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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, Human Normal University, China	1986

Research Interests

- Microarray-based microbial functional genomics, proteomics and their applications
- Bioinformatics, computer programming, and database design and management
- Microbial gene functions, regulations and network modeling under environmental stresses
- Microbial physiology, biochemistry, molecular genetics and bioremediation

Professional Experience

Adjunct Associate Professor/Research Scientist , Department of Botany and Microbiology	Nov 2005 – Present
Associate Director , Institute for Environmental Genomics, University of Oklahoma, Norman, OK	
Research Assistant Professor & Bioinformatics Team Leader	Sep 2005 – Oct 2005
University of Tennessee/ORNL, Oak Ridge, Tennessee, USA	
Postdoctoral Associate & Bioinformatics Team Leader	Feb 2003 – Aug 2005
Oak Ridge National Laboratory (ORNL), Oak Ridge, Tennessee, USA	
Postdoctoral Research Associate and Software Developer	Oct 1998 - Dec 2002
University of Guelph, Guelph, Ontario, Canada	
Researcher	Dec 1997 – Sep 1998
Research Institute of Innovative Technology for the Earth, Kyoto, Japan	

Selected Publications

(More than 40 publications in bioinformatics, genomics, microbiology, microbial ecology, and molecular biology, and more than 10 manuscripts are in review or in preparation)

• Ten most closely related publications

1. 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. X514 via isotopic labeling. *Applied and Environmental Microbiology* **75**:5001-5008.
2. Walker CB, **He Z**, Yang ZK, Stolyar SS, Jacobsen J, Ringbauer Jr JA, Wall JD, Zhou J, Arkin AP, and Stahl DA. 2009. Energy conservation by *Desulfovibrio vulgaris* in syntrophic growth with a hydrogenotrophic methanogen. *Journal of Bacteriology* **191**:5793-5801.
3. 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. 2009. GeoChip-based Analysis of Metabolic Diversity of Microbial Communities at the Juan de Fuca Ridge Hydrothermal Vent. 2009. GeoChip-based analysis of metabolic diversity of microbial communities at the Juan de Fuca Ridge hydrothermal vent. *Proceedings of National Academy of Sciences of the United States of America* **106**: 4840–4845.
4. **He Z** and Zhou J. 2008. Empirical evaluation of a new method for calculating signal to noise ratio (SNR) for microarray data analysis. *Applied and Environmental Microbiology* **74**:2957-2966.
5. **He Z**, Gentry TJ, Schadt CW, Wu L, Liebich J, Chong SC, Huang Z, Wu W, Gu B, Jardine P, Criddle C, and Zhou J. 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**).
6. Mukhopadhyay A, **He Z**, Yen HC, Alm EJ, He Q, Huang K, Baidoo EE, Chen W, Borglin SC, Redding A, Holman HY, Sun J, Joyner DC, Keller M, Zhou J, Arkin AP, Hazen TC, Wall JD, and Keasling JD. 2006. Salt stress in *Desulfovibrio vulgaris* Hildenborough: An integrated genomics approach. *Journal of Bacteriology* **188**:4068-4078.
7. He Q, Huang KH, **He Z**, Alm EJ, Fields MW, Hazen TC, Arkin AP, Wall JD, and Zhou J. 2006. Energetic consequences of nitrite stress in *Desulfovibrio vulgaris* Hildenborough inferred from global transcriptional analysis. *Applied and Environmental Microbiology* **72**:4370-4381.

8. **He Z**, Wu L, Li X, Fields MW and Zhou J. 2005. Empirical establishment of oligonucleotide probe design criteria. *Applied and Environmental Microbiology* **71**:3753-3760 (**One of the top 20 papers most requested in 2005 by AEM**).
 9. Li X*, **He Z*** and Zhou J. 2005. Selection of optimal oligonucleotide probes for microarrays using multiple criteria, global alignment and parameter estimation (*co-first author). *Nucleic Acids Research* **33**:6114-6123.
 10. **He Z**, Wu L, Fields MW and Zhou J. 2005. Comparison of microarray performance with different probe sizes for monitoring gene expression. *Applied and Environmental Microbiology* **71**:5154-5162.
- **Ten other related publications**
1. Andersen G, **He Z**, DeSantis T, Brodie E, and Zhou J. 2009. The Use of Microarrays in Microbial Ecology (An invited book chapter, in press).
 2. Walker CB, Stolyar S, Chivian D, Pinel N, Gabster JA, Dehal PS, **He Z**, Yang ZK, Yen HCB, Zhou J, Wall JD, Hazen TC, Arkin AP, and Stahl DA. 2009. Contribution of mobile genetic elements to *Desulfovibrio vulgaris* genome plasticity. *Environmental Microbiology* **9**:2244-2252.
 3. 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. *Environmental Science & Technology* **43**:3529-3534.
 4. **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).
 5. 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).
 6. 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. *The ISME Journal* **1**:163-179.
 7. 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.
 8. Gentry TJ, Wickham JS, Schadt CW, **He Z**, and Zhou J. 2006. Microarray Applications in Microbial Ecology Research. *Microbial Ecology* **52**:159-175 (Invited review).
 9. 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 of *Desulfovibrio vulgaris* Hildenborough transition into stationary phase during electron donor depletion. *Applied and Environmental Microbiology* **72**:5578-5588.
 10. Liebich J, Schadt CW, Chong SC, **He Z**, Rhee SK and Zhou J. 2006. Improvement of oligonucleotide design criteria for the development of functional gene microarrays for environmental applications. *Applied and Environmental Microbiology* **72**:1688-1691.

Software

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| • Package for functional gene array design and data analysis | Dec 2006 - present |
| • Genomic DNA-based microarray data analysis – <i>GMADA</i> | Aug 2006 - present |
| • Environmental sequence and genome analysis systems - <i>ESGAS</i> | Apr 2004 – Oct 2005 |
| • Oligonucleotide probe design program - <i>CommOligo</i> | Jul 2003 - Jun 2004 |

Synergistic Activities and memberships

- Member of Editorial Board for *Applied and Environmental Microbiology*(AEM)
- Reviewer for *Applied and Environmental Microbiology*, *ISME Journal*, *Bioinformatics*, *BMC Bioinformatics*, *Gene*, *Applied Biotechnology Microbiology*, *Canadian Journal of Microbiology*, *Current Microbiology*, and *Journal of Virological Methods*
- Member of *American Society for Microbiology* (ASM) and *American Association for the Advancement of Science* (AAAS)