

CHRISTOPHER WARREN SCHADT

Biosciences Division
Oak Ridge National Laboratory
MS 6038, PO Box 2008
Oak Ridge, TN 37830
Email: schadtcw@ornl.gov

Department of Microbiology
University of Tennessee
307 Ken & Blair Mossman Bldg.
Knoxville, TN 37996-1937
Email: cschadt@utk.edu

EDUCATION

University of Colorado, Biology, Ph.D. May 2002
University of Washington, Botany, B.S. March 1996

PROFESSIONAL POSITIONS

Senior Staff Scientist, Biosciences Division, Oak Ridge Natl. Laboratory, 2012-Pres.
Joint Faculty Associate Professor, Dept. of Microbiology & Bredesen Center for Interdisciplinary Graduate Education, Univ. of Tenn, 2010-Pres.
Staff Scientist, Biosciences Division, Oak Ridge National Laboratory, 2007-12.
Adjunct Professor, Univ. of Tennessee, Genome Science and Technology, 2007-Pres.
Adjunct Professor, Univ. of Tennessee, Dept. of Microbiology, 2007-2010
Group Leader for Molecular Microbial Ecology, ORNL, 2007-2012
Associate Staff Scientist, Environmental Sciences Division, ORNL, 2005-06
Postdoctoral Research Associate, Environmental Sciences Division, ORNL, 2003-05
Postdoctoral Research Associate, University of Colorado, 2002-03

GRANTS AND AWARDS

Co-PI, DOE-BSSD Program – 2022-2025 (1M annual) “Uncovering the microbial networks that degrade plant-derived phenolic compounds and their role in peatland soil carbon sequestration - revisiting the 'enzyme latch' hypothesis”.

Co-PI, DOE-BSSD Program – 2020-2022 (1M annual) “Bio-Scales Pilot Project: Defining gene function and its connection to ecosystem processes”

PI, ORNL-LDRD Program – 2016-18 (390K annual) “Understanding the microbially-driven mechanisms behind the rapid responses of soils to short-term disturbance events that result in large nitrous oxide emission pulses”

PI, ORNL-LDRD Program – 2015 (35K total funding) “Targeted Metagenomic Analysis of the Novel Bacterial Phylum AD3 from Walker Branch Watershed Shallow Subsurface Soils”

Co-PI, DOE-TES Program – 2014-17 (350K annual) “Toward A Predictive Understanding of the Response of Belowground Microbial Carbon Turnover to Climate Change Drivers in a Boreal Peatland”

Co-PI, DOE-TES Program – 2011-13 (350K annual) “The response of soil carbon storage and microbially mediated carbon turnover to simulated climatic disturbance in a northern peatland forest: revisiting the concept of soil organic matter recalcitrance”

Co-PI, DOE Genomic Sciences Program – 2009-Present (6.5M annual) “ORNL Scientific Focus Area in Plant-Microbe Interfaces”

Co-PI, DOE Terrestrial Ecosystem Sciences Program 2009-Present (8.25M annual)

“ORNL Scientific Focus Area in Terrestrial Ecosystems Sciences”
Co-PI & ORNL lead, DOD/SERDP Program – 2010-12 (550K annual) “Mechanisms and Permanence of Sequestered Pb and As in soils: Impact on Human Bioavailability”
PI, ORNL-LDRD Program – 2007-09 (350K annual funding) “Carbon Drivers of the Microbe Switchgrass Rhizosphere Interface”
Co-PI, DOE-ERSP Program – 2007-2012 (1.3M annual funding) “Multiscale Investigations on the Rates and Mechanisms of Targeted Immobilization and Natural Attenuation of Metal, Radionuclide and Co-Contaminants in the Subsurface”
Co-PI, DOE-GtL Program – 2006-10 (3.5M annual funding) “Virtual Institute for Microbial Stress and Survival – Environmental Stress Pathways Project”
Co-PI, ORNL-LDRD Program – 2005-07 (350 K annual funding) “Disentangling Soil Respiration Using Genomic Techniques”
Co-PI, DOE-PER Program – 2005-08. (1.2M annual funding) “Hierarchical Experimental Responses at Macromolecular to Ecosystem Scales”
Co-PI, DOE-NABIR Program – 2004-07 (450K annual funding) “An Integrated Assessment of Geochemical and Community Structure Determinants of Metal Reduction Rates in Subsurface Sediments”
Co-PI, DOE-TCP Program – 2004-12. (1.8M annual funding) “Consortium for enhancing Carbon Sequestration in Terrestrial Ecosystems”
University of Colorado Graduate Student Travel Grants (0.5K) - 1998 & 2000
Beverly Sears Graduate Student Research Grant (2K)- 1997 & 99
Edna Bailey Sussman Graduate Student Research Grant (1K) - 1998

TEACHING EXPERIENCE

Joint Faculty Assoc. Professor, University of Tennessee, 2008-Present

Courses:

GST 520 - Advanced Genetics/Genomics (units on Microbial Diversity; Microbial Comparative Genomics; and Metagenomics – team taught; I conducted 2-3 lectures per semester each fall for 3 years)

GST 541 - Graduate Student Colloquium (Organize graduate student research presentations, lead paper discussions, etc.), Spring Semester 2013

MICRO 620/EEB 630 – Special Topics Course: Fungal Ecology and Systems. Co-taught with Brandon Matheny (EEB), Spring Semester 2015

Graduate Teaching Assistant, University of Colorado, 1996-1998

Introductory Biology Laboratory (2 semesters)

Genetics Recitation (1 Semester)

General Microbiology Laboratory (2 semesters)

SUPERVISION, MENTORING AND GRADUATE COMMITTEES

Dissertation Advisor or Co-Advisor for: Emily Austin (Ecology and Evolutionary Biology UTK, Ph.D. 2013) Migun Shakya (Genome Science and Technology UTK, Ph.D. 2013), and Jessica Velez (Bredesen Center UTK/ORNL, Ph.D. 2020),

Graduate committee member for: Sean Berthrong (PhD, Duke Univ., 2009); Alisha Campbell (PhD, Univ. of Tenn., 2012); Patrick Chanton (MSc, Georgia Tech Univ.

2014); Mellissa Cregger (PhD, Univ. of Tenn., 2012); Emily Hollister (PhD, Texas A&M Univ., 2008); Zabrenna Griffiths (Univ. of Tenn, in progress), Puja Jastoria (PhD Florida State Univ, 2016); Steven Higgins (PhD, Univ. of Tenn, 2018); Lillian Mubitha (Univ. of Tenn., Pending); Diliya Murtazina (Univ. of Tenn., Pending); Chance Noffsinger (Univ. of Tenn, Pending); Jennifer Reeve (Ph.D, Washington State Univ., 2008), Enid Rodriguez (MSc, Univ. of Puerto Rico Mayaguez, 2006); Katherine Sides (MSc, Univ. of Tenn., 2009); Tianze Song (PhD, Georgia Tech, 2022); Sophia Turner (Univ. of Tenn., in progress) Sagar Uturkar (PhD, Univ. of Tenn., 2016); Ian Ware (PhD, Univ. of Tenn., 2019); Mellissa Warren (MSc, Georgia Tech Univ. 2015); Devon Lagueux (Univ. of Houston, in progress);
Postdoctoral/Postmasters Advisor for: William Argiroff (ORNL-Current), Hector Castro (Univ. of Tennessee), Melissa Cregger (ORNL Staff Scientist), Huihai Chen (Sun Yat-Sen University), Marie-Anne De Graaff (Boise State Univ.), Nicholas Dove (AgBiome, Inc.), Sanghoon Kang (Rice University), Laurel Kluber (Novozymes, Inc.), Thomas Gihring (Univ. of Wisconsin, Madison), Eric Johnston (Schneider, Inc.), Yongchao Li (Univ. of Oklahoma), Mike Robeson (Univ. of Arkansas), Spencer Roth (current-ORNL) Jessica (Meg) Steinweg (Roanoke College), Tarah Sullivan (Washington State University), Allison Veach (Univ. of Texas San Antonio), Amudhan Venkateswaran (Pioneer Hybrid Corp.), Daniel Yip (Microbes Biosciences, Inc.), Tingfen Yan (Univ. of Maryland), Gengxin Zhang (Chinese Acad. of Sci.)
Hosted and Advised: 4 visiting faculty/scientists; 5 visiting postdoctoral students; 8 visiting graduate students; 2 high school science teachers; 36 undergraduate students; & 3 high school students, for research internships of 3-12 months at ORNL through the Oak Ridge Institute for Science and Education (ORISE) and other programs.
Group Leader for Molecular Microbial Ecology Group at ORNL 2007-2012.
Organization included 3 Staff Scientists; 2 Technical Staff; 7 full-time Postdoctoral Associates; 3 Graduate Student Researchers, 1 Administrative Assistant, as well as graduate students, undergraduate students and multiple temporary appointments of visiting scientists

PROFESSIONAL SERVICE

Chair, Emerging Ecological Issues Committee, Ecological Society of America – 2022-24
Review Panel Member, PNNL/EMSL, Directors CD1 review for Microbial Molecular Phenotyping Capability – 2022
Co-Organizer, DOE-ESS Workshop “Emerging technologies for investigation of soil-plant-microbe dynamics” - 2021
Associate Editor for mSystems Journal – 2020-23
Member, Science Committee, Ecological Society of America – 2019-21
Elected Chair of Soil Ecology Section & ESA Council Member, Ecological Society of America – 2017-19
Review Panel Member, GEM graduate fellowship program, 2018, 19 & 20
Review Panel Member, DOE JGI User Programs – 2017, 18 & 20
Review Panel Member, DOE EPSCoR, Genomic Sciences, and TES Programs – 2016, 18, 21

Elected Vice Chair, Soil Ecology Section, Ecological Society of America – 2015-17
Deputy Section Editor for BMC Microbiology – 2016-17
Associate Editor for BMC Microbiology – 2013-16
Review Panel Member, ORAU Powe Fellowship – 2015-16
Review Panel Member, PNNL Environmental Molecular Sciences Laboratory User Facility – 2014-16, 2018
Invited Session Chair and Organizer for 2013 Fungal Genetics meeting session on “Ecological Metagenomics”
ORNL Internal Seed Money Proposal Review Committee – 2009-10
Biological and Environmental Sciences Directorate Seminar Committee – 2007-09 (Chair 2008-2009)
Convener and Organizer for 2009 ASM General Meeting Colloquium on “Model Microbial Systems – A tractable and manipulable bridge between organismal and environmental studies”
Steering Committee for NSF RCN Network “Fungal Environmental Science and Informatics Networks”, PI - Tom Bruns, UC Berkeley – 2007-09
Steering Committee Member, LSP-JGI Fungal Genome Sequencing Program – 2006-07
Review Panel Member, Ecosystems Program, EPSCoR Program, and Polar Programs National Science Foundation – 2007, 11,13,15,16, 20
Review Panel Member, National Institute of Environmental and Health Sciences, 2014
Add Hoc Reviewer, various National Science Foundation programs – 2006 to Present
Add Hoc Reviewer for NASA postdoctoral fellowship program – 2009,10
Regular reviewer for the journals: *Applied and Environmental Microbiology*; *BMC Microbiology*; *Environmental Microbiology*; *Environmental Science and Technology*; *ISME Journal*; *Microbial Ecology*; *Molecular Ecology*; *New Phytologist*; *PLOS One*; *Soil Biology and Biogeochemistry*;
Univ. of Colorado, Elected, Graduate Student Government Representative – 1998,99

PROFESSIONAL SOCIETIES

American Society for Microbiology
Ecological Society of America
Soil Ecology Society

COMMUNITY SERVICE

Regional Board Member & Area Referee Administrator, American Youth Soccer Organization – 2016 to Present
Referee for the American Youth Soccer Organization, United States Soccer Federation and Tennessee Secondary School Athletic Association – 2014 to Present
Volunteer, Invasive Plant Survey Crew, Knox County Parks and Recreation – 2014 & 2015
Volunteer, Tennessee Valley Unitarian Universalist Church – 2013 to 2017

PEER REVIEWED PUBLICATIONS ([Google Scholar Link](#))

2022

1. Chen, H., Ma, K., Lu, C., Fu, Q., Qiu, Y., Zhao, J., Huang, Y., Yang, Y. **Schadt**,

- C.W.**, and Chen, H., (2022). Functional redundancy in soil microbial community based on metagenomics across the globe. *Frontiers in Microbiology*. <https://doi.org/10.3389/fmicb.2022.878978>
2. Chen, H., Ma, K., Huang, Y., Fu, Q., Qiu, Y., Lin, J., **Schadt, C.W.** and Chen, H., (2022). Lower functional redundancy in “narrow” than “broad” functions in global soil metagenomics. *Soil*. <https://doi.org/10.5194/soil-8-297-2022>
 3. Dove, N.C., Carrell, A.A., Engle, N.L., Klingeman, D.M., Rodriguez, M., Wahl, T., Tschaplinski, T.J., Muchero, W., **Schadt, C.W.** and Cregger, M.A., (2022). Relationships between Sphaerulina musiva Infection and the Populus Microbiome and Metabolome. *Msystems*, <https://doi.org/10.1128/msystems.00120-22>
 4. Fremin, et al. (2022). Thousands of small, novel genes predicted in global phage genomes. *Cell Reports*. <https://doi.org/10.1016/j.celrep.2022.110984>
 5. Watmough, et al. (2022). Variation in carbon and nitrogen concentrations among peatland categories at the global scale. *PLoS One*. <https://doi.org/10.1371/journal.pone.0275149>
- 2021**
6. Bear, S.E., Seward, J.D., Lamit, L.J., Basiliko, N., Moore, T., Lilleskov, E., Yavitt, J.B., **Schadt, C.W.**, Smith, D.S., Mclaughlin, J. and Siljanen, H., Mykytczuk, N, Williams, S., Roulet, N., Harris, L., Carson, M.A., Watmough, S., Bräuer, S.L. (2021). Beyond the usual suspects: methanogenic communities in eastern North American peatlands are also influenced by nickel and copper concentrations. *FEMS Microbiology Letters*. <https://doi.org/10.1093/femsle/fnab151>
 7. Cregger, M., Carper, D.L., Christel, S., Doktycz, M., Labbe, J., Michener, J., Dove, N., Johnston, E.R., Moore, J., Velez, J., Morrell-Falvey, J., Muchero, W., Pelletier, D., Retterer, S., Tschaplinski, T., Tuskan, G., Weston, D., and **C. Schadt**. (2021). Plant-microbe interactions: from genes to ecosystems using Populus as a model system. *Phytobiomes Journal*, <https://doi.org/10.1094/PBIOMES-01-20-0009-FI>
 8. Carper, D. L., Weston, D. J., Barde, A., Timm, C. M., Lu, T-Y., Burdick, L. H., Jawdy, S. S., Klingeman, D. M., Robeson, M. S. II, Veach, A. M., Cregger, M. A., Kalluri, U. C., **Schadt, C. W.**, Podar, M., Doktycz, M. J., and Pelletier, D. A. (2020). Cultivating the Bacterial Microbiota of *Populus* roots. *mSystems*. <https://doi.org/10.1128/mSystems.01306-20>
 9. Dove, N.C., Klingeman, D.M., Carrell, A.A., Cregger, M.A. and **C.W. Schadt**. (2021). Fire alters plant microbiome assembly patterns: integrating the plant and soil microbial response to disturbance. *New Phytologist*, <https://doi.org/10.1111/nph.17248>
 10. Dove NC, Veach AM, Muchero W, Wahl T, Stegen JC, **Schadt CW** and Cregger MA. (2021). Assembly of the *Populus* microbiome is temporally dynamic and determined by selective and stochastic factors. *mSphere* <https://doi.org/10.1128/mSphere.01316-20>
 11. Liang, J., Wang, G., Singh, S., Jagadamma, S., Gu, L., **Schadt, C.W.**, Wood, J.D., Hanson, P.J., and Mayes, M.A. (2021). Intensified Soil Moisture Extremes Decrease Soil Organic Carbon Decomposition: A Mechanistic Modeling Analysis. *Journal of Geophysical Research: Biogeosciences*. <https://doi.org/10.1029/2021JG006392>

12. Nayfach, S., et al. (2021). A genomic catalog of Earth's microbiomes. *Nature Biotechnology*. <https://doi.org/10.1038/s41587-020-0718-6>
13. Ricciuto, D.M., Xu, X., Shi, X., Wang, Y., Song, X., **Schadt, C.W.**, Griffiths, N.A., Mao, J., Warren, J.M., Thornton, P.E., Chanton, J., Keller, J.K., Bridgham, S.D., Gutknecht, J., Sebastyen, S.D., Finzi, A., Kolka, R., and P.J. Hanson. (2021). "An integrative model for soil biogeochemistry and methane processes: I. Model structure and sensitivity analysis." *Journal of Geophysical Research: Biogeosciences*. <https://doi.org/10.1029/2020JG005963>.
14. Salmon, V.G., Brice, D.J., Bridgham, S., Childs, J., Graham, J., Griffiths, N.A., Hofmockel, K., Iversen, C.M., Jicha, T.M., Kolka, R.K., Kostka, J.E., Malhorta A. Norby, R.J., Phillips J.R., Riccuto, D., **Schadt C.W.**, Sebastyen, S.D., Shi, X., Walker, A.P., Warren, J.M., Weston, D.J., Yang, X, and P.J. Hanson. (2021). Nitrogen and phosphorus cycling in an ombrotrophic peatland: a benchmark for assessing change. *Plant and Soil*, <https://doi.org/10.1007/s11104-021-05065-x>
15. Singh, S., Jagadamma, S., Liang, J., Kivlin, S.N., Wood, J., Wang, G., **Schadt, C.W.**, DuPont, J.I., Gowda, P. and Mayes, M.A., (2021). Differential Organic Carbon Mineralization Responses to Soil Moisture in Three Different Soil Orders Under Mixed Forested System. *Frontiers in Environmental Science*, <https://doi.org/10.3389/fenvs.2021.682450>
16. Ter Horst, A.M., Santos-Medellín, C., Sorensen, J.W., Zinke, L.A., Wilson, R.M., Johnston, E.R., Trubl, G., Pett-Ridge, J., Blazewicz, S.J., Hanson, P.J. and Chanton, J.P., **Schadt, C.W.**, Kostka, J.E., Emerson, J.B. (2021). Minnesota peat viromes reveal terrestrial and aquatic niche partitioning for local and global viral populations. *Microbiome*. <https://doi.org/10.1186/s40168-021-01156-0>
17. Van Nuland, M., I. Ware, **C. Schadt**, Z. Yang, J. Bailey and J. Schweitzer. (2021). Natural soil microbiome variation affects spring foliar phenology with consequences for plant productivity and climate-driven range shifts. *New Phytologist*, <https://doi.org/10.1111/nph.17599>
18. Veach, A.M., Morris, R., Yip, D.Z., Yang, Z.K., Engle, N.L., Cregger, M.A., Tschaplinski, T.J. and **C.W. Schadt**. (2021). Correction to: Rhizosphere microbiomes diverge among *Populus trichocarpa* plant-host genotypes and chemotypes, but it depends on soil origin. *Microbiome*, 9(1), <https://doi.org/10.1186/s40168-019-0668-8>
19. Vélez, J.M., Morris, R.M., Vilgalys, R., Labbé, J. and **C.W. Schadt**. (2021). Phylogenetic diversity of 200+ isolates of the ectomycorrhizal fungus *Cenococcum geophilum* associated with *Populus trichocarpa* soils in the Pacific Northwest, USA and comparison to globally distributed representatives. *PLoS ONE*, 16(1), <https://doi.org/10.1371/journal.pone.0231367>
20. Ware, IA, ME Van Nuland, ZK Yang, **CW Schadt**, JA Schweitzer and JK Bailey. (2021). Climate-driven divergence in plant-microbiome interactions generates range-wide variation in bud break phenology. *Communications Biology*. <https://doi.org/10.1038/s42003-021-02244-5>
21. Wilson, R., Tfaily, M, Kolton, M., Johnston, E., Petro, C., Zalman, C., Hanson, P., Heyman, H., Kyle, J., Hoyt, D., Eder, E., Purvine, S., Kolka, R., Sebastyen, S., Griffiths, N., **Schadt, C.**, Keller, J., Bridgham, S., Chanton, J., and Kostka, J. (2021). Soil metabolome response to whole ecosystem warming at the Spruce

and Peatland Responses Under Changing Environments experiment. *Proceedings of the National Academy of Sciences*.
<https://doi.org/10.1073/pnas.2004192118>

22. Zhang, H., Deng, Q., **Schadt, C.W.**, Mayes, M.A., Zhang, D. and Hui, D., (2021). Precipitation and nitrogen application stimulate soil nitrous oxide emission. *Nutrient Cycling in Agroecosystems*, <http://doi.org/10.1007/s10705-021-10155-4>.

2020

23. Carper, D.L., **Schadt, C.W.**, Burdick, L.H., Kalluri, U.C. and Pelletier, D.A., (2020). Draft Genome Sequence of *Tumebacillus* sp. Strain BK434, Isolated from the Roots of Eastern Cottonwood. *Microbiology Resource Announcements*, 9(22).
24. Chen, H., Dai, Z., Veach, A.M., Zheng, J., Xu, J. and **C.W. Schadt. (2020)**. Global meta-analyses show that conservation tillage practices promote soil fungal and bacterial biomass. *Agriculture, Ecosystems & Environment*, 293, p.106841.
25. He, Z., Deng, Y., Xu, M., Li, J., Liang, J., Xiong, J., Yu, H., Wu, B., Wu, L., Xue, K. and Shi, S., Carillo, Y., Van Nostrand, J.D., Hobbie, S.E., Reich, P.B., **Schadt, C.W.**, Kent, A.D., Pendall, E., Wallenstein, M., Luo, Y., Yan, Q., and Zhou, J. (2020). Microbial functional genes commonly respond to elevated carbon dioxide. *Environment international*, 144, p.106068.
26. Hui, D., Porter, W., Phillips, J.R., Aidar, M.P., Lebreux, S.J., **Schadt, C.W.** and Mayes, M.A., (2020). Phosphorus rather than nitrogen enhances CO₂ emissions in tropical forest soils: Evidence from a laboratory incubation study. *European Journal of Soil Science*, 71(3), pp.495-510.
27. Jian, S., Li, J., Wang, G., Kluber, L.A., **Schadt, C.W.**, Liang, J. and Mayes, M.A., (2020). Multi-year incubation experiments boost confidence in model projections of long-term soil carbon dynamics. *Nature Communications*, 11(1), pp.1-9.
28. Kluber, L.A., Johnston, E.R., Allen, S.A., Hendershot, J.N., Hanson, P.J. and **Schadt, C.W.**, (2020). Constraints on microbial communities, decomposition and methane production in deep peat deposits. *PloS ONE*, 15(2), p.e0223744.
29. Nash, J., Laushman, R. and **Schadt, C.W.** (2020). Ectomycorrhizal fungal diversity interacts with soil nutrients to predict plant growth despite weak plant-soil feedbacks. *Plant and Soil*, pp.1-14.
30. Pelletier, D.A., Burdick, L.H., Podar, M., **Schadt, C.W.** and Kalluri, U.C., (2020). Draft Genome Sequence of *Larkinella* sp. Strain BK230, Isolated from *Populus deltoides* Roots. *Microbiology Resource Announcements*, 9(12).
31. Seward, J., Carson, M.A., Lamit, L.J., Basiliko, N., Yavitt, J.B., Lilleskov, E., **Schadt, C.W.**, Smith, D.S., Mclaughlin, J., Mykytczuk, N. and Willims-Johnson, S., (2020). Peatland Microbial Community Composition Is Driven by a Natural Climate Gradient. *Microbial Ecology*.
32. Veach, A.M., Chen, H., Yang, Z.K., Labbe, A.D., Engle, N.L., Tschaplinski, T.J., **Schadt, C.W.** and Cregger, M.A., (2020). Plant Hosts Modify Belowground Microbial Community Response to Extreme Drought. *mSystems*, 5(3).

2019

33. Barba, J, MA Bradford, PE Brewer, D Bruhn, K Covey, J van Haren, JP Megonigal,

- TN Mikkelsen, SR Pangala, M Pihlatie, B Poulter, A Rivas-Ubach, **CW Schadt**, K Terazawa, DL Warner, Z Zhang, and R Vargas. (2019). Methane emissions from tree stems: a new frontier in the global carbon cycle. *New Phytologist*. **222**:18-28. DOI: 10.1111/nph.15582
34. Bonito, G, GMN Benucci, K Hameed, D Weighill, P Jones, K-H Chen, D Jacobson, **CW Schadt** and R Vilgalys. (2019). Fungal-Bacterial Networks in the *Populus* Rhizobiome are Impacted by Soil Properties and Host Genotype. *Frontiers in Microbiology*. **10**:481. DOI:10.3389/fmicb.2019.00481
35. Chen, H, Dai Z, Jager HI, Wullschlegler SD, Xu J, and **Schadt CW**. (2019). Influences of nitrogen fertilization and climate regime on the above-ground biomass yields of miscanthus and switchgrass: A meta-analysis. *Renewable and Sustainable Energy Reviews*. **108**:303-311. DOI:10.1016/j.rser.2019.03.037
36. Chen, H, ZK Yang, D Yip, RH Morris, SJ Lebreux, MA Cregger, DM Klingeman, S Hui, RL Hettich, SW Wilhelm, G Wang, FE Loeffler and **CW Schadt**. (2019). One-time nitrogen fertilization shifts switchgrass soil microbiomes within a context of larger spatial and temporal variation. *PLoS ONE* **14**:e0211310. DOI:10.1371/journal.pone.0211310
37. Liao, HL, G Bonito, JA Rojas, K Hameed, S Wu, **CW Schadt**, JL Labbe, G Tuskan, FM Martin, IV Grigoriev and R Vilgalys. (2019). Fungal endophytes of *Populus trichocarpa* alter host phenotype, gene expression and rhizobiome composition. *Molecular Plant-Microbe Interactions*. DOI:10.1094/MPMI-05-18-0133-R
38. Veach, AM, RH Morris, DZ Yip, ZK Yang, NL Engle, MA Cregger, TJ Tschaplinski, **CW Schadt**. (2019). Rhizosphere microbiomes diverge among *Populus trichocarpa* plant-host genotypes and chemotypes, but it depends on soil origin. *Microbiome*. **7**:76. DOI:10.1186/s40168-019-0668-8
39. Ware, IM, ME Van Nuland, JA Schweitzer, Z Yang, **CW Schadt**, LC Sidak-Loftis, NE Stone, JD Busch, DM Wagner and JK Bailey. (2019). Climate-driven reduction of genetic variation in plant phenology alters soil communities and nutrient pools. *Global Change Biology*. **25**:1514-1528. DOI:10.1111/gcb.14553
40. *Yip, DZ, *AM Veach, ZK Yang, MA Cregger and ***CW Schadt**. (2019). Methanogenic Archaea dominate mature heartwood habitats of Eastern Cottonwood (*Populus deltoides*). *New Phytologist* **222**:115-121. DOI:10.1111/nph.15346 (*equal contribution).

2018

41. *Cregger, MA, *AM Veach, ZK Yang, MJ Crouch, R Vilgalys, GA Tuskan, and **CW Schadt**. (2018). The *Populus* holobiont: dissecting the effects of plant niches and genotype on the microbiome. *Microbiome* **6**:31 (*equal contribution).
42. Dai, Z, W Su, H Chen, A Barberán, H Zhao, M Yu, L Yu, PC Brookes, **CW Schadt**, SX Chang and J Xu. (2018). Long-term nitrogen fertilization decreases bacterial diversity and favors the growth of Actinobacteria and Proteobacteria in agroecosystems across the globe. *Global Change Biology*. **24**:3452–3461
43. Higgins SD, **CW Schadt**, PB Matheny and FE Löffler. (2018). Phylogenomics reveals the dynamic evolution of fungal nitric oxide reductases and their relationship to secondary metabolism. *Genome Biology and Evolution*. DOI: 10.1093/gbe/evy187

44. Karpinets, TV, V Gopalakrishnan, J Wargo, AP Futreal, **CW Schadt**, and J Zhang. (2018). Linking associations of rare low-abundance species to their environments by association networks. *Frontiers in Microbiology*. **9**:297.
45. Steinweg, JM, JE Kostka, PJ Hanson and **CW Schadt**. (2018). Temperature sensitivity of extracellular enzymes differs with peat depth but not with season in an ombrotrophic bog. *Soil Biology and Biochemistry*. **125**:244-250
46. Timm, CM, KR Carter, AA Carrell, SR Jun, SS Jawdy, JM Vélez, LE Gunter, ZK Yang, I Nookaew, NL Engle, TY Lu, **CW Schadt**, TJ Tschaplinski, MJ Doktycz, GA Tuskan, DA Pelletier and DJ Weston. (2018). Abiotic Stresses Shift Belowground Populus-Associated Bacteria Toward a Core Stress Microbiome. *mSystems*. **3**:e00070-17.
47. Veach, AM, DZ Yip, NL Engle, ZK Yang, A Bible, J Morrell-Falvey, TJ Tschaplinski, UC Kalluri and **CW Schadt**. (2018). Modification of plant cell wall chemistry impacts metabolome and microbiome composition in *Populus PdKOR1* RNAi plants. *Plant and Soil*. DOI:10.1007/s1110
48. Yu, H, Z He, A Wang, J Xie, L Wu, J Van Nostrand, D Jin, Z Shao, **CW Schadt**, J Zhou and Y Deng. (2018). Divergent responses of forest soil microbial communities under elevated CO₂ in different depths of upper soil layers. *Applied and Environmental Microbiology*. **84**:e01694-17

2017

49. Bonito G, K Hameed, R Healy, M Toome, C Reid, HL Liao, **CW Schadt** and R Vilgalys. (2017). *Atractiella rhizophila*, an endorhizal fungus isolated from the *Populus* root microbiome. *Mycologia*, **109**:18-26
50. Uehling J, A Gryganskyi, K Hameed, T Tschaplinski, PK Misztal, S Wu, A Desirò, N Vande Pol, Z Du, A Zienkiewicz, K Zienkiewicz, E Morin, E Tisserant, R Splivallo, M Hainaut, B Henrissat, R Ohm, A Kuo, J Yan, A Lipzen, M Nolan, K LaButti, K Barry, AH Goldstein, J Labbé, **C Schadt**, G Tuskan, I Grigoriev, F Martin, R Vilgalys and G Bonito. (2017) Comparative genomics of *Mortierella elongata* and its bacterial endosymbiont *Mycoavidus cysteinexigens*. *Environmental Microbiology* **19**:2964-2983
51. Warren MJ, X Lin, JC Gaby, CB Kretz, M Kolton, J Pett-Ridge, PL Morton, DJ Weston, **CW Schadt**, JE Kostka, JB Glass. (2017). Molybdenum-based diazotrophy in a *Sphagnum* peatland in northern Minnesota. *Applied and Environmental Microbiology* **83**: e01174-17
52. Velez J, TJ Tschaplinski, R Vilgalys, **CW Schadt**, G Bonito, K Hameed, N Engle and CE Hamilton. (2017). Characterization of a novel, ubiquitous fungal endophyte from the rhizosphere and root endosphere of *Populus* trees. *Fungal Ecology*, **27**:78-86
53. Zhang P, Z He, JD Van Nostrand, Y Qin, Y Deng, L Wu, Q Tu, J Wang, **CW Schadt**, M Fields, TC Hazen, A Arkin and J Zhou. (2017). Dynamic Succession of Groundwater Sulfate-Reducing Communities during Prolonged Reduction of Uranium in a Contaminated Aquifer. *Environmental Science & Technology* **51**:3609-3620

2016

54. Bible AN, SJ Fletcher, DA Pelletier, **CW Schadt**, SS Jawdy, DJ Weston, LN Engle, T

- Tschaplinski, R Masyuko, S Poliseti, PW Bohn, TA Coutinho, MJ Doktycz and JL Morrell-Falvey. (2016). A Carotenoid-Deficient Mutant in *Pantoea* sp. YR343, a Bacteria Isolated from the Rhizosphere of *Populus deltoides*, is Defective in Root Colonization. *Frontiers in Microbiology* **7**:491
55. Bonito G, K Hameed, R Ventura, J Krishnan, **CW Schadt**, and R Vilgalys, (2016). Isolating a functionally relevant guild of fungi from the root microbiome of *Populus*. *Fungal Ecology*, **22**:35-42.
56. Deng, Y, Z He, J Xiong, H Yu, M Xu, SE Hobbie, PB Reich, **CW Schadt**, A Kent, E Pendall, M Wallenstein, Z He, and J Zhou. (2016). Elevated carbon dioxide accelerates the spatial turnover of soil microbial communities. *Global Change Biology*, **22**(2):957-964.
57. Deng Y, P Zhang, Y Qin, Q Tu, Y Yang, Z He, **C Schadt** and J Zhou. (2016). Network succession reveals the importance of competition in response to emulsified vegetable oil amendment for uranium bioremediation. *Environmental Microbiology* **18**(1):205-218
58. Higgins SA, A Welsh, LH Orellana, KT Konstantinidis, JC Chee-Sanford, RA Sanford, **CW Schadt**, and FE Löffler. (2016). Detection and Diversity of Fungal Nitric Oxide Reductase Genes (p450nor) in Agricultural Soils. *Applied and Environmental Microbiology*, **82**(10), pp.2919-2928.
59. Jun, SR., TM Wassenaar, I Nookaew, L Hauser, V Wanchai, M Land, CM Timm, TYS Lu, **CW Schadt**, MJ Doktycz and DA Pelletier. (2016) Diversity of *Pseudomonas* Genomes, Including *Populus*-Associated Isolates, as Revealed by Comparative Genome Analysis. *Applied and Environmental Microbiology*, **82**(1): 375-383.
60. Utturkar SM, WN Cude, MS Robeson, ZK Yang, DM Klingeman, ML Land, SL Allman, TYS Lu, SD Brown, **CW Schadt**. M Podar and DA Pelletier. (2016). Enrichment of root endophytic bacteria from *Populus deltoides* and single-cell genomics analysis. *Applied and Environmental Microbiology*, **82**(18): 5698-5708.
61. Wilson RM, AM Hopple, MM Tfaily, SD Sebestyen, CW Schadt, L Pfeifer-Meister, C Medvedeff, KJ McFarlane, JE Kostka, M Kolton, R Kolka, LA Kluber, JK Keller, TP Guilderson, NA Griffiths, JP Chanton, SD Bridgham, and PJ Hanson. (2016). Stability of Peatland Carbon to Rising Temperatures. *Nature Communications*, **7**: 13723.

2015

62. Hacquard S and **CW Schadt*** (2015). Towards a holistic understanding of the beneficial interactions across the *Populus* microbiome. *New Phytologist*, **205**(4): 1424-1430. [*equal contribution]
63. Klingeman DM, S Utturkar, TYS Lu, **CW Schadt**, DA Pelletier and SD Brown (2015). Draft Genome Sequences of Four *Streptomyces* Isolates from the *Populus trichocarpa* Root Endosphere and Rhizosphere. *Genome Announcements*, **3**(6): e01344-15.
64. Jun, SR, MS Robeson, LJ Hauser, **CW Schadt** and AA Gorin. (2015). PanFP: Pangenome-based functional profiles for microbial communities. *BMC Research Notes*. **8**: 479.
65. Naujokas, MF, NT Basta, Z Cheng, GM Hettiarachchi, M Maddaloni, **CW Schadt**,

- KG Scheckel, C Attanayake and H Henry. (2015). Bioavailability-based In Situ Remediation to Meet Future Lead (Pb) Standards in Urban Soils and Gardens. *Environmental Science & Technology*. **49**(15):8948–8958
66. **Schadt, CW** and A Rosling. (2015). Comment on “Global diversity and geography of soil fungi”. *Science*. **348**(6242):1438.
67. Timm, C.M., Campbell, A.G., Utturkar, S.M., Jun, S.R., Parales, R.E., Tan, W.A., Robeson, M.S., Lu, T.Y.S., Jawdy, S., Brown, S.D. and Ussery, D.W., **Schadt, C.W.** (2015). Metabolic functions of *Pseudomonas fluorescens* strains from *Populus deltoides* depend on rhizosphere or endosphere isolation compartment. *Frontiers in Microbiology*, **6**: 1118
68. Wang, G, S Jagadamma, MA Mayes, **CW Schadt**, JM Steinweg, L Gu and WM Post. (2015). Microbial dormancy improves development and experimental validation of ecosystem model. *ISME Journal*. **9**: 226-237.
69. Zhang, P, WM Wu, JD Van Nostrand, Y Deng, Z He, T Gihring, G Zhang, **CW Schadt**, D Watson, P Jardine, CS Criddle, S Brooks, TL Marsh, JM Tiedje, AP Arkin and J Zhou. (2015). Dynamic succession of groundwater functional microbial communities in response to emulsified vegetable oil amendment during sustained in situ U (VI) reduction. *Applied and Environmental Microbiology*. **81**(12): 4164-4172.

2014

70. Bonito, G, H Reynolds, M Robeson, J Nelson, B Hodkinson, G Tuskan, **CW Schadt** and R Vilgalys. (2014). Plant host and soil origin influence fungal and bacterial assemblages in the roots of woody plants. *Molecular Ecology*: **23**(13): 3356-3370.
71. Jastoria, P, SJ Green, A Canion, WA Overholt, O Prakash, D Wafula, D Hubbard, DB Watson, **CW Schadt**, SC Brooks and JE Kostka. (2014). Watershed scale fungal community characterization along a pH gradient in a subsurface environment co-contaminated with uranium and nitrate. *Applied and Environmental Microbiology*, **80**:1810-1820.
72. Lin, X, MM Tfaily, JM Steinweg, P Chanton, K Esson, ZK Yang, JP Chanton, W Cooper, **CW Schadt** and JE Kostka (2014). Microbial metabolic potential in carbon degradation and nutrient acquisition (N, P) in an ombrotrophic peatland. *Applied and Environmental Microbiology*, **80**:3531-3540.
73. Lin, X, MM Tfaily, SJ Green, JM Steinweg, P Chanton, A Invittaya, JP Chanton, W Cooper, **CW Schadt** and JE Kostka (2014). Microbial community stratification linked to variation in organic matter properties in a boreal peatland. *Applied and Environmental Microbiology*, **80**:3518-3530.
74. Tfaily, MM, WT Cooper, JE Kostka, PR Chanton, **CW Schadt**, PJ Hanson, CM Iversen and JP Chanton. (2014). Organic matter transformation in the peat column at Marcell Experimental forest: Humification and vertical stratification. *Journal of Geophysical Research: Biogeosciences*, **119**:661-675.
75. Utturkar, SM, DM Klingeman, ML Land, **CW Schadt**, MJ Doktycz, DA Pelletier and SD Brown (2014). Evaluation and validation of *de novo* and hybrid assembly techniques to derive high quality genome sequences. *Bioinformatics*. **30**(19): 2709-2716.

76. Wang, G, MA Mayes, L Gu, and **CW Schadt**. (2014). Representation of Dormant and Active Microbial Dynamics for Ecosystem Modeling. *PLoS ONE* **9**:e89252.

2013

77. De Graaff, MA, J Six, J Jastrow, J Phillips, **CW Schadt** and SD Wulfschleger. (2013). Variation in root architecture among switchgrass cultivars impacts root decomposition rates. *Soil Biology and Biochemistry* **58**:198-206.
78. Guevara, G, G Bonito, J Trappe, E Cazares, G Williams, RA Healy, **CW Schadt** and R Vilgalys. (2013). New North American truffles (*Tuber* spp.) species and their ectomycorrhizal associations. *Mycologia* **105**:194–209.
79. Shakya, M, C Quince, JH Campbell, ZK Yang, **CW Schadt** and M Podar. (2013). Comparative metagenomic and rRNA microbial diversity characterization using Archaeal and Bacterial synthetic communities. *Environmental Microbiology* **15**:1882-1889.
80. Shakya M, N Gottel, H Castro, ZK Yang, L Gunter, J Labbe, W Muchero, G Bonito, R Vilgalys, G Tuskan, M Podar and **CW Schadt**. (2013) A Multifactor Analysis of Fungal and Bacterial Community Structure in the Root Microbiome of Mature *Populus deltoides* Trees. *PLoS ONE* **8**:e76382.
81. Tang, GP, W-M Wu, DB Watson, JC Parker, **CW Schadt**, X Shi, and SC Brooks. (2013). U(VI) Bioreduction with Emulsified Vegetable Oil as the Electron Donor – Microcosm Tests and Model Development. *Environmental Science and Technology*. **47**:3209–3217.
82. Tang, GP, DB Watson, W-M Wu, **CW Schadt**, JC Parker and SC Brooks. (2013) U(VI) Bioreduction with Emulsified Vegetable Oil as the Electron Donor – Model Application to a Field Test. *Environmental Science and Technology*. **47**:3218–3225.
83. Watson, DB, W Wu, T Mehlhorn, G Tang, J Earles, K Lowe, TM Gihring, G Zhang, J Phillips, MI Boyanov, BP Spalding, **CW Schadt**, KM Kemner, CS Criddle, PM Jardine and SC Brooks. (2013). In situ bioremediation of uranium with emulsified vegetable oil as the electron donor. *Environmental Science & Technology* **47**:6440-6448.

2012

84. Brown SD, DM Kingeman, TS Lu, CM Johnson, SM Utturkar, ML Land, **CW Schadt**, MJ Doktycz and DA Pelletier. (2012). Genome Announcement: Draft genome sequence of *Rhizobium* sp. strain PDO-076, a bacterium isolated from *Populus deltoides*. *Journal of Bacteriology*, **194**:2383-2384.
85. Brown SD, SM Utturkar, DM Klingeman, CM Johnson, M Stanton, ML Land, TY Lu, **CW Schadt**, MJ Doktycz and DA Pelletier. (2012). Genome Announcement: Twenty One *Pseudomonas* Genomes and Nineteen Genomes from Diverse Bacteria Isolated from the Rhizosphere and Endosphere of *Populus deltoides*. *Journal of Bacteriology* **194**:5991-5993.
86. Castro HF, AT Classen, EE Austin, KM Crawford and **CW Schadt**. (2012). Development and validation of a citrate synthase directed quantitative PCR marker for soil bacterial communities. *Applied Soil Ecology* **61**:69-75.
87. Cregger, MA, **CW Schadt**, NG McDowell, WT Pockman and AT Classen. (2012).

- Soil microbial community response to precipitation change in a semi-arid ecosystem. *Applied and Environmental Microbiology* **78**:8587-8594.
88. Dunbar J, SA Eichorst, L Gallegos-Graves, S Silva, G Xie, NW Hengartner, RD Evans, BA Hungate, RB Jackson, JP Magonigal, **CW Schadt**, R Vilgalys, DR Zak, and CR Kuske (2012) Common bacterial responses in six ecosystems exposed to ten years of elevated atmospheric carbon dioxide. *Environmental Microbiology* **14**:1145-1158.
 89. Gihring TM, SJ Green and **CW Schadt**. (2012). Massively-parallel rRNA gene sequencing exacerbates the potential for biased community diversity comparisons due to variable library sizes. *Environmental Microbiology*, **14**:285-289.
 90. Green SJ, O Prakash, P Jasrotia, W Overholt, EA Cardenas, D Hubbard, J Tiedje, DB Watson, **CW Schadt**, SC Brooks and JE Kostka. (2012). Denitrifying bacteria in the genus *Rhodanobacter* dominate bacterial communities in the highly contaminated subsurface of a nuclear legacy waste site. *Applied and Environmental Microbiology*, **78**:1039-1047.
 91. Hodkinson BP, NR Gottel, **CW Schadt**, and F Lutzoni. (2012). Photoautotrophic symbiont and geography are major factors affecting highly structured and diverse bacterial communities in the lichen microbiome. *Environmental Microbiology*, **14**:147-161.
 92. Li Y, TJ Tshaplinski, NL Engle, CY Hamilton, M Rodriguez Jr., JC Liao, **CW Schadt**, AM Guss, Y Yang and DE Graham. (2012). Combined inactivation of the *Clostridium cellulolyticum* lactate and malate dehydrogenase genes substantially increases ethanol yields from cellulose and switchgrass fermentations. *Journal of Biotechnology for Biofuels* **5**:2-13.
 93. Mosher JJ, TJ Phelps, M Podar, RA Hurt, JH Campbell, MM Drake, JG Moberly, **CW Schadt**, SD Brown, TC Hazen, AV Palumbo, BA Faybishenko and DA Elias. (2012). Microbial Community Succession during Lactate Amendment and Electron-acceptor Limitation Reveals a Predominance of Metal-reducing *Pelosinus* spp. *Applied and Environmental Microbiology* **78**:2082-2091.
 94. Sullivan, TS, NR Gottel, N Basta, PM Jardine and **CW Schadt**. (2012). Firing range soils yield a diverse array of fungal isolates capable of organic acid production and Pb-mineral solubilization. *Applied and Environmental Microbiology* **78**:6078-6086 (Images featured on journal cover, Dec Issue 2012).
 95. Weston DJ, DA Pelletier, JL Morrell-Falvey, TJ Tschaplinski, SJ Jawdy, TY Lu, SM Allen, A Karve, SJ Melton, MZ Martin, **CW Schadt**, JG Chen, X Yang, MJ Doktycz and G Tuskan. (2012). *Pseudomonas fluorescens* induces strain-dependent and strain-independent host plant responses in defense networks, primary metabolism, photosynthesis and fitness. *Molecular Plant Microbe Interactions* **25**:765-778.

2011

96. DeGraaff MA, **CW Schadt**, K Rula, J Six, JA Schwietzer and AT Classen. (2011). Elevated CO₂ and plant species diversity interact to alter root decomposition. *Soil Biology and Biochemistry* **43**:2347-2354.
97. Garten Jr. CT, DJ Brice, HF Castro, RL Graham, MA Mayes, JR Phillips, WM Post, **CW Schadt**, SD Wullschleger, DD Tyler, PM Jardine, JD Jastrow, R Matamala, RM Miller, KK Moran, TW Vugteveen, RC Izaurralde, AM Thomson, TO West, JE

- Amonette, VL Bailey, FB Metting and JL Smith. (2011). Response of “Alamo” switchgrass tissue chemistry and biomass to nitrogen fertilization in West Tennessee, USA. *Agriculture Ecosystems and Environment* **140**: 289-297.
98. Gihring TM, G Zhang, CC Brandt, SC Brooks, JH Campbell, S Carroll, CS Criddle, SJ Green, P Jardine, JE Kostka, K Lowe, TL Mehlhorn, W Overholt, DB Watson, ZK Yang, W-M Wu, and **CW Schadt**. A limited microbial consortium is responsible for extended bioreduction of uranium in a contaminated aquifer. *Applied and Environmental Microbiology*, **77**:5955-5965.
99. Gilmour CC, DA Elias, AM Kucken, SD Brown, AV Palumbo, **CW Schadt** and JD Wall. (2011). The sulfate-reducing bacterium *Desulfovibrio desulfuricans* ND132 as a model for understanding bacterial mercury methylation. *Applied and Environmental Microbiology*, **77**:3938–3951,
100. Gittel, NR, HF Castro, M Kerley, ZK Yang, DA Pelletier, M Podar, T Karpinets E Uberbacher, GA Tuskan, R Vilgalys, MJ Doktycz, **CW Schadt**. (2011). *Populus deltoides* roots harbor distinct microbial communities within the endosphere and rhizosphere across contrasting soil types. *Applied and Environmental Microbiology*, **77**:5934-5944.
101. Weber CF, DR Zak, BA Hungate, RB Jackson, R Vilgalys, RD Evans, **CW Schadt**, JP Megonigal and CR Kuske. (2011). Responses of soil cellulolytic fungal communities to elevated atmospheric CO₂ are complex and variable across five ecosystems. *Environmental Microbiology*, **13**:2778-2793.

2010

102. Castro HF, AT Classen, EE Austin, RJ Norby and **CW Schadt**. (2010) Soil microbial community responses to multiple climate change drivers. *Applied and Environmental Microbiology* **76**:999-1007.
103. Degraff MA, AT Classen, HF Castro and **CW Schadt**. (2010) Labile soil carbon inputs mediate the soil microbial community composition and plant residue decomposition rates. *New Phytologist*. **188**:1055-1064
104. Garten Jr, CT Jr., JL Smith, DD Tyler, JE Amonette, VL Bailey, DJ Brice, HF Castro, RL Graham, CA Gunderson, RC Izaurralde, PM Jardine, JD Jastrow, MK Kerley, R Matamala, MA Mayes, FB Metting, RM Miller, KK Moran, WM Post III, RD Sands, **CW Schadt**, JR Phillips, AM Thomson, T Vugteveen, TO West, and SD Wullschlegel. (2010) Intra-annual changes in biomass, carbon, and nitrogen dynamics at 4-year old switchgrass field trials in west Tennessee, USA. *Agriculture Ecosystems and Environment* **136**:177-184.
105. Hemme CL, H Mouttaki, Y-J Lee, L Goodwin, S Lucas, A Copeland, A Lapidus, T Glavina del Rio, H Tice, E Saunders, T Brettin, JC Detter, CS Han, S Pitluck, ML Land, LJ Hauser, N Krypides, N Mikhailova, Z He, L Wu, JD Van Nostrand, B Henrissat, Q He, PA Lawson, RS Tanner, LR Lynd, J Wiegel, MW Fields, AP Arkin, **CW Schadt**, BS Stevenson, MJ McInerney, Y Yang, H Dong, RL Huhnke, JR Mielenz, S-Y Ding, ME Himmel, S Taghavi, D. van der Lelie, EM Rubin, and J-Z Zhou. (2010) Genome Announcement: Sequencing of Multiple Clostridia Genomes Related to Biomass Conversion and Biofuels Production. *Journal of Bacteriology*, **192**:6494-6496.
106. Hollister EE, **CW Schadt**, R Ansley, AV Palumbo and TW Boutton. (2010)

Structural and functional diversity of soil bacterial and fungal communities following woody plant encroachment in the southern Great Plains. *Soil Biology and Biochemistry*. **10**:1816-1824.

107. Miller LD, JJ Mosher, A Venkateswaran, ZK Yang, AV Palumbo, TJ Phelps, M Podar, **CW Schadt** and M Keller. (2010) Establishment and metabolic analysis of a model microbial community for understanding trophic and electron accepting interactions of subsurface anaerobic environments. *BMC Microbiology* **10**:149.
108. Reganold, JP, PK Andrews, JR Reeve, L Carpenter-Boggs, **CW Schadt**, JR Alldredge, CF Ross, NM Davies, and J Zhou (2010) Fruit and soil quality of organic and conventional strawberry agroecosystems. *PLoS ONE*. **5**:e12346.
109. Reeve J, **CW Schadt**, L Carpenter-Boggs, S Kang, J Zhou and JP Reganold. (2010) Effects of soil type and farm management on soil ecological functional genes and microbial activities. *ISME Journal* **4**:1099–1107.
110. Zhang F, W-M Wu, JC Parker, T Mehlhorn, SD Kelly, KM Kemner, G Zhang, **CW Schadt**, SC Brooks, CS Criddle, DB Watson and PM Jardine (2010) Kinetic analysis and modeling of oleate and ethanol stimulated uranium (VI) bio-reduction in contaminate sediments under sulfate reduction conditions. *Journal of Hazardous Materials* **183**:482-489.

2009

111. Austin, EA, HF Castro, KT Sides, **CW Schadt** and AT Classen. (2009) Assessment of 10 years of CO₂ fumigation on soil microbial communities and function in a sweetgum plantation. *Soil Biology and Biogeochemistry*, **41**:514-520.
112. Berthrong, ST, **CW Schadt**, G Piñeiro and RB Jackson. (2009) Afforestation Alters the Composition of Functional Genes in Soil and Biogeochemical Processes in South American Grasslands. *Applied and Environmental Microbiology*, **75**:6240-6248.
113. Madden AS, Palumbo AV, Ravel B, Vishnivetskaya TA, Phelps TJ, **Schadt CW**, and CC Brandt (2009) Donor-dependent extent of uranium reduction for bioremediation of contaminated sediment microcosms, *Journal of Environmental Quality*, **38**:53-60.
114. Waldron, PJ, L-Y Wu, JD Van Nostrand, **CW Schadt**, DB Watson, PM Jardine, AV Palumbo, TC Hazen, J-Z Zhou. (2009) Functional gene array-based analysis of microbial community structure in groundwaters with a gradient of contaminant levels. *Environmental Science and Technology*. **43**:3529-3534.

2008

115. Baker SE, Thykaer J, Adney WS, Brettin TS, Brockman FJ, D'haeseleer P, Diego A Martinez, Miller RM, Rokhsar DS, **Schadt CW**, Torok T, Tuskan G, Bennett J, Berka RM, Briggs SP, Heitman J, Taylor J, Turgeon BG, Werner-Washburne M and ME Himmel. (2008) Fungal Genome Sequencing and Bioenergy. *Fungal Biology Reviews*. **22**:1-5.
116. Nemergut DR, Townsend AR, Sattin SR, Freeman KR, Fierer N, Neff JC, Bowman WD, **Schadt CW**, Weintraub MN and SK Schmidt. (2008) The effects of chronic nitrogen fertilization on alpine tundra soil microbial communities: Implications for carbon and nitrogen cycling. *Environmental Microbiology*, **10**:3093–3105.

117. Porter TM*, **Schadt CW***, Rizvi L, Martin AP; Schmidt SK; Scott-Denton L; Vilgalys R, and JM Moncalvo. (2008) Widespread occurrence and phylogenetic placement of a soil clone group adds a prominent new branch to the fungal tree of life. *Molecular Phylogenetics and Evolution*. **46**:635-644 (*Equal Contribution).
118. Schmidt SK, Sobieniak–Wiseman LC, Kageyama SA, Halloy SRP and **CW Schadt**. (2008) Mycorrhizal and dark-septate fungi in plant roots above 4720 meters elevation in the Andes and Rocky Mountains. *Arctic, Antarctic and Alpine Research*. **40**:576-583.
119. Zhou JZ, Kang S, **Schadt CW**, and CT Garten. (2008) Spatial Scaling of Functional Gene Diversity across Various Microbial Taxa. *Proceedings of the National Academy of Sciences*, **105**:7768-7773.

2007

120. He Z, Gentry TJ, **Schadt CW**, Wu L, Liebich J, Chong SC, Wu WM, Gu B, Jardine P, Criddle CS, and J-Z Zhou. (2007) GeoChip: A novel comprehensive microarray for investigating biogeochemical and environmental processes. *ISME Journal* **1**:67-77 (>250 citations).
121. Garten CT, Kang SH, **Schadt CW**, Brice DJ, and J-Z Zhou. (2007) Variability in Forest Soil Properties and Processes at Spatial Scales from One Meter to One Kilometer. *Soil Biology and Biogeochemistry*, **39**:2621-2627.
122. Gao H, Yang ZK, Gentry TJ, Wu L, **Schadt CW**, and J-Z Zhou. (2007). Microarray-based Analysis of Microbial Community RNAs by Whole Community RNA Amplification (WCRA). *Applied and Environmental Microbiology*, **73**:563-571.

2006

123. Rodríguez-Martínez EM, Pérez EX, **Schadt CW**, Zhou J, and A Massol-Deyá. (2006) Microbial Diversity and Bioremediation of a Hydrocarbon-Contaminated Aquifer in Vega Baja, Puerto Rico. *International Journal of Environmental Research and Public Health*, **3**:292-300.
124. Gentry TJ, Wickham, GS, **Schadt CW**, He Z, and J Zhou. (2006) Microarray Applications in Microbial Ecology Research. *Microbial Ecology*, **52**:159-175. (>100 citations).
125. Hwang C, Wu WM, Gentry TJ, Carley J, **Schadt CW**, Carroll SL, Watson D, Jardine PM, Zhou J, Hickey RF, Criddle CS, and MW Fields. (2006) Changes in bacterial community structure correlate with initial operating conditions of a field-scale denitrifying fluidized bed reactor, *Applied Microbiology and Biotechnology*, **71**:748-760.
126. Wu L, Liu X, **Schadt CW**, and J Zhou. (2006) Microarray-based analysis of subpicogram quantities of microbial community DNA. *Applied and Environmental Microbiology*, **72**:4931-4941.
127. Liebich J., **Schadt CW**, Chong SC, Rhee SK, and J Zhou. (2006) Improvement of oligonucleotide probe design criteria for the development of functional gene microarrays for environmental applications. *Applied and Environmental Microbiology*, **72**:1688-1691.

2005 and Older

128. Meyer AF, Lipson DA, Martin AP, **Schadt CW**, and SK Schmidt. (2004) Molecular

- and metabolic characterization of cold tolerant, alpine soil *Pseudomonas sensu stricto*. *Applied and Environmental Microbiology*. **70**:483-489 .
129. **Schadt CW**, Martin AP, Lipson DA and SK Schmidt. (2003). Seasonal dynamics of previously unknown fungal lineages in tundra soils. *Science* **301**:1359-1361.
130. Lipson DA, **Schadt CW** and SK Schmidt. (2002) Changes in soil microbial community structure and function in an alpine dry meadow following spring snow melt. *Microbial Ecology* **43**:307-314.
131. **Schadt CW**, Mullen RB and SK Schmidt. (2001) Isolation and phylogenetic identification of a dark septate endophyte of the alpine plant *Ranunculus adoneus*. *New Phytologist* **150**:747-754.
132. Lipson DA, **Schadt CW**, Schmidt SK and RK Monson. (1999) Ectomycorrhizal transfer of amino acid-nitrogen to the alpine sedge *Kobresia myosuroides*. *New Phytologist* **142**:163-167.

BOOK CHAPTERS

133. Reganold JP, Andrews PK, Reeve JR, Carpenter-Boggs L, **Schadt CW**, Alldredge JR, Ross CF, Davies NM and JZ Zhou. (2013). Organic Versus Conventional Strawberry Agroecosystems. In: *Sustainable Soil Management* (D. Rooney, ed). CRC Press, Pg185-212.
134. Keller M, **Schadt CW** and AV Palumbo. (2008). Single Cell Genomics. In: *Accessing Uncultivated Microorganisms* (K. Zengler, ed) American Society for Microbiology Press, Washington DC.
135. Schmidt SK, Wilson K, Meyer AF, **Schadt CW**, Porter TM and JM Moncalvo. (2008) The Missing Fungi – New Insights from Culture-Independent Molecular Studies of Soil. In: *Accessing Uncultivated Microorganisms* (K. Zengler, ed) American Society for Microbiology Press, Washington DC.
136. Gentry TJ, **Schadt CW**, He Z, and J Zhou. (2007). Functional Gene Arrays for Microbial Community Analysis. In: *Manual of Environmental Microbiology* (Crawford et al., eds) American Society for Microbiology Press, Washington DC.
137. **Schadt CW** and J Zhou. Advances in Microarrays for Soil Microbial Community Analyses. (2006) In *Soil Biology Volume 8: Nucleic Acids and Proteins in Soil* (Nannipieri, P. & Smalla K., eds). Springer-Verlag, Pp189-203.
138. **Schadt CW**, Leibich J, Chong SC, Gentry TJ, He Z, Pan H, and J Zhou. (2005) Design and Use of Functional Gene Microarrays (FGAs) for the Characterization of Microbial Communities. In *Methods in Microbiology Volume 33: Microbial Imaging* (Savidge & Pothoulakis, eds). Academic Press, Pg331-368.

DISSERTATION

- Schadt CW**. (2002) Studies on the fungal associations of the alpine sedge *Kobresia myosuroides*. Ph.D. Dissertation, University of Colorado-Boulder.

OTHER PUBLICATIONS

- Schadt, CW** and AT Classen (2007) Book Review: Soil Microbiology, Ecology and Biochemistry.: EA Paul (ed). *Soil Science Society of America Journal*, **71**:1420
- Schadt, CW**. (2014). New found 'silence' on a southern, suburban, summer night. *Belle Rêve Literary Journal* **14**(3):54-56.

PATENTS

Pelletier DA, Weston DJ, **Schadt CW**, Doktycz MJ and GA Tuskan J. 2013. Plant Growth Promoting Rhizobacterium. Filed January 2013 (No. 13/747,995), Granted August 2015 (No. US9101144 B2).

INVITED AND CONTRIBUTED PRESENTATIONS & SEMINARS

Ecological Society of America Meeting, virtual, August 2021, Invited
Sun Yat-Sen University, July 2021, Invited
Ecological Society of America, Portland OR, August 2019, Invited
10th Soil Metagenomics Meeting, Argonne Illinois, October 2017, Invited
Ecological Society of America Meeting, Ft. Lauderdale FL, August 2016, Contributed
University of Texas-Austin, Dept. of Integrative Biology, April 2016, Invited
University of Tennessee, Dept. of Civil & Environmental Engineering, March 2016, Invited
University of Nebraska-Center for Biotechnology, Feb 2016, Invited
Phytobiomes Meeting, Washington DC, July 2015, Invited
International Union of Forest Research Organizations, Florence, Italy, June 2015, Invited
Mid-Atlantic States Mycological Conference, Keynote Speaker, April 2014, Invited.
University of Tennessee, Ecology & Evolutionary Biology Departmental Seminar, August 2013, Invited
American Chemical Society Meeting, September 2013, Invited
DOE Joint Genome Institute User Meeting, March 2013, Invited
Ecological Society of America, Annual Meeting, August 2012, Contributed
DOE Joint Genome Institute Seminar, Walnut Creek CA, January 2012, Invited
DOE Subsurface Biogeochemical Research Meeting, Washington DC, April 2011, Invited
Latin American Congress of Microbiology, Uruguay, Sept. 2010, Invited
Ecological Society of America, Annual Meeting, August 2010, Contributed
Ecological Society of America, Annual Meeting, August 2009, Invited
World of Coal Ash Meeting, Lexington Kentucky, May 2009, Contributed
Duke University, Nicholas School of the Environment Seminar, April 2009, Invited
Michigan State University, Dept. Seminar in Microbiology & Molecular Biology, Jan 2009, Invited
University of Tennessee, Departmental Seminar in Civil Engineering, Oct 2008, Invited
Ecological Society of America, Annual Meeting, Aug 2008, Contributed
Texas A&M University, Dept. Seminar in Rangeland Ecology & Management, April 2008, Invited
Fungal Environmental Sampling & Informatics Network, Copenhagen Denmark, Sept 2007, Invited
Ecological Society of America, Annual Meeting, Aug 2007, Invited
American Society of Microbiology General Meeting, May 2007, Invited
University of Tennessee, Departmental Seminar in Microbiology, Dec 2006, Invited
Long Term Ecological Research Network Meeting, Estes Park Colorado, Sept 2006, Invited

Univ. of Oklahoma, Plant & Microbial Sciences, Department Seminar, June 2006,
Invited

University of Puerto Rico-Mayaguez, Biology Departmental Seminar, May 2006, Invited

Appalachian State University, Biology Departmental Seminar, Oct 2005, Invited

Ecological Society of America, Annual Meeting, Aug 2005, Contributed

Mycological Society of America, Annual Meeting, Aug 2005, Contributed

Soil Ecology Society Meeting, May 2005 (Keynote Address for Day 3), Invited