> Genome Conference of DOE Genome Joint Institute, Santa Fe, NM, March 29–April 2, 2003.
- 2003 “Development and evaluation of oligonucleotide-based functional gene arrays for bioremediation”. The 6<sup>th</sup> Annual PI Meeting, Natural and Accelerated Bioremediation Program (NABIR), Warrenton, VA, March 17–19, 2003.
- 2003 “Microarray-based genomic technology for microbial community analysis”. Montreal Microarray Symposium, Montreal, Canada, March 12-15, 2003.
- 2003 “Microarray technology for gene expression analysis”. DOE Genome To Life Workshop, Washington DC, February 10-12, 2003.
- 2002 “Microarray-based genomic technology and microbial ecology”. The Advisory Committee Meeting for Natural and Accelerated Bioremediation Program (NABIR), Baltimore, MD, November 7, 2002.
- 2002 “Microbial genomics, genomic technology and environmental applications”, Department of Microbiology, University of Alabama, Birmingham, AL, October 24-25, 2002.
- 2002 “Microbial genomics, genomic technology and environmental applications”, Pacific Northwest National Laboratory, Richland, WA, October 15, 2002.
- 2002 “Microbial genomics, genomic technology and environmental applications”, Washington State University, Pullman, WA, October 14, 2002.
- 2002 “Microbial genomics and ecology”, on an international Workshop entitled An Ecological Perspective of Genomics: Assessing Ecological Risk Through Partnerships. Pensacola Florida, FL, September 22–25, 2002.
- 2002 “Development and evaluation of microarray-based genomics technology for microbial detection”. The Genomic Workshop on Environmental Biotechnology,

- Idaho Falls, ID, September 19–20, 2002.
- 2002 “Microarray-based whole genome analysis for metal-reducing and radiation-resistant bacteria”. The US-Japan Workshop on System Biology, Tsuruoka, Yamagata, Japan, September 14–18, 2002.
- 2002 “Development of Novel Attachment Strategy for Immobilizing Oligonucleotides and Proteins on Microarrays”, The 10<sup>th</sup> International Conference on Small Genomes, Lake Arrowhead, CA, September 14–18, 2002.
- 2002 “Development and evaluation of 16S rRNA-based oligonucleotide microarrays for microbial detection”. The X<sup>th</sup> International Congress of Bacteriology and Applied Microbiology, Paris, France, July 27–August 1, 2002.
- 2002 “Microbial genomics, genomic technology and environmental applications”, The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, UK, July 22, 2002.
- 2002 “Development and evaluation of microarray-based genomics technology for microbial detection”. The 102<sup>nd</sup> General Meeting of American Society for Microbiology, Salt Lake City, UT, July 27–August 1, 2002.
- 2002 “Development of microarray-based genomics technology for microbial community analysis”. Department of Microbiology, North Carolina State University, Raleigh, NC, March 28, 2002.
- 2002 “Development of microarray-based genomics technology for microbial community analysis”. Department of Biology, Duke University, Durham, NC, March 27, 2002.
- 2002 “Molecular microbial diversity of NABIR Field Research Center, Oak Ridge, TN”. The 5<sup>th</sup> Annual PI Meeting, Natural and Accelerated Bioremediation Program (NABIR), Warrenton, VA, March 18–20, 2002.
- 2002 “Integrated analysis of genes and proteins involved in anaerobic energy metabolism of *Shewanella oneidensis* MR-1”. The 9<sup>th</sup> Genome Contractor and Grantee Workshop, Department of Energy, Oakland, CA, January 27–31, 2002.
- 2002 “Environmental microbial genomics, genomic technology and detection”, Department of Pharmaceutics and Pharmacodynamics, University of Illinois, Chicago, IL, January 16, 2002.
- 2002 “Microbial genomics, genomic technology and environmental applications”, Biotechnology research Institute, National Research Council Canada, Montreal, Quebec, Canada, February 1, 2002.
- 2001 “Development of Microarray-based genomic technology for environmental detection”, American Society for Microbiology Southeastern Branch Annual Meeting, Birmingham, AL, November 8–10, 2001.
- 2001 “Application of genomic technology to microbial ecology”, The 9<sup>th</sup> International Symposium on Microbial Ecology, August 26–31, 2001, Amsterdam, The Netherlands.
- 2001 “Functional gene arrays and community gene arrays”, The 101<sup>st</sup> General Meeting of American Society for Microbiology, Orlando, FL, May 20–24, 2001.
- 2000 “Metal reduction by extremophiles”, American Geophysical Union, Session B19 on Metal reduction, San Francisco, CA, December 15–19, 2000.
- 2000 “Developing microarray-based genomic technology for environmental studies,” a special symposium at the American Society of Agronomy meetings, Minneapolis, MN, November 6–9, 2000.
- 2000 “Genome-wide functional analysis of metal-reducing bacteria *Shewanella oneidensis* MR-1”, The 8<sup>th</sup> International Conference on Small Genomes, Lake Arrowhead, CA,

- September 24–28, 2000.
- 2000 “Microbial model organisms and DOE’s mission”, Oak Ridge National Laboratory, September 20, 2000.
- 2000 “Microbial genomics of metal-reducing bacteria”, Life Sciences Division, Oak Ridge National Laboratory, August 15, 2000.
- 2000 “Genomics and toxicology,” Shanghai Institute of Medicine, Shanghai, China, June 23, 2000.
- 2000 “Genomics, genomic technology and their impacts,” Zhejiang University, Hangzhou, China, June 21, 2000.
- 2000 “Genomics, genomic technology and their applications,” Hunan Normal University, Changsha, China, June 20, 2000.
- 2000 “Microarray-based microbial detection,” Hunan Agricultural University, Changsha, Hunan, China, June 13, 2000.
- 2000 “Recent advances in bioremediation,” Eco-Environmental Research Center, Chinese Academy of Sciences, Beijing, China, June 12, 2000.
- 2000 Keynote speech, “Genomics, genomic technology and applications,” Northeastern Forest University, Harbin, P.R. China, June 10, 2000.
- 2000 “Microarray-based genomic technology for environmental studies,” NASA/JPL, Pasadena, CA, May 25, 2000.
- 2000 “Microbial genomics and ecology”, Life Sciences Division, Oak Ridge National Laboratory, April 5, 2000.
- 2000 “Development of microarray-based genomic technology for environmental studies,” Ohio State University, Columbus, OH, April 15, 2000.
- 1999 “DNA microarrays for characterizing microbial communities,” DOE NABIR Workshop in Application of Genomic Technology to Bioremediation, Washington, DC, December 5–7, 1999.
- 1999 “Ecological, physiological and genomic diversity of metal-reducing bacteria,” The 7<sup>th</sup> Conference on Small Genomes, Washington, DC, November 13–17, 1999.
- 1999 “Molecular microbial diversity and controlling mechanisms in subsurface environments,” The 99<sup>th</sup> General Meeting of American Society for Microbiology, Chicago, IL, May 29–June 3, 1999.
- 1999 “Bioremediation, genomic technology and data analysis,” Life Sciences Division, Oak Ridge National Laboratory, November 25, 1999.
- 1998 “Recent advances of nucleic acid technology for measuring microbial biomass and activities,” DOE NABIR Workshop, Bethesda, MD, November 17, 1998.
- 1998 “Unusual microbial community diversity in soils and its controlling mechanisms,” in the Session of Microbial Community Dynamics, the VII International Congress of Ecology, Florence, Italy, July 18–26, 1998.
- 1998 Keynote speech, “Extremophilic iron-reducing bacteria: their implications for possible life in extraterrestrial environments,” The Third Symposium of Chinese Young Scientists, Beijing, P.R. China, August 19–22, 1998.
- 1998 Keynote speech, “Genomics and bioremediation,” The workshop for environmental technology, The Ministry of Chinese Sciences and Technology, Beijing, P.R. China, September 1–2, 1998.
- 1998 “Microbial genomics,” Institute of Microbiology, Chinese Academia of Sciences, Beijing, China, August 23, 1998.
- 1998 “Trends in ecology,” Eco-Environmental Research Center, Chinese Academia of

- Sciences, Beijing, China, August 24, 1998.
- 1998 “Bioremediation of hydrogen carbons, chlorinated solvents and heavy metals,” Eco-Environmental Research Center, Chinese Academia of Sciences, Beijing, China, August 25, 1998.
- 1998 “Application of molecular techniques to environmental studies,” Northeastern Forestry University, Harbin, China, August 27–29, 1998.
- 1995 “Ecological and phylogenetical diversity of toluene-degrading bacteria,” Hunan Agricultural University, Changsha, China, December 22, 1995.
- 1995 “Applications of molecular techniques to microbial community analysis,” Institute of Microbiology, Chinese Academy of Sciences, Beijing, China, December 20, 1995.
- 1995 “Recent advances in microbial ecology,” Eco-Environmental Research Center, Chinese Academy of Sciences, Beijing, China, December 19, 1995.

## **PUBLICATIONS**

### **Published/in press (Citations > 6300, H index, 44)**

1. Sundararajan, A., J. Kurowski, T. Yan, D. M. Klingman, M.P. Joachimiak, **J.-Z. Zhou**, B. Naranjo, J. A. Gralnick, and M. W. Fields. 2011. A *Shewanella oneidensis* MR-1 Sensory Box Protein Involved in Aerobic and Anoxic Growth, *Appl. Environ. Microbiol.*, in revision.
2. **Zhou, J.-Z.**\*, L.-Y. Wu\*, Y. Deng, X.-Y. Zhi, Y.-H. Jiang, Q.-C. Tu, J.-P. Xie, J. D. Van Nostrand, Z.-H. He, and Y.-F. Yang. 2011. Reproducibility and Quantitation of Amplicon Sequencing-Based Detection. *The ISME J.*, in press. \*Equal distribution.
3. Wang, J., J. D. Van Nostrand, L. Wu, Z. He, G. Li, and **J.-Z. Zhou**. 2011. Evaluation of whole-community genome DNA amplification methods with microarrays. *Appl. Environ. Microbiol.*, in revision.
4. Van Nostrand\*, J.D., L.Y. Wu\*, W.-M. Wu, Z.J. Huang, T. J. Gentry, Y. Deng, J. Carley, S. Carroll, Z.-H. He, B.H. Gu, J. Luo, C. S. Criddle, D. B. Watson, P. M. Jardine, T. L. Marsh, J.M. Tiedje, T. C. Hazen, and **J.Z. Zhou**. 2010. Dynamics of microbial community functional structure visualized by GeoChip during the *in-situ* bioremediation of a uranium-contaminated aquifer. *Appl. Environ. Microbiol.*, in revision, \*Equal distribution.
5. Hazen, T. C., E. Dubinsky, T. DeSantis, G. Andersen, Y. Piceno, N. Singh, J. Jansson, A. Probst, S. Borglin, J. Fortney, W. Stringfellow, M. Bill, M. Conrad, L. Tom, K. Chavarria, T. Alusi, R. Lamendella, D. Joyner, C. Spier, J. Baelum, M. Auer, M. Zemla, R. Chakraborty, E. Sonnenthal, P. D'haeseleer, H.-Y. Holman, S. Osman, Z.M. Lu, J. van Nostrand, Y. Deng, **J.Z. Zhou**, and O. U. Mason. 2010. Deep-sea oil plume enriches Indigenous oil-degrading bacteria. *Science*, 330: 204-208.
6. Wu, WM, J. Carley, D. Watson, B.H. Gu, S. Brooks, S. S. Kelly, K. Kemner, J. D. van Nostrand, L. Wu, M. Xu, **J.-Z. Zhou**, J. Luo, E. Cardenas, C. Hwang, M. W. Fields, T. L. Marsh, J. M. Tiedje, S. J. Green, J. E. Kostka, P. K. Kitanidis, P. M. Jardine, C. S. Criddle. 2010. Bioreduction and immobilization of uranium in situ: a case study at a USA Department of Energy radioactive waste site, Oak Ridge, Tennessee. *Acta Scientiae Circumstantiae*. In press
7. Gihring, T.M., C.W. Schadt, G.-L. Zhang, Z. Yang, S. Carroll, K. Lowe, T.-L. Mehlhorn, P. Jardine, D. Watson, S.C. Brooks, W. Wu, J.E. Kostka, W. Overholt, S.J. Green, **J.-Z. Zhou**, P. Zhang, J. van Nostrand. 2010. Changes in microbial community structure and activity during amendment with long-term electron donor sources for bioreduction of groundwater contaminants. *Geochimica et Cosmochimica Acta*. 74: A329-A329.

8. Mason, O. U., T. Nakagawa, M. Rosner, J. D. Van Nostrand, **J.-Z. Zhou**, A. Maruyama<sup>5</sup>, M. R. Fisk, S. J. Giovannoni. 2010. First Investigation of the Microbiology of the Deepest Layer of Ocean Crust. PLoS One, in press
9. Hemme, C. L., H. Mouttaki, Y.-J. Lee, L. Goodwin, S. Lucas, A. Copeland, A. Lapidus, T. G. d. Rio, H. Tice, E. Saunders, T. Brettin, J. C. Detter, C. S. Han, S. Pitluck, M. L. Land, L. J. Hauser, N. Krypides, N. Mikhailova, Z. He, L. Wu, J. D. V. Nostrand, B. Henrissat, Q. He, P. A. Lawson, R. S. Tanner, L. R. Lynd, J. Wiegel, M. W. Fields, A. P. Arkin, C. W. Schadt, B. S. Stevenson, M. J. McInerney, Y. Yang, H. Dong, Denfeng Xing, Nanqi Ren, Aijie Wang, R. L. Huhnke, J. R. Mielenz, S.-Y. Ding, M. E. Himmel, S. Taghavi, D. v. d. Lelie, E. M. Rubin, and **J.-Z. Zhou**. 2010. Sequencing of Multiple Clostridia Genomes Related to Biomass Conversion and Biofuels Production. Journal of Bacteriology, 192: 6494-6496.
10. Xie, J.P. Z.H. He, X.X. Liu, X.D. Liu, J. D. Van Nostrand, Y. Deng, L.Y. Wu, **J.-Z. Zhou**, and G.-Z. Qiu. 2010. GeoChip-based analysis of the functional gene diversity and metabolic potential of microbial communities in acid mine drainage. Appl. Environ. Microbiol, in press.
11. Wang, A.J., L.F. Gao, N.Q. Ren, J.F. Xu, C. Liu, G.-L. Cao, H. Yu, W.Z. Liu, C. L. Hemme, Z.H. He, and **J.-Z. Zhou**. 2010. Isolation and characterization of *Shigella flexneri* G3 for effective cellulosic saccharification under mesophilic conditions. Appl. Environ. Microbiol, in press.
12. Epelde, L., J. M. Becerril, G. A. Kowalchuk, Y. Deng, **J.-Z. Zhou**, and C. Garbisu. 2010. Impact of metal pollution and *thlaspi caerulescens* phytoextraction on soil microbial communities. Appl. Environ. Microbiol, 76: 7843-7853.
13. Wang, A.J., W.Z., Liu WZ, N. Q. Ren, **J.-Z. Zhou**, and A.A. Cheng 2010. Key factors affecting microbial anode potential in a microbial electrolysis cell for H<sub>2</sub> production. International Journal of Hydrogen Energy. 35: 13481-13487
14. Yang, Y., L. A. McCue, A. B. Parsons, C. X. Guan, S. Feng and **J.-Z. Zhou**. 2010. The tricarboxylic acid cycle in *Shewanella oneidensis* is independent of Fur and RyhB control. BMC Microbiology 10: 264.
15. **Zhou, J.-Z.**, Q. He, Z.H. He, T. C. Hazen, J. Wall. A. Arkin. 2010. Stress Responses of Sulfate Reducing Bacteria: from Genomes to Ecosystems. Nature Review in Microbiology, in press (**Invited**).
16. **Zhou\***, **J.-Z.**, Y. Deng\*, F. Luo, Z.-H. He, Q. Tu, and X.Y. Zhi. 2010. Functional Molecular Ecological Networks. mBio 1(4):e00169-10. doi:10.1128/mBio.00169-10.\*equal contribution.
17. Gao, H., X. Wang, Z.K. Yang, J. Chen, Y. Liang, H. Chen, T. Palzkill, and **J.-Z. Zhou**. 2010. Physiological roles of ArcA, Crp, and EtrA and their interactive control on aerobic and anaerobic respiration in *Shewanella oneidensis*. PLoS ONE In Press.
18. Parnell, J. J., G. Rompato, L. C. Latta IV, M. E. Pfrender, D. Naftz, J. VanNostrand, Z.H. He, **J.-Z. Zhou**, G. Andersen, P. Champagne, B. Ganesan, and B. C. Weimer. 2010. Functional Biogeography as Evidence of Gene Transfer in Hypersaline Microbial Communities. PLoS ONE 5, e12919. doi:10.1371/journal.pone.0012919
19. Xiong, J.B., L.Y. Wu, S.X. Tu, J. D. van Nostrand, Z.H. He, **J.-Z. Zhou**, and G.J. Wang. 2010. Diversity of microbial communities associated with soil arsenic contamination and rhizosphere of the arsenic hyper-accumulating plant *Pteris vittata* L. Appl. Environ. Microbiol, 76: 7277-7284.

20. He, Z.H., Q. He, J. van Nostrand, and **Z.-J. Zhou**. 2010. Applications of GeoChip-based metagenomic technology to environmental sciences and engineering. *Frontier in Environmental Sciences*, in press
21. Liu, W.Z., A.J. Wang, Sh. Cheng, B. E. Logan, H. Yu, Y. Deng, J. D. van Nostrand, L.Y. Wu, Z.H. He and **J.-Z. Zhou**. 2010. Geochip-based Functional Gene analysis of anodophilic communities in microbial electrolysis cells under Different Operational modes. *Environ. Sci. & Technol.*, 44: 7729-7735.
22. Lu L., H.H. Song, Y.T. Ji, Z.H. He, Y.T. Pu, **J.-Z. Zhou**, and J. Xu. 2010. Ultrasound-mediated DNA transformation in thermophilic Gram-positive anaerobes. *PLoS One*, in press
23. Liang, Y.T. J. D. van Nostrand, Y. Deng, Z.H. He, L.Y. Wu, X. Zhang, G.H. Li and **J.-Z. Zhou**. 2010. Functional gene diversity of soil microbial communities from oil-contaminated fields in China. *The ISME J.* in press
24. Yan, T.F., T., T. J. Gentry, D. B. Watson, P. M. Jardine, M. A. Bogle, A. V. Palumbo, T. C. Hazen, **J.-Z. Zhou**, and C. W. Schadt. 2010. pH Drives Extreme Shifts in Microbial Community Characteristics within a Contaminated Primary Watershed. *Environ Microbiol.*, in press
25. Reganold, J.P., P.K. Andrews, J.R. Reeve, L. Carpenter-Boggs, C.W. Schadt, J.R. Alldredge, C.F. Ross, N.M. Davies, and **J.-Z. Zhou**. 2010. Fruit and soil quality of organic and conventional strawberry agroecosystems. *PLoS ONE* 5: e12346, doi:10.1371/journal.pone.0012346.
26. Cardenas, E., W.-M. Wu, M. B. Leigh, J. Carley, S. Carroll, T. Gentry, J. Luo, D. Watson, B. Gu, M. Ginder-Vogel, P. K. Kitanidis, P. M. Jardine, **J.-Z. Zhou**, C. S. Criddle, T. L. Marsh, and J. M. Tiedje. 2010. A combined massive parallel sequencing - indicator species approach for the study of microbial communities in a uranium remediation site. *Appl. Environ. Microbiol*, 76: 6778-6786.
27. Andersen, G. L., Z. He, T.Z. DeSantis, E. L. Brodie, **J.-Z. Zhou**. 2010. The Use of Microarrays in Microbial Ecology. In: *Environmental Molecular Microbiology* (Liu, WT; Jansson, JK, eds), pp. 87-109, Caister Academic Press, Wymondham, UK.
28. Gao, H., S. Barua, Y. Liang, L. Wu, Y. Dong, S. Reed, J. Chen, D. Culley, D. Kennedy, Y. Yang, Z. He, K. H. Nealson, J. K. Fredrickson, J. M. Tiedje, M. Romine and **J.-Z. Zhou**. 2010. Impacts of *Shewanella oneidensis* c-type cytochromes on aerobic and anaerobic respiration. *Microbial Biotech.* 3(4): 455-466.
29. Liang, Y., H. Gao, J. Chen, Y. Dong, L. Wu, Z. He, X. Liu, G. Qiu, and **J.-Z. Zhou**. 2010. Pellicle formation in *Shewanella oneidensis*. *BMC Microbiol.* 10: 291.
30. Wu, M.-M., J. Carley, S. J. Green, J. Luo, S. D. Kelly, J. D. van Nostrand, K. Lowe, T. Mehlhorn, S. Carroll, B. Boonchayanant, F.E. Löffler, D. Watson, K.M. Kemner, **J.-Z. Zhou**, P. K. Kitanidis, J. E. Kostka, P. M. Jardine, and C. S. Criddle. 2010. Effects of nitrate on the stability of uranium in a bio-reduced region of the subsurface. *Environ Sci & Technol.*, 44: 5104-5111.
31. He, Q., Z. He, D. C. Joyner, M. Joachimiak, M. N. Price, Z. K. Yang, H.-C. B. Yen, C. L. Hemme, R. Chakraborty, W. Chen, M. M. Fields, D. A. Stahl, J. D. Keasling, M. Keller, A. P. Arkin, T. C. Hazen, J. D. Wall, and **J.-Z. Zhou**. 2010. Impact of elevated nitrate on sulfate-reducing bacteria: Implications of inhibitory mechanisms in addition to osmotic stress. *The ISME J.*, 4: 1386-1397.
32. He, Z., Y. Deng, J. D. Van Nostrand, Q. Tu, M. Xu, C. Hemme, X. Li, L. Wu, T. J. Gentry, Y.F. Yin, J. Liebich, T. C. Hazen, and **J.-Z. Zhou**. 2010. GeoChip 3.0 as a high throughput tool for analyzing microbial community structure, composition, and functional activity. *ISME J.*, 4: 1167-1179.

33. Van Nostrand, J.D., Z. He, and **J.-Z. Zhou**. 2010. New developments and applications of microarrays for microbial community analysis in natural and impacted ecosystems. In: M. Moo-Young (ed) *Comprehensive Biotechnology*, 2e. Elsevier, Amsterdam, The Netherlands, pp in press.
34. Van Nostrand, J.D., Z. He, **J.-Z. Zhou**. 2010. GeoChip: A high throughput metagenomics technology for dissecting microbial community functional structure. In: F.J. de Bruijn (ed) *Handbook of Molecular Microbial Ecology II: Metagenomics in Different Habitats*. John Wiley & Sons, New Jersey, pp to be determined. In Press.
35. Xu, M.Y., W.-M. Wu, L.Y. Wu, Zhili He, Joy D. Van Nostrand, Y. Deng, J. Luo, J. Carley, M. A. Ginder-Vogel, T. Gentry, B. Gu, D. Watson, P. M. Jardine, C. S. Criddle, and **J.-Z. Zhou**. 2010. Functional understanding of microbial community structures in sediments during *in situ* bioremediation/immobilization of uranium at a uranium contaminated site. *The ISME J*, 4: 1060-1070
36. Zhou, A.-F, Z.H. He, A. M. Redding, A. Mukhopadhyay, C. L. Hemme, M. P. Joachimiak, K. S. Bender, J. D. Keasling, D. A. Stahl, M. W. Fields, T. C. Hazen, A. P. Arkin, J. D. Wall, and **J.-Z. Zhou**. 2010. Hydrogen peroxide-induced oxidative stress responses in *Desulfovibrio vulgaris* Hildenborough. *Environ Microbiol*, 12: 2645-2657.
- Zhou, J.-Z.**, Z.H. He, J. D. Van Nostrand, L.Y. Wu, and Y. Deng. 2010. Applying GeoChip Analysis to Disparate Microbial Communities. *Microbe*, 5:60-64.
37. Huang, Y., W.M. Zong, X. Yan, R.F. Wang, C.L. Hemme, **J.-Z. Zhou**, Z.H. Zhou. 2010. Succession of the Bacterial Community and Dynamics of Hydrogen Producers in a Hydrogen-Producing Bioreactor. *Appl. Environ. Microbiol*, **76**: 3387-3390.
- Gao, W.M., T. J. Gentry, T. L. Mehlhorn, S. L. Carroll, P. M. Jardine, and **J.-Z. Zhou**. 2010. Characterization of Co(III) EDTA reducing bacteria in metal- and radionuclide-contaminated groundwater. *Geomicrobiology Journal*, 27: **93-100**.
38. Liang. Y.T., Z. H. He, L. Y. Wu, Y. Deng, G.H. Li, and **J.-Z. Zhou**. 2010. Development of a common oligo reference standard (CORS) for microarray data normalization and comparison across different microbial communities. *Appl. Environ. Microbiol*, **76**: 1088-1094.
39. He, Z.H., A.F. Zhou, E. Baidoo, Q. He, M. P. Joachimiak, P. Benke, R. Phan, A. Mukhopadhyay, K. Huang, E. J. Alm, M. W. Fields, J. Wall, D. Stahl, T. C. Hazen, J. D. Keasling, A. P. Arkin, and **J.-Z. Zhou**. 2010. Global transcriptional, physiological and metabolite analyses of *Desulfovibrio vulgaris* Hildenborough responses to salt adaptation. *Appl. Environ. Microbiol*, 76:1574-1586..
40. Reeve, J., C. W. Schadt, L. Carpenter-Boggs, S.H. Kang, **J.-Z. Zhou**, and J. P. Reganold. 2010. Effects of soil type and farm management on soil ecological functional genes and microbial activities. *The ISME J*, 4, 1099-1107.
41. Kimes, N. E., J. D. Van Nostrand, E. Weil, **J.-Z. Zhou**, and P.J. Morris. 2010. Microbial functional structure of *Montastraea faveolata*, an important Caribbean reef-building coral, differs between healthy and yellow-band diseased colonies. *Environ. Microbiol*. 12: 541-556.
42. Van Nostrand, J. D., S. Kang, Y. Deng, Y. Liang, Z. He, and **J.-Z. Zhou**. 2010. Monitoring Microbial Activity with GeoChip. In: *Microbial Metal and Metalloid Metabolism: Advances and Applications*. ASM Press, Washington DC, pp to be determined. (Invited book chapter, Submitted)
43. Hemme, C. L., Y. Deng, T. J. Gentry, M. W. Fields, L. Wu, Z. Fang, S. Barua, K. Barry, S. Green-Tringe, D. B. Watson, Z. He, T. C. Hazen, J. M. Tiedje, E. M. Rubin and **J.-Z. Zhou**. 2010. Metagenomic insights into evolution of a uranium-contaminated groundwater

- microbial community. The ISME J, 5: 660-672. (Highlighted by The Scientist, <http://www.the-scientist.com/blog/display/57342/>)
44. Van Nostrand, J. D., Z. He, and **J.-Z. Zhou**. 2010. Microarray analysis of environmental samples. In: Environmental Microbiology: Current Technology and Water Applications. Horizon Scientific, Norwich, UK, pp to be determined. (Invited book chapter, In Press).
  45. He, Z.H., M. Xu, D. Ye, S. Kang, L. Kellogg, L.Y. Wu, J. D. Van Nostrand, S. E. Hobbie, P. B. Reich, and **J.-Z. Zhou**. 2010. Elevated CO<sub>2</sub> Drives Marked Divergence in Soil Microbial Community Composition and Functional Structure. Ecol. Lett, 13: 564-575.
  46. Van Nostrand, J. D., Z. He, and **J.-Z. Zhou**. 2010. Analysis of microbial communities by functional gene Arrays. In: L. Barton, M. Mandl and A. Loy (eds) Geomicrobiology: Molecular and Environmental Perspective. Springer, New York, (Invited book chapter, In press).
  47. Van Nostrand, J. D, L. Wu, Z. He, and **J.-Z. Zhou**. 2010. GeoChips for analysis of microbial functional communities. In: J. R. van der Meer (ed) Handbook of Hydrocarbon and Lipid Microbiology, vol 4, Experimental Protocols and Appendices. Springer, New York, pp to be determined. (Invited book chapter, In press)
  48. Van Nostrand, J. D, Y. Liang, Z. He, G. Li, and **J.-Z. Zhou**. 2010. GeoChip: A high throughput genomic tool for linking community structure to functions. In: K. N. Timmis (ed) Handbook of Hydrocarbon and Lipid Microbiology, vol 3, Consequences of microbial interactions with hydrocarbons, oils, and lipids. Springer, New York, pp to be determined. (Invited book chapter, In press)
  49. Luo. W.S., S. D. Kelly, K. M. Kemner, D. Watson , **J.-Z. Zhou**, P.M. Jardine, and B.H. Gu . 2009. Sequestering Uranium and Technetium through Co-Precipitation with Aluminum in a Contaminated Acidic Environment. Environ Sci & Technol., 43: 7516-7522.
  50. Liebich, J. T. Wachtmeister, **J.-Z. Zhou**, and P. 2009. Degradation of Diffuse Pesticide Contaminants: Screening for Microbial Potential Using a Functional Gene Microarray. VADOSE ZONE JOURNA, 8 : 703-710.
  51. Brajesh K. Singh, B.K., C. D. Campbell, S. J. Sorenson, and **J.-Z. Zhou**. 2009. Soil genomics is the way forward. Nat. Microbiol. Rev., 7: 10 , DOI: 10.1038/nrmicro2119-c1| ISSN 1740-1526.
  52. Gentry, T.J., Z. He, and **J.-Z. Zhou**. 2009. Detection and Characterization of Uncultivated Microorganisms using Microarrays (An invited book chapter). MICROBIOLOGY MONOGRAPHS 10:35-58.
  53. Tas, N., M. H.A. van Eekert, G. Schraa, **J.-Z. Zhou**, W. M. de Vos, and H. Smidt. 2009. Tracking Functional Guilds: *Dehalococcoides* spp. in European River Basins Contaminated with Hexachlorobenzene. Appl. Environ. Microbiol., 75: 4696-4704.
  54. Liang, Y.L., Z.L. He, H.C. Gao HC, G.Z. Qiu, **J.-Z. Zhou**, and X.-D. Liu XD. 2009. Characterization of cytochrome mutants for pellicle formation in *Shewanella oneidensis* MR-1. *Transactions of Nonferrous Metals Society of China* 19: 700-706.
  55. Liang, Y.T, G. Li, J. D. Van Nostrand, Z.-L. He, L.Y. Wu, Y. Deng, X. Zhang, and **J.-Z. Zhou**. 2009. Microarray-based analysis of microbial functional diversity along an oil contamination gradient in oil field. FEMS Microbiol. Ecol., 70: 324-333.
  56. Walker, C. B., Z.L. He, Z. K. Yang, J. A. Ringbauer, Jr., **J.-Z. Zhou**, G. Voordouw, J. D. Wall, A. P. Arkin, T.C. Hazen, S. Stolyar, and D. A. Stahl. 2009. The Electron Transfer System of Syntrophically Grown *Desulfovibrio vulgaris*. J. Bacteriol. 191: 5793-5801.
  57. Feng, X.Y., H. Mouttaki, L. Lin, R. Huang, B. Wu, C. L. Hemme, Z.H. He, B. Zhang, L. Hicks, J. Xu, **J.-Z. Zhou**, and Y. J. Tang. 2009. Characterization of the Central Metabolic Pathways in *Thermoanaerobacter* sp. X514 via Isotopomer-Assisted Metabolite Analysis.

- Appl. Environ. Microbiol, 75: 5001-5008.
58. He, Q., P. M. Lokken, and **J.-Z. Zhou**. 2009. Characterization of the Impact of Acetate and Lactate on Ethanol Fermentation by *Thermoanaerobacter ethanolicus*. *Bioresource Technology*, 100: 5955-5965.
  59. Gao, H., Z.K Yang, S. Barua, S. B. Reed, M. F. Romine, K. H. Nealson, J. K. Fredrickson, J. M. Tiedje, and **J.-Z. Zhou**. 2009. Reduction of nitrate in *Shewanella oneidensis* depends on atypical NAP and NRF systems with NapB as a preferred electron transport protein from CymA to NapA. *The ISME J.*, 3: 966-976.
  60. Ning, J., J. Liebich, M. Kastner, **J.-Z. Zhou**, A. Schaffer, P. and Burauel. 2009. Different influences of DNA purity indices and quantity on PCR-based DGGE and functional gene microarray in soil microbial community study. *Appl. Microbiol. Biotechnol.*, 82: 983-993
  61. Van Nostrand, J. D, W.-M. Wu, L. Wu, Y. Deng, J. Carley, S. Carroll, Z. He, B. Gu, J. Luo, C. Criddle, P. Jardine, J. M. Tiedje, T. C. Hazen, **J.-Z. Zhou**. 2009. GeoChip-based analysis of functional microbial communities in a bioreduced uranium-contaminated aquifer during reoxidation by oxygen. *Environ. Microbiol.*, 11: 2611-2626.
  62. Waldron, P. J., J. D. Van Nostrand, D. B. Watson, Z. He, L. Wu, P. M. Jardine, T. C. Hazen, and **J.-Z. Zhou**. 2009. GeoChip analysis of subsurface microbial communities impacted by heavy metal and nitrate contamination. *Environ. Sci. Technol.*, 43: 3529-3534.
  63. Wang, A.J., W. Z., Liu, S.A. Cheng, D.F. Xing, **J.-Z. Zhou**, and B. E. Logan. 2009. Source of methane and methods to control its formation in single chamber microbial electrolysis cells. *International Journal of Hydrogen Energy*, 34: **3653-3658**.
  64. Walker C, S. S. Stolyar, D. Chivian, N. Pinel, J. A. Gabster, P. S. Dehal, Z. He, Z. K. Yang, H. B. Yen, **J.-Z. Zhou**, J. D. Wall, T. C. Hazen, A. P. Arkin, D. A. Stahl. 2009. Contribution of mobile genetic elements to *Desulfovibrio vulgaris* genome plasticity. *Environ Microbiol.*, 11: 2244-2252.
  65. Yang Y. , D. P. Harris, F. Luo, W. Xiong, M. Joachimiak, L. Wu, P. Dehal, J. Jacobsen, Z. Yang, A. V. Palumbo, A. P. Arkin, and **J.-Z. Zhou**. 2009. Snapshot of Iron Response in *Shewanella oneidensis* by Gene Network Reconstruction. *BMC Genomics*, *BMC Genomics* 2009, **10**:131 doi:10.1186/1471-2164-10-131.
  66. He, Z., and **J.-Z. Zhou**. 2009. Selection of oligonucleotide probes for microarrays. *Molecular Microbial Ecology Manual 2nd* (Invited review, in press).
  67. Wang, F., H. Zhou, J. Meng, X.T. Peng, L. Jiang, P. Sun, C. Zhang, J. D. Van Nostrand, Y. Deng, Z. He, L. Wu, **J.-Z. Zhou**, X. Xiao. 2009. GeoChip-based Analysis of Metabolic Diversity of Microbial Communities at the Juan de Fuca Ridge Hydrothermal Vent. *Proc Nat. Acad. Sci*, 106: 4840-4845
  68. Liang, Y., J. Wang, J. D. Van Nostrand, **J.-Z. Zhou**, X. Zhang, G. Li. 2009. Microarray-based functional gene analysis of soil microbial communities in ozonation and biodegradation of crude oil. *Chemosphere*, 75: 193-199.
  69. **Zhou, J.-Z.**, 2009. Predictive Microbial Ecology. *Microbial Biotechnology*, **2**, 154–156
  70. Yin, H., L. Cao, M. Xie, Q. Chen, G. Qiu, **J.-Z. Zhou**, L. Wu, D. Wang, X. Liu. 2008. Bacterial diversity based on 16S rRNA and gyrB genes at Yinshan mine, China. *Syst. & Appl. Microbiol.* 31: 302-311.
  71. Mason, O. U., C. A DiMeo-Savoie, J. D. Van Nostrand, **J.-Z. Zhou**, M. R. Fisk, and S. J. Giovannoni. 2009. Prokaryotic diversity, distribution, and preliminary insights into their role in biogeochemical cycling in marine basalts. *ISME J*, 3: 231-242.
  72. He, Z, J. D. Van Nostrand, L. Wu, and **J.-Z. Zhou**. 2008. Development and application of functional gene arrays for microbial community analysis. *Transactions of Nonferrous Metals Society of China* **18**: 1319-1327 (Invited review).

73. Deng, Y., Z. He, J. D. Van Nostrand, **J.-Z. Zhou**. 2008. Design and analysis of mismatch probes for long oligonucleotide microarrays. *BMC Genomics*, *BMC Genomics* 2008, **9**:491doi:10.1186/1471-2164-9-491
74. Van Nostrand, Joy, D., Y. Liang, Z. He, and J.-Z. Zhou. 2008. GeoChip: A high throughput genomic tool for linking community structure to functions. Pp. ?-?. In: J. R. van der Meer (ed) *Handbook of Hydrocarbon and Lipid Microbiology*, vol 4, *Experimental Protocols and Appendices*. Springer, New York (**Invited**).
75. Van Nostrand, J. D, Y. Liang, Z. He, G. Li, and **J.-Z. Zhou**. GeoChip: A high throughput genomic tool for linking community structure to functions. Pp. ?-?. In: K. N. Timmis (ed) *Handbook of Hydrocarbon and Lipid Microbiology*, vol 3, *Consequences of microbial interactions with hydrocarbons, oils, and lipids*. Springer, New York. (**Invited**).
76. Rodrigues, D. F., N. Ivannova, Z. He, M. Huebner, **J.-Z. Zhou** and J. M. Tiedje. 2008. Architecture of thermal adaptation in an *Exiguobacterium sibiricum* strain isolated from 3 million year old permafrost: A genome and transcriptome approach. *BMC Genomics* 2008, **9**:547doi:10.1186/1471-2164-9-547.
77. Gao, H., D. Pattison, T. Yan, D. M. Klingeman, X. Wang, J. Petrosino, L. Hemphill, X. Wan, A.B. Leaphart, G. Weinstock, T. Palzkill, and **J.-Z. Zhou**. 2008. Generation and Validation of a *Shewanella oneidensis* MR-1 Clone Set for Protein Expression and Phage Display. *PLoS One*, **3**(8):e2983.
78. Wang, X., H. Gao, Y. Shen, G. M. Weinstock, **J.-Z. Zhou**, and T. Palzkill. 2008. A High-throughput Percentage-of-Binding Strategy to Measure Binding Energies in DNA-Protein Interactions: Application to Genome Scale Site Discovery. *Nucl. Acids Res.*, **36**: 4863-4871
79. Hwang, C., W. Wu, T.J. Gentry, J. Carley, S.L. Carroll, D. Watson, P.M. Jardine, **J.-Z. Zhou**, C.S. Criddle, and M.W. Fields:2008. Bacterial Community Succession During in situ Uranium Bioremediation: Spatial Similarities Along Controlled Flow Paths. *The ISME J*, **3**: 47-64.
80. **Zhou, J.-Z\***, S. Kang\*, C. W. Schadt, and C.T. Garten, Jr. 2008. Spatial Scaling of Functional Gene Diversity across Various Microbial Taxa. *Proc Nat. Acad. Sci*, **105**: 7768-7773. \*equal contribution
81. Wu\*, L., L. Kellogg, A.H. Devol, A.V. Palumbo, J.M. Tiedje, and **J.-Z. Zhou\***. 2008. Microarray-Based Characterization of Microbial Community Functional Structure and Heterogeneity in Marine Sediments From the Gulf of Mexico. *Appl. Environ. Microbiol*, **74**: 4516-4529. \*equal contribution.
82. Yang, Y., M. Zhu, L. Wu, and **J.-Z. Zhou**. 2008. Assessment of Data Processing to Improve Reliability of Microarray Experiments Using Genomic DNA Reference. *BMC Genomics* 2008, **9**(Suppl 2):S5doi:10.1186/1471-2164-9-S2-S5.
83. Cardenas, E., W. Wu, M.B. Leigh, J. Carley, S. Carroll, T. Gentry, J. Luo, D. Watson, B. Gu, M. Ginder-Vogel, P. K. Kitanidis, P.M. Jardine, **J.-Z., Zhou**, C.S. Criddle, T.L. Marsh and J.M. Tiedje. 2008. Microbial Communities in Contaminated Sediments Associated with Bioremediation of Uranium to Submicromolar Levels. *Appl. Environ. Microbiol*, **74**: 3718-3729.
84. Wu, LY., X.D. Liu, M.W. Fields, D.K. Thompson, C.E. Bagwell, J.M. Tiedje, T.C. Hazen, and **J.-Z. Zhou**. 2008. Microarray-based whole-genome hybridization as a tool for determining prokaryotic species relatedness. *The ISME J*, **2**, 642–655.
85. He, Z.L., and **J.-Z. Zhou**. 2008. Empirical determination of signal to noise ratio (SNR) thresholds for microarray analysis. *Appl. Environ. Microbiol*. **74**: 2957–2966.
86. Gao, H.C., X.H. Wang, Z.K. Yang, T. Palzkill, and **J.-Z. Zhou**. 2008. Probing Regulon of ArcA in *Shewanella oneidensis* MR-1 by Integrated Genomic Analyses. *BMC Genomics*, **9**:

42 (17 pages)

87. Yang, Y.F., D.P. Harris, F. Luo, L.Y. Wu, A.B. Parsons, A. V. Palumbo and **J.-Z. Zhou**. 2008. Characterization of the *Shewanella oneidensis* Fur Gene: Roles in Iron and Acid Tolerance Response. *BMC Genomics* 2008, **9**(Suppl 1):S11.
88. Pereira, P.M. Q.He, A.V. Xavier, **J.-Z. Zhou**, I.A. C. Pereira and R. O. Louro. 2008. Transcriptional Response of *Desulfovibrio vulgaris* Hildenborough to Oxidative Stress Mimicking Environmental Conditions. *Archives of Microbiology*, 189: 451-461
89. Pereira, P. M., Q. He, F. M. A. Valente, A. V. Xavier, **J.-Z. Zhou**, I. A. C. Pereira & R. O. Louro. 2008. Energy metabolism in *Desulfovibrio vulgaris* Hildenborough: insights from transcriptome analysis. *Antonie van Leeuwenhoek International Journal of General and Molecular Microbiology*, 93:347-362.
90. Yin, H.Q., L. Cao, G. Qiu, D. Wang, L. Kellogg, **J.-Z. Zhou**, X. Liu, Z. Dai, J. Ding X. Liu. 2008. Molecular diversity of 16S rRNA and gyrB genes in copper mines. *Archives of Microbiology*, 189: 101-110.
91. Huang, Z., C. Zhang, B.P. Hedlund, J. Wiegel, **J.-Z. Zhou**. 2007. Molecular phylogeny of uncultivated Crenarchaeota in Great Basin hot springs of moderately elevated temperature. *Geomicrobiology J.* 24: 535-542.
92. Amos, B. K., Y. Sung, K. E. Fletcher, T. J. Gentry, **J.-Z. Zhou**, and F. E. Löffler. 2007. Detection and Quantification of *Geobacter lovleyi* Strain SZ: Implications for Bioremediation at Tetrachloroethene- (PCE-) and Uranium-Impacted Sites. *Appl. Environ. Microbiol.*, 73: 6898-6904.
93. Wang F., J. Meng, X. Xiao, X. Peng, H. Zhou , Z. He, **J.-Z. Zhou** 2007. The metabolic diversity and dynamics of deep-sea hydrothermal vent microbial communities revealed by molecular approaches. *Journal of China University of Geosciences*, 18:360.
- Bretschger, O., A. Obraztsova, C. A. Sturm, I. Chang, Y. A. Gorby, S. B. Reed, D. E. Culley, C. L. Reardon, S. Barua, M.F. Romine, **J.-Z. Zhou**, A.S. Beliaev, R. Bouhenni, D. Saffarini, F. Mansfeld, B.H. Kim, J. K. Fredrickson, and K.H. Nealson. 2007. An exploration of current production and metal oxide reduction by *Shewanella oneidensis* MR-1 wild-type and mutants. ***Appl. Environ. Microbiol.*, 73:7003-7012.**
94. Wu, W., J. Carley, J. Luo, M. A. Ginder-Vogel, E. Cardenas, M.B. Leigh, C.C. Hwang, S. D. Kelly, C. Ruan, L. Wu, J. Van Nostrand, T. Gentry, K. Lowe, T. Mehlhorn, S. Carroll, M. W. Fields, B. Gu, D. Watson, K. M. Kemner, T. Marsh, J.M. Tiedje, **J.-Z. Zhou**, Scott Fendorf, Peter K. Kitanidis, Philip M. Jardine, and Craig S. Criddle. 2007. In Situ Bioreduction of Uranium (VI) to Submicromolar Levels and Reoxidation by Dissolved Oxygen. *Environ.Sci.Technol.* 41: 5716-5723.
95. Stolyar, S., Q. He, M.P. Joachimiak, Z. He, Z. K. Yang, S. E. Borglin, D.C. Joyner, K. Huang, E. Alm, T. C. Hazen, **J.-Z. Zhou**, J.D. Wall, A.P. Arkin, and D.A. Stahl. 2007. Response of *Desulfovibrio vulgaris* to alkaline stress. *J. Bacteriol.* 189: 8944-8952
96. Mukhopadhyay A., A.M. Redding, M.P. Joachimiak, A.P. Arkin, S.E. Borglin, P.S. Dehal, R. Chakraborty, J.T. Geller, T.C. Hazen, Q.He, D.C. Joyner, V.J. J. Martin, J.D. Wall, Z. K. Yang, **J.-Z. Zhou**, and J.D. Keasling. 2007. Cell wide responses to low oxygen exposure in *Desulfovibrio vulgaris* Hildenborough. *J. Bacteriol.*, 189:5996-6010.
97. Luo, W., W. Wu, T. Yan, C. S. Criddle, P. M. Jardine, **J.-Z. Zhou**, and B. Gu. 2007. Influence of Bicarbonate, Sulfate, and Electron Donors on Biological reduction of Uranium and Microbial Community Composition. *Applied Microbiology and Biotechnology*: 77: 713-721
98. Yin, H., L. Cao, G. Qiu, D. Wang, L. Kellogg, **J.-Z. Zhou**, Z. Dai, X. Liu, 2007. Development and evaluation of 50-mer oligonucleotide arrays for detecting microbial

- populations in Acid Mine Drainages and bioleaching systems. *J. Microbiol. Methods*, 70: 165-178.
99. Yang Y., M.Wan, W. Shi, H. Peng, G. Qiu, **J.-Z. Zhou**, X. Liu. 2007. Bacterial diversity and community structure in acid mine drainage from Dabaoshan Mine, China. *Aquatic Microbial Ecology*, 47: 141-151.
  100. Luo, F., D. Yang, J. Zhong, H. Gao, L. Khan, D. K. Thompson and **J.-Z. Zhou**. 2007. Constructing gene co-expression networks and predicting functions of unknown genes by random matrix theory. *BMC Bioinformatics*, 8:299 (17 pages). \*Equal contribution.
  101. Butler, J. E., Q. He, K. P. Nevin, Z. He, **J.-Z. Zhou**, D. R. Lovley. 2007. Genomic and microarray analysis of aromatics degradation in *Geobacter metallireducens* and comparison to a *Geobacter* isolate from a contaminated field site *BMC Genomics* 8:180
  102. Caffrey, S., H. S. Park, J. Voordouw, Z. He, **J.-Z. Zhou**, and Gerrit Voordouw. 2007. Function of Periplasmic Hydrogenases in the Sulfate-Reducing Bacterium *Desulfovibrio vulgaris* Hildenborough. *J. Bacteriol.* 89: 6159–6167
  - Bender, K.S., H. Yen, C. L. Hemme, Z Yang, Z. He, Q. He, J.-Z. Zhou, K. Huang, E. J. Alm, T. C. Hazen, A. P. Arkin, and J. D. Wall. 2007.** Analysis of a Ferric Uptake Regulator (Fur) Mutant of *Desulfovibrio vulgaris* Hildenborough. *Appl. Environ. Microbiol.* 73: 5389-5400.
  103. Garten, C.T., S. Kang, D.J. Brice, C. W. Schadt, and **J.-Z. Zhou**. 2007. Variability in Soil Properties at Different Spatial Scales (1 m to 1 km) in a Deciduous Forest Ecosystem. *Soil Biol & Biochem.* 39: 2621-2627.
  104. Zhang, Y., X. Zhang, X. Liu, Y. Xiao, L. Qu, L. Wu, **J.-Z. Zhou**, 2007. Microarray-based analysis of changes in diversity of microbial genes involved in organic carbon decomposition following land use/cover changes. *FEMS Microbiology Letters* 266: 144-151.
  105. Leigh, M.B., V.H. Pellizari, O. Uhlik, R. Sutka, J. Rodrigues, N. E. Ostrom, **J.-Z. Zhou**, and J. M. Tiedje, 2007. Biphenyl-utilizing bacteria and their functional genes in a pine root zone contaminated with polychlorinated biphenyls (PCBs). *The ISME J*, 1: 134-148.
  106. Yergeau, E., Kang, S., He, **J.-Z., Zhou**, and G. A. Kowalchuk. 2007. Functional microarray analysis of nitrogen and carbon cycling genes across an Antarctic latitudinal transect. *The ISME J*. 1: 163-179
  - 107.** Gentry,T., C. Schadt, and **J.-Z. Zhou**. 2007. Functional gene array for microbial community analysis. Pp. 1052-1062. In Hurst, C.J, Crawford, R. L., Mills, A. L., Garland, J.L., Stetzenbach, L. D., and Lipson, D. A. (eds), *The 3<sup>rd</sup> edition of the ASM Manual of Environmental Microbiology*, (**Invited**), ASM Press, Washington DC.
  108. Anderssen, G., Z. He, and **J.-Z. Zhou**. 2007. Microarrays for environmental applications. In *Molecular Environmental Microbiology*, edited by W.-T. Liu and J. Janssen. In press, (invited)
  109. Gentry, T., Z. He, and **J.-Z. Zhou**. 2007. Detecting and enumerating uncultivated microorganisms: functional DNA arrays. In: *Uncultivated Microorganism*, Edited by S. Epstein, Springer, (Invited review, in press)
  110. He, Z., T. J. Gentry, C. W. Schadt, L. Wu, J. Liebich, S. C. Chong, W.M. Wu, B. Gu, P. Jardine, C. Criddle, and **J.-Z. Zhou**. 2007. GeoChip: A comprehensive microarray for investigating biogeochemical, ecological, and environmental processes. *The ISME Journal*, 1: 67-77 (**News Release by Nature Press Office: ([http://www.nature.com/ismej/press\\_releases/index.html](http://www.nature.com/ismej/press_releases/index.html))**)
  111. Luo, F., Y. Yang, C. Chen, **J.-Z. Zhou**, R. H. Scheuermann. 2007. Modular Organization of Protein Interaction Networks. *Bioinformatics.* 23: 207-214.

112. Gao, H., Z. K. Yang, T. J. Gentry, L. Wu, C. W. Schadt, and **J.-Z. Zhou**. 2007. Microarray-based Analysis of Microbial Community RNAs by Whole Community RNA Amplification (WCRA). *Appl. Environ. Microbiol.* 73: 563-571. **(The 8<sup>th</sup> of the top 20 papers most requested in 2007 (January to March) by AEM)**.
113. Wagner M., H. Smidt, A. Loy, **J.-Z. Zhou**. 2007. Unravelling Microbial Communities with DNA-Microarrays: Challenges and Future Directions. *Microb Ecol* 53:498-506
114. Zhu, M., Q. Wu, Y. Yang, **J.-Z. Zhou**. 2006. A New Approach to Identify Functional Modules Using Random Matrix Theory. *IEEE Symposium on Computational Intelligence in Bioinformatics and Computational Biology*, 1:117-123.
115. Walker, C. B., S. S. Stolyar, N. Pinel, H. Yen, Z. He, **J.-Z. Zhou**, J. D. Wall, D. A. Stahl. 2006. Recovery of temperate *Desulfovibrio vulgaris* bacteriophage using a novel host strain. *Environ. Microbiol.*, **8**:1950-1959.
- Zhou, X., and **J.-Z. Zhou**. 2006. The Arts for fabricating protein microarray. Pp. 257-270. Rampal, J. (ed), in *Microarrays: Methods and Protocols*, *Methods in Molecular Biology*, The Humana Press Inc, New Jersey, USA **(Invited)**
116. Van Nostrand, J. D., T.V. Khijniak, T.J. Gentry, M.T. Novak, A.G. Sowder, **J.-Z. Zhou**, P.M. Bertsch and P.J. Morris. 2006. Isolation and Characterization of Four Gram-Positive Nickel-Tolerant Microorganisms from Contaminated Riparian Sediments. *Microb. Ecol.* 53: 670-682.
117. Mukhopadhyay A., Z. He , E. J. Alm, A.P. Arkin, E.E. Baidoo, S.C. Borglin, W.Chen, T.C. Hazen, Q. He, H.Y.Holman, K. Huang, R. Huang, D.C. Joyner, N. Katz, M. Keller, P. Oeller, A. Redding, J. Sun, J. D. Wall, J. Wei, Z. M Yang, H. Yen , **J.-Z. Zhou** and J.D. Keasling. 2006. Salt stress in *Desulfovibrio vulgaris* Hildenborough: An integrated genomics approach. *J. Bacteriol.* 188: 4068-4078.
118. Clark, M.E., Q. He, Z. He, K. Huang, E.J. Alm, X. Wan, T.C. Hazen, A.P. Arkin, J.D. Wall, **J.-Z. Zhou**, and M.W. Fields. 2006. Temporal transcriptomic analysis of *Desulfovibrio vulgaris* Hildenborough transition into stationary phase growth during electron donor depletion. *Appl. Environ. Microbiol.* 72: 5578-5588.
119. Gentry, T., C. Schadt, and **J.-Z. Zhou**. 2006. Microarrays in microbial ecology research. *Microbial Ecology*, 52 : 159-175 **(Invited)**
120. Chourey, K., M. Thompson, J. Morrell-Falvey, N. C. VerBerkmoes, S. D. Brown, M. Shah, **J.-Z. Zhou**, M. Doktycz, R. L. Hettich, and D. K. Thompson. 2006. Global molecular and morphological effects of 24-hour chromium (VI) exposure on *Shewanella oneidensis* MR-1. *Appl. Environ. Microbiol.* 72: 6331-6344
121. Rodríguez-Martínez, E.M., E. X. Pérez, C.W. Schadt, **J.-Z. Zhou**, and A.A. Massol-Deyá. 2006. Microbial Diversity and Bioremediation of a Hydrocarbon-Contaminated Aquifer in Vega Baja, Puerto Rico. *International Journal of Environmental Research and Public Health*: 3:292-300.
122. Yan, T., **J.-Z. Zhou**, and C. Zhang. 2006. Diversity of functional genes for methanotrophs in sediments associated with gas hydrates and hydrocarbon seeps in the Gulf of Mexico. *FEMS Microbiology Ecology*: 57: 251-259.
123. Gao, H., A. Obraztova, N. Stewart, R. Popa, J. K. Fredrickson, J. M. Tiedje, K., H. Neilson, and **J.-Z. Zhou**. 2006. *Shewanella loihica* sp. nov., isolated from iron-rich microbial mats in Pacific Ocean. *Int J Syst Evol Microbiol*; 56: 1911-1916.
124. Luo, F., J. Zhong, Y. Yang, R. H. Scheuermann, and **J.-Z. Zhou**. 2006. Application of random matrix theory to biological networks. *Physics Letters A*: 357: 420-423.

125. Gao, H., Z. K. Yang, L. Wu, D. K. Thompson, and **J.-Z. Zhou**. 2006. Global Transcriptome Analysis of the Cold Shock Response of *Shewanella oneidensis* MR-1 and mutational analysis of its classical cold-shock proteins. *J. Bacteriol.*, 188:4560-4569.
126. Fields, M.F., C.E. Bagwell, S.L. Carroll, T. Yan, X. Liu, D.B. Watson, P.M. Jardine, C.S. Criddle, T.C. Hazen, and **J.-Z. Zhou**. 2006. Phylogenetic and functional biomarkers as indicators of bacterial community responses to mixed-waste contamination. *Environ. Sci. & Tech.* 40: 2601-2607.
127. Cho, C. M., T. Yan, X. Liu, L. Wu, **J.-Z. Zhou**, and L.Y. Stein. 2006. Transcriptome of *Nitrosomonas europaea* with a disrupted nitrite reductase (*nirK*) gene. *Appl. Environ. Microbiol.* 70:4450-4454.
- Wu, W.M., J. Carley, T. Gentry, M. A. Ginder-Vogel, M. Fienen, T. Mehlhorn, H. Yan, S. Carroll, J. Nyman, J. Luo, M. E. Gentile, M. W. Fields, R. F. Hickey, D. Watson, S. Fendorf, **J.-Z. Zhou**, P. Kitanidis, P. M. Jardine, and C. S. Criddle. 2006. Field-scale bioremediation of uranium in a highly contaminated aquifer II: geochemical control of U(VI) bioavailability and evidence of U(VI) reduction. *Environ. Sci. & Tech.* 40: 3986-3995.
128. Brown, S. D., M. R. Thompson, N. C. VerBerkmoes, K. Chourey, M. Shah, **J.-Z. Zhou**, R. L. Hettich, and D. K. Thompson. 2006. Molecular Dynamics of the *Shewanella oneidensis* Response to Chromate Stress. *Molecular and Cellular Proteomics.* 5: 1054-1071.
129. Gao, W., Y. Liu, C. S. Giometti, L. Wu, X. Liu, T. Yan, D. Stanek, D. Xu, Y. Xu, M. W. Fields, and **J.-Z. Zhou**. 2006. Functional annotation of a conserved hypothetical protein in *Shewanella oneidensis* MR-1: a PHB-like protein involved in iron homeostasis and oxidative damage protection. *BMC Genomics*, 7:76.
130. Leaphart, A. B., D. K. Thompson, K. Huang, E. Alm, X. Wan, A. Arkin, S. D. Brown, L. Wu, T. Yan, X. Liu, G. S. Wickham, and **J.-Z. Zhou**. 2006. Transcriptome Profiling of *Shewanella oneidensis* Gene Expression Following Exposure to Acidic and Alkaline pH. *J. Bacteriol.* 188:1633-42.
131. He, Q., K. Huang, Z. He, E. Alm, M. W. Fields, T. C. Hazen, A. Arkin, J. D. Wall, and **J.-Z. Zhou**. 2006. Energetic Consequences of Nitrite Stress in *Desulfovibrio vulgaris* Hildenborough Inferred from Global Transcriptional Analysis. *Appl. Environ. Microbiol.* 72:4370-4381.
- 132.** Luo, F., J. Zhong, Y. Yang, **J.-Z. Zhou**. 2006. Application of Random Matrix Theory to Microarray Profiles for Discovering Functional Gene Modules. *Physical Review E*, 73 (031924), 1-5.
133. Roh, Y., H. Gao, H. Vali, D. W. Kennedy, Z. K. Yang, W. Gao, A. C. Dohnalkova, R. D. Stapleton, J. W. Moon, T. J. Phelps, J. K. Fredrickson, and **J.-Z. Zhou**. 2006. Metal Reduction and Iron Biomineralization by a Psychrotolerant Fe(III)-Reducing Bacterium *Shewanella* sp. PV-4. *Appl. & Environ. Microbiol.* 72:3236-3244.
- 134.** Chhabra, S.R., Q. He, K. H. Huang, S. P. Gaucher, E. J. Alm, Z. He, M. Z. Hadi, T.C. Hazen, J. D. Wall, **J.-Z. Zhou**, A. P. Arkin, and A.K. Singh. 2006. Global Analysis of Heat Shock Response in *Desulfovibrio vulgaris* Hildenborough. *J. Bacteriol.* 188: 1817-1828.
135. Qiu, X., M. J. Daly, A. Vasilenko, M. V. Omelchenko, E. K. Gaidamakova, L. Wu, **J.-Z. Zhou**, G. W. Sundin and J. M. Tiedje. 2006. Transcriptome Analysis Applied to Survival of *Shewanella oneidensis* MR-1 Exposed to Ionizing Radiation and Comparison to *Deinococcus radiodurans*. *J. Bacteriol.* 188:1199-1204.

136. Wei, X., T. Yan, N. G. Hommes, X. Liu, L. Wu, C. McAlvin, M.G. Klotz, L.A. Sayavedra-Soto, **J.-Z. Zhou**, and D. J. Arp. 2006. Transcript profile of *Nitrosomonas europaea* during growth and ammonia/carbonate deprivation. *FEMS Microbiology Lett.* 257:76-83.
137. Windt, W.D, H. Gao, W. Krömer, J. Dick, N. Boon, **J.-Z. Zhou**, and W. Verstraete. 2006. Molecular characterization of an autoaggregating mutant of *Shewanella oneidensis*. *Microbiology*, 152: 721-729.
138. Brown, S. D., M. Martin, K. Huang, E. Alm, Y. Yang, A. Arkin, **J.-Z. Zhou**, and D. K. Thompson. 2006. Cellular Response of *Shewanella oneidensis* to Strontium Stress. *Appl. Environ. Microbiol.*, 72: 890-900.
139. Liebich, J., S. C. Chong, C. Schadt, Z. He, and **J.-Z. Zhou**. 2006. Improvement of oligonucleotide probe design criteria for the development of functional gene microarrays for environmental applications. *Appl. Environ. Microbiol.* 72:1688-1691.
140. Hwang, C., W. Wu, T. J. Gentry, J. Carley, S. L. Carroll, C. Schadt, D. Watson, P. M. Jardine, **J.-Z. Zhou**, R. F. Hickey, C. S. Criddle, and M.W. Fields. 2006. Changes in bacterial community structure correlate with initial operating conditions of a fieldscale denitrifying fluidized bed reactor. *Applied Microbiology and Biotechnology*, 71: 748-760.
141. Fields, M.W., J. Schryver, C. C. Brandt, T. Yan, **J.-Z. Zhou**, and A.V. Palumbo. 2006. Confidence intervals for similarity values achieved from direct sequence determination of cloned SSU rRNA genes from environmental samples. *J. Microbiol. Methods*, 65: 144-152.
142. Zhou, X., and **J.-Z. Zhou**. 2006. Characterization of Carbohydrate-Protein Interaction by Oligosaccharides (Carbohydrate) Microarrays fabricated on Aminoxyacetyl -Functionalized Glass Surface. *Biosensors & Bioelectronics*, 21: 1451-1458.
143. Gentile, M, T. Yan, S. M. Tiquia, M. W. Fields, J. Nyman, **J.-Z. Zhou**, and C. S. Criddle. 2006. Stability and Resilience in a Denitrifying Fluidized Bed Reactor. *Microbial Ecology*, 52: 311-321.
144. Gentry, T., and **J.-Z. Zhou**. 2006. Microarrays-based microbial detection and characterization. In *Advanced Techniques in Diagnostic Microbiology*, Edited by Yi-Wei Tang and Charles W. Stratton, pp 276-290. Springer, New York, NY (Invited).
145. Wu\*, L., X. Liu, C. W. Schadt, and **J.-Z. Zhou\***. 2006. Microarray-based analysis of sub-nanogram quantities of microbial community DNAs using Whole Community Genome Amplification (WCGA). *Appl. Environ. Microbiol.* 72:4931-4941. \*equal contribution. **(The 11<sup>th</sup> of the top 20 papers most requested in 2006 (October to December) by AEM)**
146. Bagwell, C. E., X. Liu, L. Wu, and **J.-Z. Zhou**. 2006. Effects of legacy nuclear waste on the compositional diversity and distributions of sulfate-reducing bacteria in a terrestrial subsurface aquifer. *FEMS Microbiology Ecology*, 55:424-431.
147. Wan, X., **J.-Z. Zhou**, and D. Xu. 2006. CodonO: a new informatics method for measuring synonymous codon usage bias within and across genomes. *International Journal of General Systems*. 35:109-125.
148. Li, X., Z. He, and **J.-Z. Zhou**. 2005. Selection of optimal oligonucleotide probes for microarrays using multiple criteria, global alignment and parameter estimation. *Nucl. Acids Res.* 33:6114-6123
149. Zhou, X., **J.-Z. Zhou**. 2005. Protein microarrays for multianalyte detection fabricated on polymeric thin film assembled with polyelectrolytes, *Proteomics*, 6:1415-1426.
150. Kataeva, I., J. Chang, H. Xu, C. Luan, **J.-Z. Zhou**, V. N. Uversky, D. Lin, P. Horanyi, Z. Liu, L. G. Ljungdahl, J. Rose, M. Luo, and B. Wang. 2005. Improving solubility of *Shewanella oneidensis* MR-1 and *Clostridium thermocellum* JW-20 proteins expressed into *Escherichia coli*. *J. Proteome Res.* 2005 4:1942-1951.

151. Mukhopadhyay, A., Z. He, E. Alm, Q. He, B. Yen, K. Huang, E., Baidoo, W. Chen, S. Borglin, A. Redding, H.Y. Holman, J. Sun, D. Joyner, N. Katz, M. Keller, **J.-Z. Zhou**, A. P. Arkin, T. C., Hazen, J. Wall, J.D. Keasling. 2005. The anatomy of salt stress in *Desulfovibrio vulgaris* Hildenborough. *Molecular & Cellular Proteomics*: 4: S384-S384.
152. Hu, S. X. Chen, C. Tu, F. Louws, **J.-Z. Zhou**, D. Shuew. 2005. High soil microbial diversity correlates with pathogen invasion but suppresses pathogen activity. *Phytopathology*, 95: S45-S45
153. Bencheikh-Latmani, R., S. M. Williams, L. Haucke, C. S. Criddle, L. Wu, **J.-Z. Zhou**, B. M. Tebo. 2005. Global Transcriptional Profiling of *Shewanella oneidensis* MR-1 During Cr(VI) and U(VI) Reduction. *Appl. Environ. Microbiol.*, 71:7453-7460.
154. Beliaev, A. S., D. M. Stanek, J. A. Klappenbach, L. Wu, D. A. Saffarini, M. F. Romine, K. H. Nealson, J. K. Fredrickson, and **J.-Z. Zhou**. 2005. Electron Acceptor-Induced Shifts in *Shewanella oneidensis* MR-1 Gene Expression Profiles. *J. Bacteriol.*, 187:7138-7145.
155. Oda, Y., S. K. Samanta, L. Wu, X. Liu, T. Yan, **J.-Z. Zhou**, C. S. Harwood. 2005. A functional genomic analysis of three nitrogenase isozymes in the photosynthetic bacterium *Rhodospseudomonas palustris*. *J. Bacteriol.*, 187: 7784-7794
156. Gu, B., W. Wu, M. A. Ginder-Vogel, H. Yan, M. W. Fields, **J.-Z. Zhou**, S. Fendorf, C. S. Criddle, and P. M. Jardine. 2005. Bioreduction of Uranium in a Contaminated Soil Column. *Environ Sci & Tech.*, 39, 4841-4847.
157. He, Z., L. Wu, M. W. Fields, **J.-Z. Zhou**. 2005. Use of Microarrays with Different Probe Sizes for Monitoring Gene Expression. *Appl. & Environ. Microbiol.*, 71: 5154–5162.
158. He, Z., L. Wu, X. Li, M. W. Fields, **J.-Z. Zhou**. 2005. Empirical establishment of oligonucleotide probe design criteria using perfect match and mismatch probes and artificial targets. *Appl. & Environ. Microbiol.*, 71:3753-3760. (**Listed as one of the top 20 papers most requested in 2005 by AEM**).
159. Wu, W., B. Gu, M. W. Fields, M. Gentile, Y. Ku, H. Yan, S. Tiquia, T. Yan, J. Nyman, **J.-Z. Zhou**, P.M. Jardine, C. S. Criddle. 2005. Reduction and Sorption of Uranium(VI) by Microbial Biomass from a Denitrifying Fluidized Bed Reactor. *Bioremediation J.*, 9:49-61.
160. Kolker, E., A. F. Picone, M. Y. Galperin, M. F. Romine, R. Higdon, K. S. Makarova, N. Kolker, G. A. Anderson, K. J. Auberry, G. Babnigg, A. S. Beliaev, P. Edlefsen, D. A. Elias, Y. Gorby, T. Holzman, J. Klappenbach, K. T. Konstantinidis, M. L. Land, M. S. Lipton, L. McCue, M. Monroe, L. Pasa-Tolic, G. Pinchuk, S. Purvine, X Qiu, M. Serres, S. Tsapin, B. A. Zakrajsek, W. Zhu, **J.-Z. Zhou**, F. W. Larimer, C. Lawrence, M. Riley, F. R. Collart, J. R. Yates, III, R. D. Smith, C. Giometti, K. Nealson, J. K. Fredrickson, and J. M. Tiedje. 2005. Global Profiling of *Shewanella oneidensis* MR-1: Expression of ‘Hypothetical’ Genes and Improved Functional Annotations. *Proc Nat. Acad. Sci.*102: 2099-2104.
161. Qiu, X., G. W. Sundin, L. Wu, **J.-Z. Zhou**, and J. M. Tiedje. 2005. Comparative analysis of differentially expressed genes in *Shewanella oneidensis* MR-1 following UVA-, UVB- and UVC exposure. *J. Bacteriol.*, 187: 3556-3564.
162. Liu, Y., W. Gao, T. Yan, L. Wu, X. Liu, E. Alm, S. Wang, A. Arkin, M. W. Fields, D. K. Thompson, and **J.-Z. Zhou**. 2005. Transcriptome Analysis of *Shewanella oneidensis* MR-1 in Response to Elevated Salt Conditions. *J. Bacteriol.*, 187: 2901-2907.

- Gao, W., Y. Liu, **J.-Z. Zhou**, and H. Pan. 2005. Effects of a Strong Static Magnetic Field on Bacterium *Shewanella oneidensis*: An Assessment by Using Whole Genome Microarray. *Bioelectromagnetics*, 26:2-6.
- 163.** Stapleton, R., Z. L. Sabree, A. V. Palumbo, C. Moyer, A. Devol, Y. Roh, and **J.-Z. Zhou**. 2005. Metal reduction at cold temperatures by *Shewanella* isolates from various marine environments. *Aquatic Microbiol.*, 38: 81–91.
164. Schadt C. W., and **J.-Z. Zhou**. Advances in Microarrays for Soil Microbial Community Analyses. (2006) In *Soil Biology Volume8: Nucleic Acids and Proteins in Soil* (Nannipieri, P. & Smalla K., eds). Springer-Verlag, Pp189-203.
165. Schadt, C. W., J. Liebich, S. C. Chong, T. J. Gentry, Z. He, H. Pan and **J.-Z. Zhou**. 2005. Design and Use of Functional Gene Microarrays (FGAs) for the Characterization of Microbial Communities. In: Savidge T, Pothulakis H (eds) *Methods in Microbiology V34: Microbial Imaging*, pp331-368, Academic Press, London (**Invited**).
166. Tiquia, S.M., M.W. Fields, and **J.-Z. Zhou**. 2004. Oligonucleotide-based functional gene arrays for analysis of microbial communities in the environment. *Molecular Microbial Ecology Manual*. Kowalchuk, G.G.; de Bruijn, F.J.; Head, I.M.; Akkermans, A.D.; van Elsas, J.D. (Eds.), Kluwer Academic Publishers, pp. 1743-1763.
167. Fields, M.W., T. Yan, S. K. Rhee, S. L. Carroll, P. Jardine, C. S. Criddle and **J.-Z. Zhou**. 2005. Impacts on microbial communities and cultivable isolates from ground water contaminated with high levels of nitric acid–uranium waste. *FEMS Microbiol. Ecol.* 53: 417–428
168. Wu, L., D. K. Thompson, X. Liu, M. W. Fields, C. E. Bagwell, J. M. Tiedje, and **J.-Z. Zhou**. 2004. Development and evaluation of microarray-based whole-genome hybridization for detection of microorganisms within the context of environmental applications. *Environ Sci & Tech.*, 38: 6775-6782.
169. Post, V.M, R.C. Izaurrealde, J.D. Jastrow, B.A. McCarl, J.E. Amonette, V.L. Bailey, P.M. Jardine, T.O. West, **J.-Z. Zhou**. 2004. Enhancement of Carbon Sequestration in U.S. Soils. *BioScience*, 54:895-908.
170. Zhou, X., L. Wu, **J.-Z. Zhou**. 2004. Fabrication of DNA microarrays on nanoengineered polymeric ultrathin film prepared by self-assembly of polyelectrolyte multilayers. *Langmuir*, 20: 8877-8885.
- Qiu, X., R. A. Hurt, L. Wu, C. Chen, J. M. Tiedje, and **J.-Z. Zhou**. 2004. Detection and quantification of copper-denitrifying bacteria by quantitative competitive PCR. *J. Microbiol Methods*, 59:199-210.
171. Ye, Q., Y. Roh, S. L. Carroll, B. Blair, **J.-Z. Zhou**, C. Zhang and M. W. Fields. 2004. Alkaline, anaerobic respiration: isolation and characterization of a novel, alkaliphilic, metal-reducing bacterium. *Appl. Environ. Microbiol.* 70:5595-5602.
172. Zhou, X., and **J.-Z. Zhou**. 2004. Improving the signal sensitivity and photostability of DNA hybridizations on microarrays by using dye-doped core-shell silica nanoparticles. *Anal. Chem.*, 76:5302-5312.
173. Gao, H., Y. Wang, X. Liu, T. Yan, L. Wu, E. Alm, A. Arkin, D. K. Thompson, and **J.-Z. Zhou**. 2004. Global Transcriptome Analysis of the Heat Shock Response of *Shewanella oneidensis*. *J. Bacteriol.*, 186: 7796-7803.
174. Wan, X., N.C. VerBerkmoes, L. A. McCue, D. Stanek, H. Connelly, L. Wu, X. Liu, T. Yan, A. Leaphart, R. L. Hettich, **J.-Z. Zhou**, and D. K. Thompson. 2004. Defining the *Shewanella oneidensis* FUR Regulon: Integration of Genome-Wide Expression Analysis,

- Proteome Characterization, and Regulatory Motif Discovery. \*Equal contribution. *J. Bacteriol.* 186: 8385-8400.
175. Wan, X., D. Xu, A. Kleinhofs and **J.-Z. Zhou**. 2004. Quantitative relationship between synonymous codon usage bias and GC composition across the unicellular genomes. *BMC Evolutionary Biology* 2004, 4:19
  176. Palumbo, A.V., J. Schryver, M. Fields, C. Bagwell, and **J.-Z. Zhou**, T. Yan, X. Liu, and C. T. Brandt. 2004. Coupling of Functional Gene Diversity and Geochemical Data from Environmental Samples. *Appl. Environ. Microbiol.* 70:6525-6534.
  177. Luo, F., L. Khan, F. Bastani, I. Yen and **J.-Z. Zhou**. 2004. A Dynamically Growing Self-organizing Tree (DGSOT) for Hierarchical Clustering Gene Expression Profiles. *Bioinformatics*, 20: 2605-2617.
  178. Rhee\*, S.K, X. Liu, L. Wu, S. C. Chong, X. Wan and **J.-Z. Zhou\***. 2004. Detection of genes involved in biodegradation and biotransformation in microbial communities using 50-mer oligonucleotide microarrays. *Appl. Environ. Microbiol.* 70:4303-4317. \*Equal contribution.
  179. Tiquia, S.M., L.Wu, S.C. Chong, S. Passovets, D. Xu, Y. Xu, and **J.-Z. Zhou**. 2004. Evaluation of 50-mer oligonucleotide arrays for detecting microbial populations in environmental samples. *Biotechniques*. 36: 664-675.
  180. **Zhou, J.-Z.**, B. Xia, H. Huang, A.V. Palumbo, and J. M. Tiedje. 2004. Microbial diversity and heterogeneity in sandy subsurface soils. *Appl. Environ. Microbiol.*, 70: 1723-1734.
  181. **Zhou, J.-Z.**, and D. K. Thompson, 2004. Microarray technology and applications in environmental microbiology. Vol 82: pp 183-268. D.L. Sparks (Editor-in-Chief), *Advances in Agronomy*. Academic Press, New York (**Invited**).
  182. Liu, Y., A. Venkateswaran, and **J.-Z. Zhou**, 2004. Functional Genomic Analysis of *Deinococcus radiodurans* Resistance to Ionizing Radiation. European Symposium on Environmental Biotechnology on April 25-28, 2004.
  183. Liu, X., C. Bagwell, L. Wu, A. H. Devol, and **J.-Z. Zhou**. 2003. Molecular Diversity of Sulfate-Reducing Bacteria from Two Different Continental Margin Habitats. *Appl. Environ. Microbiol.*, 69:6073-6081. \*Equal contribution.
  - Zhou, J.-Z.**, B. Xia, H. Huang, D. S. Treves, L. J. Hauser, R. J. Mural, A. V. Palumbo, and J. M. Tiedje. 2003. Bacterial phylogenetic diversity and a novel candidate division of two humid region, sandy surface soils. *Soil Biology and Biochemistry*, 35:915-924.
  184. Wan, X., D. Xu, and **J.-Z. Zhou**. 2003. A new informatics method for measuring synonymous codon usage bias. In *Intelligent engineering systems through artificial neural networks*, vol 13, eds. Dagli et al., p1101-1018. New York, NY: ASME Press
  185. Liu\*, Y., **J.-Z. Zhou\***, M. Omelchenko, A. Beliaev, A. Venkateswaran, J. Stair, L. Wu, D. K. Thompson, D. Xu, I. B. Rogozin, E. K. Gaidamakova, M. Zhai, K. S. Makarova, E. V. Koonin, and M. J. Daly. 2003. Transcriptome dynamics of *Deinococcus radiodurans* recovering from ionizing radiation. *PNAS*, 100: 4191-4196. \*equal contribution. (Commentary by Jeremy S. Edwards and John R. Battista. 2003. *TRENDS in Biotechnology*: 21: 381-382).
  186. Liu, X., S. M. Tiquia, G. Holguin, L. Wu, S. C. Nold, A. H. Devol, K. Luo, A. V. Palumbo, J. M. Tiedje, and **J.-Z. Zhou**. 2003. Molecular diversity of denitrifying genes in continental margin sediments within the oxygen deficient zone of the Pacific Coast of Mexico. *Appl. Environ. Microbiol.*, 69:3549-3560.
  187. **Zhou, J.-Z.** 2003. Microarrays for bacterial detection and microbial community analysis. *Curr Opin. Microbiol.* 6:288-294. (**Invited**)

- 188.** Yost, C., L. Hauser, F. Larimer, D.K. Thompson, A. Beliaev, **J.-Z. Zhou**, Y. Xu, and D. Xu. 2003. A computational study of *Shewanella oneidensis* MR-1: Structural prediction and functional inference of hypothetical proteins. *Omics: A Journal of Integrative Biology*.7:177-191.
189. Palumbo, A.V., S. Fisher, J. R. Tarver, W. L. Daniels, Z. Yang, S. M. Tiquia, L. Wu, and J.-Z. Zhou, and J. Amonette,. 2003. Issues with the Use of Fly Ash for Carbon Sequestration Proceedings of the Second National Conference on Carbon Sequestration. Hilton Mark Center, Alexandria, Virginia. May 5-8, 2003.
190. Yan, T., M. W. Fields, L. Wu, Y. Zu, J. M. Tiedje and **J.-Z. Zhou**. 2003. Molecular diversity and characterization of nitrite reductase gene fragments (*nirK* and *nirS*) from nitrate- and uranium-contaminated groundwater. *Environ. Microbiol.*, 5:13-24. \*equal contribution.
191. Roh, Y., C. Zhang, H. Vali, R.J. Lauf, **J.-Z. Zhou**, and T. J. Phelps. 2003. Biogeochemical and environmental factors in Fe biomineralization: magnetite and siderite formation. *Clays and Clay Minerals*. 51: 83-95.
192. Treves, D. S., B. Xia, **J.-Z. Zhou** and J. M. Tiedje. 2003. Spatial isolation maintains microbial diversity in a large particle matrix. *Microbial Ecol.*, 45:20-8.
193. **Zhou, J.-Z.**, and D. K. Thompson. 2002. Microarrays: Application in environmental microbiology. p. 1968-1979. Bitton, G. (Editor in Chief), *The Encyclopedia in Environmental Microbiology*, John Wiley & Sons, New York. **(Invited)**
194. Roh, Y., S. Liu, G. Li, H. Huang, T. J. Phelps, and **J.-Z. Zhou**. 2002. Isolation and characterization of metal-reducing Thermoanaerobacter strains from deep subsurface environments. *Appl. Environ. Microbiol.*, 68:6013-6020.
195. **Zhou, J.-Z.**, and J. H. Miller. 2002. Microbial genomics, challenges and opportunities — The 9<sup>th</sup> International Conference on Microbial Genomes. *J. Bacteriol.*, 184: 4327-4333 **(Invited)**.
196. Beliaev, A. S., D. K. Thompson, M. Fields, L. Wu, D. P. Lies, K. H. Nealson, and **J.-Z. Zhou**. 2002. Microarray Transcription Profiling of a *Shewanella oneidensis* *etrA* Mutant. *J. Bacteriol.* 184: 4612-4616.
197. Xu, D., G. Li, L. Wu, **J.-Z. Zhou**, and Y. Xu. 2002. PRIMEGENS: A Computer Program for Robust and Efficient Design of Gene-Specific Targets on Microarrays. *Bioinformatics*, 18:1432-1437, 2002.
198. **Zhou, J.-Z.**, and D. K. Thompson. 2002. Challenges in applying microarrays to environmental studies. *Curr. Opin. Biotech.* 13:204-207. **(Invited)**
199. Taranenko N. I., R. Hurt, **J.-Z. Zhou**, N. R. Isola, H. Huang, S.H. Lee, C. H. Chen. 2002. Laser desorption mass spectrometry for microbial DNA analysis. *J. Microbiol. Methods* 48: 101-106.
200. **Zhou, J.-Z.**, and J. M. Tiedje. 2002. New DOE program expands dramatically beyond microbial genomics. *ASM News*: 68:110-111. **(Invited)**
201. **Zhou, J.-Z.**, B. Xia, D. S. Treves, T. L. Marsh, R. V. O'Neill, L. Wu, A. V. Palumbo and J. M. Tiedje. 2002. Spatial and resource factors influencing high soil microbial diversity. *Appl. Environ. Microbiol.* 68: 326-334.
202. Thompson D.K., A. S. Beliaev, C. S. Giometti, S. L. Tollaksen, T. Khare, D. P. Lies, K. H. Nealson, H. Lim, J. Yates III, C. C. Brandt, J. M. Tiedje, and **J.-Z. Zhou** 2002. Transcriptional and Proteomic Analysis of a Ferric Uptake Regulator (Fur) Mutant of *Shewanella oneidensis*: Possible Involvement of Fur in Energy Metabolism, Transcriptional Regulation, and Oxidative Stress. *Appl. Environ. Microbiol.* 68:881-892.

203. Beliaev, A. S., D. K. Thompson, C. S. Giometti, G. Li, J. Yates III, K. H. Nealson, J.M. Tiedje, J. F. Heidelberg, and **J.-Z. Zhou**. 2002. Gene and Protein Expression Profiles of *Shewanella oneidensis* During Anaerobic Growth with Different Electron Acceptors. *Omics: A Journal of Integrative Biology* 6: 39-60.
204. Schut, G. J., **J.-Z. Zhou**, and M. W. Adams. 2002. DNA microarray analysis of the hyperthermophilic archaeon *Pyrococcus furiosus*: Evidence for a new type of sulfur-reducing enzyme complex. *J. Bacteriology* 183: 7027-7036.
205. Gu, B., D. B. Watson, L. Wu, D. H. Phillips, D. C. White, and **J.-Z. Zhou**. 2002. Microbiological characteristics in a zero-valent iron reactive barrier. *Environ. Monitoring Assessment*: 77: 293-309.
206. Wu, L., D. Thompson, G. Li, R. Hurt, H. Huang, J. M. Tiedje, and **J.-Z. Zhou**. 2001. Development and Evaluation of Functional Gene Arrays for Detection of Selected Genes in the Environment. *Appl. Environ. Microbiol.* 67: 5780-5790.
207. Murray, A. E., D. Lies, G. Li, K. Nealson, **J.-Z. Zhou**, J. M. Tiedje. 2001. DNA:DNA hybridization to microarrays reveals gene-specific differences between closely related microbial genomes. *PNAS*, 98: 9853-9858.
208. Hurt, R. A., X. Qiu, L. Wu, Y. Roh, A. V. Palumbo, J. M. Tiedje, and **J.-Z. Zhou**. 2001. Simultaneous Extraction of RNA and DNA from Environmental Samples. *Appl. Environ. Microbiol.* 67: 4495-4503.
209. Sepulveda-Torres, L. C., **J.-Z. Zhou**, C. Guasp, J. Lalucat, D. Knaebel, J. L. Plank and C. S. Criddle. 2001. Pseudomonas strain KC represents a new genomovar within *Pseudomonas stutzeri*. *Int. Syst. J. Bact.* 51: 2013-2019.
210. Qiu, X., L. Wu, H. Huang, P. E. McDonel, A.V. Palumbo, J. M. Tiedje, and **J.-Z. Zhou**. 2001. Evaluation of PCR-generated chimeras, mutations, and heteroduplexes with 16S rRNA gene-based cloning. *Appl. Environ. Microbiol.* 67: 880-887.
211. Xia, B., D. S. Treves, **J.-Z. Zhou**, J. M. Tiedje. 2001. Soil microbial community diversity and driving mechanisms. *Prog. Nat. Sci.* 11: 818-824.
212. Zhang, C., J. Horita, D. R. Cole, **J.-Z. Zhou**, D. R. Lovley, and T. J. Phelps. 2001. Temperature-dependent oxygen and carbon isotope fractions of biogenic siderite. *Geochimica et Cosmochimica Acta.* 65: 2257-2271.
213. Palumbo A. V., **J.-Z. Zhou**, C. Zhang, R. D. Stapleton, B. L. Kinsall, and T. M. Phelps. 2001. Biotransformations and biodegradation in extreme environments. P. 549-571. In *Biotransformations: Bioremediation Technology for Health and Environmental Protection* (eds. Singh, V. P. and Stapleton, R. D.). Elsevier, London.
214. Gruntzig, V., S. C. Nold, **J.-Z. Zhou**, and J. M. Tiedje. 2001. *Pseudomonas stutzeri* nitrite reductase gene abundance in environmental samples measured by real-time PCR. *Appl. Environ. Microbiol.* 67: 760-768.
215. **Zhou, J.-Z.**, S. Liu, B. Xia, C. Zhang, A. V. Palumbo, and T. J. Phelps. 2001. Molecular characterization of thermophilic iron-reducing enrichment cultures from deep subsurface environments. *Journal of Applied Microbiology* 90: 96-105.
216. **Zhou, J.-Z.** and A. V. Palumbo. 2000. Sequence to function: The 7<sup>th</sup> Conference on Small Genomes. *Genetica* 108: vii-ix.
217. Tiedje J. M., J. Cho, A. Murray, D. Treves, B. Xia, and **J.-Z. Zhou**. 2001. Soil Teaming with Life: New Frontiers for Soil Science. p. 393-412. In *Sustainable Management of Soil Organic Matter* (eds, R. M. Rees, B. C. Ball, C. D. Campbell and C. A. Watson), CABI International.

218. Nold, S. C., **J.-Z. Zhou**, A. H. Devol, and J. M. Tiedje. 2000. Pacific Northwest marine sediments contain-Proteobacterial ammonia oxidizing bacteria. *Appl. Environ. Microbiol.* 66: 4532-4535.
219. Xu, D., Y. Xu, G. Li, and **J.-Z. Zhou**. 2000. A computer program for generating gene-specific fragments for microarrays. P. 3-4, In Miyano, S., R. Shamir, and T. Takagi (eds), *Currents in Computational Molecular Biology*, Universal Academy Press, Inc, Tokyo, Japan.
220. **Zhou, J.-Z.**, B. Xia, L. Wu, R. V. O'Neill, A. V. Palumbo, and J. M. Tiedje. 2000. Unusual diversity in soil microbial communities. The 6<sup>th</sup> Chinese Society of Ecology. P. 29-40, **(Invited)**
221. Braker, G., **J.-Z. Zhou**, L. Wu, A. H. Devol, and J. M. Tiedje. 2000. Nitrite Reductase Genes (*nirK* and *nirS*) as Functional Markers to Investigate Diversity of Denitrifying Bacteria in Marine Sediment Communities. *Appl. Environ. Microbiol.* 66: 2096-2104.
222. Xia, B., **J.-Z. Zhou**, J. M. Tiedje. 2000, Structure of bacterial community in soil environment and its ecological characteristics, *Acta Ecologica Sinica* 20(4): 1201-1209.
223. Zhang C., R. Stapleton, **J.-Z. Zhou**, A. V. Palumbo, and T. J. Phelps. 1999. Iron reduction by psychrophilic enrichment cultures. *FEMS Microbial Ecology* 30: 367-371.
224. Song, B., M. M. Haggblom, **J.-Z. Zhou**, J. M. Tiedje, and N. J. Palleroni. 1999. Taxonomic characterization of aromatics-degrading denitrifying bacteria: Description of *Azoarcus* sp. nov. and *Azoarcus* sp. nov. *Int. Syst. J. Bact.* 49: 1129-1140.
225. Li, G., and **J.-Z. Zhou**. 1999. Genomics, microarray-based genomic technology and potential ecological applications. The 3<sup>rd</sup> Conference on Molecular Ecology, Beijing, P. 29-40, **(Invited)**.
226. Palumbo, A. V., **J.-Z. Zhou**, T. J. Phelps, B. Kinsall, C. Zhang, E. L. Majer, J. E. Peterson, T. Griffin, S. M. Pfiffner. 1999. Ecology and bioremediation: a staged approach to site characterization. Uzochukwu and Reddy (eds), *Proceedings of the 1998 National Conference on Environmental Remediation Science and Technology*. Battelle Press, pp. 195-202.
227. Deysh, S. N., N. S. Panikov, W. Liesack, R. Grobkopf, **J.-Z. Zhou**, and J. M. Tiedje. 1998. Isolation of acidophilic methane-oxidizing bacteria from northern peat wetlands. *Science* 282: 281-284.
228. **Zhou, J.-Z.**, A. V. Palumbo and J. M. Strong-Gunderson. 1999. Phylogenetic characterization of a mixed microbial community capable of degrading carbon tetrachloride. *Appl. Biochem. Biotechnol.* 80: 243-253.
229. Liu, S., **J.-Z. Zhou**, C. Zhang, D. R. Cole and T. J. Phelps. 1997. Thermophilic Fe(III)-reducing bacteria from the deep subsurface: The evolutionary implications. *Science* 277: 1106-1109.
230. **Zhou, J.-Z.**, S. V. Liu, C. Zhang, A. V. Palumbo, and T. J. Phelps. 1998. Extremophilic iron-reducing bacteria: Their implications for possible life in extraterrestrial environments. *The Third Symposium of Chinese Young Scientists*, p. 47-52, Beijing, P. R. China.
231. Xia, B., **J.-Z. Zhou**, J. M. Tiedje 1998. Effect of vegetation on structure of soil microbial community. *Chinese Journal of Applied Ecology* 9(3): 296-300
232. Xia, B., **J.-Z. Zhou**, J. M. Tiedje. 1998. Application of molecular methods in microbial ecology. *Acta Scientiarum Naturalium Universitatis Sunyatseni* 37(2): 97-101
233. Xia, B., **J.-Z. Zhou**, J. M. Tiedje. 1998. Effect of overlying vegetation on soil microbial community structure and their activity. *Acta Scientiarum Naturalium Universitatis Sunyatseni* 37(3): 94-98

234. **Zhou, J.-Z.**, M. E. Davey, J. B. Figueras, E. Rivkina, D. Gilichinsky, and J. M. Tiedje. 1997. Phylogenetic diversity of a bacterial community determined from Siberian tundra soil DNA. *Microbiology* 143:3913-3919.
235. Tiedje, J. M., **J.-Z. Zhou**, K. Nusslein, C. Moyer and R. R. Fulthorpe. 1997. Extent and patterns of soil microbial diversity. P. 35-41. In Martins, M. T. et al. (eds). *Progress in Microbial Ecology*, Brazilian Society for Microbiology, Sao Paulo.
236. **Zhou, J.-Z.**, A. V. Palumbo, and J. M. Tiedje. 1997. Sensitive detection of a novel class of toluene-degrading denitrifiers, *Azoarcus tolulyticus* using SSU rRNA primers and probes. *Appl. Environ. Microbiol.* 63: 2384-2390.
237. Massol-Deya, A., R. Weller, L. Rio-Hernandez, **J.-Z. Zhou**, R. F. Hickey, and J. M. Tiedje. 1997. Succession and convergence of biofilm communities in fixed-film reactors treating aromatic hydrocarbons in groundwater. *Appl. Environ. Microbiol.* 63: 270-276.
238. **Zhou, J.-Z.**, and A. Kleinhofs. 1996. Molecular evolution of nitrate reductase genes. *J. Mol. Evol.* 42: 432-442.
239. **Zhou, J.-Z.**, M. A. Bruns, and J. M. Tiedje. 1996. DNA recovery from soils of diverse composition. *Appl. Environ. Microbiol.* 62: 316-322. **(Among the most highly cited 20 papers for all papers published in Applied and Environmental Microbiology, since January, 2008)**
240. **Zhou, J.-Z.**, S. Ma, and G. W. Hinman. 1996. Ecological exergy analysis — A new method for ecological energetics study. *Ecological Modeling* 84: 291-303.
241. Shih, C. C., M. E. Davey, **J.-Z. Zhou**, J. M. Tiedje, and C. S. Criddle. 1996. Effects of phenol feeding pattern on microbial community structure and cometabolism of trichloroethylene. *Appl. Environ. Microbiol.* 62: 2953-2960.
242. Chee-Sanford, J.C., J. W. Frost, M. R. Fries, **J.-Z. Zhou**, and J. M. Tiedje. 1996. Evidence for acetyl coenzyme A and cinnamoyl coenzyme A in the anaerobic toluene mineralization pathway in *Azoarcus tolulyticus* Tol-4. *Appl. Environ. Microbiol.* 62: 964-973.
243. Tiedje, J. M., and **J.-Z. Zhou**. 1996. Analysis of non-culturable bacteria. pp. 53-65. In *Methods for the examination of organismal diversity in soils and sediments*, (G. S. Hall, ed). CAB International, New York.
244. **Zhou, J.-Z.**, M. R. Fries, J. C. Chee-Sanford, and J. M. Tiedje. 1995. Phylogenetic analyses of a new group of denitrifiers capable of anaerobic growth on toluene: Description of *Azoarcus tolulyticus* sp. nov. *Int. J. Syst. Bacteriol.* 45: 500-506.
245. **Zhou, J.-Z.**, and J. M. Tiedje. 1995. Development of phylogenetic probes specific to *Burkholderia cepacia* G4. pp. 65-75. In Hincee, R. E., Douglas, G. S. and Ong, S. K. (eds), *Monitoring and Verification of Bioremediation*, Battelle Press, Columbus.
246. **Zhou, J.-Z.**, and J. M. Tiedje. 1995. Gene transfer from a bacterium injected into an aquifer to an indigenous bacterium. *Mol. Ecol.* 4: 613-638.
247. **Zhou, J.-Z.**, A. Kilian, R. L. Warner, and A. Kleinhofs. 1995. Variation of nitrate reductases genes in grass species. *Genome* 38: 919-927.
248. Fries, M. R., **J.-Z. Zhou**, J. C. Chee-Sanford, and J. M. Tiedje. 1994. Isolation, characterization and distribution of denitrifying toluene degraders from a variety of habitats. *Appl. Environ. Microbiol.* 60: 2802-2810.
249. **Zhou, J.-Z.**, A. Kilian, R. L. Warner, and A. Kleinhofs. 1994. An NADH nitrate reductase gene copy appears to have been deleted in barley. *Theor. Appl. Genetics* 88: 589-592.
250. **Zhou, J.-Z.**, S. Ma, and C. Chen. 1991. An index of ecosystem diversity. *Ecol. Modeling* 59: 151-163.
251. **Zhou, J.-Z.** and S. Ma. 1990. Ecosystem stability. pp. 54-71. In *Perspectives on Modern Ecology*, Edited by Shijun M. China Science and Technology Press.

252. **Zhou, J.-Z.** 1987. On ecological engineering. The proceeding of Symposium of Ecological Society of China. Chengdu, China.
253. **Zhou, J.-Z.**, and C. Chen. 1987. Studies on predation and simulation models of Wolf spider *Lycosa pseudoannulata* to Brown planthopper *Nilaparvata lugens* III. Selective predation. *Acta Ecologia Sinica* 7: 228-237.
254. **Zhou, J.-Z.**, and C. Chen. 1987. Studies on predation and simulation models of Wolf spider *Lycosa pseudoannulata* to Brown planthopper *Nilaparvata lugens* IV. Simulation model and stability analysis of the monopredator-two prey species system. *Acta Ecologia Sinica* 7: 349-358.
255. **Zhou, J.-Z.**, and C. Chen. 1987. Quantitative measurement of selectivity of predator for prey. *Acta Ecologia Sinica*, 7: 50-56.
256. **Zhou, J.-Z.**, and C. Chen. 1987. Studies on predation and simulation models of *Cyrtarrhinus lividipennis* to Brown planthopper *Nilaparvata lugens*. *Hunan Agri. Sci.* 36: 35-46.
257. **Zhou, J.-Z.** 1986. A general model for insect population simulation. The proceeding of the Symposium of Youth Ecologists of China, Zhangjiajie, China.
258. **Zhou, J.-Z.**, and C. Chen. 1986. Studies on predation and simulation models of Wolf spider *Lycosa pseudoannulata* to Brown planthopper *Nilaparvata lugens* I. Functional response. *Chinese J. Biol. Control*, 2(1): 2-9.
259. **Zhou, J.-Z.**, and C.M. Chen. 1986. Studies on predation and simulation models of Wolf spider *Lycosa pseudoannulata* to Brown planthopper *Nilaparvata lugens* II. Simulation model and stability analysis of the monopredator-monoprey species system. *Acta Ecologia Sinica* 6: 238-247.

## **BOOKS**

**Zhou, J.-Z.**, D.K. Thompson, Y. Xu, and James M. Tiedje. 2004. *Microbial Functional Genomics*. 624pp. John Wiley & Sons, Hoboken, New Jersey. **(Was the first comprehensive book in this field)**

## **PATENTS & PETENT APPLICATIONS**

1. **Zhou, J.-Z.**, L. Wu, and X. Liu. 2010. Method for analyzing microbial communities. US Patent No. 7,759,057.

## **KEY MANUSCRIPTS SUBMITTED FOR REVIEW**

1. **Zhou, J.-Z.**, J. P. Xie, L. Y. Wu, K. Xue, Z. H. He, YiQ. Luo. Microbial Mediation of Carbon Cycle Feedback to Climate Warming (Under review in *Science*)
2. **Zhou, J.-Z.**, L. Wu, Y. Deng, X.Y. Zhi, Y.H. Jiang, Q.C. Tu, J.P. Xie, J. D. Van Nostrand, Y.F. Yang, and Z.L. He. 2010. Reproducibility and Quantitation of Amplicon Sequencing-Based Detection. *The ISME J.*
3. **Zhou, J.-Z.**, Y. Deng, Feng Luo, and Z.L. He. Phylogenetic Molecular Ecological Networks in Response to Elevated CO<sub>2</sub>. *Nature Climate Change*
4. Hemme, C. L., M. W. Fields, Q. He, Y. Deng, L. L., Qichao Tu, H. Mouttaki, X.Y. Feng, Z. Zuo, B.D. Ramsey, Z.L. He, K. Barry, E. Saunders, H. Sun, M. Land, Y.J. Chang, L.Y Wu, J. Van Nostrand, L. Hauser, A. Lapidus, C. S. Han, J. Xu, Y.J. Tang, J. Wiegel,

- T. J. Phelps, E. Rubin, and **J.Z. Zhou**. Comparative Genomics of Ethanol-Producing *Thermoanaerobacter* Species. Nature Communications, under review.
5. Lu, Z.M., Y. Deng, J. D. Van Nostrand, Z.-L. He, J. Voordeckers, A.F. Zhou, Y.-J. Lee, O. Mason, E. Dubinsky, K. Chavarria, L. Tom, J. Fortney, R. Lamendella, J. K. Jansson, P. D'haeseleer, T. C. Hazen, and J.-Z. Zhou. Rapid Succession and Adaptation of Microbial Community Functional Structure Response to Oil Plume. PNAS, under review
  6. He, Z.H., Y. Piceno, Y. Deng, M.Y. Xu, Z.M. Lu, T. DeSantis, G. Andersen, S. Hobbie, P. Reich, and **J.-Z. Zhou**. Phylogenetic diversity, composition and structure of soil microbial communities in response to elevated CO<sub>2</sub>. The ISME J,
  7. Hemme, C. L., P. A. Lawson, S. Lucas, A. Copeland, A. Lapidus, T. Glavina del Rio, H. Tice, E. Saunders, T. Brettin, C. Detter, C. S. Han, L. Goodwin, S. Pitluck, Miriam Land, L. Hauser, N. Krypides, N. Mikhailova, Z. He, L.Wu, J. van Nostrand, Eddy Rubin, and **J.-Z. Zhou**. 2010. Phylogenomic Analysis of Clostridia. Submitted to BMC Genomics
  8. Liang, Y., J. Wang, J. D. Van Nostrand, **J.-Z. Zhou**, X. Zhang, G. Li. Microarray-based functional gene analysis of soil microbial communities in ozonation and biodegradation of crude oil. (Submitted, Chemosphere.)
  9. Mason, O. U., T. Nakagawa, M. Rosner, J. D. Van Nostrand, **J.-Z. Zhou**, A. Maruyama, M. R. Fisk, S. J. Giovannoni, and the Integrated Ocean Drilling Program Expeditions 304/305 Science Party. 2010. Hydrocarbon utilizing prokaryotes in plutonic ocean crust sampled from the Atlantis Massif, 30 °N, 42 °W. (Submitted, Environ. Microbiol.)
  10. Liang Y., J. D. Van Nostrand, L. A. N'Guessan, A. D. Peacock, Y. Deng, P. E. Long, C. T. Resch, L. Wu, Z. He, **T. C. Hazen**, G. Li, D. R. Lovley, and **J.-Z. Zhou**. Microarray-based functional analysis of microbial communities for in-situ uranium reduction under sulfate-reducing vs. Fe-reducing conditions. (To be submitted to Environ Sci & Technol).
  11. Leigh, M. B., E. Cardenas, W.-M. Wu, O. Uhlik, J. Carley, S. Carroll, T. Gentry, T. L. Marsh, **J.-Z. Zhou**, P. Jardine, C. S. Criddle, and J. M. Tiedje. Ethanol-biostimulated **microbial** communities in aquifer sediments active in uranium (VI) bioreduction. (Submitted to Microbial Ecology)
  12. Ning, J., J. Liebich, L. Dai, N. Li, S., Leder, M. Kästner, **J.-Z. Zhou**, and A. Schäffer, and P. Burauel. Seasonal influence on the **bacterial** community structure and functions in a planted constructed wetland. To be submitted to FEMS Microbiology Ecology
  13. Fang, Z., H. He, H. Jiang, C. Hemme, Z. He, **J.-Z. Zhou**. Enhanced Ethanol Production from Cellulose Fermentation by Thermophilic Co-cultures. (To be submitted to AEM)
  14. Neslihan Tas, N., M. H.A. van Eekert, J. D. Van Nostrand, Y. Deng, L. Wu, Z.H. He, **J.-Z. Zhou** and H. Smidt. Magnifying glass for ecosystems: Functional gene array analysis of polluted river sediments. (To be submitted to AEM).
  15. Yergeau, E., S. Bokhorst, S. Kang, W. H. van der Putten, **J.-Z. Zhou**, and G. A. Kowalchuk. Rapid functional responses of Antarctic soil microorganisms to simulated global warming. (To be submitted to ISME J).
  16. Yin, H, L.H Cao, G.Z. Qiu, M. Xie, Q.J. Chen, Z.L. He, L.Y. Wu, D. Z. Wang, **J.-Z. Zhou**, and X.D. Liu.. Microarray-based analysis of microbial communities at nine sites associated with acid mine drainages. (To be submitted to The ISME J.).
  17. Fang, Z.G., Q. He, H.L. Jiang, C. Hemme, Z.L. He, **J.-Z. Zhou**. Enhanced Ethanol Production from Cellulose Fermentation by Thermophilic Co-cultures. (To be submitted, Appl Environ Microbiol)

18. Wang, J., Y. Zhou, J. D. Von Nostrand, X. Zhang, J.-Z. Zhou, G. H. Li. Effects of ozonation on residual oils, soil organic matters and indigenous microorganisms in bioremediated soil. (To be submitted to EST)

## PROJECTS

### Currently funded projects

1. Experimental Macroecology: Effects of Temperature on Biodiversity. NSF Macrosystems, Co-PI with James Brown, Mike Kaspari et al (\$4.5M in total, \$1.8M for J. Zhou) (July 1, 2011 to June 30, 2015),
2. HuMiChip to detect and characterize the human microbiome. Co-PI with He. OCAST, \$300K (February 1, 2011 to January 31, 2014)
3. From Community Structure to Functions: Metagenomics-Enabled Predictive Understanding of Temperature Sensitivity of Soil Carbon Decomposition to Climate Warming, Department of Energy, PI, \$3M (July 1, 2010 - June 30, 2013)
4. Plant Stimulation of Soil Microbial Community Succession: How Sequential Expression Mediates Soil Carbon Stabilization and Turnover, Department of Energy, Co-PI with Mary Firestone et al, \$0.5M for J. Zhou (July 1, 2010 - June 30, 2013)
5. Development of Microarrays-based Metagenomics Technology for Monitoring Sulfate-Reducing Bacteria in Subsurface Environments. PI, DOE STTR/SBIR, \$100K (June 19, 2010- March 18, 2011)
6. Development of Novel Random Network Theory-Based Approaches to Identify Network Interactions Among Nitrifying Bacteria. PI, DOE STTR/SBIR, \$100K (June 19, 2010- March 18, 2011)
7. Institute for Environmental Genomics, PI with Z.L. He, \$375K (January 1, 2008 --- December 31, 2013).
8. Microbial Enhanced Hydrocarbon Recovery (MEHR) Systems Biology Program. Energy BioSciences Institute, Co-PI with Hazen et al, \$1.5M for J. Zhou (Oct 1, 2008 – Sept 30, 2017).
9. Extending Knowledge of Anaerobic Hydrocarbon Metabolism: Linking Metabolism, Functional Gene Molecular Markers and the GeoChip. ConoPhilipps, Co-PI with Joseph Suflita et al (\$2 M in total), \$ 403K for J. Zhou (Oct 1, 2008 –December 30, 2010)
10. Oklahoma EPSCoR Research Infrastructure Improvement Plan Building Oklahoma's Leadership Role in Cellulosic Bioenergy. NSF EPSCoR Program (\$8.7M in total), PI with Ray Huhnke (Director) et al, \$2,117K for J. Zhou (Oct 1, 2008-Sept 30, 2013)
11. Characterization of an H<sub>2</sub> Producing Biological System operating at 1 nM H<sub>2</sub> Concentration. Co-PI with Krumholtz et al (\$900K in total). DOE BES, \$250K for J. Zhou (Oct 1, 2008-Sept 30, 2011)
12. Whole genome DNA arrays for bacterial identification and detection, Co-PI with Wu et al. OCAST, \$300K (February 1, 2008 to January 31, 2011)
- 13.** Isolation and characterization of novel microbial catalysts for direct fermentation of lignocellulose to ethanol. PI with Liyou Wu, Zhili He, Oklahoma Bioenergy Center, \$400K (February 1, 2008, January 31, 2011)

- 14.** Genomics-enabled understanding of microbial interactions and regulatory networks of microbial consortia for efficient cellulosic ethanol production. Co-PI with Zhili He, Liyou Wu et al, Oklahoma Bioenergy Center, \$830K (February 1, 2008, January 31, 2011)
- 15.** Linking community structure to functions: Metagenomic analysis of Feedstock-Related Microbial Communities using GeoChip and Pyrosequencing. Co-PI with Liyou Wu, Zhili He, Yiqi Luo, Oklahoma Bioenergy Center, \$1030K (February 1, 2008, January 31, 2010)
- 16.** The Joint BioEnergy Institute (JBEI) (\$125M in total), \$400K for J. Zhou (October 1, 2007 – September 30, 2012)
- 17.** Trajectories of microbial community function in response to accelerated remediation of subsurface metal contaminants. Co-PI with Mary Firestone et al. DOE ERSP program, ~ \$1350 K (October 1, 2007 – September 30, 2010), \$210K for J. Zhou.
18. MO: A Genomics-enabled FACE Microbial Observatory: Changes in Microbial Diversity and Functions in responding to elevated CO<sub>2</sub>, Nitrogen Deposition and Plant Diversity. NSF-USDA Microbial Observatories Program, PI with Zhili He, \$866K (July 1, 2007 – June 30, 2011).
19. Rapid Deduction of Stress Response Pathways in Metal and Radionuclide Reducing Bacteria Phase 2: Molecular Determinants of Community Activity, Stability and Ecology (MDCASE) (ESPP 2), DOE Genomics:GTL Program (\$35M in total), PI with Adam Arkins (Director), Terry Hazen, Judy Wall, David Stahl, et al, \$4,000K (October 1, 2007 – September 30, 2012).
- 20.** Metagenomics-enabled understanding of the functions and activities of microbial communities at ERSP Field Research Center at Oak Ridge, TN. Co-PI with Tiedje and Marsh. DOE NABIR program, ~ \$1500 K (October 1, 2006 – March 30, 2012), \$750K for J. Zhou.
21. Integrated genome-based studies of Shewanella ecophysiology. DOE Genomics:GTL program (\$15M) PI with J. Fredrickson (Director), K. Nealson, J.M Tiedje, and et al. ), \$1000K (October 1, 2006– September 30, 2009). DOE Genomics:GTL program, October 1, 2006– September 30, 2012
22. Multiscale Investigations on the Rates and Mechanisms of Targeted Immobilization and Natural Attenuation of Metal, Radionuclide and Co-Contaminants in the Subsurface. Co-PI with Jardine, Watson, Criddle, Gu et al. \$15M, (October 1, 2006 --- September 30, 2011), \$150K for Zhou.

### Funded projects in China

1. The Fund for Foreign Scholars in University Research and Teaching Programs supported by The Ministry of Education of China and The State Administration of Foreign Experts Affairs of China, \$5M Chinese yuan (Januray 1, 2007 --- December 31, 2011)
2. Special award for Oversea Young Scientist, \$120K Chinese Yuan (July 1, 2004 --- June 30, 2007).

### **Ongoing genome sequencing projects:**

1. Genomic Sequencing of Multiple Species of Class *Clostridia* Relevant to the Production of Bioethanol from Cellulosic Feedstocks. 2006. (PI with Hemme, He et al). The genome will be sequenced by DOE Joint Genome Institute.
2. Sequencing *Clostridium cellulolyticum* to advance understanding plant biomass degradation and energy production, 2005. (Qing He, and J.-Z. Zhou). The genome will be sequenced by DOE Joint Genome Institute.
3. Genome sequencing of multiple Anaeromyxobacter species: comparative genomics for insight into the ecophysiology, genetics and evolution of metal-reducing and halo-respiring bacteria. 2005. (Robert A. Sanford, Matthew W. Fields, Frank E. Löffler, John R. Kirby, J.-Z. Zhou, James K. Fredrickson, and Alexander S. Beliaev). Three genomes will be sequenced by DOE Joint Genome Institute.
4. Genome-level understanding of the diversity and structure of a groundwater microbial community in the NABIR Research Field Research Center. 2004. (Zhou, PI, Fields, co-PI). The entire community with about 20 species in highly contaminated site will be sequenced by DOE Joint Genome Institute in 2005.
5. Whole-genome sequence determination of novel, extremophilic, metal-reducing bacteria important to bioremediation and energy production. 2003. (Fields, Zhou). 3 gram-positive extremophilic iron reducing bacteria isolated at ORNL are under sequencing.
6. Sequence multiple strains of *Shewanella* to advance understanding their metal-reducing physiology and ecological potential. 2004. (Fredrickson, Nealson, DiChristina, Tiedje, Zhou et al.). 16 *Shewanella* strains are under sequencing by JGI. Two of these strains were isolated at ORNL.

### **Accomplished projects**

1. Development of Comprehensive Functional Gene Arrays for Microbial Community Analysis, Co-PI with He. OCAST, \$300K (October 1, 2006 to Sept 30, 2009)
2. Microarray analysis and functional assays to assess microbial ecology and disease suppression in soils under organic or sustainable management. Co-PI with Louws and Hu, USDA, \$160K (October 1, 2006 ---September 30, 2008)
3. Development of microbial consortia for efficient ethanol production from plant biomass, PI, Department of Energy, Oklahoma, \$200K (April 1, 2007 --- March 31, 2009)
4. Identification of Molecular and Cellular Responses of *Desulfovibrio vulgaris* Biofilms under Culture Conditions Relevant to Field Conditions for Bioreduction of Heavy Metals, Co-PI with Matthew Fields, Judy Wall, DOE ERSP Program, \$300K (October 1, 2005 to Sept 30, 2008).
5. Deduction and analysis of the interacting stress response pathways of metal/radionuclide-reducing bacteria, DOE Genomics:GTL Program, PI with Adam Arkins (Director), Terry Hazen, Judy Wall, David Stahl, et al (\$30M in total), \$5,010K for J. Zhou (July 1, 2002 – September 30, 2007).
6. Molecular Approaches to Understanding C and N Dynamics and their Role in the Global Carbon Cycle. Co-PI, with Tiedje, Devol, and Massol-Deya, DOE Biotechnological Investigations — Ocean Margin Program. ~ \$1,500 K (October 1, 2003 – September 30, 2006). \$600K for J. Zhou.

7. Towards Understanding Population Dynamics of Metal and Radionuclide Reducers at Field Remediation Sites. Co-PI with Tiedje and Treves. DOE NABIR program, ~ \$900 K (October 1, 2003 – September 30, 2006), \$450K for J. Zhou.
8. Development and Use of Integrated Microarray-based Genomic Technologies for Assessing Microbial Community Composition and Dynamics. PI, DOE NABIR program, ~ \$900 K (October 1, 2003 – September 30, 2006).
9. Elucidating the Molecular Basis of Chromium(VI) Reduction by *Shewanella oneidensis* MR-1 and Resistance to Metal Toxicity Using Integrated Biochemical, Proteomic, and Comparative Genomics Approaches. Co-PI with Thompson and Hettich. DOE NABIR program, ~ \$820 K (October 1, 2003 – September 30, 2006).
10. Integrated analysis of protein complexes and regulatory networks involved in anaerobic energy metabolism of *Shewanella oneidensis* MR-1, PI, with Larimer, Nealson, Thompson, et al., DOE Microbial Cell Project, \$4,500K (October 1, 2001– September 30, 2006).
11. Field-scale evaluation of biostimulation for remediation of uranium-contaminated groundwater at a proposed NABIR Field research center in Oak Ridge TN, Co-PI, with Criddle, Jardine, Kitanidis, Hopkins. DOE NABIR program, ~ \$3,250 K (October 1, 2000 – September 30, 2004). \$540K for J. Zhou.
12. Center for research on enhancing carbon sequestration in terrestrial ecosystems (Co-PI, with Jacobs et al.) (\$10M in total), \$900K for J. Zhou (October 1, 1999 – September 30, 2005).
13. The *Rhodopseudomonas palustris* Microbial Cell Project, Co-PI, with Tabita, Thompson, et al., DOE Microbial Cell Project (\$2.1M in total), \$150K for J. Zhou (October 1, 2001– September 30, 2006).
14. The dynamics of cellular stress responses in *Deinococcus radiodurans*, Co-PI, with Mike Daly et al., DOE Microbial Cell Project (\$900K in total), \$240K (October 1, 2001– September 30, 2004).
15. Microbially mediated immobilization of contaminants through in situ biostimulation: Scale up of EMSP project 55267, Co-PI with Jardine and Brooks, DOE EM Science Program, \$1,427K (October 1, 2000 – September 30, 2004). \$140K for J. Zhou.
16. Use of DNA Microarrays for Understanding the Genetic and Metabolic Regulation of Carbon Dioxide Fixation and Hydrogen Production in *Rhodopseudomonas palustris*. Co-PI with Harwood and Thompson. DOE Microbial Genome Program (\$1.8M in total), \$750K for J. Zhou (October 1, 2001– September 30, 2004).
17. Gene Expression Profiles in *Nitrosomonas europaea*, an Obligate Chemolitho- autotroph. Co-PI with Arp and Klotz, DOE Microbial Genome Program, \$600K for J. Zhou (October 1, 2001– September 30, 2004).
18. Genomic Characterization of Belowground Ecosystem Responses to Climate Change. Co-PI with DiFazio, Fields, et al., ORNL Laboratory Directed Development and Research Program, \$545K (October 1, 2002– September 30, 2004).
19. Community-Wide Analysis of Unique Sequences and Functions from Uncultured Microorganisms, Co-PI with Fields, ORNL Laboratory Directed Development and Research Program, \$500K, (October 1, 2001– September 30, 2003).
20. Coupling process and microbial community studies to understand the mechanisms controlling carbon preservation and nitrogen loss in marine sediments. Co-PI, with Tiedje, Devol, Massol-Deya and Palumbo, DOE Biotechnological Investigations — Ocean Margin Program. ~ \$1,650 K (October 1, 2000 – September 30, 2003). \$600K for J. Zhou.

21. Understanding the roles of spatial isolation and carbon in microbial community structure dynamics, and activity for bioremediation, Co-PI with Tiedje and Treves. DOE NABIR program, ~ \$1,250 K (October 1, 2000 – September 30, 2003), \$650K for J. Zhou.
22. Development and use of 16S rRNA gene-based oligonucleotide microarrays for Assessing Microbial Community Composition and Dynamics. PI with Thompson, Hurt, Xu and Xu, DOE NABIR program, ~ \$1,200 K (October 1, 2000 – September 30, 2003). \$900K for J. Zhou.
23. Enhancing carbon sequestration and reclamation of degraded lands with fossil fuel combustion byproducts, Co-PI with Palumbo et al., DOE Fossil Energy Program, ~1,100K (October 1, 2000 – September 30, 2003).
24. Computational structure characterization of metal-reduction proteins in microbe, Co-PI with Ying Xu, Dong Xu et al., DOE Experimental and Computational Structural Biology, ~ \$1,100K (October 1, 2000 – September 30, 2003).
25. *Shewanella putrefaciens*: Regulation of the genes and proteins involved in metal reduction pathways, Co-PI with Carol Giometti, DOE NABIR Program, \$210K (October 1, 1999 – September 30, 2002).
26. Linking genomics to cellular responses and mechanisms for radiation resistance in *Deinococcus radiodurans*, PI, with Hettich, Burlage, Beliaev, and Thompson, Laboratory Directed Research and Development Program, Oak Ridge National Laboratory, \$867K (October 1, 2000 – September 30, 2002).
27. Development of microchip-based detection methods: a high throughput microbial detection tool for bioremediation and carbon sequestration. PI, Seed Money Program, Oak Ridge National Laboratory, 100K (February 1, 2000 – September 30, 2001).
28. Exploring whole genome sequence information for defining the functions of unknown genes and regulatory networks in dissimilatory metal reduction pathways. PI, with Neilson and Tiedje, DOE Microbial Genome Program, \$1,350K (October 1, 1998 – September 30, 2001).
29. Noncompetitive diversity patterns in soils: their causes and implications. Co-PI with Tiedje, O'Neill and Palumbo, DOE NABIR program, ~ \$1,100 K (October 1, 97 – September 30, 2000)
30. Linking process and population studies to understand the nitrogen loss mechanisms of Pacific Northwest marine sediments. Co-PI with Tiedje, Devol, Massol-Deya and Palumbo, DOE Biotechnological Investigations — Ocean Margin Program. ~ \$1,300 K (October 1, 1997 – September 30, 2000).
31. Rapid gene probe for microorganisms monitoring by novel MS approaches. Co-PI with W. Chen, DOE NABIR program, ~ \$800 K (October 1, 1999 – September 30, 2002).
32. Isolation of Proteins Involved in Metal Reduction from *Shewanella oneidensis* MR-1 with Mass Spectrometry, LDRD Program, Oak Ridge National Laboratory, \$50K (March 1, 2000 – September 30, 2000)
33. Development and testing of molecular probes that distinguish effective TCE-cooxidizers from ineffective TCE-cooxidizers: a potential tool for site assessment and management. Co-PI with Tiedje, Department of Defense, \$150K (September 1, 1996 to September 1, 1998).
34. Enzymes from extremophiles in bioremediation and bioprocessing. Co-PI with Woodward and Palumbo et al., Oak Ridge National Laboratory, ~ \$800K (September 1, 1996 to August 31, 1998).
35. Development of gene probes for nitrate reductase in environmental media: a tool to evaluate nitrogen retention in watersheds. Co-PI with Mulholland and Garten, Oak Ridge National Laboratory, 92K (January 1, 1998 to December 30, 1998).

**Current staff**

	From	Time	Position
Zhili He	Australian National Univ, Australia	2005.11	Research Associate Professor
Liyou Wu	Hunan Agricultural Univ	2005.11	Research Associate Professor
Missy Lee		2007.5	Administrative Assistant

**Current postdoc**

Postdoctorals	From	Start time	
Aifen Zhou	Shandong Univ	2005.12	
Joy Van Nostrand	Univ of South Carolina Medical School	2006.4	
Sanghoon Kang	Univ of Virginia	2004.9	
Christopher Hemme	Univ of Missouri, Columbus	2003.4	
Ye Deng	Zhejiang Univ	2007.11	
Dongru Qiu	Keio Univ, Japan	2008.4	
Kai Xue	Cornell Univ	2009.1	
Ping Zhang	University of Arkansas	2009.8	
Youngjin Lee	University of Georgia	2009.8	
James Voordeckers	Rutgers University	2009.8	
Yi-Huei Jiang	National Tsinghua University, Taiwan	2009.8	
Lei Chen	North Carolina State Univ	2010.5	
Tong Yuan	University of Oklahoma	2010.7	
Jin Zhang	Iowa State Univ	2010.10	

**Current graduate students**

	From	Start time	
Wenbin Liu	Central South Univ, China	2008.1	Ph.D candidate
Feifei Liu	Central South Univ, China	2008.1	Ph.D candidate
Qichao (Philloid) Tu	Zhejiang Univ	2008.8	Ph.D candidate
Min Xie	Central South Univ	2009.1	Ph.D candidate
Yue Wang	Shanghai Institute of Plant Physiology and	2009.1	Ph.D candidate

	Ecology		
Yujia Qin	Harbin Institute of Technology	2009.1	Ph.D candidate
Rong Song	Virginia Tech	2010.6-	Ph.D candidate
Zhou Shi	Yunnan Univ	2010.8-	Ph.D candidate
Su Xu	Wuhan Univ	2010.8-	Ph.D candidate
Mark H. Pinkerton	Drexel Univ	2010.8-	

### **Current visiting scholars and students**

	From	Start	
Zhengmei Lu	Zhangjiang Univ	2008.12	Associate Professor
Linfang Gao	Harbin Institute of Technology	2009.1	Ph.D candidate
Shijie Bai	Xiamen University	2009.10	Ph.D candidate
Pigang Liu	Harbin Institute of Technology	2009.11	Associate Professor

### **Master students mentored**

Patricia J. Waldron	Univ of Massachusetts	2006.8-2000.1	
Jingrong Chen	Nanjing Univ, China	2006.8-2009.5	MS
Yunyu (Irene) Chen	Nanjing Agricultural Univ	2007.8-2010.9	MS

### **POSTDOCTORAL TRAINED**

Postdoctorals	From	Time period	Present position
Raymond D. Stapleton	Univ of Tenn, Knox	1998.4-1999.8	Staff Scientist, Merck & Co Pharmaceutical Company, VA
Guangshan (Gary) Li	Virginia Tech	1998.10-2000.9	Staff Scientist, Dow Corning, NY
Richard Hurt	Univ of Tenn, Knox	1998.4-2001.9	Staff Scientist, Atomic Sciences, Oak Ridge, TN
Dorothea Thompson	Univ of Maryland	1999.12-2001.9	Assistant Prof, Purdue Univ
Gina Holguin	Univ of Waterloo	2000.12-2001.6	Staff Scientist, Centrode Investigaciones Biológicas del No-roeste, CIBNOR, LaPaz 23090, BCS, Mexico
Mathew Fields	Cornell Univ	2000.12-2000.9	Assistant Prof, Montana State Univ

Christopher Bagwell	Univ of South Carolina	2001.3-2002.8	Staff Scientist, Savannah River National Lab, Aiken, SC.
Alex Beliaev	Univ of Massettutes	1999.12-2002.9	Staff Scientist, Pacific Northwest National Laboratory, Richland, WA
Adam Leaphart	Univ of South Carolina	2002.6-2003.9	Staff Scientist, State Department of Health, SC.
Sonia Maraya Tiquia	Univ of Hongkong	2001.9-2003.8	Assistant Profe, Univ of Michigan, Dearborne, MI.
Sung-Keun Rhee	Rutgers University	2002.3-2003.8	Staff Scientist, Biotechnology Center, South Korea.
Xiufeng Wan	Univ of Mississippi	2001.12-2003-11	Staff Scientist, Center for Disease Control, Atlanta, GA
Yongqing Liu	Noble Foundation, OK	2000.3-2003.12	Research Assist Prof, University of Louisville, Louisville, KY
Ting Li,	Univ of Kenturky	2002.3-2003.12	Postdoc, Univ of Georgia, Athens, GA
Song Chong	Oregon Polytech	2002.3-2003.9	Scientist, private company, Korea
Jost Liebich		2003.1-2004.7	Postdoc, Institute of Chemistry and Dynamics of the Geosphere IV, Forschungszentrum Jülich GmbH, Germany
Crystal Bickley McAlvin	Univ of Tenn, Knox	2003.3-2004.11	Postdoc, Univ of Tenn, Knox
Yunfeng (David) Yang	Albert Einstein College of Medicine, Bronx, NY	2003.2-2005.11	Staff Scientist, Oak Ridge National Lab
Christopher Schadt	Univ of Colorado	2003.1-2005.11	Staff Scientist, Oak Ridge National Lab
Steve Brown	Univ of Otago, Dunedin, New Zealand	2002.10-2005.11	Staff Scientist, Oak Ridge National Lab
Terry Gentry	Univ of Arizona	2003.8-2005.11	Assist Prof, Texas A&M Univ

Xichun Zhou	Univ of Singapore	2001.8-2005.11	Staff Scientist, Adatech Inc, Denver, CO
Haichun Gao	Purdue Univ	2002.2-2008.4	Professor, Zhejiang Univ
Zhili He	Australian National Univ, Australia	2003.2-2005.11	Research Assist Prof, Univ of Oklahoma
Weimin Gao	Penn State Univ	2001.9-2005.3	Staff Scientist, Brookhaven National Lab
Soumitra Barua	Nagoya Univ Graduate School of Medicine	2003.9-2006.9	Postdoc, Univ of Oklahoma Medical School
Qiang He	Univ of Illinois at Urbana-Champaign	2003.8-2005.8	Assist Prof, Univ of Tenn, Knoxville
Amudhan Venkateswaran	Uniformed Services University of the Health Sciences (USUHS), Bethesda, Maryland	2003.1-2004.2	Postdoc, Oak Ridge National Lab
Tingfen Yan	Northeastern Forestry Univ., Harbin China	2003.1-2005.11	Postdoc, Oak Ridge National Lab
Youlboong Sung	Georgia Institute of Technology	2004.8-2006.8	Staff Scientist, Biotechnology Center, South Korea.
Gene Wickam	Univ of Indiana	2003.8-2005.11	Private firm
Laurie Kellogg	Univ of Minnesota	2005.12-2007.9	Law School, Univ of Minnesota
Hongchen Jiang	Miami Univ	2007.11-2008.10	Assistant Professor, China GeoSciences University
Helong Jiang	Univ of Singapore	2006.9-2008.10	One Hundred Scholar, Professor, Institute of Lake and River, Chinese Academy of Science
Housna Mouttaki	Univ of Oklahoma	2007.11-2008.10	France
Aihua Liu	Tohoku University, Japan	2008.11-2009.10	Chinese Academy of Sciences
Yuting Liang	Tsinghua University	2009.8-2010.7	Changzhou Technology Univ, China

#### **Postmasters or BS trained**

	From		Current position
Heshu Huang	Univ of Georgia	1997.3-2000.4	Private firm

Xiaoyun Qiu	Fudan Univ, China	1998.8-1999.9	Ph.D candidate, Mich State Univ
Julia Stair	Univ of Tennessee	2001.5-2001.11	Research scientist, Univ of Tennessee
Debra Beth Arnett	Univ of Tennessee	2001.4-2002.5	Private firm
Hongbin Pan		2003.4-2004.9	Oak Ridge National Lab
Dawn Stanek	Univ of Georgia		Research scientist, Oak Ridge National Lab
Lisa Fagan	BS, Univ of Tennessee	2002.1-2003.12	Technician, Oak Ridge National Lab
Joy M. Pelfrey	BS, Univ of Oklahoma	2006.1-2007.1	Private firm

**Past visiting Ph.D or MS students mentored (Did thesis in my lab)**

	From	Time periods	Present position
Xueduan Liu	Ph.D, Central South Univ	2000.8-2003.11	Shenhua scholar, Central South Univ
Liyu Wu	Ph.D, Hunan Agricultural Univ	1997.11-2001.12	Research assistant Prof, Univ of Oklahoma
Huaquang Hua	Central South Univ	2004.5-2007.5	Assistant prof, Central South Univ
Laurel Crosby	Stanford Univ		Postdoc, Stanford Univ
Xiaohu Wang	Baylor College of Medicine		Postdoc, Baylor College of Medicine
Yi Wen	Stanford Univ		Stanford Univ
Feng Luo	University of Texas, Dallas		Clemson Univ, SC
Qi Ye	Univ of Georgia		Univ of Georgia
Ye Deng	Zhejiang Univ	2005.12-2007.12	Postdoc at OU
Qichao (Philloid) Tu	Zhejiang Univ	2007.8-2008.8	Ph.D student at OU
Yili Liang	Central South Univ	2006.3-2009.1	Central South Univ
Yuting Liang	Tsinghua Univ	2006.12-2009.3	Tsinghua Univ
Jian Wang	Tsinghua Univ	2008.10-2009.9	Ph. D Candidate at Tsinghua Univ
Xiaoyang Zhi	Yunnan Univ	2008.11-2010.5	Ph. D Candidate at Yunnan Univ
Lin Lu	Qingdao Institute of Biomass Energy and	2008.7-2010.6	Ph.D candidate

	Bioprocessing Technology, Chinese Academy of Sciences		
Shengmu Xiao	Donghua University	2009.4-2010.2	Donghua University, Shanghai
Yanfei Chen	Zhejiang Univ	2010.2-2010.8	Ph.D candidate
Jianping Xie	Central South Univ	2007.5-2010.9	Ph.D candidate
Wenzhong Liu	Harbin Institute of Technology	2008.4-2010.10	Ph.D candidate
Hao Yu	Harbin Institute of Technology	2008.9-2010.10	Ph.D candidate
Jinbo Xiong	Huazhong Agricultural Univ	2008.9-2010.9	Ph. D Candidate

### **Ph.D committee member**

	From	Time periods	Current position
Xiaoyun Qiu	Michigan State Univ		Postdoc, Harvard Univ
Laurel Crosby	Stanford Univ		Postdoc, Stanford Univ
Wim De Windt	Ghent University, Belgium		Private firm, Belgium

### **Past visiting scholars and students**

	From	Time periods	Current position
Beicheng Xia	Zhongshan Univ	1998.8-2000.9	Prof, Zhongsha Univ
Zhijian Wang,	Zhongshan University	2004.8-2005.10	Assistant Prof, Zhongshan University
Huiwen Zhang	Institute of Applied Ecology, Chinese Academy of Sciences	2004.11-2005.11	Institute of Applied Ecology, Chinese Academy of Sciences
Wen-Tso Liu,	Singapore University	2004.1-2004.4	Prof, Singapore University
Yimin Wang	Savannah River Ecology Laboratory, Aiken, SC.	2004.1-2004.12	Private firm
Zhiyong Huang	Univ of Georgia	2004.4-2004.8	Univ of Georgia
Tingfen Yan	Northeastern Forestry University, Harbin, China	2000.11-2004.4	Oak Ridge National Lab
Lara Martin	Virginia Tech	1998.8-1999.8	
Matthew Wallenstein	Duke Univ	2002.6-2003.8	
Fengping Wang	The 3 <sup>rd</sup> Institute of Oceanography	2006.11-2007.3	The 3 <sup>rd</sup> Institute of Oceanography
Etienne Yergeau	Netherlands Institute of	2005.12-2006.2	Netherlands Institute of

	Ecology, The Netherlands		Ecology, The Netherlands
Neslihan Tas	Wageningen Univ, The Netherlands	2006.12-2007.5	Wageningen Univ, The Netherlands
Gina La Spada	Istituto Sperimentale Talassografico, CNR, Messina, Italy	2006.12-2007.5	Istituto Sperimentale Talassografico, CNR, Messina, Italy
Aijie Wang	Harbin Institute of Technology	2007.7-2007.8	Professor, Harbin Institute of Technology
Olivia Mason	Oregon State Univ	2007.9-2007.10	Oregon State Univ
Yuting Liang	Tsinhua Univ, Beijing, China	2006.12-2007.12	Tsinhua Univ, Beijing, China
Zhiguo Fang	Eco-Environmental Research Center Chinese Academy of Science	2006.8-2008.4	Associate Professor, Hangzhou Industrial Univ
Di Liu	Institute of Microbiology, Chinese Academy of Science (CAS)	2008.2-2008.5	Scientist, CAS,
Jie Yu	Chinese Academy of Science (CAS)	2008.3-2008.5	CAS
Manuela di Lorenzo	Centre for Terrestrial Ecology, Netherlands Institute of Ecology	2008.5-2008.5	Centre for Terrestrial Ecology, Netherlands Institute of Ecology
Lur Epelde	Netherlands Institute of Ecology, The Netherlands	2008.7-2008.7	Netherlands Institute of Ecology, The Netherlands
Eiko Kuramae	Netherlands Institute of Ecology, The Netherlands	2008.7-2008.7	Netherlands Institute of Ecology, The Netherlands
Guochun Ding	Julius Kühn-Institut Bundesforschungsinstitut für Kulturpflanzen Institut für Epidemiologie und Pathogendiagnostik	2008.6-2008.7	Julius Kühn-Institut Bundesforschungsinstitut für Kulturpflanzen Institut für Epidemiologie und Pathogendiagnostik
Zhiguo Fang	Eco-Environmental Research Center, Chinese Academy of Sciences	2006.8-2008.5	Assistant Professor, Zhejiang Industrial Univ
Meiying Xu	Guangzhou Institute of Microbiology	2006.8-2008.9	Associate Professor, Guangzhou Institute of Microbiology
Tuyong Yi	Huanan Agri Univ	2008.9-2009.12	Associate Professor
Xinyu Li	Shengyang Institute of Ecology, CAS	2010.4-2010.9	Associaite Professor
Jiangtao Li	Tongji University	2010.10-12	Lecturer

Fabiana Paula	University of Sao Paulo	2010.10-12	Ph.D candidate

**Past visiting undergraduate students and interns**

Patrick E. McDonel	University of Indiana at South Bend	1998.8-1999.8	Ph.D candidate, Univ of Calif, Berkeley
Zakee Sabree	Florida A&M Univ	1998.8-1998.12	Univ of Wisconsin, Madison, WI
Jestus Kim	Emory University	1999.6-1999.8	Emory Univ
Nicholas Laszio		2001.9-12	
Jon Brooks Boroughs		2000.6-2000.8	High School Teacher
Daree Russell		2000.4-2001.3	
Roshitha V. Dunstan		2001.6-2001.8	
Shreni Keniya		2001.8-2001.12	
Katie Bergman		2001.6-2001.8	
Samantha Danielle		2002.5-2002.8	
Scott J. Pesek	Univ of Tennessee	2003.8-2003.12	Univ of Tennessee
Funjun Zhou	Univ of Tennessee	2004.8-2004.12	Univ of Tennessee
Kevin Kuhaida		2000.10-2000.12	
Rachel Lynch		2004.5-2004.8	
Melissa Schuyler		2004.5-2004.8	