**LIYOU WU**

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**EDUCATION and TRANING**

Rothamsted Research, Harpenden, Hertfordshire, UK, Functions and Diversity of Soil Microbiology, Underwood Fellow, Biotechnology and Biological Sciences Research Council, September, 2009-February, 2010

Oak Ridge National Laboratory, TN, USA, Genomics and Environmental Microbiology, Postdoctoral Training, 2001-2002

Hunan Agricultural University & Michigan State University, Molecular and Environmental Microbiology, Joint program, PhD, 2001

Hunan Agricultural University, Plant Pathology, M.S., 1987

Hunan Agricultural University, Plant Pathology, B.S., 1982

**PROFESSIONAL POSITIONS**

Adjunct Associate professor/Research Scientist (highest level), the Department of Botany/Microbiology & the

Institute for Environmental Genomics, University of Oklahoma, 2007-present

Research Assistant Professor, University of Oklahoma, 2006-2007

Staff Scientist, Oak Ridge National Laboratory, 2002-2006

Postdoctoral Research Associate, Oak Ridge National Laboratory, 2001-2002

Visiting Scientist, Michigan State University & Oak Ridge National Laboratory, 1997-2001

Professor, Hunan Agricultural University, 1998-present

Associate Professor, Hunan Agricultural University, 1993-1997

Lecturer, Hunan Agricultural University, 1988-1993

Teaching Assistant, Hunan Agricultural University, 1987-1988

Graduate Research and Teaching Assistant, Hunan Agricultural University, 1984-1987

Research Assistant, Taojiang Agricultural Institute, 1982-1984

**RESEARCH PROJECTS**

1. From Community Structure to Functions: Metagenomic-Enabled predictive Understanding of Temperature Sensitivity jof Soil Carbon Decompossition to Climate Warming. $1,000,000 for the period of 10/1/2010-9/30/2013, co-PI, Department of Energy
2. Systems-Level Understanding of Factors Controlling Feedstock. $480,000 for the period of 09/1/2009-08/31/2011, **Principal Investigator**, Oklahoma Bioenergy Center.
3. Linking community structure to functions: Metagenomic analysis of Feedstock-Related Microbial Communities using GeoChip and Pyrosequencing. $761,982 for the period of 1/1/2008-12/31/2009, **Principal Investigator**, Oklahoma Bioenergy Center.
4. Whole genomic DNA Array for Bacteria Detection and Identification. $300,000 for the period of 2/1/2008-1/302011, **Principal Investigator**, Oklahoma Applied Research Support (OARS) Program of Oklahoma Center for the Advancement of Science & Technology (OCAST).
5. Microbial Diversity Observation in Grassland under different Agricultural Practices. £48,200, March 5, 2009-April 4, 2010, **Principal Investigator,** Biotechnology and Biological Science Research Council, UK, Underwood Fellowship
6. Isolation and Characterization of novel microbial catalysts for direct fermentation of lignocellulose to ethanol. $294 K for the period of 1/1/2008 - 12/31/2009, **Co- Principal Investigator**, Oklahoma Bioenergy Center.
7. Improvement of the Performance of Novel Microbial Catalysts for Direct Fermentation of Lignocellulose to Ethanol. $300K for the period of 09/01/2009-8/31/2011, **Co- Principal Investigator**, Oklahoma Bioenergy Center.
8. Integrated genome-based studies of Shewanella ecophysiology. $1,000K for the period of 10/1/2006-9/30/2009 **Co- Principal Investigator**, Genomics: GTL program, the Department of Energy.
9. METASOIL3 - An NSF/USDA contribution to the worldwide TERRAGENOME project. Pending, about $600K for the period of 09/1/2009-08/31/2012 was requested, **Co- Principal Investigator,** USDA & NSF, Agriculture and Food Research Initiative - Microbial Genomics: Genome Sequencing.
10. From Community Structure to Functions: Metagenomics-Enabled Predictive Understanding of Temperature Sensitivity of Soil Carbon Decomposition to Climate Warming. Pending, $2,998,407 was requested for the period of 1/1/2010-12/31/2012, **Co-Principal Investigator**, Genomics: GTL program, the Department of Energy.

**Synergistic Activities**

1. **Associate Editor, BMC Microbiology, 2009-present**
2. Facility manager, the Institute for Environmental Genomics, the University of Oklahoma
3. Occasional reviewer: Journal of Microbiological Methods, Applied Microbiology and Biotechnology, Current Microbiology, and the Minnesota Sea Grant.

**AWARDS AND HONORS**

1. US patent: Method for analyzing microbial communities. patent # 7759057
2. **R&D 100 award, OU Geochip, R&D Magazine, 2009**
3. Second Prize from Hunan Education Committee for the Project of Reforming Teaching Model of Phytopathology, 1997.
4. Second Prize from Huadong Area Society of Publication Committee for the book, Breeding Technique of Virus-free Fruit Trees, 1996.
5. First Prize from Hunan Science and Technology Committee for the Project of Establishment of Virus-free Citrus Propagation System in Hunan Province, 1994.

**EXPERTISE AND RELEVANT EXPERIENCE**

Molecular and environmental microbiology, microbial ecology, microbial community analysis using microarray technology and other genomic technology

**PUBLICATIONS**

1. Zhou, J. Z., **L. Y. Wu\* (co-first author**), X. Y. Zhi, Y. Deng, Q. C. Tu, J. P. Xie, J. D. Van Nostrand, and Z. L. He. (2011). Reproducibility and Quantitation of Pyro-Tag Sequencing-based Detection. ISME journal 5(1): 1751-7362.
2. Xie, J. P., Z. L. He, X. X. Liu, X. D. Liu, J. D. Van Nostrand, Y. Deng, L. Y. Wu, J. Z. Zhou and G. Z. Qiu (2011). "GeoChip-Based Analysis of the Functional Gene Diversity and Metabolic Potential of Microbial Communities in Acid Mine Drainage." Applied and Environmental Microbiology 77(3): 991-999.
3. Liu, A.H., **L. Y. Wu (co-first co-corresponding author)**, Z. L. He, and J. Z. Zhou. 2010. Development of highly fluorescent dye-chemically-doped silica nanoparticle for sensitive DNA microarray detection. Biosensor Bioelectronics, in press.
4. Van Nostrand, J. D., **L. Y. Wu (co-first co-corresponding author),** W.-M. Wu, T. J. Gentry, Z. J. Huang, Y. Deng, J. Carley, S. Carroll, Z. L. 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 composition and function during the in-situ bioremediation of a uranium-contaminated aquifer. Applied and Environmental Microbiology, in press.
5. He, Z. L., Y. Deng, J. D. Van Nostrand, Q. C. Tu, M. Y. Xu, C. L. Hemme, X. Y. Li, **L. Y. 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 composition, structure and functional activity." Isme Journal 4(9): 1167-1179.
6. He ZL, Xu MY, Deng Y, Kang SH, Kellogg **L, Wu LY** et al (2010). Metagenomic analysis reveals a marked divergence in the structure of belowground microbial communities at elevated CO2. Ecology Letters 13: 564-575.
7. Hemme, C. L., Y. Deng, T. J. Gentry, M. W. Fields, **L. Y. Wu**, S. Barua, K. Barry, S. G. Tringe, D. B. Watson, Z. L. He, T. C. Hazen, J. M. Tiedje, E. M. Rubin and J. Z. Zhou (2010). "Metagenomic insights into evolution of a heavy metal-contaminated groundwater microbial community." Isme Journal 4(5): 660-672.
8. Hemme, C. L., H. Mouttaki, Y. J. Lee, G. X. Zhang, L. Goodwin, S. Lucas, A. Copeland, A. Lapidus, T. G. del Rio, H. Tice, E. Saunders, T. Brettin, J. C. Detter, C. S. Han, S. Pitluck, M. L. Land, L. J. Hauser, N. Kyrpides, N. Mikhailova, Z. L. He, **L. Y. Wu**, J. D. Van 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. F. Yang, H. L. Dong, D. F. Xing, N. Q. Ren, A. J. Wang, R. L. Huhnke, J. R. Mielenz, S. Y. Ding, M. E. Himmel, S. Taghavi, D. van der Lelie, E. M. Rubin and J. Z. Zhou (2010). "Sequencing of Multiple Clostridial Genomes Related to Biomass Conversion and Biofuel Production." Journal of Bacteriology 192(24): 6494-6496.
9. Liang YT, He ZL, **Wu LY**, Deng Y, Li GH, Zhou JZ (2010). Development of a Common Oligonucleotide Reference Standard for Microarray Data Normalization and Comparison across Different Microbial Communities. Applied and Environmental Microbiology 76: 1088-1094.
10. Liu, W. Z., A. J. Wang, S. A. Cheng, B. E. Logan, H. Yu, Y. Deng, J. D. Van Nostrand, **L. Y. Wu**, Z. L. He and J. Z. Zhou (2010). "Geochip-Based Functional Gene Analysis of Anodophilic Communities in Microbial Electrolysis Cells under Different Operational Modes." Environmental Science & Technology 44(19): 7729-7735.
11. Xiong JB, **Wu LY**, Tu SX, Van Nostrand JD, He ZL, Zhou JZ et al (2010). Microbial Communities and Functional Genes Associated with Soil Arsenic Contamination and the Rhizosphere of the Arsenic-Hyperaccumulating Plant Pteris vittata L. Applied and Environmental Microbiology 76: 7277-7284.
12. Xu MY, Wu WM, **Wu LY**, He ZL, Van Nostrand JD, Deng Y et al (2010). Responses of microbial community functional structures to pilot-scale uranium in situ bioremediation. Isme Journal 4: 1060-1070.
13. Jianping Xie, Zhili He, Xinxing Liu, Xueduan Liu, Joy D. Van Nostrand, Ye, Deng, **Liyou Wu**, Jizhong Zhou, and Guanzhou Qiu (2010). GeoChip-based analysis of the functional gene diversity and metabolic potential of microbial communities in acid mine drainage. Applied and Environmental Microbiology. doi:10.1128/AEM.01798-10
14. Liang YL, Gao HC, Chen JR, Dong YY, **Wu L**, He ZL et al (2010). Pellicle formation in Shewanella oneidensis. Bmc Microbiology 10.
15. **Wu, L.**, L. Kellogg, A. H. Devol, J. M. Tiedje, and J. Zhou. 2008. Microarray-based characterization of microbial community functional structure and heterogeneity in marine sediments from the gulf of Mexico. Applied and Environmental Microbiology 74:4516-4529.
16. **Wu, L. Y.**, 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 procaryotic species relatedness. Isme Journal 2:642-655.
17. **Wu, L. Y**., X. Liu, C. W. Schadt, and J. Z. Zhou. 2006. Microarray-based analysis of subnanogram quantities of microbial community DNAs by using whole-community genome amplification. Applied and Environmental Microbiology 72:4931-4941.
18. He, Z. L., **L. Y. Wu**, X. Y. Li, M. W. Fields, and J. Z. Zhou. 2005. Empirical establishment of oligonucleotide probe design criteria. Applied and Environmental Microbiology 71:3753-3760.
19. He, Z. L., **L. Y. Wu**, M. W. Fields, and J. Z. Zhou. 2005. Use of microarrays with different probe sizes for monitoring gene expression. Applied and Environmental Microbiology 71:5154-5162.
20. **Wu, L. Y.**, D. K. Thompson, X. D. 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. Environmental Science & Technology 38:6775-6782.
21. Tiquia, S. M., **L. Y. Wu (co-first author)**, 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-+.
22. **Wu, L. Y.**, D. K. Thompson, G. S. Li, R. A. Hurt, J. M. Tiedje, and J. Z. Zhou. 2001. Development and evaluation of functional gene arrays for detection of selected genes in the environment. Applied and Environmental Microbiology 67:5780-5790.
23. Yang, Y. F., D. P. Harris, F. Luo, W. L. Xiong, M. Joachimiak, **L. Y. Wu**, P. Dehal, J. Jacobsen, Z. M. 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 10.
24. Wang, F. P., H. Y. Zhou, J. Meng, X. T. Peng, L. J. Jiang, P. Sun, C. L. Zhang, J. D. Van Nostrand, Y. Deng, Z. L. He, **L. Y. Wu**, J. H. Zhou, and X. Xiao. 2009. GeoChip-based analysis of metabolic diversity of microbial communities at the Juan de Fuca Ridge hydrothermal vent. Proceedings of the National Academy of Sciences of the United States of America 106:4840-4845.
25. Waldron, P. J., **L. Y. Wu**, J. D. Van Nostrand, C. W. Schadt, Z. L. He, D. B. Watson, P. M. Jardine, A. V. Palumbo, T. C. Hazen, and J. Z. Zhou. 2009. Functional Gene Array-Based Analysis of Microbial Community Structure in Groundwaters with a Gradient of Contaminant Levels. Environmental Science & Technology 43:3529-3534.
26. Van Nostrand, J. D., W. M. Wu, **L. Y. Wu**, Y. Deng, J. Carley, S. Carroll, Z. L. 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. 2009. GeoChip-based analysis of functional microbial communities during the reoxidation of a bioreduced uranium-contaminated aquifer. Environmental Microbiology 11:2611-2626.
27. Liang, Y. T., G. H. Li, J. D. Van Nostrand, Z. L. He, **L. Y. Wu**, Y. Den, X. Zhang, and J. Z. Zhou. 2009. Microarray-based analysis of microbial functional diversity along an oil contamination gradient in oil field. Fems Microbiology Ecology 70:324-333.
28. Yin, H. Q., L. H. Cao, M. Xie, Q. J. Chen, G. Z. Qiu, J. Z. Zhou, **L. Y. Wu**, D. Z. Wang, and X. D. Liu. 2008. Bacterial diversity based on 16S rRNA and gyrB genes at Yinshan mine, China. Systematic and Applied Microbiology 31:302-311.
29. Yin, H. Q., G. Z. Qiu, **L. Y. Wu**, M. Xie, J. H. Zhou, Z. M. Dai, D. Z. Wang, L. Kellogg, L. H. Cao, and X. D. Liu. 2008. Microbial community diversity and changes associated with a mine drainage gradient at the Dexing copper mine, China. Aquatic Microbial Ecology 51:67-76.
30. He, Z. L., J. D. Van Nostrand, **L. Y. Wu**, and J. Z. Zhou. 2008.
31. Zhang, Y. G., X. Q. Zhang, X. D. Liu, Y. Xiao, L. J. Qu, **L. Y. Wu**, and 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.
32. Yang, Y. F., M. X. Zhu, **L. Y. Wu**, and J. Z. Zhou. 2007. Assessment of data processing to improve reliability of microarray experiments using genomic DNA reference. Bmc Genomics 9.
33. Yang, Y. F., D. P. Harris, F. Luo, **L. Y. Wu**, A. B. Parsons, A. V. Palumbo, and J. Z. Zhou. 2007. Characterization of the Shewanella oneidensis Fur gene: roles in iron and acid tolerance response. Bmc Genomics 9.
34. Wu, W. M., J. Carley, J. Luo, M. A. Ginder-Vogel, E. Cardenas, M. B. Leigh, C. C. Hwang, S. D. Kelly, C. M. Ruan, **L. Y. Wu**, J. Van Nostrand, T. Gentry, K. Lowe, T. Mehlhorn, S. Carroll, W. S. Luo, M. W. Fields, B. H. Gu, D. Watson, K. M. Kemner, T. Marsh, J. Tiedje, J. Z. Zhou, S. Fendorf, P. K. Kitanidis, P. M. Jardine, and C. S. Criddle. 2007. In situ bioreduction of uranium (VI) to submicromolar levels and reoxidation by dissolved oxygen. Environmental Science & Technology 41:5716-5723.
35. He, Z. L., T. J. Gentry, C. W. Schadt, **L. Y. Wu**, J. Liebich, S. C. Chong, Z. J. Huang, W. M. Wu, B. H. Gu, P. Jardine, C. Criddle, and J. Zhou. 2007. GeoChip: a comprehensive microarray for investigating biogeochemical, ecological and environmental processes. Isme Journal 1:67-77.
36. Gao, H. C., Z. M. K. Yang, T. J. Gentry, **L. Y. Wu**, C. W. Schadt, and J. Z. Zhou. 2007. Microarray-based analysis of microbial community RNAs by whole-community RNA amplification. Applied and Environmental Microbiology 73:563-571.
37. Wei, X. M., T. F. Yan, N. G. Hommes, X. D. Liu, **L. Y. Wu**, C. McAlvin, M. G. Klotz, L. A. Sayavedra-Soto, J. Z. Zhou, and D. J. Arp. 2006. Transcript profiles of Nitrosomonas europaea during growth and upon deprivation of ammonia and carbonate. Fems Microbiology Letters 257:76-83.
38. Qiu, X. Y., M. J. Daly, A. Vasilenko, M. V. Omelchenko, E. K. Gaidamakova, **L. Y. 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. Journal of Bacteriology 188:1199-1204.
39. Leaphart, A. B., D. K. Thompson, K. Huang, E. Alm, X. F. Wan, A. Arkin, S. D. Brown, **L. Y. Wu**, T. F. Yan, X. D. Liu, G. S. Wickham, and J. Z. Zhou. 2006. Transcriptome profiling of Shewanella oneidensis gene expression following exposure to acidic and alkaline pH. Journal of Bacteriology 188:1633-1642.
40. Gao, W. M., Y. Q. Liu, C. S. Giometti, S. L. Tollaksen, T. Khare, **L. Y. Wu**, D. M. Klingeman, M. W. Fields, and J. Zhou. 2006. Knock-out of SO1377 gene, which encodes the member of a conserved hypothetical bacterial protein family COG2268, results in alteration of iron metabolism, increased spontaneous mutation and hydrogen peroxide sensitivity in Shewanella oneidensis MR-1. Bmc Genomics 7.
41. Gao, H. C., Z. M. K. Yang, **L. Y. 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. Journal of Bacteriology 188:4560-4569.
42. Cho, C. M. H., T. F. Yan, X. D. Liu, **L. Y. Wu**, J. Z. Zhou, and L. Y. Stein. 2006. Transcriptome of a Nitrosomonas europaea mutant with a disrupted nitrite reductase gene (nirK). Applied and Environmental Microbiology 72:4450-4454.
43. Brown, S. D., M. Martin, S. Deshpande, S. Seal, K. Huang, E. Alm, Y. F. Yang, **L. Y. Wu**, T. F. Yan, X. D. Liu, A. Arkin, K. Chourey, J. Z. Zhou, and D. K. Thompson. 2006. Cellular response of Shewanella oneidensis to strontium stress. Applied and Environmental Microbiology 72:890-900.
44. Bagwell, C. E., X. Liu, L. Wu, and J. 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.
45. Qiu, X. Y., G. W. Sundin, **L. Y. Wu**, J. Z. Zhou, and J. M. Tiedje. 2005. Comparative analysis of differentially expressed genes in Shewanella oneidensis MR-1 following exposure to UVC, UVB, and UVA radiation. Journal of Bacteriology 187:3556-3564.
46. Oda, Y., S. K. Samanta, F. E. Rey, **L. Y. Wu**, X. D. Liu, T. F. Yan, J. Z. Zhou, and C. S. Harwood. 2005. Functional genomic analysis of three nitrogenase isozymes in the photosynthetic bacterium Rhodopseudomonas palustris. Journal of Bacteriology 187:7784-7794.
47. Liu, Y. Q., W. M. Gao, Y. Wang, **L. Y. Wu**, X. D. Liu, T. F. Yan, E. Alm, A. Arkin, D. K. Thompson, M. W. Fields, and J. Z. Zhou. 2005. Transcriptome analysis of Shewanella oneidensis MR-1 in response to elevated salt conditions. Journal of Bacteriology 187:2501-2507.
48. Bencheikh-Latmani, R., S. M. Williams, L. Haucke, C. S. Criddle, **L. Y. Wu**, J. Z. Zhou, and B. M. Tebo. 2005. Global transcriptional profiling of Shewanella oneidensis MR-1 during Cr(VI) and U(VI) reduction. Applied and Environmental Microbiology 71:7453-7460.
49. Beliaev, A. S., D. M. Klingeman, J. A. Klappenbach, L. Wu, M. F. Romine, J. A. Tiedje, K. H. Nealson, J. K. Fredrickson, and J. Zhou. 2005. Global transcriptome analysis of Shewanella oneidensis MR-1 exposed to different terminal electron acceptors. Journal of Bacteriology 187:7138-7145.
50. Zhou, X. C., **L. Y. Wu**, and J. Z. Zhou. 2004. Fabrication of DNA microarrays on nanoengineered polymeric ultrathin film prepared by self-assembly of polyelectrolyte multilayers. Langmuir 20:8877-88
51. Wan, X. F., N. C. VerBerkmoes, L. A. McCue, D. Stanek, H. Connelly, L. J. Hauser, **L. Y. Wu**, X. D. Liu, T. F. Yan, A. Leaphart, R. L. Hettich, J. Z. Zhou, and D. K. Thompson. 2004. Transcriptomic and proteomic characterization of the fur modulon in the metal-reducing bacterium Shewanella oneidensis. Journal of Bacteriology 186:8385-8400.
52. Rhee, S. K., X. D. Liu, **L. Y. Wu**, S. C. Chong, X. F. Wan, and J. Z. Zhou. 2004. Detection of genes involved in biodegradation and biotransformation in microbial communities by using 50-mer oligonucleotide microarrays. Applied and Environmental Microbiology 70:4303-4317.
53. Qiu, X. Y., R. A. Hurt, **L. Y. Wu**, C. H. Chen, J. M. Tiedje, and Z. Zhou. 2004. Detection and quantification of copper-denitrifying bacteria by quantitative competitive PCR. Journal of Microbiological Methods 59:199-210.
54. Gao, H. C., Y. Wang, X. D. Liu, T. F. Yan, **L. Y. Wu**, E. Alm, A. Arkin, D. K. Thompson, and J. Z. Zhou. 2004.
55. Gao, H. C., Y. Wang, X. D. Liu, T. F. Yan, **L. Y. Wu**, E. Alm, A. Arkin, D. K. Thompson, and J. Z. Zhou. 2004. Global transcriptome analysis of the heat shock response of Shewanella oneidensis. Journal of Bacteriology 186:7796-7803.
56. Yan, T. F., M. W. Fields, **L. Y. Wu**, Y. G. 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. Environmental Microbiology 5:13-24.
57. Liu, Y. Q., J. Z. Zhou, M. V. Omelchenko, A. S. Beliaev, A. Venkateswaran, J. Stair, **L. Y. 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. Proceedings of the National Academy of Sciences of the United States of America 100:4191-4196.
58. Liu, X. D., S. M. Tiquia, G. Holguin, **L. Y. 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 off the Pacific coast of Mexico. Applied and Environmental Microbiology 69:3549-3560.
59. Liu, X. D., C. E. Bagwell, **L. Y. Wu**, A. H. Devol, and J. H. Zhou. 2003. Molecular diversity of sulfate-reducing bacteria from two different continental margin habitats. Applied and Environmental Microbiology 69:6073-6081.
60. Zhou, J. Z., B. C. Xia, D. S. Treves, **L. Y. Wu**, T. L. Marsh, R. V. O'Neill, A. V. Palumbo, and J. M. Tiedje. 2002. Spatial and resource factors influencing high microbial diversity in soil. Applied and Environmental Microbiology 68:326-334.
61. Xu, D., G. S. Li, **L. Y. Wu**, J. Z. Zhou, and Y. Xu. 2002. PRIMEGENS: robust and efficient design of gene-specific probes for microarray analysis. Bioinformatics 18:1432-1437.
62. Gu, B. H., D. B. Watson, **L. Y. Wu**, D. H. Phillips, D. C. White, and J. Z. Zhou. 2002. Microbiological characteristics in a zero-valent iron reactive barrier. Environmental Monitoring and Assessment 77:293-309.
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65. Hurt, R. A., X. Y. Qiu, **L. Y. Wu**, Y. Roh, A. V. Palumbo, J. M. Tiedje, and J. H. Zhou. 2001. Simultaneous recovery of RNA and DNA from soils and sediments. Applied and Environmental Microbiology 67:4495-4503.
66. Braker, G., J. Z. Zhou, **L. Y. 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 Pacific northwest marine sediment communities. Applied and Environmental Microbiology 66:2096-2104.