

***Matthew W. Fields***

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**Education and Training**

Postdoctoral Research Associate, Oak Ridge National Laboratory 2001  
Ph.D. Microbiology, Minor: Biochemistry/Biological Engineering, Cornell University 2001  
M.S. Biological Sciences, Mississippi State University 1995  
B.S. Biology/Chemistry, Western Kentucky University 1993

**Research Experience**

Assistant Professor, Department of Microbiology, Miami University 2003-  
Develop and direct research program in bacterial physiology, biochemistry, and ecology dealing with model organisms (*Shewanella* spp., *Desulfovibrio*, *Alkaliphilus*, *Anaeromyxobacter*, field isolates) and *in situ* communities associated with bioremediation (groundwater, sediments, reactors)  
Current Laboratory 1 Postdoctoral Assoc.; 3 Ph.D. students; 4 undergraduates  
Presentations (oral/poster at national conferences) 17 in 2005; 13 in 2004; 10 in 2003

Research Staff Scientist, Oak Ridge National Laboratory 2001-2003  
Assess microbial ecology of contaminated sites using molecular- and culture-based techniques; isolation and physiological characterization of novel and unique microbes; development of functional, community, and metagenomic DNA microarrays; coordination of global transcriptomic studies with cellular physiology

Graduate Research Assistant, Department of Microbiology, Cornell University 1996-2001  
Conducted and initiated independent research combining microbial physiology and molecular biology dealing with the role and regulation of polysaccharide hydrolases from rumen bacteria; advised and coordinated undergraduate research

**Teaching Experience**

Microbial Ecology (475/575) lecture 2005-  
The course covered the basic concepts of microbial ecology, examined biotic and abiotic interactions within and between populations, and discussed the role of bacteria in maintaining steady-state conditions in natural ecosystems. Lecture material was supplemented with scientific literature for discussion-based meetings.

Biological Concepts (116) lecture (co-instructor) 2004-  
Covered basic prokaryotic and eukaryotic taxonomy, DNA replication, transcription, translation, and biotechnology.

Summer Workshop for Secondary Education Teachers (co-instructor) 2004  
Lectures covered basic microbiological concepts, practices, and experiments.

Microbial Physiology (425/525) lecture and laboratory 2003-  
The course covered principle concepts of microbial physiology including: cell composition, cell growth, electron transport, chemiosmosis, photosynthesis, central metabolism, lipids, nucleic acids, transport, gene expression, nutrient transport, and adaptive response.

Graduate Journal Club (750) course 2003-  
Consisted of weekly meetings with graduate students to discuss primary literature on stress response studies related to microbial physiology. Scientific papers were discussed in detail in an informal setting to stimulate open discussion and questions in a round-table format.

University Service

Editorial Board for <i>Applied and Environmental Microbiology</i>	2006-2009
Invited speaker at MI-ASM branch meeting	2005
Invited by DOD to attend MBT workshop and draft strategic plan	2005
Faculty Research Committee (advisory committee to University Senate)	2005-
Invited by USDA to help develop road-map for a joint NSF-USDA proposal call	2004
<i>Ad Hoc</i> reviewer for <i>Applied and Environmental Microbiology</i>	2004-
Serve on the Ecology program committee; Instrumentation Laboratory Advisory Committee	2004-
Serve as MBI advisor for Environmental Science co-major	2004-
Faculty Fellow for the Sigma Phi Epsilon fraternity	2004-
Co-PI for funded NSF equipment grant	2004-

Publications

27. Hwang, C., W.-M. Wu, T.J. Gentry, J. Carley, S.L. Carroll, C. Schadt, D. Watson, P.M. Jardine, J. Zhou, R.F. Hickey, C.S. Criddle, and M.W. Fields. 2005. Changes in bacterial community structure correlate with initial operating conditions of a field-scale denitrifying fluidized bed reactor. *Appl. Microbiol. Biotech.* (accepted)
26. Fields, M.W., J. Schryver, C.C. Brandt, T. Yan, J. Zhou, and A.V. Palumbo. 2005. Confidence intervals for similarity values achieved from direct sequence determination of cloned SSU rRNA genes from environmental samples. *J. Microbiol. Methods* (in press)
25. M. Gentile, T. Yan, S.M. Tiquia, M.W. Fields, J. Nyman, J. Zhou, and C. S. Criddle. 2005. Stability in a denitrifying fluidized bed reactor. *Microbial Ecology* (in press)
24. B. Gu, W.-M. Wu, M.A. Ginder-Vogel, H. Yan, M.W. Fields, S. Fendorf, C.S. Criddle, and P.M. Jardine. 2005. Bioreduction of uranium in a contaminated soil column. *Environ. Science. Tech.* 39:4841-4847
23. Dong, H., H. Jiang, G. Zhang, B. Yu, L.R. Chapman, C.R. Lucas, and M.W. Fields. 2005. Microbial diversity in water and sediment of Lake Qinghai: the largest inland saline lake in China. *Microbial Ecol.* (in press)
22. He, Z., L. Wu, M.W. Fields and J. Zhou. 2005. Comparison of microarrays with different probe sizes for monitoring gene expression. *Appl. Environ. Microbiol.* 71:5154-5162
21. Fields, M.W., T. Yan, S.-K. Rhee, S.L. Carroll, P.M. Jardine, D.B. Watson, C.S. Criddle and J. Zhou. 2005. Impacts on microbial communities and cultivable isolates from groundwater contaminated with high levels of nitric acid-uranium waste. *FEMS Microbiol. Ecol.* 53:417-428
20. Wu, W., B. Gu, M.W. Fields, M. Gentile, S.M. Tiquia, J. Nyman, J. Zhou, C.S. Criddle. 2005. Characterization of uranium (VI) reduction by microbial biomass from a denitrifying fluidized bed reactor. *Bioremediation J.* 9.1-13
19. Fields, M.W. and J.B. Russell. 2005. Transcriptional regulation of  $\beta$ -glucanase activity in the ruminal bacterium, *Prevotella bryantii* B<sub>14</sub>. *Curr. Microbiol.* 50:155-159
18. He, Z., L. Wu, X. Li, M.W. Fields and J. Zhou. 2005. Empirical establishment of oligonucleotide probe design criteria. *Appl. Environ. Microbiol.* 71:3753-3760
17. Liu, Y., W. Gao, L. Wu, X. Liu, T. Yan, M.W. Fields, D.K. Thompson, and J. Zhou. 2005.

Genomic expression profiling of *Shewanella oneidensis* MR-1 response to sodium salt stress. *J. Bacteriol.* 187:2501-2507

16. Palumbo, A.V., J.C. Schryver, M.W. Fields, C. E Bagwell, J. Zhou, T. Yan, X. Liu and C.C. Brandt. 2004. Coupling functional gene diversity and geochemical data from environmental samples. *Appl. Environ. Microbiol.* 70:6525-6534

15. Tiquia, S.M., S.C. Chong, M.W. Fields, and J. Zhou. 2004. Oligonucleotide-based functional gene arrays for analysis of microbial communities in the environment, *In Molecular Microbial Ecology Manual*, Kluwer Academic Press

14. Wu, L., D.K. Thompson, X. Liu, M.W. Fields, C.E. Bagwell, J.M. Tiedje, and J. Zhou. 2004. Development and evaluation of microarray-based whole-genome hybridization for detection of microorganisms within the context of environmental applications. *Environ. Sci. Technol.* 38:6775-6782

13. Ye, Q., Y.Roh, B.B. Blair, C. Zhang, J. Zhou and M.W. Fields. 2004. Isolation and characterization of a novel, alkaliphilic, metal-reducing bacterium, and possible implications for alkaline chemotrophy. *Appl. Environ. Microbiol.* 70:5595-5602

12. Yan, T., M.W. Fields, L. Wu, Y. Zu, J.M. Tiedje, and J. Zhou. 2003. Molecular diversity and characterization of nitrite reductase gene fragments (*nirS* and *nirK*) from nitrate- and uranium-contaminated groundwater. *Environ. Microbiol.* 5(1):13-24

11. Fields, M.W. and J.B. Russell. 2002. The glucomannokinase of *Prevotella bryantii* B<sub>14</sub>: sequence homology with the regulatory glucokinases of gram-positive microorganisms. *Anaerobe* 8:69-74

10. A.S. Beliaev, D.K. Thompson, M.W. Fields, L.Wu, D.P. Lies, K.H. Nealson, and J. Zhou. 2002. Microarray transcription profiling of a *Shewanella oneidensis* *etrA* mutant. *J. Bacteriol.* 184:4612-16

9. Roh, Y., R. Stapleton, J. Zhou, C. Zhang, A.V. Palumbo, T.J. Phelps, and M.W. Fields. 2002. Iron reduction by extremophiles: Geochemical and biotechnological implications, *In The Biogeochemistry of Iron Cycling in the Environment*, C. Zhang and J. D. Coates (eds.): Kluwer Academic Press

8. Fields, M.W. and J.B. Russell. 2001. Purification and characterization of a novel glucomannokinase of *Prevotella bryantii* B<sub>14</sub>, and its possible role in  $\beta$ -glucanase expression. *Microbiol.* 147:1035-1043

7. Jarvis, G.N., M.W. Fields, D.A. Adamovich, C.E. Arthurs, and J.B. Russell. 2001. The mechanism of carbonate killing of *Escherichia coli*. *Letts. Appl. Microbiol.* 33:196-200

6. Fields, M.W., S. Mallik, and J.B. Russell. 2000. *Fibrobacter succinogenes* S85 ferments cellulose just as fast as cellobiose until limited by cellulose surface area. *Appl. Microbiol. Biotech.* 54:570-574

5. Fields, M.W. and J.B. Russell. 2000. Alternative pathways of glucose transport in *Prevotella bryantii* B<sub>14</sub>. *FEMS Microbiol. Letts.* 183:137-142

4. Fields, M.W. and J.B. Russell. 1998. The role of ruminal carboxymethylcellulases in the degradation of  $\beta$ -glucans from cereal grains. *FEMS Microbiol. Ecol.* 27:261-268

3. Fields, M.W., D.B. Wilson, and J.B. Russell. 1997. A mutant of *Prevotella ruminicola* B<sub>14</sub> deficient in  $\beta$ -1,4-endoglucanase and mannanase activities. FEMS Microbiol. Letts. 154:9-15
2. Gardner, R.G., J.E. Wells, M.W. Fields, D.B. Wilson, and J.B. Russell. 1997. A *Prevotella ruminicola* B<sub>14</sub> operon encoding extracellular polysaccharide hydrolases. Curr. Microbiol. 35:274-277
1. Fields, M.W., P.E. Ryals, and K.L. Anderson. 1997. Polysaccharide-inducible outer membrane proteins of *Bacteroides xylanolyticus* X5-1. Anaerobe 3:43-48

### Manuscripts

H. Jiang, G. Zhang, L. Chapman, B. Yu, M.W. Fields, and H. Dong. Microbial diversity in water and sediment of lake chaka: an inland hypersaline lake in northwestern china. Appl. Environ. Microbiol. (in revision)

Nowlin, W.H., M.J. González, M.H.H. Stevens, M.J. Vanni, M.W. Fields, J.J. Valente. Periodical cicadas affect dynamics, productivity and stability of woodland pond ecosystems. Ecol. Letts (submitted)

Kurowski, J., A. Sundararaja, A. Klonowska, T. Yan, D.M. Klingman, M. Duley, J. Zhou, and M. W. Fields. Deletion of a multi-domain PAS protein causes pleiotropic effects in *Shewanella oneidensis* MR-1. J. Bacteriol. (in review)

Fields, M.W., C.E. Bagwell, S.L. Carroll, T. Yan, X. Liu, D.B. Watson, P.M. Jaridne, C.S. Criddle, T.C. Hazen, and J. Zhou. Gene sequences as indicators of bacterial community responses to mixed-waste contamination. Environ. Sci. Technol. (in review)

He, Q. et al. Energetic consequences of nitrite stress in *Desulfovibrio vulgaris* Hildenborough inferred from global transcriptional analysis. Mol. Microbiol. (submitted)

Wu, W. et al. Field-scale bioremediation of uranium in a highly contaminated aquifer II: reduction of U(VI) and geochemical control of U(VI) bioavailability. Environ. Sci. Technol. (submitted)

Clark, M.E., Q. He, Z. He, E. Alm, K. Huang, T.C. Hazen, A. Arkin, J.D. Wall, J. Zhou, and M.W. Fields. Temporal transcriptomic analyses of *Desulfovibrio vulgaris* Hildenborough grown under electron acceptor excess conditions. J. Bacteriol. (in preparation)

### Current Grant Support

PI – Construction of whole genome microarrays, and expression analysis of *Desulfovibrio vulgaris* cells in metal-reducing conditions (uranium and chromium), DOE-ER63765

Co-PI - Integrated analysis of protein complexes and regulatory networks involved in anaerobic energy metabolism of *Shewanella oneidensis* MR-1, LAB 01-20, DOE Microbial Cell Project

Co-PI – Rapid deduction of stress response pathways in metal/radionuclide reducing bacteria, LAB 02-13, DOE Genomes to Life program

Co-PI – Effects of 17 year cicada emergence on aquatic food webs, NSF 04-2, DEB-Ecology

PI - Whole-genome sequence determination of novel, extremophilic, metal-reducing bacteria, DOE Community Sequencing Program

Co-PI - Genome-level understanding of the diversity and structure of a groundwater microbial community in the NABIR Research Field Research Center, DOE Community Sequencing Program

PI - Identification of Molecular and Cellular Responses of *Desulfovibrio vulgaris* Biofilms under Culture Conditions Relevant to Field Conditions for Bioreduction of Heavy Metals, DOE-DE-FG01-05 ER05-05