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Professional Profile

I am an Adjunct Professor and a University Research Scientist of Microbiology, and the Associate Director of Institute for Environmental Genomics at the University of Oklahoma. I have been conducting interdisciplinary research activities in microbial ecology, functional genomics, and molecular microbiology using cutting edge technologies and approaches, which has resulted in more than **87** refereed publications in professional journals such as *Ecology Letters*, *Current Opinion in Biotechnology*, *the ISME Journal*, *Nature Reviews Microbiology*, *Proceedings of National Academy of Sciences of the United States of America*, *Nucleic Acids Research*, *Environmental Microbiology*, *Applied and Environmental Microbiology*, *Journal of Bacteriology*, *Environmental Science & Technology*, *FEMS Microbial Ecology*, and *BMC Genomics* as well as *Plant Physiology*. I have served as a member of Editorial Board of *Applied and Environmental Microbiology* since 2006 and *TheScientificWorldJOURNAL* (Genomics) since 2011. I have been a reviewer for many professional journals and proposals in microbiology, microbial ecology, genomics, molecular biology, and bioinformatics. A unique microarray-based genomics technology developed at the Institute for Environmental Genomics of University of Oklahoma, and OU GeoChip won an R&D 100 Award of 2009 and an Innovator of the Year 2010 Award. I have secured tens of millions research funding from National Science Foundation (NSF), US Department of Energy (US DOE), US Department of Agriculture (USDA), ConocoPhillips, and the State of Oklahoma as a principle investigator (PI) or co-PI since October 2006.

My research interests are to understand the microbial ecology, genomics/metagenomics, physiology, and molecular mechanisms underlying important microbial processes in nature and controlled environments. This includes three directions: (i) Microbial ecology to understand the diversity, composition, structure, interaction, dynamics and evolution of microbial communities related to the global climate change, long-term sustainability of bioenergy crops, and bioremediation using high throughput metagenomic technologies, such as microarrays (e.g., GeoChip, PhyloChip) and next generation sequencing; (ii) Systems microbiology and microbial functional genomics to understand gene functions, regulations, and networks of model organisms or near-model organisms, such as *Desulfovibrio vulgaris* Hildenborough, and *Shewanella oneidensis* MR-1 for bioremediation, and *Clostridium* and *Thermoanaerobacter* species for biofuels production using a consolidated bioprocessing (CBP); and (iii) Development of microarray-based biotechnologies and bioinformatics tools to achieve my research goals. Those directions unify my research into an interactive and cohesive research theme, which embeds basic research components, public interests, and an applied component. To efficiently implement such interdisciplinary research activities, I have established collaboration with researchers from USA, Europe, Canada, and China in those fields.

Education and Certificates

Bioinformatics	Certified Bioinformatics Specialist (CBS) and Master (CBM)	2002
BA	Computing and Information Science, University of Guelph, ON, Canada	2001
PhD	Research School of Biological Sciences, Australian National University, Australia	1998
MS	Shanghai Institute of Plant Physiology, the Chinese Academy of Science, China	1989
BS	Department of Biology, Hunan Normal University, China	1986

Interests

- Microbial ecology, physiology, and evolution related to the global climate change, bioenergy, stress responses and bioremediation
- Systems microbiology and microbial functional genomics for single organisms and microbial communities to understand gene functions, regulations and networks.
- Biotechnology with focuses on array-based genomic applications (e.g., GeoChip), and the generation of biofuels by mixed cultures.
- Bioinformatics in computer programming, applications of bioinformatics tools, database design and management, and software tools for biological uses.

Professional Experience

Adjunct Professor, Department of Botany and Microbiology Associate Director, Institute for Environmental Genomics Research Scientist IV, University of Oklahoma, Norman OK, USA	Sep 2011– present
Adjunct Associate Professor, Department of Botany and Microbiology Associate Director, Institute for Environmental Genomics Research Scientist IV, University of Oklahoma, Norman OK, USA	Sep 2007 – Aug 2011
Research Assistant Professor, Department of Botany and Microbiology Associate Director, Institute for Environmental Genomics Research Scientist IV, University of Oklahoma, Norman OK, USA	Oct 2005 – Aug 2006
Research Assistant Professor & Bioinformatics Team Leader University of Tennessee/ORNL, Oak Ridge, Tennessee, USA	Sep 2005 – Sep 2005
Postdoctoral Associate & Bioinformatics Team Leader Oak Ridge National Laboratory (ORNL), Oak Ridge, Tennessee, USA	Feb 2003 – Aug 2005
Bioinformatics Instructor (part-time) Xintra Computer College, Scarborough/Toronto, Ontario, Canada	Sep 2002 – Jan 2003
Software Developer/Tester (part-time) Research in Motion, Waterloo, Ontario, Canada	Nov 2001 – Jan 2003
Postdoctoral Research Associate University of Guelph, Guelph, Ontario, Canada (<i>Confidential contracts and NO publications were allowed.</i>)	Oct 1998 - Dec 2002
Researcher Research Institute of Innovative Technology for the Earth, Kyoto, Japan	Dec 1997 – Sep 1998

Junior Researcher/Research Scientist

Aug 1989 - Mar 1994

Shanghai Institute of Plant Physiology, the Chinese Academy of Sciences, Shanghai, China

Selected Publications

(i) Manuscripts submitted

1. Li X, Deng Y, Li Q, Lu C, Wang J, Zhang H, Zhu J, Zhou J, and **He Z***. Responses of soil microbial communities to elevated ozone and wheat (*Triticum aestivum* L) cultivars revealed by GeoChip-based analysis (*Corresponding author, submitted to *The ISME Journal*).
2. Frank Reith F, Brugger J, Zammit CM, Gregg AL, Goldfarb KC, Andersen GL, DeSantis TZ, Piceno YM, Brodie EL, Lu Z, **He Z**, Zhou J, and Wakelin SA. Influence of geogenic factors on microbial communities in metallogenic Australian soils (Submitted to *The ISME Journal*).
3. Yang Y, Wu L, Lin Q, Yuan M, Xu D, Yu H, Hu Y, Duan J, Li X, **He Z**, Xue K, Van Nostrand JD, Wang S, and Zhou J. Responses of the functional structure of soil microbial community to livestock grazing in Tibetan alpine grassland (Submitted to *The ISME Journal*).
4. Walker CB, Redding-Johanson AM, Baidoo EE, Rajeev L, He Z, Hendrickson EL, Joachimiak MP, Stolyar S, Arkin AP, Leigh JA, Zhou J, Keasling JD, Mukhopadhyay A, and Stahl DA. Functional responses of methanogenic archaea to syntrophic growth (Submitted to *The ISME Journal*).
5. Wang H, Lu Z, **He Z**, Zhou J, Xu X, Van Nostrand JD, and Zhang Z. Sediment Carbon and Phosphorus Biogeochemical Cycles and the Functional Gene Shifts of Wetlands Subjected to Experimental Warming (Submitted to *Applied and Environmental Microbiology*).
6. Xu M, **He Z**, Deng Y, Wu L, Van Nostrand JD, Hobbie SE, Reich PB, and Zhou J. Elevated CO₂ alters soil microbial functional structure and potential in carbon and nitrogen cycling (Submitted to *Applied and Environmental Microbiology*).
7. Jiang H, **He Z**, He Q, Hemme CL, Wu L, and Zhou J. Performance of cellulose conversion to ethanol by fed-batch co-culture fermentation (Submitted to *Applied and Environmental Microbiology*).
8. Zhou J, Liu W, Deng Y, Jiang YH, Xue K, **He Z**, Van Nostrand JD, Yang Y, and Wang A. Stochastic assembly leads to alternative communities with distinct functions (Submitted to *PNAS*).
9. Lu Z, **He Z**, Parisi V, Kang S, Deng Y, Van Nostrand JD, Masoner J, Cozzarelli I, Suflita JM, and Zhou J. GeoChip-based analysis of microbial functional gene diversity in a landfill leachate-contaminated aquifer (Submitted to *Environmental Science & Technology*).
10. Kang S, Van Nostrand JD, Gough HL, **He Z**, Hazen TC, Stahl DA, and Zhou J. Functional gene array-based analysis of microbial communities in heavy metals contaminated lake sediments (Submitted to *Environmental Microbiology*).

(ii) Published peer-review articles and book chapters (87 publications in microbial functional genomics, microbial physiology and ecology, molecular biology, and bioinformatics, H index = 22 with more than 1600 citations up to December 31, 2011)

2012

1. Clark ME, **He Z**, Redding AM, Joachimiak MP, Keasling JD, Zhou J, Arkin AP, Mukhopadhyay A, and Fields MW. 2012. Transcriptomic and proteomic analyses of *Desulfovibrio vulgaris* biofilms: carbon and energy flow contribute to the distinct biofilm growth state. *BMC Genomics* (in press).
2. **He Z**, Van Nostrand JD, and Zhou J. 2012. Applications of functional gene microarrays for profiling microbial communities. *Curr Opin Biotechnol* (Invited review, in press, DOI 10.1016/j.copbio.2011.12.021).
3. **He Z***, Deng Y, and Zhou J. 2012. Development of functional gene microarrays for microbial community analysis. *Curr Opin Biotechnol* **23**: 49–55 (*corresponding author, invited review).
4. **He Z**, Piceno Y, Deng Y, Xu M, Lu Z, DeSantis T, Andersen G, Hobbie SE, Reich PB, and Zhou J. 2012. The phylogenetic composition and structure of soil microbial communities shifts in response to elevated carbon dioxide. *ISME J* **6**: 259-272.
5. Deng Y*, **He Z***, Xu M, Qin Y, Van Nostrand JD, Wu L, Roe BA, Wiley G, Hobbie SE, Reich PB, and Zhou J. Pyrosequencing of 16S rRNA genes reveals a shift of soil microbial composition and structure under elevated carbon dioxide. *Appl Environ Microbiol* (in press).
6. Liang Y, Van Nostrand JD, N'Guessan LA, Peacock AD, Deng Y, Long PE, Resch T, Wu L, **He Z**, Li G, Hazen, Lovley DR, and Zhou J. Microbial Functional Gene Diversity with a Shift of Subsurface Redox Condition. *Appl Environ Microbiol* (in press).
7. Zhou J, Xue K, Xie J, Deng Y, Wu L, Cheng X, Fei S, Deng S, **He Z**, Van Nostrand JD, and Luo Y. Microbial mediation of carbon cycle feedbacks to climate warming. *Nature Climate Change* (in press, DOI: 10.1038/NCLIMATE1331).
8. Trivedi P, **He Z**, Van Nostrand JD, Zhou J, Albrigo G, and Wang N. 2012. Huanglongbing alters the structure and functional diversity of microbial communities associated with citrus rhizosphere. *ISME J* **6**: 363-383.
9. Lu Z , Deng Y, Van Nostrand JD, **He Z**, Voordeckers J, Zhou A, Lee YJ, Mason OU, Dubinsky EA, Chavarria KL, Tom LM, Fortney JL, Lamendella R, Jansson JK, D'haeseleer P, Hazen TC, and Zhou J. 2012. Microbial gene functions enriched in the Deepwater Horizon deep-sea oil plume. *ISME J* **6**: 451-460.
10. Zhou A, Chen Y, Zane GM, **He Z**, Hemme CL, Joachimiak MP, Baumoh J, He Q, Fields MW, Arkin AP, Wall JD, Hazen TC, and Zhou J. 2012. Functional characterization of Crp/Fnr-type global transcriptional regulators in *Desulfovibrio vulgaris* Hildenborough. *Appl Environ Microbiol* **78**:1168-117.

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11. **He Z**, Van Nostrand JD, Deng Y, and Zhou J. 2011. Development and applications of functional gene microarrays in the analysis of the functional diversity, composition, and structure of microbial communities. *Front Environ Sci Engin China* **5**: 1-20 (Invited Feature Article).
12. Xie J, **He Z**, Liu X, Liu X, Van Nostrand JD, Deng Y, Wu L, Zhou J, and Qiu G. 2011. GeoChip-based analysis of the functional gene diversity and metabolic potential of microbial communities in acid mine drainage. *Appl Environ Microbiol* **77**: 991-999.

13. Hemme CL, Fields MW, He Q, Deng Y, Lin L, Tu Q, Mouttaki H, **He Z**, Barry K, Saunders E, Sun H, Land M, Hauser L, Lapidus A, Han CS, Xu J, Wiegel J, Phelps TJ, Rubin E, and Zhou J. 2011. Correlation of genomic and physiological traits of *Thermoanaerobacter* species with biofuel yields. *Appl Environ Microbiol* **77**: 7998-8008.
14. Lin L, Song H, Tu Q, Qin Y, Zhou A, Liu W, **He Z**, Zhou J, and Xu J. 2011. Thermoanaerobic glycobiome reveals mechanisms of pentose and hexose co-utilization in bacteria. *PLoS Genet* **7**: e1002318 (doi:10.1371/journal.pgen.1002318).
15. Liu A, Wu L, **He Z**, and Zhou J. 2011. Development of highly fluorescent silica nanoparticles chemically doped with organic dye for sensitive DNA microarray detection. *Anal Bioanal Chem* **401**: 2003–2011.
16. He Q, Hemme CL, Jiang H, **He Z**, and Zhou J. 2011. Mechanisms of enhanced cellulosic bioethanol fermentation by co-cultivation of *Clostridium* and *Thermoanaerobacter* spp. *Bioresour Technol* **102**: 9586–9592.
17. Wang J, Van Nostrand JD, Wu L, **He Z**, Li G, and Zhou J. Microarray-based evaluation of whole-community genome DNA amplification methods. *Appl Environ Microbiol* **77**: 4241–4245.
18. Van Nostrand JD, Wu L, Wu W, Huang Z, Gentry TJ, Deng Y, Carley J, Carroll S, **He Z**, Gu B, Luo J, Criddle CS, Watson DB, Jardine PM, Marsh TL, Tiedje JM, Hazen TC, and Zhou J. Dynamics of microbial community composition and function during *in situ* bioremediation of a uranium-contaminated aquifer. *Appl Environ Microbiol* **77**: 3860–3869.
19. Zhou J, Deng Y, Luo F, **He Z**, and Yang Y. 2011. Phylogenetic molecular ecological network of soil microbial communities in response to elevated CO₂. *mBio* **2**: doi:10.1128/mBio.00122-11.
20. Zhou J, He Q, Hemme CL, Mukhopadhyay A, Hillesland K., Zhou A, **He Z**, Van Nostrand JD, Hazen TC, Stahl DA, Wall JD, and Arkin AP. 2011. How sulphate-reducing microorganisms cope with stress: lessons from systems biology. *Nat Rev Microbiol* **9**: 452-466.
21. Zhou J, Wu L, Deng Y, Zhi X, Jiang YH, Tu Q, Xie J, Van Nostrand JD, **He Z**, and Yang Y. 2011. Reproducibility and quantitation of amplicon sequencing-based detection. *ISME J* **5**: 1303–1313.
22. Wang A, Gao L, Ren N, Xu J, Liu C, Gao G, Yu H, Liu W, Hemme CL, **He Z**, and Zhou J. 2011. Isolation and characterization of *Shigella flexneri* G3 for effective cellulosic saccharification under mesophilic conditions. *Appl Environ Microbiol* **77**: 517-523.
23. Liang Y, Van Nostrand JD, Deng Y, **He Z**, Wu L, Zhang X, Li G, and Zhou J. 2011. Functional gene diversity of soil microbial communities from oil-contaminated fields in China. *ISME J* **5**: 403-413.
24. Van Nostrand JD, Kang S, Deng Y, Liang Y, **He Z**, and Zhou J. 2011. Monitoring microbial activity with GeoChip. In JF Stolz and RS Oremland (eds), *Microbial Metal and Metalloid Metabolism: Advances and Applications*, pp261-282. ASM Press, Washington DC (Invited book chapter).

25. Van Nostrand JD, **He Z**, and Zhou J. 2011. Metagenomics analysis of below-ground microbial communities using microarrays. In: D. Marco (ed) *Metagenomics: Current Innovations and Future Trends*, Caister Academic. pp 265-288.
26. Van Nostrand JD, **He Z**, and Zhou J. 2011. 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.
27. Van Nostrand JD, **He Z**, Zhou J. 2011. 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 509-520.

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28. **He Z**, Xu M, Deng Y, Kang S, Kellogg L, Wu L, Van Nostrand JD, Hobbie SE, Reich PB, and Zhou J. 2010. Metagenomic analysis reveals a marked divergence in the structure of belowground microbial communities at elevated CO₂. *Ecol Lett* **13**: 564-575.
29. **He Z**, Deng Y, Van Nostrand JD, Tu Q, Xu M, Hemme CL, Li X, Wu L, Hazen TC, and Zhou J. 2010. GeoChip 3.0 as a high throughput tool for analyzing microbial community composition, structure, and functional activity. *ISME J* **4**: 1167-1179.
30. **He Z**, Zhou A, Baidoo E, He Q, Joachimiak MP, Benke P, Phan R, Mukhopadhyay A, Hemme CL, Huang K, Alm EJ, Fields MW, Wall JD, Stahl D, Hazen TC, Keasling JD, Arkin, AP, and Zhou J. 2010. Global transcriptional, physiological and metabolite analyses of *Desulfovibrio vulgaris* Hildenborough responses to salt adaptation. *Appl Environ Microbiol* **76**: 1574-1586.
31. Liang Y*, **He Z***, Wu L, Deng Y, Li G, and Zhou J. 2010. Development of a common oligonucleotide reference standard for microarray data normalization and comparison across different microbial communities. *Appl Environ Microbiol* **76**: 1088-1094 (*co-first authors).
32. Zhou J, **He Z**, Van Nostrand JD, Wu L, and Deng Y. 2010. Applying GeoChip analysis to disparate microbial communities. *Microbe* **5**: 60-65 (Invited review).
33. Zhou A, **He Z**, Redding AM, Mukhopadhyay A, Hemme CL, Joachimiak MP, He Q, Bender KS, Keasling JD, Stahl D, Fields MW, Hazen TC, Arkin, AP, Wall JD, and Zhou J. 2010. Hydrogen peroxide-induced oxidative stress responses in *Desulfovibrio vulgaris* Hildenborough. *Environ Microbiol* **12**: 2645-2657.
34. He Q, **He Z**, Joyner DC, Price MN, Yang ZK, Yen HB, Chakraborty R, Chen W, Keller M, Arkin AP, Hazen TC, Wall JD, and Zhou J. 2010. Impact of elevated nitrate on sulfate-reducing bacteria: implications of inhibitory mechanisms in addition to osmotic stress. *ISME J* **4**: 1386-1397.
35. Zhou J, Deng Y, Luo F, **He Z**, Tu Q, and Zhi X. 2010. Functional molecular ecological networks. *mBio* **1**: e00169-10 (doi:10.1128/mBio.00169-10).
36. Liang Y, Gao H, Chen J, Dong Y, Wu L, **He Z**, Liu X, Qiu G, and Zhou J. 2010. Pellicle formation in *Shewanella oneidensis*. *BMC Microbiol* **10**: 291.
37. Liu W, Wang A, Cheng S, Logan B, Yu H, Deng Y, Van Nostrand JD, Wu L, **He Z**, and Zhou J. 2010. GeoChip-based functional gene analysis of anodophilic communities in microbial electrolysis cells under different operational modes. *Environ Sci Technol* **44**: 7729-7735.

38. Hemme CL, Mouttaki H, Lee YJ, Goodwin L, Lucas S, Copeland A, Lapidus A, del Rio TG, Tice H, Saunders E, Brettin T, Detter JC, Han CS, Pitluck S, Land ML, Hauser LJ, Krypides N, Mikhailova N, **He Z**, Wu L, Van Nostrand JD, Henrissat B, He Q, Lawson PA, Tanner RS, Lynd LR, Wiegel J, Fields MW, Arkin AP, Schadt CW, Stevenson BS, McInerney MJ, Yang Y, Dong H, Huhnke RL, Mielenz JR, Ding SY, Himmel ME, Taghavi S, van der Lelie D, Rubin EM, and Zhou J. 2010. Genome announcement: sequencing of multiple Clostridia genomes related to biomass conversion and biofuels production. *J Bacteriol* **192**: 6494-6496.
39. Xiong J, Wu L, Tu S, Van Nostrand JD, **He Z**, Zhou J, and Wang G. 2010. Microbial communities and functional genes associated with soil arsenic contamination and rhizosphere of the arsenic hyper-accumulating plant *Pteris vittata* L. *Appl Environ Microbiol* **76**: 7277-7284.
40. Parnell JJ, Rompato G, Latta LC IV, Pfrender ME, Van Nostrand JD, **He Z**, Zhou J, Andersen G, Champine P, Ganesan B, and Weimer1BC. 2010. Functional Biogeography as Evidence of Gene Transfer in Hypersaline Microbial Communities. *PLoS ONE* **5**: e12919.
41. Lin L, Song H, Ji Y, **He Z**, Pu Y, Zhou J, and Xu J. 2010. Ultrasound-mediated DNA transformation in thermophilic Gram-positive anaerobes. *PLoS ONE* **5**: e12582.
42. Gao H, Barua S, Liang Y, Wu L, Dong Y, Reed S, Chen J, Culley D, Kennedy D, Yang Y, **He Z**, Nealon KH, Fredrickson JK, Tiedje JM, Romine M, and J Zhou. 2010. Impacts of *Shewanella onedensis* c-type cytochromes on aerobic and anaerobic respiration. *Microb Biotechnol* **3**: 455-466.
43. Xu M, Wu W, Wu L, **He Z**, Van Nostrand JD, Deng Y, Luo J, Carley J, Ginder-Vogel M, Gentry TJ, Gu B, Watson D, Jardine PM, Marsh TL, Tiedje JM, Hazen TC, Criddle CS, and Zhou J. 2010. Functional understanding of microbial community structures in contaminated sediments during in situ bioremediation/immobilization of uranium. *ISME J* **4**: 1060-1070.
44. Hemme CL, Wu L, Deng Y, Gentry TJ, Fields MW, Fang Z, Barua S, Watson D, **He Z**, Richardson P, Hazen TC, Tiedje JM, Rubin E, and Zhou J. 2010. Metagenomic insights into evolution of a heavy metal-contaminated groundwater microbial community. *ISME J* **4**: 660-672.
45. Andersen G, **He Z**, DeSantis T, Brodie E, and Zhou J. 2010. The Use of Microarrays in Microbial Ecology in *Environmental Molecular Microbiology*, pp87-110 (Edited by Wen-Tso Liu and Janet K. Jansson), Caister Academic Press, Norfolk, UK.
46. Van Nostrand JD, Liang Y, **He Z**, Li G, and Zhou J. 2010. GeoChip: A high throughput genomic tool for linking community structure to functions. In *Handbook of Hydrocarbon and Lipid Microbiology*, pp.2677-2685. Springer Berlin Heidelberg, Germany.
47. Van Nostrand, JD, **He Z**, and Zhou J. 2010. Analysis of microbial communities by functional gene Arrays. In: L. Barton, M. Mandl and A. Loy (eds) in *Geomicrobiology: Molecular and Environmental Perspective*, pp109-126. Springer, New York (Invited book chapter).

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48. Liang Y, Li G, Van Nostrand JD, **He Z**, Wu L, Deng Y, Zhang X, and Zhou J. 2009. Microarray-based analysis of microbial functional diversity along an oil contamination gradient in oil field. *FEMS Microb Ecol* **70**: 324-333.

49. Van Nostrand JD, Wu W, Wu L, Deng Y, Carley J, Carroll S, **He Z**, Gu B, Luo J, Criddle CS, Watson DB, Jardine PM, Marsh TL, Tiedje JM, Hazen TC, and Zhou J. 2009. GeoChip-based analysis of functional microbial communities in a bioreduced uranium-contaminated aquifer during reoxidation by oxygen. *Environ Microbiol* **11**: 2611-2626.
50. Walker CB, **He Z**, Yang ZK, Stolyar SS, Jacobsen J, Ringbauer Jr JA, Wall JD, Zhou J, Arkin AP, and Stahl DA. 2009. The electron transfer system of syntrophically grown *Desulfovibrio vulgaris*. *J Bacteriol* **191**: 5793-5801.
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52. Feng X, Mouttaki H, Lin L, Huang R, Wu B, Hemme CL, **He Z**, Zhang B, Hicks LM, Xu J, Zhou J, and Tang YJ. 2009. Characterization of the central metabolic pathways in *Thermoanaerobacter* sp. strain X514 via isotopomer-assisted metabolite analysis. *Appl Environ Microbiol* **75**: 5001-5008.
53. Liang Y, **He Z**, Gao H, Qiu G, Zhou J and Liu X. 2009. Characterization of cytochrome mutants for pellicle formation in *Shewanella onedensis* MR-1. *Trans Nonferrous Met Soc China* **19**: 700-706.
54. Waldron PJ, Wu L, Van Nostrand JD, Schadt CW, **He Z**, Watson DB, Jardine PM, Palumbo AV, Hazen TC, Zhou J. 2009. Functional gene array-based analysis of microbial community structure in groundwaters with a gradient of contaminant levels. *Environ Sci Technol* **43**: 3529-3534.
55. Wang F, Zhou H, Meng J, Peng X, Jiang L, Sun P, Zhang C, Van Nostrand JD, Deng Y, **He Z**, Wu L, Zhou J, and Xiao X. GeoChip-based analysis of metabolic diversity of microbial communities at the Juan de Fuca Ridge hydrothermal vent. *Proc Natl Acad Sci USA* **106**: 4840-4845.
56. Van Nostrand JD, Wu L, **He Z**, and Zhou J. 2009. 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 4039-4050 (Invited book chapter).
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59. **He Z***, Van Nostrand JD, Wu L, and Zhou J. 2008. Development and application of functional gene arrays for microbial community analysis. *Transactions of Nonferrous Metals Society of China* **18**: 1319-1327 (Invited review, *corresponding author).
60. Deng Y, **He Z***, Van Nostrand JD, Zhou J*. 2008. Design and analysis of mismatch probes for long oligonucleotide microarrays. *BMC Genomics* **9**: 491 (*corresponding author).

61. Rodrigues DF, Ivanova N, **He Z**, Huebner M, Zhou J, and Tiedje JM. 2008. Architecture of thermal adaptation in an *Exiguobacterium sibiricum* strain isolated from 3 million year old permafrost: A genome and transcriptome approach. *BMC Genomics* **9**: 547.

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64. Yergeau E, Kang S, **He Z**, Zhou J, and Kowalchuk GA. 2007. Functional microarray analysis of nitrogen and carbon cycling genes across an Antarctic latitudinal transect. *ISME J* **1**: 163-179.
65. Butler J, He Q, Nevin PK, **He Z**, Zhou J, and Lovley D. 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.
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70. Gentry TJ, Wickham JS, Schadt CW, **He Z**, and Zhou J. 2006. Microarray applications in microbial ecology research. *Microb Ecol* **52**: 159-175 (Invited review).
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72. Clark ME, He Q, **He Z**, Huang KH, Alm EJ, Wan X, Hazen TC, Arkin AP, Wall JD, Zhou J, and Fields MW. 2006. Temporal transcriptomic analysis as *Desulfovibrio vulgaris* Hildenborough transitions into stationary phase during electron donor depletion. *Appl Environ Microbiol* **72**: 5578-5588.
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81. **He Z** and Zhou J. 2004. Selection of oligonucleotide probes for microarrays. *Molecular Microbial Ecology Manual*, pp1880-1891. Springer Netherlands.
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Most Recent Oral/Poster Presentations (since 2008)

(i) Oral presentations

1. Exploration of microbial interactions via 16S rRNA gene pyrosequences (Invited speaker by Guangdong Institute of Microbiology, September 2011, Guangzhou, China).
2. Analysis of microbial communities in response to elevated CO₂ and uranium contamination using GeoChip technologies (Invited speaker by Lanzhou University, September 2011, Lanzhou, China).
3. Conversion of lignocellulosic biomass to biofuels by a novel fungus *Penicillium expansum* YT02 (Invited speaker by Institute of Tropical Bioscience and Biotechnology, the Chinese Academy of Tropical Agricultural Sciences, September 2011, Haikou, China)
4. A novel fungus efficiently converts cellulosic biomass into soluble sugars (Invited speaker, 2011 EPSCoR Annual Meeting, Norman, OK, USA, April 2011).
5. Detection and functional characterization of microbial communities using metagenomic approaches (Invited speaker by Agriculture and Agri-Food Canada, January 2011, Lethbridge, Alberta, Canada)
6. Metagenomic analysis of alterations in the soil microbial community structure and functional potential under elevated CO₂ (The 13th International Symposium on Microbial Ecology, Seattle, WA, USA, August 2010).
7. GeoChip 3.0: a high throughput metagenomic tool for analyzing microbial community structure, composition, and functional activity (Invited speaker, the First Meeting of SCOR WG134 Microbial Carbon Pump in the Ocean, October 2009, Xiamen, China).
8. Metagenomics approaches and applications (Invited speaker by Guangdong Institute of Microbiology, November 2009, Guangzhou, China).
9. Development of GeoChip 3.0 for Microbial Community Analysis (The 12th International Symposium on Microbial Ecology, Cairns, Australia, August 2008).
10. From Single Microorganisms to Communities: Genomics-Based Understanding of Microbial Stress Responses and Adaptation (Invited speaker by Monsanto, May 2008, St. Louis, MO, USA).
11. GeoChip Development and Its Applications in Microbial Community Analysis (Keynote speaker, December 2007, the 10th Environmental Microbiology Conference, Guangzhou, China).
12. **35** other oral presentations at regional and national meetings or conferences.

(ii) Poster presentations since 2008

2011

1. More than **three** posters at the Annual ENIGMA Retreat (Berkeley, CA, September 2011)
2. **One** poster at the Applied and Environmental Microbiology Meeting (Gordon Research Conference, South Hadley, MA, July 2011)

3. **18** poster presentations at the 2011 ASM General Meeting (May 2011, the 111th General Meeting of American Society for Microbiology, New Orleans, LA, USA)
4. **Five** poster presentations at the 2011 Genomics:GTL Annual Meeting (April 2011, Washington DC, USA)
5. **One** poster presentation at the 6th Department of Energy Subsurface Biogeochemical Research PI Meeting (Washington DC, USA, April 2011)

2010

1. **19** poster presentations at the 13th International Symposium on Microbial Ecology (August 2010, Seattle, WA, USA).
2. **Five** poster presentations at the 2010 Genomics:GTL Annual Meeting (February 2010, Crystal City, VA, USA).
3. **Three** poster presentations at the 5th Department of Energy's Environmental Remediation Science Program (ERSP) Annual Principal Investigator (PI) Meeting of (March 2010, Washington DC, USA).
4. **20** poster presentations at the 2010 ASM General Meeting (May 2010, the 110th General Meeting of American Society for Microbiology, San Diego, CA, USA).

2009

1. **Six** poster presentations at the 2009 Genomics:GTL Annual Meeting (February 2009, Washington DC, USA).
2. **29** poster presentations at the 2009 ASM (May 2009, the 109th General Meeting of American Society for Microbiology, Philadelphia, PA, USA).
3. **Three** poster presentations at the 17th Annual International Conference on Microbial Genomics (October 2009, Flintstone, MD, USA).

2008

1. **Seven** poster presentations at the 2008 Genomics:GTL Annual Meeting (February 2008, Washington DC, USA).
2. **21** poster presentations at the 2008 ASM (May 2008, the 108th General Meeting of American Society for Microbiology, Boston, MA, USA).
3. **Four** poster presentations at the Grow Biofuels Conference (November 2008, Oklahoma City, OK, USA).

Software

- IEG Microbial Community Network Analysis Pipeline – *IMCNAP* May 2009–present
- Genomic DNA-based Microarray Data Analysis – *GMADA* Aug 2007–present
- Environmental Sequence and Genome Analysis Systems - *ESGAS* Apr 2004–Dec 2008
- Oligonucleotide probe design program - *CommOligo* Jul 2003–Jun 2004
- Web Blackberry Client Systems Nov 2001–Dec 2002

Professional Services and Memberships

- A member of the Editorial Board of *Applied and Environmental Microbiology* (AEM)
- A member of the Editorial Board of The Scientific World JOURNAL (Genomics) (TSWJ)
- The American Society for Microbiology (ASM)
- The American Association for the Advancement of Science (AAAS)
- The International Society for Microbial Ecology (ISME)
- Reviewer for a variety of journals, including *Applied and Environmental Microbiology* (AEM), *Applied Microbiology Biotechnology* (AMB), *the ISME Journal*, *Journal of Bacteriology*, *Microbiology*, *Canadian Journal of Microbiology*, *Current Microbiology*, *Bioinformatics*, *BMC Bioinformatics*, *Gene*, *Journal of Virological Methods*, and *Journal of Phytopathology*
- Reviewer of DOE and NSF proposals

Awards

- **2009 R&D 100 Award** by R&D Magazine for *OU GeoChip* developed by Jizhong Zhou, **Zhili He**, Liyou Wu, Joy D. Van Nostrand, and Ye Deng at the Institute for Environmental Genomics and Department of Botany and Microbiology, University of Oklahoma. This is a prestigious award for providing a mark of excellence known to industry, government, and academia as proof that the product is one of the most innovative ideas of the year (2009).
- **An Innovator of the Year 2010 Award** by The Journal Record for the development of GeoChip and associated technologies in Oklahoma. This program recognizes businesses, organizations and individuals who embrace both the entrepreneurialism and innovation that make Oklahoma such a special place to live and work (2010).