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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

Adjunct Research Fellow , National Center for Genome Resources	2012-
Associate Professor , Department of Microbiology, Center for Biofilm Engineering, MSU	2011-
Assistant Professor , Department of Microbiology, Center for Biofilm Engineering, MSU	2007-
Assistant Professor , Department of Microbiology, Miami University	2003-2006
Research Staff Scientist , Oak Ridge National Laboratory	2001-2003

Teaching Experience

Advanced Genetics; Microbial Ecology; General Microbiology; Biological Concepts; Microbial Physiology; Graduate Journal Reading; Undergraduate Research; Summer Workshop for Secondary Education Teachers

Service and Awards (2009-)

AAAS Review Panel	2012
College Curriculum Committee	2012-
Specialty Editor- <i>FIM-Microbiotechnology, Ecotoxicology & Bioremediation</i>	2011-
Wiley Faculty Award for Meritorious Research	2011
Molecular Biosciences Program-Advisory Committee Chair	2010-
Thermal Biology Institute Advisory Board	2010-
Molecular Biosciences Program Advisory Committee	2009-
MSU Award of Excellence	2010
Review Board for DOE-EMSL User Facility	2009-
DOE-CESD Panel Review	2009
Center for Biofilm Engineering Faculty Research Award	2009
ASM Branch Lectureship Program	2009-2011
Editorial Board for <i>Applied and Environmental Microbiology</i>	2006-

Publications

57. Bowen De León, K., M.L. Young, L.B. Camilleri, S.D Brown, J.M. Skerker, A.M. Deutschbauer, A.P. Arkin, and **M.W. Fields**. 2012. Draft genome sequence of *Pelosinus fermentans* JBW45 isolated during *in situ* stimulation for Cr(VI) reduction. *J. Bacteriol.* 194:5456-57.

56. Valenzuela, J., A. Mazurie, R. Carlson, R. Gerlach, K.E. Cooksey, B.M. Peyton, and **M.W. Fields**. 2012. Potential role of multiple carbon fixation pathways during lipid accumulation in *Phaeodactylum tricorutum*. *Biotechnol. Biofuels* 5:40.

55. Bowen-De León, K., B.D. Ramsay, and **M.W. Fields**. 2012. Quality-score refinement of SSU rRNA gene pyrosequencing differs across gene region for environmental samples. *Microbial Ecol.* 64:499–508.
54. Clark, M.E., Z. He, A.M. Redding, M.P. Joachimiak, J.D. Keasling, J.-Z. Zhou, A.P. Arkin, A. Mukhopadhyay, and **M.W. Fields**. 2012. Transcriptomic and proteomic analyses of *Desulfovibrio vulgaris* biofilms: carbon and energy flow contribute to the distinct biofilm growth state. *BMC Genomics* 13 :138
53. Lorenz, L.A., B.D. Ramsay, D.M. Goeres, **M.W. Fields**, C.A. Zapka, D.R. Macinga. 2012. Evaluation and remediation of bulk soap dispensers for biofilm. *Biofouling* 28: 99–109.
52. Gardner, R., K.E. Cooksey, F. Mus, R. Macur, K. Moll, E. Eustance, R.P. Carlson, R. Gerlach, **M.W. Fields**, B.M. Peyton. 2012. Use of sodium bicarbonate to stimulate triacylglycerol accumulation in the chlorophyte *Scenedesmus* sp. and the diatom *Phaeodactylum tricorutum*. *J. Appl. Phycol.* (doi:10.1007/s10811-011-9782-0).
51. Zhou, A., Y.I. Chen, G.M. Zane, Z. He, C.L. Hemme, M.P. Joachimiak, J. Baumohl, Q. He, **M.W. Fields**, A.P. Arkin, J.D. Wall, T.C. Hazen and J. Zhou. 2012. Functional characterization of Crp/Fnr-type global transcriptional regulators in *Desulfovibrio vulgaris* Hildenborough. *Appl. Environ. Microbiol.* 78:1168-1177.
50. Hemme, C.L., **M.W. Fields**, Q. He, Y. Deng, Q. Tu, H. Mouttaki, Z. He, K. Barry, E. Saunders, H. Sun, M. Land, L. Hauser, A. Lapidus, C.S. Han, E. Rubin and J. Zhou. 2011. Correlation of genomic and physiological traits of *Thermoanaerobacter* Species with biofuel yields. *Appl. Environ. Microbiol.* 77:7998-8008.
49. Sundararajan, A., J. Kurowski, T. Yan, D. M. Klingeman, M.P. Joachimiak, J. 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.* 77:4647-4656.
48. Elias, D.A. and **Fields, M.W.** 2011. Transcriptomic studies in metal-reducing bacteria. *In* *Microbial Metal and Metalloid Metabolism: Advances and Applications*, Eds. Stolz and Oremland, Chapter 12, 211-244, American Society for Microbiology Press, Washington, D.C.
47. Wu, W.-M., J. Carley, D. Watson, B. Gu, S. Brooks, S.D. Kelly, K. Kemner, J. D. van Nostrand, L. Wu, M. Xu, J. 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. 2011. 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 Chinese). 31:449-459.
46. Hemme, C.L. *et al.*, 2010. Sequencing of multiple *Clostridia* genomes related to biomass conversion and biofuels production. *J. Bacteriol.* 192:6494–6496.
45. Zhou, A., Z. He, A.M. Redding-Johanson, A. Mukhopadhyay, C.L. Hemme, M.P. Joachimiak, F. Luo, Y. Deng, K.S. Bender, Q. He, J.D. Keasling, D.A. Stahl, **M.W. Fields**, T.C. Hazen, A.P. Arkin, J.D. Wall, and J. Zhou. 2010. Hydrogen peroxide-induced oxidative stress responses in *Desulfovibrio vulgaris* Hildenborough. *Environ. Microbiol.* 12: 2645–2657.
44. He, Q., Z. He, D.C. Joyner, M. Joachimiak, M.N. Price Z.K. Yang, H.-C.B. Yen, C.L. Hemme, W. Chen, **M.W. Fields**, D.A. Stahl, J.D. Keasling, M. Keller, A.P. Arkin, T.C. Hazen, J.D. Wall and J. Zhou.

2010. Impact of elevated nitrate on sulfate-reducing bacteria: a comparative study of *Desulfovibrio vulgaris*. *Nature ISME J.* 4:1386-1397.
43. Hemme, C.L., Y. Deng, T.J. Gentry, **M.W. Fields**, L. Wu, S. Barua, K. Barry, S.G. Tringe, D.B. Watson, Z. He, T.C. Hazen, J.M. Tiedje, E.M. Rubin and J. Zhou. 2010. Metagenomic insights into evolution of a heavy metal-contaminated groundwater microbial community. *Nature ISME J.* 4:660-672.
42. He, Z., A. Zhou, E. Baidoo, Q. He, M.P. Joachimiak, P. Benke, R. Phan, A. Mukhopadhyay, C.L. Hemme, K. Huang, E.J. Alm, **M.W. Fields**, J.D. Wall, D.A. Stahl, T.C. Hazen, J.D. Keasling, A.P. Arkin, and J. Zhou. 2010. Global transcriptional, physiological, and metabolite analyses of the responses of *Desulfovibrio vulgaris* Hildenborough to salt adaptation. *Appl. Environ. Microbiol.* 76:1574–1586.
41. Holman, H.Y.N., E. Wozei, L. Comolli, Z. Lin, S. Boglin, K.H. Downing, **M.W. Fields**, T.C. Hazen. 2009. Real-time monitoring of hydrogen-bond dynamics during oxygen-stress adaptive response in strict anaerobes. *Proc. Natl. Acad. Sci. USA* 106:12599-12604.
40. Elias, D.A., E.C. Drury, A.M. Redding, A. Mukhopadhyay, H.-C. B.Yen, **M.W. Fields**, T.C. Hazen, A.P. Arkin, J.D. Keasling, and J.D. Wall. 2009. Expression profiling of hypothetical genes in *Desulfovibrio vulgaris* leads to improved functional annotation. *Nucleic Acids Res.* 37:2926–2939.
39. Hwang, C., W. Wu, T.J. Gentry, J. Carley, G.A. Corbin, S.L. Carroll, D.B. Watson, P.M. Jardine, J. Zhou, C.S. Criddle, and **M.W. Fields**. 2009. Bacterial community succession during *in situ* uranium bioremediation: spatial similarities along controlled flow paths. *Nature ISME J.* 3:47–64.
38. Wu, L., X. Liu, **M.W. Fields**, D.K. Thompson, C.E. Bagwell, J.M. Tiedje, T.C. Hazen, and J. Zhou. 2008. Microarray-based whole-genome hybridization as a tool for determining prokaryotic species relatedness. *Nature ISME J.* 2 :1-14.
37. Klonowska, A., M.E. Clark, S.B. Thieman, B.J. Giles, J.D. Wall and **M.W. Fields**. 2008. Hexavalent chromium reduction in *Desulfovibrio vulgaris* Hildenborough causes transitory inhibition of sulfate reduction and cell growth. *Appl. Microbiol. Biotechnol.* 78:1007-1016.
36. Wu, W., et al. 2007. Bioreduction of uranium (VI) *in situ* and stability of immobilized uranium: impact of dissolved oxygen. *Environ. Sci. Technol.* 41:5716-5723.
35. Clark, M.E., R.E. Edelman, M.L. Duley, J.D. Wall, and **M.W. Fields**. 2007. Biofilm formation in *Desulfovibrio vulgaris* Hildenborough is dependent upon protein filaments. *Environ. Microbiol.* 9:2844-2854.
34. Nowlin, W.H., M.J. González, M.H.H. Stevens, M.J. Vanni, **M.W. Fields**, J.J. Valente. 2007. Periodical cicadas affect dynamics, productivity and stability of woodland pond ecosystems. *Ecol.* 88:2174–2186.
33. Clark, M.E., Q. He, Z. He, E.J. Alm, K.H. Huang, T.C. Hazen, A.P. Arkin, J.D. Wall, J. Zhou, and **M.W. Fields**. 2006. Temporal transcriptomic analyses of *Desulfovibrio vulgaris* Hildenborough during electron donor depletion. *Appl. Environ. Microbiol.* 72:5578-5588.
32. He, Q., K.H. Huang, Z. He, E.J. Alm, **M.W. Fields**, T.C. Hazen, A.P. Arkin, J.D. Wall, and J. Zhou. 2006. Energetic consequences of nitrite stress in *Desulfovibrio vulgaris* Hildenborough inferred from global transcriptional analysis. *Appl. Environ. Microbiol.* 72:4370-438.

31. Gao, W., Y. Liu, C.S. Giometti, S.L. Tollaksen, T. Khare, L. Wu, D.M. Klingeman, **M.W. Fields** and J. Zhou. 2006. Knock-out of a prohibitin-like protein results in alteration of iron metabolism, increased spontaneous mutation and hydrogen peroxide sensitivity in the bacterium *Shewanella oneidensis*. *BMC Genomics* 7:76.
30. Wu, W. et al. 2006. 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.* 40:3986-3995.
29. Dong, H., H. Jiang, G. Zhang, L. Chapman, B. Yu, and **M.W. Fields**. 2006. Microbial diversity in water and sediment of Lake Chaka: an inland hypersaline lake in northwestern china. *Appl. Environ. Microbiol.* 72: 3832–3845.
28. **Fields, M.W.**, C.E. Bagwell, S.L. Carroll, T. Yan, X. Liu, D.B. Watson, P.M. Jardine, C.S. Criddle, T.C. Hazen, and J. Zhou. 2006. Phylogenetic and functional biomarkers as indicators of bacterial community responses to mixed-waste contamination. *Environ. Sci. Technol.* 40:2601-2607.
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**. 2006. Changes in bacterial community structure correlate with initial operating conditions of a field-scale denitrifying fluidized bed reactor. *Appl. Microbiol. Biotech.* 71:748–760.
26. **Fields, M.W.**, J. Schryver, C.C. Brandt, T. Yan, J. 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. Meth.* 65:144– 152.
25. Dong, H., H. Jiang, G. Zhang, B. Yu, L.R. Chapman, C.R. Lucas, and **M.W. Fields**. 2006. Microbial diversity in water and sediment of Lake Qinghai: the largest inland saline lake in China. *Microbial Ecol.* 51:65-82.
24. Gentile, M., T. Yan, S.M. Tiquia, **M.W. Fields**, J. Nyman, J. Zhou, and C. S. Criddle. 2006. Stability in a denitrifying fluidized bed reactor. *Microbial Ecol.* 52:311-321.
23. Gu, B., 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. Sci. Technol.* 39:4841-4847.
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 β -glucanase activity in the ruminal bacterium, *Prevotella bryantii* B₁₄. *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, E. Alm, A.P. Arkin, D.K. Thompson, **M.W. Fields**, 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.
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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 the Gram-negative ruminal bacterium, *Prevotella bryantii* B₁₄, and its sequence conservation with regulatory glucokinases of Gram-positive bacteria. *Anaerobe* 8:69-74
10. Beliaev, A.S., 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* B₁₄, and its possible role in β -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* B₁₄. *FEMS Microbiol. Letts.* 183:137-142

4. **Fields, M.W.** and J.B. Russell. 1998. The role of ruminal carboxymethylcellulases in the degradation of β -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* B₁₄ deficient in β -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* B₁₄ 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