Eoin L. Brodie

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Education and Training

B.S. Microbiology, University College Dublin, Ireland	1996
Ph.D. Microbial Ecology, University College Dublin, Ireland	2001
Postdoctoral, Microbial Ecology, University of California, Berkeley	2002-2004
Postdoctoral, Molecular Microbiology, Lawrence Berkeley National Laboratory	2004-2005
UC Berkeley/Berkeley Lab, Leadership Development Program, UC Center for Executive Education	2010

Research and Professional Experience

Program Co-Lead, Environmental and Biological System Sciences, LBNL	2014-present
Assistant Adjunct Professor, University of California, Berkeley	2012-present
Staff Scientist, Lawrence Berkeley National Lab	2009-present
Research Scientist, Lawrence Berkeley National Lab	2008-2009
Scientific Engineering Associate, Lawrence Berkeley National Lab	2005-2008
Postdoctoral Research Fellow, Lawrence Berkeley National Lab	2004-2005
Guest lecturer UC Berkeley (ESPM131, ESPM112)	2002-present
Postdoctoral Research Fellow, University of California, Berkeley	2002-2004
Enterprise Ireland Graduate Research Fellowship, University College Dublin	1996-2000

Honors and awards

Royal Netherlands Academy of Arts and Sciences, Visiting Professor	2014-2015
LBNL Outstanding Performance Award	2009
R&D 100 award for Berkeley Lab PhyloChip	2008
Wall Street Journal Technology Innovation Award (PhyloChip)	
- Winner Best New Technology (Environment Category)	2008
- Bronze Best New Technology (Overall)	2008
Pollution Engineering Magazine Number 1 New Technology for 2008 (PhyloChip)	2008
Promega Prize, Society for General Microbiology.	2001
Faculty of Science Graduate Symposium, UC Dublin.	2000
Enterprise Ireland Basic Research Award	1996-1999

Service to scholarly journals

Editorial Board: Microbiome	2012-present
Academic Editorial Board: Peer J.	2012-present
Associate Editor: Frontiers in Terrestrial Microbiology	2011-present

Reviewer for: Applied and Environmental Microbiology, Soil Biology and Biochemistry, Chemosphere, Journal of Microbiological Methods, Geomicrobiology Journal, Ecology Letters, Ecosystems, Molecular Ecology Notes, Fungal Ecology, Ground Water Monitoring and Remediation, Microbial Ecology, FEMS Microbiology Ecology, Environmental Microbiology, BMC Genomics, PloS One, Genome Research, Environmental Science and Technology, Journal of Geophysical Research, Environmental Science and Pollution Research, Journal of Proteome Research, ISME Journal, PNAS.

Other Professional activities

Scientific advisory board of Second Genome	2011-present
Current member of the 'greengenes' 16S rRNA database development team	2004-present
Co-developer of the Berkeley Lab PhyloChip and MycoChip	2004-present

Sessions convened at national meetings

"Integrating Microbial Processes Into Ecosystem Models of Carbon and Nitrogen Cycling", AGU Fall Meeting, San Francisco, December, 2012.

"Beyond the Black Box: Integrating Advanced Microbial Characterization Data with Subsurface Reactive Transport Models", Computational Methods in Water Resources, XVII, San Francisco, July 2008.

"From Black Box to Can of Worms: Advances in Molecular Analysis of Microbial Communities" American Geophysical Union Fall Meeting December, San Francisco, December 2007.

Proposal reviewing activities

DOE JGI Community Sequencing Program	2011, 2013
DOE EMSL user program	2011, 2012
Israel Science Foundation	2011
DOE Science Graduate Fellowship	2010
UK National Environmental Research Council	2010, 2013
NSF Geobiology and Low-Temperature Geochemistry Program	2009, 2013
USDA NRICGP Soil Processes program	2008
DOE Experimental Program to Stimulate Competitive Research	2007

Invited panelist

National Science Foundation: "Microscale Approaches to Macroscale Issues in Terrestrial Ecosystem Ecology", Washington DC, April 2007.

Department of Energy: "Carbon cycling and biosequestration", Rockville, MD, March 2008.

"Novel Ecosystems and Climate Change", in association with the Ecological Society of America Meeting in Albuquerque, NM, August 2009. Department of Energy, Climate Research Roadmap Workshop, Arlington, VA, May 2010.

Invited presentations

"Environmental microbiology research portfolio", UCB Superfund Research Program Retreat, San Jose, June 2014.

"Genome-enabled watershed simulation capability – GEWaSC", Plenary presentation at SBR/TES Joint PI meeting, Potomac, MD, May 2014.

""Challenges, advances and opportunities in modeling plant and microbial communities", presentation at DOE-BER Computational Challenges in Mechanistic Modeling of Terrestrial Ecosystems (CCMMTE) with David Weston, Germantown, MD, April 2014.

"Challenges, advances and opportunities in modeling microbial communities", presentation to DOE BER management, remote presentation, Germantown, MD, March 2014.

"Single colony home with great potential and easy access to nearby carbon sources". Advanced Light Source Science Café, Berkeley, CA, August 2013.

“Current topics in sequencing and the human microbiome”. Institute of Infectious Diseases and Molecular Medicine, University of Cape Town, South Africa, November 2012.

“Water Potential and the Life of a Soil Microbe”. Institute of Infectious Diseases and Molecular Medicine, University of Cape Town, South Africa, November 2012.

“Hope and Change: Water Potential and the Life of a Soil Microbe”. Department of Ecology & Evolutionary Biology, UC Irvine, CA November 2012.

“Challenges for Understanding and Modeling Carbon and Nutrient Cycling and Microbiological Processes in Terrestrial Ecosystems” Invited plenary session presentation at DOE Subsurface Biogeochemical Research program Annual PI meeting, Washington D.C. May, 2012.

“Mediterranean Grassland Soil Metagenome (MGSM): Enabling a systems view of soil carbon and nitrogen biogeochemistry under a changing climate” at DOE Joint Genome Institute, Community Sequencing Program, Plant-Soil-Microbe interaction workshop. January 2012, Walnut Creek, CA

“We know more about the movement of the celestial bodies than about the soil underfoot” at the Lawrence Berkeley National Laboratory, Life Sciences Division retreat, January 2012, Lafayette, CA.

Secrets of the Soil: Science at the Theater, November 2011, Berkeley Repertory Theater, Berkeley, CA.

“Distinct resuscitation patterns of soil microbes following early-season wet-up” at the 2011 Argonne Soils Workshop, October 2011, Indian Lakes, IL.

“Coordinating activities in climate related soils research at Berkeley Lab” at LBNL Earth Sciences Division Town Hall meeting, October 2011. Berkeley, CA.

“Top-down approaches to identifying conserved traits among soil microorganisms” at DOE Subsurface Biogeochemical Research program Annual PI meeting, April, 2011, Washington D.C.

“Understanding and predicting the response of soil microbial communities to global change”. DOE Genomic Sciences Contractor-Grantee Workshop, Session on Integrated Omics Approaches to Understand Environmental Processes February 2010, Washington D.C.

“Are There Predictable Soil Microbial Community Responses to Climate Change?" Subsurface Biosphere Initiative seminar series, College of Oceanic and Atmospheric Sciences, March 2009, Oregon State University, Corvallis, OR.

“PhyloChip: A high-density phylogenetic microarray for analysis of microbial community composition and activity”. Plant and Animal Genome XVII Conference, January 2009, San Diego, CA.

“Teasing apart a microbes life with help from the molecular toolbox”. Invited Plenary Presentation at NSF sponsored workshop “Microscale Approaches to Macroscale Issues in Terrestrial Ecosystem Ecology” April 2007, Washington DC.

"Molecular Tools in Environmental Microbiology". Invited presentation. April 2007, Adjuntas, PR. Advances in Environmental Remediation, Instituto Comunitario de Biodiversidad y Cultura Casa Pueblo de Adjuntas, Programa de Biotecnología Industrial, Universidad de Puerto Rico – Mayaguez.

"Characterization and monitoring of prokaryotic communities using phylogenetic high density DNA microarrays (PhyloChip)". April 2007, Adjuntas, PR. Advances in Environmental Remediation, Instituto Comunitario de Biodiversidad y Cultura Casa Pueblo de Adjuntas, Programa de Biotecnología Industrial, Universidad de Puerto Rico – Mayaguez.

"Microbial detection technologies using genetic signatures". March 2007, Berkeley, CA. ASTAR Advanced Judicial Institute on Nanotechnology, Synthetic Biology and Environmental Biotechnology Platform B Workshop.

"Case Study: Monitoring aerosols for intentional release of agents: Tularemia fatality". March 2007, Berkeley, CA. ASTAR Advanced Judicial Institute on Nanotechnology, Synthetic Biology and Environmental Biotechnology Platform B Workshop.

"Integration of the Omics, Bioinformatics and Biogeochemistry: A New Frontier for Environmental Biotechnology" at Battelle International Meeting on Remediation of Chlorinated and Recalcitrant Compounds, Monterey, CA May 2006.

"Advances in Bioremediation of Soils and Sediments Polluted with Metals and Radionuclides: Field Research on Bioremediation of Metals and Radionuclides" also at Battelle International Meeting on Remediation of Chlorinated and Recalcitrant Compounds, Monterey, CA May 2006.

"High Density Microarrays for Microbial Population Dynamics" presented to University of California, San Francisco, Department of Anesthesia and Perioperative Care and the Pulmonary and Critical Care Division, CA June 2006.

Short courses taught
Introduction to bioinformatics for metagenomics. Institute of Infectious Diseases and Molecular Medicine, University of Cape Town, South Africa, November 2012.

Membership in professional societies
Member of the American Society for Microbiology, American Geophysical Union, International Society for Microbial Ecology, International Society for Subsurface Microbiology.

Teaching activities
Guest lecturer at University of California, Berkeley, Department of Environmental Science Policy and Management and Microbial Biology Program (Soil Microbiology, ESPM131; Microbial Ecology, ESPM112)

Research supervision
Graduate students
Co-advisor: Heejung Cho, Ph.D. candidate, UCB-PMB (2014-present)
Co-advisor: Rebecca Daly, Ph.D. candidate, UCB-PMB (2006-deferred).
Committee: (Ph.D. thesis): Steven Blazewicz UCB-ESPM (graduated 2012). Erin Nuccio UCB-ESPM (graduated 2013). Chris Brown UCB-PMB (expected 2016)
Committee (quals): Manisha Anantharaman, Ph.D. candidate, UCB-ESPM (2009-). Steven Blazewicz UCB-ESPM (graduated 2012). Chris Brown UCB-PMB (expected 2016)

Ad hoc research mentor to UC Berkeley doctoral candidates Eric Dubinsky (2004-2007), Kristen DeAngelis (2006-2007), David Johnson (2005-2007), Christine Sun (2006-2007), Karelyn Cruz (2005-2009), Patrick Lee (2006-2008), Kimberlee West (2006-2011), Sarah Placella (2005-2011), Kelly Wrighton (2006-2010), Nhu Nguyen (2006-2011).

Research mentor to: Alex Hangsterfer (2008-2010) Scripps Institution of Oceanography; Brandon Briggs, Oregon State University (2008-2011), Ana Maldonado-Contreras (University of Puerto Rico, Rio-Piedres, 2008-2011), Filipa Godoy-Vitorino, (University of Puerto Rico, Rio-Piedres, 2008-2011), Eva Lloret-Sevilla (Spanish National Research Council, 2010-2012). George Wells, Stanford University (2008-2009).

Mentor for undergraduate fellows (Catherine Fontana, Albion College, MI, 2008; Christopher Lambert, University of Portland, 2009) through the DOE SURE GCEP summer fellowship program.

Mentor for graduate fellows (Catherine Fontana, Yale University) under DOE GREF graduate fellowship program.

Postdoctoral fellows

- Eric King (2014-present)
- Kateryna Zhalnina (2014-present)
- Javier Ceja Navarro (2010-present)
- Ulisses Nunes da Rocha (2011-2013). Currently a postdoc at VU Amsterdam.
- Mari Nyyssonen (2010-2013). Currently a Scientist at VTT Technical Research Center of Finland
- Nicholas Bouskill (2009-2012). Currently a Research Scientist at LBNL.
- Ulas Karaoz (2008-2013). Currently a Project Scientist at LBNL.
- Ruyang Han (2008-2013). Currently a research scientist at USDA.
- Holly Ganz (UC Berkeley, 2007-2011). Currently a research scientist at UC Davis.

Visiting faculty

Mentor for Faculty (Arturo Massol) from the University of Puerto Rico through the DOE/NSF FaST program (June-August 2006), Steven Wakelin (CSIRO Australia, July 2008), Bjorn Johansson, Fulbright Fellow (U Minho, Portugal).

Undergraduate students

Supervisor of UC Berkeley undergraduate student interns, Seung Baek (2003-2005), Calvin Myint (2005-2006), Byron Ma (2007-2008), Tiffany Kwak (2009-2011), Marina Volegova (2010-present). Sara Marie Komenan (LA Valley College – Transfer to Excellence Program, June – August 2012), Badamtseteg Jargalsaikhan (UC Berkeley, September 2012 to May 2013), Rozina Hossainkhil (UC Berkeley, September 2012 to May 2013), Dinh Ly (UC Berkeley, September 2012 to May 2013), Severin Ouedraogo (UC Berkeley September 2012 to May 2013), Yen Nguyen (UC Berkeley, September 2012 to date).

Mentor for undergraduate students from the University of Puerto Rico through the DOE/NSF FaST program (June-August 2006).
Mentor for undergraduate interns through the DOE CSEE and GREF programs (2006-present).

High school students

Mentor for summer high school interns through the DOE SULI and LBNL HSSRPP programs

and the (2006-2012).

High school teachers
Summer 2013: Marcel Degas (San Francisco International High School) summer internship at LBNL through the Industry Initiatives for Science and Math Education (IISME) program supported through the LBNL Center for Science and Engineering Education (CSEE).

Peer Reviewed Publications. (H-index 39: Dec 8th 2014; total citations 8448)

1. Beller, H. R., L. Yang, C. Varadharajan, R. Han, H. C. Lim, U. Karaoz, S. Molins, M. A. Marcus, **E. L. Brodie**, C. I. Steefel and P.S. Nico. 2014. Divergent aquifer biogeochemical systems converge on similar and unexpected Cr (VI) reduction products. Environmental Science & Technology **48**:10699-10706.
2. Berlemont, R., S. D. Allison, C. Weihe, Y. Lu, **E. L. Brodie**, J. B. Martiny, and A. C. Martiny. 2014. Cellulolytic potential under environmental changes in microbial communities from grassland litter. Frontiers in Microbiology **5**:639.
3. Closek, C. J., S. Sunagawa, M. K. DeSalvo, Y. M. Piceno, T. Z. DeSantis, **E. L. Brodie**, M. X. Weber, C. R. Voolstra, G. L. Andersen, and M. Medina. 2014. Coral transcriptome and bacterial community profiles reveal distinct Yellow Band Disease states in Orbicella faveolata. Isme J.
4. Vandehey, N. T., T. R. Northen, **E. L. Brodie**, and J. P. O'Neil. 2014. Noninvasive Mapping of Photosynthetic Heterogeneity in Biological Soil Crusts by Positron Emission Tomography: Carbon Fixation. Environmental Science & Technology Letters **1**:393-398.
5. Ganz HH, Turner WC, **Brodie EL**, Kusters M, Shi Y, et al. (2014) Interactions between Bacillus anthracis and Plants May Promote Anthrax Transmission. PLoS Negl Trop Dis 8(6): e2903. doi:10.1371/journal.pntd.0002903
6. Wells, G. F., C. H. Wu, Y. M. Piceno, B. Eggleston, **E. L. Brodie**, T. Z. DeSantis, G. L. Andersen, T. C. Hazen, C. A. Francis, and C. S. Criddle. 2014. Microbial biogeography across a full-scale wastewater treatment plant transect: evidence for immigration between coupled processes. Applied microbiology and biotechnology 98:4723-4736.
7. Ma, Y., R. Madupu, U. Karaoz, C. W. Nossa, L. Yang, S. Yooseph, P. S. Yachimski, **E. L. Brodie**, K. E. Nelson, and Z. Pei. 2014. Human Papillomavirus Community in Healthy Persons, Defined by Metagenomics Analysis of Human Microbiome Project Shotgun Sequencing Data Sets. Journal of virology 88:4786-4797.
8. Druhan, J. L., M. Bill, H. Lim, C. Wu, M. E. Conrad, K. H. Williams, D. J. DePaolo, and **E. L. Brodie**. 2014. A large column analog experiment of stable isotope variations during reactive transport: II. Carbon mass balance, microbial community structure and predation. Geochimica et Cosmochimica Acta 124:394-409.
9. Wakelin, S. A., B. I. Barratt, E. Gerard, A. L. Gregg, **E. L. Brodie**, G. L. Andersen, T. Z. DeSantis, J. Zhou, Z. He, and G. A. Kowalchuk. 2013. Shifts in the phylogenetic structure and functional capacity of soil microbial communities follow alteration of native tussock grassland ecosystems. Soil Biology and Biochemistry 57:675-682.
10. Rajeev, L., U. N. da Rocha, N. Klitgord, E. G. Luning, J. Fortney, S. D. Axen, P. M. Shih, N. J. Bouskill, B. P. Bowen, and C. A. Kerfeld, Ferran Garcia-Pichel, **E.L. Brodie**, T.R. Northen, and A. Mukhopadhyay. 2013. Dynamic cyanobacterial response to hydration and dehydration in a desert biological soil crust. The ISME journal.
11. Nyyssönen, M., H. M. Tran, U. Karaoz, C. Weihe, M. Z. Hadi, J. B. Martiny, A. C. Martiny, and **E. L. Brodie**. 2013. Coupled high-throughput functional screening and next generation sequencing for identification of plant polymer decomposing enzymes in metagenomic libraries. Frontiers in microbiology 4.

12. Close, H. G., S. R. Shah, A. E. Ingalls, A. F. Diefendorf, **E. L. Brodie**, R. L. Hansman, K. H. Freeman, L. I. Aluwihare, and A. Pearson. 2013. Export of submicron particulate organic matter to mesopelagic depth in an oligotrophic gyre. Proceedings of the National Academy of Sciences 110:12565-12570.
13. Ceja-Navarro, J. A., N. H. Nguyen, U. Karaoz, S. R. Gross, D. J. Herman, G. L. Andersen, T. D. Bruns, J. Pett-Ridge, M. Blackwell, and **E. L. Brodie**. 2013. Compartmentalized microbial composition, oxygen gradients and nitrogen fixation in the gut of Odontotaenius disjunctus. The ISME journal.
14. Briggs, B. R., M. Graw, **E. L. Brodie**, J.-J. Bahk, S.-H. Kim, J.-H. Hyun, J.-H. Kim, M. Torres, and F. S. Colwell. 2013b. Microbial distributions detected by an oligonucleotide microarray across geochemical zones associated with methane in marine sediments from the Ulleung Basin. Marine and Petroleum Geology 47:147-154.
15. Briggs, B. R., **E. L. Brodie**, L. M. Tom, H. Dong, H. Jiang, Q. Huang, S. Wang, W. Hou, G. Wu, and L. Huang. 2013a. Seasonal patterns in microbial communities inhabiting the hot springs of Tengchong, Yunnan Province, China. Environmental microbiology.
16. Druhan, J. L., M. Bill, H. Lim, C. Wu, M. E. Conrad, K. H. Williams, D. J. DePaolo, and **E. L. Brodie.** (2013). A large column analog experiment of stable isotope variations during reactive transport: II. Carbon mass balance, microbial community structure and predation. Geochimica et Cosmochimica Acta. In press.
17. Nyyssönen, M., Tran, H. M., Karaoz, U., Weihe, C., Hadi, M. Z., Martiny, J. B., Martiny, A.C. and **Brodie, E.L**. (2013). Coupled high-throughput functional screening and next generation sequencing for identification of plant polymer decomposing enzymes in metagenomic libraries. *Frontiers in Microbiology*, *4*.
18. Lau S.C., Zhang R, **Brodie E.L.**, Piceno Y.M., Andersen G, Liu W.T. (2013). Biogeography of bacterioplankton in the tropical seawaters of Singapore. *FEMS Microbiol. Ecol.* 84(2):259-269.
19. Rajeev L, da Rocha UN, Klitgord N, Luning EG, Fortney J, Axen SD, Shih PM, Bouskill NJ, Bowen BP, Kerfeld CA, Garcia-Pichel, F., **Brodie, E. L.**, Northen, T. R. Mukhopadhyay, A. (2013). Dynamic cyanobacterial response to hydration and dehydration in a desert biological soil crust. *ISME J.*
20. Beller, H. R., Han, R., Karaoz, U., Lim, H. C., & **Brodie, E. L.** (2013). Genomic and physiological characterization of the chromate-reducing, aquifer-derived firmicute Pelosinus sp. strain HCF1. *Applied and Environmental Microbiology*, *79*(1), 63–73.
21. Lynch, S. V, Goldfarb, K. C., Wild, Y. K., Kong, W., De Lisle, R. C., & **Brodie, E. L**. (2013). Cystic fibrosis transmembrane conductance regulator knockout mice exhibit aberrant gastrointestinal microbiota. *Gut Microbes*, *4*(1), 3–9.
22. Bouskill, NJ, Lim, HC, Borglin, S, Salve, R, Wood, T, Silver, WL, **Brodie, EL**. (2013) Pre-exposure to drought increases the resistance of tropical forest soil bacterial communities to extended drought. *ISME J.*, 7:384–394.
23. Ceja-Navarro, J. A., **Brodie, E. L.**, & Vega, F. E. (2012). A technique to dissect the alimentary canal of the coffee berry borer (Hypothenemus hampei), with isolation of internal microorganisms. *Journal of Entomological and Acarological Research*, *44*(3), e21.
24. Bouskill, NJ, Tang, J, Riley, WJ, **Brodie, EL**. (2012) Trait based representation of biological nitrification: model development, testing and predicted community composition. Frontiers in Aquatic Microbiology. 3: 364.
25. Brisson, V. L., K. A. West, P. K. H. Lee, S. G. Tringe, **E. L. Brodie**, and L. Alvarez-Cohen. 2012. Metagenomic analysis of a stable trichloroethene-degrading microbial community. Isme J.
26. Ganz, H., U. Karaoz, W. Getz, W. Versfeld, and **E.L. Brodie**. 2012. Diversity and structure of soil bacterial communities associated with vultures in an African savanna. Ecosphere 3 (6): 47.

27. Hayden, H. L., P. M. Mele, D. S. Bougoure, C. Y. Allan, S. Norng, Y. M. Piceno, **E. L. Brodie**, T. Z. DeSantis, G. L. Andersen, and A. L. Williams. 2012. Changes in the microbial community structure of bacteria, archaea and fungi in response to elevated CO2 and warming in an Australian native grassland soil. Environmental Microbiology.
28. Placella, S. A., **E. L. Brodie**, and M. K. Firestone. 2012. Rainfall-induced carbon dioxide pulses result from sequential resuscitation of phylogenetically clustered microbial groups. Proceedings of the National Academy of Sciences 109:10931-10936.
29. Reith, F., J. Brugger, C. M. Zammit, A. L. Gregg, K. C. Goldfarb, G. L. Andersen, T. Z. DeSantis, Y. M. Piceno, **E. L. Brodie**, Z. Lu, Z. He, J. Zhou and S.A. Wakelin. 2012. Influence of geogenic factors on microbial communities in metallogenic Australian soils. Isme J.
30. Russo, S. E., R. Legge, K. A. Weber, **E. L. Brodie**, K. C. Goldfarb, A. K. Benson, and S. Tan. 2012. Bacterial community structure of contrasting soils underlying Bornean rain forests: Inferences from microarray and next-generation sequencing methods. Soil Biology and Biochemistry.
31. Wakelin, S. A., R. R. Anand, F. Reith, A. L. Gregg, R. R. P. Noble, K. C. Goldfarb, G. L. Andersen, T. Z. DeSantis, Y. M. Piceno, and **E. L. Brodie**. 2012. Bacterial communities associated with a mineral weathering profile at a sulphidic mine tailings dump in arid Western Australia. Fems Microbiology Ecology.
32. Wakelin, S. A., B. I. P. Barratt, E. Gerard, A. L. Gregg, **E. L. Brodie**, G. L. Andersen, T. Z. DeSantis, J. Zhou, Z. He, and G. A. Kowalchuk. 2012. Shifts in the phylogenetic structure and functional capacity of soil microbial communities follow alteration of native tussock grassland ecosystems. Soil Biology and Biochemistry.

33. Godoy-Vitorino, F. Leal, SJ., Diaz, WA, Rosales, J., Goldfarb, KC, Garcia-Amado, MA, Michelangeli, F., **Brodie, EL**, Domínguez-Bello, MG. 2012. Differences in crop bacterial community structure between hoatzins from different geographical locations, Res Microbiol, 10.1016/j.resmic.2012.01.001.

34. Sridevi G, Minocha R, Turlapati SA, Goldfarb KC, **Brodie EL**, Tisa LS, Minocha SC. 2012.Soil bacterial communities of a calcium-supplemented and a reference watershed at the Hubbard Brook Experimental Forest (HBEF), New Hampshire, USA. FEMS Microbiol Ecol. 79:728-40. PubMed PMID:22098093.

35. Wakelin SA, Anand RR, Reith F, Gregg AL, Noble RR, Goldfarb KC, Andersen GL, Desantis TZ, Piceno YM, **Brodie EL**. Bacterial communities associated with a mineral weathering profile at a sulphidic mine tailings dump in arid Western Australia. 2012. FEMS Microbiol Ecol. 79:298-311. PubMed PMID:22092956.

36. Lee PK, Warnecke F, **Brodie EL**, Macbeth TW, Conrad ME, Andersen GL, Alvarez-Cohen L. 2012. Phylogenetic Microarray Analysis of a Microbial Community Performing Reductive Dechlorination at a TCE-Contaminated Site. Environ Sci Technol. 46:1044-54. PubMed PMID:22091783.

37. Mayali X, Weber PK, **Brodie EL**, Mabery S, Hoeprich PD, Pett-Ridge J. High-throughput isotopic analysis of RNA microarrays to quantify microbial resource use. ISME J. 2011 Dec 8; PubMed PMID:22158395.

38. Treseder, KK, Balser, TC, Bradford, MA, **Brodie, EL**, Dubinsky, EA, Eviner, VT, Hofmockel, KS, Lennon, JT, Levine, UY, MacGregor, BJ, Pett-Ridge, J, Waldrop, M. (2011) Integrating microbial ecology into ecosystem models: challenges and priorities. Biogeochemistry: 1-12. DOI: 10.1007/s10533-011-9636-5

39. Paszczynski AJ, Paidisetti R, Johnson AK, Crawford RL, Colwell FS, Green T, Delwiche M, Lee H, Newby D, **Brodie EL**, Conrad M. Proteomic and targeted qPCR analyses of subsurface microbial communities for presence of methane monooxygenase. Biodegradation. 2011 Nov; 22 (6) :1045-59. PubMed PMID:21360114.

40. **Brodie EL**, Joyner DC, Faybishenko B, Conrad ME, Rios-Velazquez C, Malave J, Martinez R, Mork B, Willett A, Koenigsberg S, Herman DJ, Firestone MK, Hazen TC. Microbial community response to addition of polylactate compounds to stimulate hexavalent chromium reduction in groundwater. Chemosphere. 2011 Oct; 85 (4) :660-5. PubMed PMID:21872904.

41. Briggs BR, Pohlman JW, Torres M, Riedel M, **Brodie EL**, Colwell FS. Macroscopic biofilms in fracture-dominated sediment that anaerobically oxidize methane. Appl Environ Microbiol. 2011 Oct; 77 (19) :6780-7. PubMed PMID:21821755; PubMed Central PMCID: PMC3187087.

42. Godoy-Vitorino F, Goldfarb KC, Karaoz U, Leal S, Garcia-Amado MA, Hugenholtz P, Tringe SG, **Brodie EL**, Dominguez-Bello MG. Comparative analyses of foregut and hindgut bacterial communities in hoatzins and cows. ISME J. 2011 Sep 22; PubMed PMID:21938024.

43. Banning NC, Gleeson DB, Grigg AH, Grant CD, Andersen GL, **Brodie EL**, Murphy DV. Soil microbial community successional patterns during forest ecosystem restoration. Appl Environ Microbiol. 2011 Sep; 77 (17) :6158-64. PubMed PMID:21724890; PubMed Central PMCID: PMC3165429.

44. DeAngelis KM, Wu CH, Beller HR, **Brodie EL**, Chakraborty R, DeSantis TZ, Fortney JL, Hazen TC, Osman SR, Singer ME, Tom LM, Andersen GL. PCR amplification-independent methods for detection of microbial communities by the high-density microarray PhyloChip. Appl Environ Microbiol. 2011 Sep; 77 (18) :6313-22. PubMed PMID:21764955; PubMed Central PMCID: PMC3187179.

45. Lee PK, Cheng D, Hu P, West KA, Dick GJ, **Brodie EL**, Andersen GL, Zinder SH, He J, Alvarez-Cohen L. Comparative genomics of two newly isolated Dehalococcoides strains and an enrichment using a genus microarray. ISME J. 2011 Jun; 5 (6) :1014-24. PubMed PMID:21228894; PubMed Central PMCID: PMC3131851.

46. DeSantis TZ, Keller K, Karaoz U, Alekseyenko AV, Singh NN, **Brodie EL**, Pei Z, Andersen GL, Larsen N. Simrank: Rapid and sensitive general-purpose k-mer search tool. BMC Ecol. 2011 Apr 27; 11:11. PubMed PMID:21524302; PubMed Central PMCID: PMC3097142.

47. Maldonado-Contreras A, Goldfarb KC, Godoy-Vitorino F, Karaoz U, Contreras M, Blaser MJ, **Brodie EL**, Dominguez-Bello MG. Structure of the human gastric bacterial community in relation to Helicobacter pylori status. ISME J. 2011 Apr; 5 (4) :574-9. PubMed PMID:20927139; PubMed Central PMCID: PMC3105737.

48. Huang YJ, Nelson CE, **Brodie EL**, Desantis TZ, Baek MS, Liu J, Woyke T, Allgaier M, Bristow J, Wiener-Kronish JP, Sutherland ER, King TS, Icitovic N, Martin RJ, Calhoun WJ, Castro M, Denlinger LC, Dimango E, Kraft M, Peters SP, Wasserman SI, Wechsler ME, Boushey HA, Lynch SV, National Heart, Lung, and Blood Institute's Asthma Clinical Research Network. Airway microbiota and bronchial hyperresponsiveness in patients with suboptimally controlled asthma. J Allergy Clin Immunol. 2011 Feb; 127 (2) :372-381.e1-3. PubMed PMID:21194740; PubMed Central PMCID: PMC3037020.

49. Goldfarb KC, Karaoz U, Hanson CA, Santee CA, Bradford MA, Treseder KK, Wallenstein MD, **Brodie EL**. Differential growth responses of soil bacterial taxa to carbon substrates of

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Book chapters

1. Nyyssönen, M., H. and **E. L. Brodie**. (2014). Chapter 2. Uncovering the Metabolic Diversity of Soil Microbial Communities Through Functional Metagenomics. In *Trends in Soil Microbiology*, Eds (DP. Singh and HB, Singh), Studium Press LLC, Houston, TX.

2. **Brodie, E.L.** and S.V. Lynch. Phyloarrays. 2013. In The Human Microbiota: How Microbial Communities Affect Health and Disease. Fredricks, D.N. (Ed). Chapter 3, pp75. Wiley Blackwell (NY).

3. **Brodie, E.L.** Phylogenetic microarrays (PhyloChips) for analysis of complex microbial communities. In: Handbook of Molecular Microbial Ecology I: Metagenomics and Complementary Approaches. Frans J. De Bruijn (Ed). Wiley-Blackwell, Hoboken, NJ.
4. Andersen, G.L., He, Z. DeSantis, T.Z., **Brodie, E.L.**, and J. Zhou. 2010. The Use of Microarrays in Microbial Ecology. Chapter 5 in Environmental Molecular Microbiology, Wen-Tso Liu and Janet K. Jansson (Eds.) Caister Academic Press.
5. Andersen, G. L., Piceno, Y. M., DeSantis, T. Z., and **E. L. Brodie.** 2006. What DNA Microarrays Can Tell Us About Bacterial Diversity: A New Light on an Old Question. In M. J. Bailey (ed.), Phyllosphere Microbiology, Oxford University Press, Oxford, U.K.

Patents and invention disclosures

1. JIB-2927. Array for Detecting Antibiotic Resistance.
2. IB-2229P4. Methods And Systems For Phylogenetic Analysis. A Persistent and Diverse Airway Microbiota Present During Chronic Obstructive Pulmonary Disease Exacerbations.
3. Chip-SIP: Quantification Of Nucleic Acid Stable Isotope Labeling With Biopolymer Microarrays And Secondary Ionization Mass Spectrometry. US Pat. App 13/023,468
4. Using Phylogenetic Probes for Quantification of Stable Isotope Labeling and Microbial Community Analysis. US Pat. App 13/023,538.

Current funding ($ per year)

<u>ACTIVE</u>

LBNL – 103024-001 10/01/2014-9/30/2017 1.5 mo
DOE LBNL-LDRD $600k/year
Project title: Harnessing the soil microbiome for food and fuel security
Project goal: Under the Berkeley Lab Microbes-to-Biomes initiative, this work targets improved understanding and manipulation of plant nutrient limitation by considering interacting environmental constraints (mineralogy, geochemistry, climate) and microbial adaptive strategies.
Role in project: Co-PI

LBNL Technology Innovation Award 03/01/2014-02/28/2015 1.0 mo
DOE LBNL-TIA $89,218
Project title: Rapid pathogen and antibiotic resistance diagnosis
Project goal: Our overarching goal is to produce a diagnostic tool for diagnosing a bacterial infection and its potential antibiotic susceptibility/resistance phenotype within a typical day shift in a clinical microbiology laboratory. We have developed a customized and targeted resequencing assay using Affymetrix GeneChip microarray platform which is a single test that can be performed directly on a clinical specimen to simultaneously detect and determine the DNA sequence of a wide range of genes characterizing 45 pathogenic organisms and their antimicrobial resistance determinants within 8 hours. This work is focused on technology transfer to a CLIA facility at UCSF.
Role in project: PI

DE-AC02-05CH11231 (Hubbard) 10/01/2013-9/30/2018 5.0 mo
DOE/BER Subsurface Biogeochemical Research Scientific Focus Area $6.8M/year
Project title: Genome-enabled Watershed Simulation Capability (GEWaSC)
*Project goal: Development of a **G**enome-**E**nabled **Wa**tershed **S**imulation **C**apability (**GEWaSC)**, which will provide a predictive framework for understanding how genomic information stored in a subsurface microbiome affects biogeochemical watershed functioning, how watershed-scale processes affect microbial functioning, and how these interactions co-evolve. I co-lead the GEWaSC modeling component of this large effort.*
Role in project: CI (Component Lead)

DE-SC0010570 (Firestone) 09/01/2013-08/31/2016 1.2 mo
DOE/BER Genomic Sciences $210k/year
Project title: *Mapping soil carbon from cradle to grave: drafting a molecular blueprint for C transformation from roots to stabilized soil organic C.*
Project goal: Our primary objective is to determine how organic carbon decomposition and stabilization processes in soil are impacted by the interactions between plant roots and the soil microbial community (bacteria, archaea, fungi, microfauna).
Role in project: Co-PI

UH2/UH3CA140233(Pei, Nelson) (Sandy Recovery) 08/01/2013-07/31/2015 0.96 mo.
Funding agency: NIH/NCI $1,378k
Project title: Foregut microbiome in development of esophageal adenocarcinoma
Major goal: The goal is to demonstrate that there is a change in the foregut microbiome at various stages of reflux disorder developing toward esophageal adenocarcinoma.
Role in project: CI

DE-AC02-05CH11231 10/01/2012-09/31/15 1.0 mo.
DOE/BER-Genome Sciences $356k/year
Project title: A Systems Biology Approach to Energy Flow Biofuel Producing Microbial Communities.
Major goal: The objective of this research is to develop an integrated analysis of energy flow in complex microbial communities for the purpose of understanding conditions leading to optimal biofuel production. We will combine biogeochemical, stable isotope probing, metatranscriptomic and computational approaches, with the aim of understanding nutrient cycling and biofuel (specifically, H2) production in microbial communities.
Role in project: Co-PI

Current Non-Monetary Research Awards

DOE Environmental Molecular Sciences Laboratory Proposal #48434 (Brodie-PI). September 2014-present.

- *Identifying the key organisms, pathways and locations of lignocellulosic biomass transformation and hydrogen production in wood-feeding Passalid beetles*

Joint DOE Environmental Molecular Sciences Laboratory (EMSL) and Joint Genome Institute Proposal #48086 (Brodie co-PI). September 2013-present

- *Mapping soil carbon from cradle to grave: using comparative transcriptomics, proteomics and metabolite analysis to identify the microbial blueprint for root-enhanced decomposition of organic matter*. Mass spectrometer allocation at EMSL for proteomics and Illumina sequencing at JGI for metatranscriptomics.

DOE-Joint Genome Institute, Community Sequencing Program #653. (Brodie PI). September 2011-present.

- *Mediterranean Grassland Soil Metagenome (MGSM): Enabling a systems view of soil carbon and nitrogen biogeochemistry under a changing climate*. 1Tb metagenome and isolate sequencing.