

## Curriculum Vitae

### Personal data

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**Name** Vincent J. Deneff  
**Office address** Department of Ecology and Evolutionary Biology  
 4060 Biological Sciences Building  
 University of Michigan  
 1105 N. University  
 Ann Arbor, MI 48109  
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### Education/Employment

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2012 – present: **Assistant Professor**, Ecology and Evolutionary Biology, University of Michigan, Ann Arbor, MI, USA.  
 2005 – 2011: **Post-doctoral researcher**, Banfield Laboratory, University of California Berkeley, USA.  
 2001 – 2005: **Ph.D.** in Applied Biological Sciences, LabMET, Universiteit Gent, Belgium.  
 2000 – 2005: **Visiting Scholar** at the Center for Microbial Ecology, Michigan State University, USA.  
 1996 – 2001: **Bachelor/Master** Bio-engineering, magna cum laude, University of Leuven, Belgium.  
 2008: **Teaching assistant**, NSF International Antarctic Biology Course, McMurdo Station, Antarctica.  
 2003: **Advanced Bacterial Genetics Summer Course** (Cold Spring Harbor Laboratory, NY, USA).  
 2002: **Microbial Diversity Summer Course** (Marine Biological Laboratory, Woods Hole, MA, USA).

### Publications

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\* Mentored undergraduate student author  
 \*\* Mentored graduate student author  
 \*\*\* Mentored post-doctoral researcher author  
 \*\*\*\* Mentored research technician author

#### **In review:**

Props, R.\*\*, Boon, N., **V.J. Deneff**, Strain-resolved analysis of a ubiquitous and abundant freshwater bacterial lineage shows larger genomic divergence across nutrient than temperature gradients. (Appl. Env. Microbiol., revised manuscript submitted January 18, 2020) [biorXiv](#)  
 Schmidt, M.L.\*\*, Biddanda, B.A., Weinke, A.D., Chiang, E.\*, Januska, F., Props, R., **V.J. Deneff**. Microhabitats shape diversity-productivity relationships in freshwater bacterial communities. (FEMS Microbiol. Ecol., in revision) [biorXiv](#)  
 Evans, J.T., and **V.J. Deneff**. To dereplicate or not to dereplicate? (mSphere, in revision) [biorXiv](#)

#### **Published:**

Jackrel, S.L.\*\*\*, K. Schmidt\*, B.J. Cardinale, and **V.J. Deneff**. 2020. Microbiomes Reduce their Host's Sensitivity to Interspecific Interactions. [mBio 11:e02657-19](#) [**mBio Editor's pick**].  
 Schulz, F., Roux, S., Paez-Espino, D., Jungbluth, S., Walsh, D., **Deneff, V.J.**, McMahon, K.D., Konstantinidis, K.T., Eloie-Fadrosh, E.A., Kyrpides, N., and Woyke, T. 2020. Giant virus diversity and host interactions through global metagenomics. [Nature](#) <https://doi.org/10.1038/s41586-020-1957-x>  
 Rubbens, P., Schmidt, M.L.\*\*\*, Props, R.\*\*, Biddanda, B.A., Boon, N., Waegeman, W., **V.J. Deneff**. 2019. Randomized lasso associates freshwater lake-system specific bacterial taxa with heterotrophic production through flow cytometry. [mSystems 4 \(5\) e00093-19](#). (Rubbens and Schmidt contributed equally)  
 Jackrel, S.L.\*\*\*, White, J., Buffin, K.\*, Hayden, K.\*, Sarnelle, O., **V.J. Deneff**. 2019. Genome Evolution and Host Microbiome Shifts Correspond with Intraspecific Niche Divergence within Harmful Algal Bloom-Forming *Microcystis aeruginosa*. [Mol Ecol, 28 \(17\)](#). [**Mol Ecol blog spotlight article**]  
 Props, R.\*\*, Monsieurs P., Vandamme, P., Leys, N., **Deneff, V.J.**, Boon, N. 2019. Gene Expansion and Positive Selection as Bacterial Adaptations to Oligotrophic Conditions. [mSphere 4 \(1\), e00011-19](#)

- Jackrel, S.L.<sup>\*\*\*</sup>, Narwani, A., Bentlage, B., Levine, R.B., Hietala, D.C., Savage, P.E., Oakley, T.H., **Deneff, V.J.**, B.J. Cardinale. 2018. Ecological engineering helps maximize function in algal bio-oil production. *Appl Environ Microbiol* 00953-18. [**AEM spotlight article**]
- Chiang, E.\* , Schmidt, M.L.<sup>\*\*</sup>, Berry, M.A.<sup>\*\*\*\*</sup>, Biddanda, B.A., Burtner, A.M., Johengen, T.H., Palladino, D., **V.J. Deneff**. 2018. Verrucomicrobia are prevalent in north-temperate freshwater lakes and display class-level preferences between lake habitats. *PLoS ONE* 13(3): e0195112.
- Deneff, V.J.** 2018. Peering into the Genetic Makeup of Natural Microbial Populations Using Metagenomics. Martin F. Polz and Om P. Rajora (eds.), *Population Genomics: Microorganisms* (Springer). [https://doi.org/10.1007/13836\\_2018\\_14](https://doi.org/10.1007/13836_2018_14)
- Props, R.<sup>\*\*</sup>, M.L. Schmidt<sup>\*\*</sup>, J. Heyse, H.A. Vanderploeg, N. Boon, and **V.J. Deneff**. 2018. Flow cytometric monitoring of bacterioplankton phenotypic diversity predicts high population- specific feeding rates by invasive dreissenid mussels. *Environ Microbiol* 20 (2), 521-534.
- Deneff V.J.**, Carrick H.J., Cavaletto J., Chiang E.\* , Johengen T.H., Vanderploeg H.A. 2017. Lake bacterial assemblage composition is sensitive to biological disturbance caused by an invasive filter feeder. *mSphere* 2 (3), e00189-17.
- Meyer, K.A., Davis, T.W., Watson, S.B., **Deneff, V.J.**, Berry, M.A.<sup>\*\*\*\*</sup>, G.J. Dick. 2017. Genome sequences of lower Great Lakes *Microcystis* sp. reveal strain-specific genes that are present and expressed in western Lake Erie blooms. *PLoS One* 12 (10), e0183859.
- Berry, M.A.<sup>\*\*\*\*</sup>, J.D. White, T.W. Davis, S. Jain, T.H. Johengen, G.J. Dick, O. Sarnelle and **V.J Deneff**. 2017. Are oligotypes meaningful ecological and phylogenetic units? A case study of *Microcystis* in freshwater lakes. *Front Microbiol*, 8: 365.
- Berry, M.A.<sup>\*\*\*\*</sup>, T.W. Davis, R.M. Cory, M.B. Duhaime, T.H. Johengen, G.W. Kling, J.A. Marino, P.A. Den Uyl, D. Gossiaux, G.J. Dick, **V.J. Deneff**. 2017. Cyanobacterial harmful algal blooms are a biological disturbance to western Lake Erie bacterial communities. *Environ Microbiol*, 19 (3), 1149-1162.
- CC Wu, S Ghosh, K Martin, AJ Pinto, **VJ Deneff**, TM Olson, N Love. (2017). The microbial colonization of activated carbon block point-of-use (PoU) filters with and without chlorinated phenol disinfection byproducts. *Environ Sci: Water Res Technol* 3, 830-843.
- Paez-Espino, D., Chen I.A., Palaniappan, K., Ratner, A., Chu, K., Szeto, E., Pillay, M., Huang, J., Markowitz, V.M. Nielsen, T., Huntemann, M., Reddy, TBK, Pavlopoulos, G.A., Sullivan, M.B., Campbell, B.J., Chen, F. McMahon, K., Hallam, S.J., **Deneff, V.J.**, Cavicchioli, R., Caffrey, S.M., Streit, W.R., Webster, J., Handley, K.M., Salekdeh, G.H., Tsessmetzis, N., Setubal, J.C., Pope, P.B., Liu, W., Rivers, A.R., Ivanova, N.N., Kyrpides, N.C. (2017). IMG/VR: a database of cultured and uncultured DNA Viruses and retroviruses. *Nucl Acids Res* 45: D457-D465.
- Fujimoto, M.<sup>\*\*\*</sup>, Cavaletto, J., Liebig, J.R., McCarthy, A.<sup>\*\*\*\*</sup>, Vanderploeg, H.A., and **V.J. Deneff**. (2016). Spatiotemporal distribution of bacterial populations along a freshwater estuary to pelagic gradient in Lake Michigan. *J Great Lakes Res* 42: 1036-1048.
- Deneff, V.J.**, M. Fujimoto<sup>\*\*\*</sup>, M.A. Berry<sup>\*\*\*\*</sup>, and M.L. Schmidt<sup>\*\*</sup>. (2016). Seasonal succession leads to habitat-dependent differentiation in ribosomal RNA:DNA ratios among freshwater lake bacteria. *Front Microbiol* 7: 606.
- Cory, R.M., Davis, T.W., Dick, G.J., Johengen, T., **Deneff, V.J.**, Berry, M.A.<sup>\*\*\*\*</sup>, Page, S.E., Watson, S.B., Yuhas, K. and G.W. Kling. (2016). Seasonal dynamics in dissolved organic matter, hydrogen peroxide, and cyanobacterial blooms in Lake Erie. *Front. Mar. Sci.* 3: 54.
- Deneff, V.J.**, R.S. Mueller, E. Chiang\*, J.R. Liebig, H.A. Vanderploeg. (2016). *Chloroflexi* CL500-11 populations that predominate deep lake hypolimnion bacterioplankton rely on nitrogen-rich DOM metabolism and C1 compound oxidation. *Appl Env Microbiol* 82(5):1423-32 [**AEM spotlight article**]
- Schmidt, M.L.<sup>\*\*</sup>, J.D. White, and **V.J. Deneff** (2016). Phylogenetic conservation of freshwater lake habitat preference varies between abundant bacterioplankton phyla. *Environ Microbiol* 18(4): 1212–1226.
- Shetty, A.R., de Gannes, V., Obi, C.C., Lucas, S., Lapidus, A., Cheng, J.F., Goodwin, L.A., Pitluck, S., Peters, L., Mikhailova, N. and Teshima, H., Han, C., Tapia, R., Land, M., Hauser, L.J., Kyrpides, N., Ivanova, N., Pagani, I., Chain, P.S.G., **Deneff, V.J.**, Woyke, T., and Hickey, W.J. (2015). Complete genome sequence of the phenanthrene-degrading soil bacterium *Delftia acidovorans* Cs1-4. *Stand Genomic Sci* 10(1):1-10.
- McCarthy, A.<sup>\*\*\*\*</sup>, Chiang\*, E., Schmidt, M.L.<sup>\*\*</sup>, and **Deneff, V.J.** (2015). RNA preservation agents and nucleic acid extraction method bias perceived bacterial community composition. *PLoS One* 10 (3), e0121659.

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- Denef V.J.**, J.F. Banfield. 2012. *In situ* evolutionary rate measurements show ecological success of recently emerged bacterial hybrids. [Science 336\(6080\):462-6](#). [recommended as being of special significance in its field by F1000 Faculty <http://f1000.com/717960409>]
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- Belnap, C.P., C. Pan, **V.J. Denef**, N.C. VerBerkmoes, N.F. Samatova, R.L. Hettich, J.F. Banfield. 2011. Quantitative proteomic analyses of the response of acidophilic microbial communities to different pH conditions. [ISME J. 5\(7\):1152-61](#).
- Morowitz, M.J., **V.J. Denef**, E. Costello, B. Thomas, D.A. Relman, J.F. Banfield. 2011. Strain-resolved community genomic analysis of gut microbial colonization in a premature infant. [Proc Natl Acad Sci U S A 108\(3\): 1128–1133](#).
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- Mueller, R.S, **V.J. Denef**, L.H. Kalnejais, K.B. Suttle, B.C. Thomas, P. Wilmes, R. Smith, D.K. Nordstrom, M.B. Shah, N.C. VerBerkmoes, R.L. Hettich, and J.F. Banfield. 2010. Ecological distribution and population physiology defined by proteomics in a natural microbial community. [Molecular Systems Biology 6:374](#).
- Denef, V.J.**, Mueller, R.S., and Banfield J.F. 2010. Winogradsky review: AMD biofilms: using model communities to study microbial evolution and ecological complexity in nature. [ISME J. 4\(5\):599-610](#).
- Denef, V.J.**, L. Kalnejais, P., Mueller, R.S., Wilmes, B. Baker, Brian C. Thomas, N.C. VerBerkmoes, R.L. Hettich, and J.F. Banfield. 2010. Proteogenomic basis for ecological divergence of closely related bacteria in natural acidophilic microbial communities. [Proc Natl Acad Sci U S A 107\(6\):2383-90](#).
- Parnell, J.J., **Denef, V.J.**, Park, J., Tsoi, T.V., and Tiedje, J.M. 2010. Environmentally Relevant Parameters Affecting PCB Degradation: Carbon Source- and Growth Phase-Mitigated Effects of the Expression of the Biphenyl Pathway and Associated Genes in *B. xenovorans* LB400. [Biodegradation 21\(1\):147-56](#).
- Goltsman, D.S.A., **V.J. Denef**, S.W. Singer, N.C. VerBerkmoes, M. Lefsrud, R. Muller, G.J. Dick, C. Sun, K. Wheeler, A. Zemla, B.J. Baker, L. Hauser, M. Land, M.B. Shah, M.P. Thelen, R.L. Hettich, and J.F. Banfield. 2009. Community genomic and proteomic analysis of chemoautotrophic, iron-oxidizing "L. rubarum" and *L. ferrodiazotrophum* in AMD biofilms. [Appl. Environ. Microbiol. 75\(13\): 4599-4615](#).
- VerBerkmoes, N.C., **V.J. Denef**, R.L. Hettich, and J.F. Banfield. 2009. Community proteomic functional analysis of natural microbial communities. [Nat. Rev. Microbiol. 7, 196-205](#).
- Wilmes, P., S.L. Simmons, **V.J. Denef**, and J.F. Banfield. 2009. The dynamic genetic repertoire of microbial communities. [FEMS Microbiol Rev 33\(1\), 109-132](#).
- Denef, V.J.**, N.C. VerBerkmoes, M.B. Shah, P. Abraham, M. Lefsrud, R.L. Hettich, and J.F. Banfield. 2009. Proteomics-inferred genome typing (PIGT) demonstrates inter-population recombination as a strategy for environmental adaptation. [Environ Microbiol. 11\(2\), 313-325](#).
- Simmons, S., G. DiBartolo, **V.J. Denef**, D.S.A. Goltsman, M.P. Thelen, and J.F. Banfield. 2008 Population genomic analysis of strain variation in *Leptospirillum* group II bacteria involved in AMD formation. [PLoS Biol. 6\(7\): e177](#).
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- Lo, I., **V.J. Denef**, N.C. Verberkmoes, M.B. Shah, D. Goltsman, G. DiBartolo, G.W. Tyson, E.E. Allen, R.J. Ram, J.C. Detter, P.M. Richardson, M.P. Thelen, R.L. Hettich, and J.F. Banfield. 2007. Strain-resolved community proteomics reveals that recombination shapes the genomes of acidophilic bacteria. [Nature 446\(7135\):537-541](#).
- Denef, V.J.** 2007. Biodegradation of organic anthropogenic pollutants by *Burkholderia* species. In:

- [Burkholderia: Molecular Biology and Genomics](#). Coenye, T. and Vandamme, P., eds. (Horizon Scientific Press, UK)
- Chain, P.S.G.\* , **V.J. Deneff\***, K.T. Konstantinidis, L.M. Vergez, L. Agullo, V.L. Reyes, L. Hauser, M. Cordova, L. Gomez, M. Gonzalez, M. Land, V. Lao, F. Larimer, J.J. LiPuma, E. Mahenthalingam, S.A. Malfatti, C.J. Marx, J.J. Parnell, A. Ramette, P. Richardson, M. Seeger, D. Smith, T. Spilker, W.J. Sul, T.V. Tsoi, L.E. Ulrich, I.B. Zhulin, and J.M. Tiedje. 2006. *Burkholderia xenovorans* LB400 harbors a multi-replicon, 9.7 M bp genome shaped for versatility. [Proc. Natl. Acad. Sc. USA 103\(42\):15280-15287](#). \* contributed equally
- Parnell, J.J., J. Park, **V.J. Deneff**, T.V. Tsoi, S.A Hashsham, J. Quensen III, and J.M. Tiedje. 2006. Coping with PCB toxicity: The physiological and genome-wide response of *Burkholderia xenovorans* LB400 to PCB (polychlorinated biphenyl)-mediated stress. [Appl. Environ. Microbiol. 72\(10\):6607-6614](#).
- Deneff, V.J.**, J.A. Klappenbach, J.L.M. Rodrigues, M.A. Patrauchan, C. Florizone, T.V. Tsoi, W. Verstraete, L.D. Eltis, and J.M. Tiedje. 2006. Genetic analysis of the three benzoate catabolic pathways and their associated oxidative stress response in *Burkholderia xenovorans* LB400. [Appl. Environ. Microbiol. 72\(1\):585-96](#).
- Deneff, V.J.**, M.A. Patrauchan, C. Florizone, J. Park, T.V. Tsoi, W. Verstraete, J.M. Tiedje, and L.D. Eltis. 2005. Carbon source and growth phase specific expression of biphenyl, benzoate and C<sub>1</sub> metabolic pathways in *Burkholderia xenovorans* LB400. [J. Bacteriol. 187\(23\):7996-8005](#).
- Deneff, V.J.**, J. Park, T.V. Tsoi, J.-M. Rouillard, H. Zhang, J.A. Wibbenmeyer, W. Verstraete, E. Gulari, S.A. Hashsham, and J.M. Tiedje. 2004. Biphenyl and benzoate metabolism in a genomic context: Outlining genome-wide metabolic networks in *Burkholderia xenovorans* LB400. [Appl Environ Microbiol 70\(8\):4961-70](#)
- Deneff, V.J.**, J. Park, J. L. Rodrigues, T. V. Tsoi, S. A. Hashsham, J. M. Tiedje. 2003. Validation of a more sensitive method for using spotted oligonucleotide DNA microarrays for functional genomics studies on bacterial communities. [Environ. Microbiol. 5\(10\):933-43](#).

## Funding Support

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### Current:

- 2019-2022:** NOAA: Linking genes to microbial traits key to the rise and demise of cyanobacterial harmful algal blooms (PI, \$950,000 - \$434,784 to VJD)
- 2017-2020:** NSF DEB Population and Community Ecology Cluster: EAGER: Importance of bacterial phenotypic plasticity relative to changes in community composition as responses to disturbance. (PI; \$199,999 to VJD)
- 2018-2021:** NOAA: Understanding the genetic traits and gene-environment interactions that determine feeding resistance to invasive dreissenid mussels by toxic cyanobacterial bloom-forming *Microcystis* in the Laurentian Great Lakes. (PI; co-PIs: Dr. Tom Johengen (UM SNRE-CILER) and Dr. Henry Vanderploeg (NOAA GLERL); \$520,192 - \$315,887 to VJD)
- 2019-2020:** Great Lakes Commission Invasive Mussels Collaborative: Invasive mussels control demonstration project. (Co-PI, PI: Dr. Harvey Bootsma, University of Wisconsin, Milwaukee: \$35,986 to VJD)
- 2018-2021:** NPS: Identifying microbiological factors driving botulism outbreaks at Sleeping Bear Dunes National Lakeshore (PI; co-PI Prof. Melissa Beth Duhaime; \$180,000 to VJD and MBD).
- 2018-2020:** NOAA: The Role of Dreissenid Mussels in Transforming Nutrient Loads into Harmful Algal Blooms (co-PI; PI: Dr. Tom Johengen (UM SNRE-CILER); \$85,000 - \$63,000 to VJD).

### Pending:

- 2020-2025:** Microbiome control over eukaryotic species coexistence. NSF Rules of Life: Microbiome Theory and Mechanisms (PI, \$2,850,000; co-PIs: Dr. Bradley Cardinale (UM SEAS), Dr. Annette Ostling (UM EEB, Dr. Nina Lin (UM Engineering))

### Past:

- 2017-2018:** NSF DEB Population and Community Ecology Cluster: DISSERTATION RESEARCH: A trait-based approach for understanding the relationship between bacterial community assembly and metabolic function. (PI; co-PI: M.L. Schmidt. (\$18,610 to MLS and VJD)
- 2012-2018:** DOE-JGI Community Sequencing Program: The bacterial component of the microbial loop in

the Laurentian Great Lakes and their role in the carbon cycle (PI; 2.0 Tbp of sequencing (16S rRNA gene, bacterial/archaeal and viral metagenomics, transcriptomics)).

- 2016-2019:** NSF EFRI-PSBR: Biodiversity & Biofuels: Finding Win-Win Scenarios for Conservation and Energy Production in the Next Century. (co-PI after transfer from Prof Todd Oakley (UCSB) ; PI: Prof. Brad Cardinale (UM SEAS), co-PIs: Phil Savage and Prof. Nina Lin (UM CEE); \$1,999,612, \$200,000 to VJD).
- 2016-2017:** University of Michigan M-Cubed Interdisciplinary Funding: Statistical analyses of cyanobacterial harmful algal blooms (Co-PI). PI: Dr. Greg Dick (UM EES); co-PI: Dr. Don Scavia (UM Graham Sustainability Institute). (\$60,000, \$30,000 to VJD)
- 2015-2016:** University of Michigan Water Center: The difference a species makes: how do quagga mussels change the benthic habitat microbiome? (PI) (\$19,078)
- 2014-2015:** University of Michigan Water Center: Environmental DNA-based quantification of dreissenid mussels and their impacts on freshwater bacterioplankton: building the foundation for a UM program focused on the interactions between freshwater invasive species and microbial community structure and function (PI); co-PI: Dr. Tom Johengen (UM SNRE-CILER). (\$49,956 - \$39,956 to VJD)
- 2014-2015:** University of Michigan Water Center: Building capacity for freshwater science: Integrating microbial genomics, environmental chemistry, and ecosystem processes to understand harmful algal blooms (co-PI); PI: Dr. Gregory Dick (UM EES); co-PI: Dr. Tom Johengen (UM SNRE-CILER). (\$249,485 - \$108,547 to VJD)
- 2014-2015:** Michigan Sea Grant (NOAA): A genomic approach to trace the sustenance of the freshwater microbial food web (PI). (\$12,909)
- 2012-2014:** University of Michigan M-Cubed Interdisciplinary Funding: Biofuels and Biodiversity (Co-PI). PI: Dr. Nina Lin (UM Chemical Engineering); co-PI: Dr. Bradley Cardinale (UM School of Natural Resources and the Environment). (\$60,000)

### **Mentees**

**PhD students:** Marian Schmidt (EEB, 2012 – 2018; current: postdoctoral researcher at the University of Texas, Austin (Ochman lab – supported by a 3-year Simons Foundation Fellowship); Ruben Props (UGent, Belgium, 2016 – 2018; current: Founder, Kytos, Ghent, Belgium); Nikesh Dahal (EEB, 2017 - ...); Jinny Yang (2018 - ...)

**Post-doctoral researchers:** Dr. Masanori Fujimoto (EEB, 2015; current: Assistant Research Professor, University of Florida); Dr. Sara Jackrel (EEB, 2016 – ...; starting as Assistant Professor, University of California, San Diego in 2020)

**Undergraduate researchers:** Chloe Turnbow (2020 - ...), James Lauer (2019-...), Dylan Baker (2018-... – M-Sci Alumnus; LSA Internship scholarship), Anna Ortega (2018-...), Kathryn Schmidt (2017-2018 – MCubed Summer Fellowship; co-author on manuscript in review, first author on manuscript in preparation), Cassandra Huerta (2017), Rachel Climer (2016-2017 – UROP best poster award winner), Kristen Hayden (2016-2017, co-author on manuscript in review), Kyle Buffin (2016-2017 – MCubed Summer Fellowship, co-author on manuscript in review), Morgan Meade (2015-2016), Amadeus Twu (2015-2016 – UROP summer fellowship), Joseph Batdorff (2014-2015), Seana Florida (2014-2015), Michelle Park (2014), Amelia Waters (2013-2015 – UROP summer fellowship), Natalie Imirzian (2013-2014), Edna Chiang (2012-2015 – ASM Undergraduate Research Fellowship, Beckman Undergraduate Research Fellowship, co-author on three papers, first author on one paper), Katherine Hunsberger (2012), Houraa Daher (2012).

### **Invited and contributed presentations (since 2012)**

Microbiomes alter competitive interactions between their hosts

*Department of Biology, University of Illinois, Chicago, IL. January 28, 2020.*

Algal microbiomes alter competitive interactions between their hosts

*16th Symposium of Aquatic Microbial Ecology (SAME16), Potsdam, Germany. September 1-6, 2019.*

Genome Evolution and Host Microbiome Shifts Drive Intraspecific Niche Divergence within Harmful Algal Bloom-Forming *Microcystis aeruginosa*.

*American Society for Microbiology Microbe Meeting, San Francisco, CA. June 20-24, 2019.*

Microbial community analysis to better understand avian botulism outbreaks.

*Sleeping Bear Dunes Coastal Monitoring and Research Symposium, Empire, MI. February 28, 2019.*

Are dreissenid mussels re-engineering lake microbial systems?

*Department of Biology, Bowling Green State University, Bowling Green, OH. November 8, 2017.*  
Cyanobacterial harmful algal blooms are a biological disturbance to western Lake Erie bacterial communities.

*Association of Environmental Engineering and Science Professors (AEESP) biennial Research and Education Conference, June 18-21, 2017.*

The difference a species makes: impact of invasive species on freshwater microbial communities.  
*Water @ Michigan, January 21, 2016.*

The difference a species makes: are invasive species tuning the invisible engine of the freshwater world.  
*14<sup>th</sup> Symposium on Aquatic Microbial Ecology, Uppsala, Sweden, August 23-28, 2015.*

Something old, something new, something borrowed, something green.  
*EDAMAME summer course, Kellogg Biological Station, June 30, 2015.*

Seasonal and spatial distribution of free living and particle-associated bacteria in Lake Michigan in the context of dreissenid mussel invasion.

*Great Lakes/HABs omics workshop, NSF- and NOAA-sponsored workshop on cyanobacterial harmful algal blooms, Bowling Green, OH, April 13-15, 2015.*

Do invasive zebra mussels alter structure of and carbon processing by bacterioplankton communities in lakes?

*Kellogg Biological Station Seminar Series, November 21, 2014*

The difference a species makes: are invasive species tuning the invisible engine of the freshwater world.  
*University of Michigan Microbial Ecology Working Group, October 30, 2014.*

Population and community genomics-based insights into eco-evolutionary microbial dynamics.  
*Ecological Society of America, 98<sup>th</sup> Annual Meeting, Minneapolis, MN, August 4-9, 2013.*

*In situ* evolutionary rate measurements show ecological success of recently emerged bacterial hybrids  
*Workshop on linking microbial ecology and evolution, Berlin, Germany. June 25-27, 2013.*

Studying evolutionary dynamics and ecological complexity of microbial communities in nature.  
*Annis Water Resources Institute, Grand Valley State University, Muskegon, MI. November 9, 2012.*

Microbial community interactions: Lessons from a natural model system  
*Microbial Metagenomics Course, Michigan State University, East Lansing, MI. June 13, 2012.*

## **Teaching (since 2012)**

**Winter 2020:** EEB 446 – Microbial Ecology; EEB300: Chloe Turnbow; James Lauer

**Fall 2019:** Bio 207 – Microbiology. EEB300: Anna Ortega; James Lauer

**Winter 2019:** EEB 446 – Microbial Ecology.

**Fall 2018:** Bio 144 – What's in your DNA? Implications for you and society; BIO200 – Undergraduate Research (Anna Ortega, Dylan Baker)

**Fall 2017:** Bio 144 – What's in your DNA? Implications for you and society; BIO200 – Undergraduate Research (Kathryn Schmidt, Kyle Buffin)

**Winter 2017:** Bio 144 – What's in your DNA? Implications for you and society; BIO200 – Undergraduate Research (Cassandra Huerta); UROP (Kristen Hayden; Rachel Climer)

**Fall 2016:** EEB 446 – Microbial Ecology; BIO200 – Undergraduate Research (Kyle Buffin); UROP (Kristen Hayden; Rachel Climer)

**Winter 2016:** Bio 144 – What's in your DNA? Implications for you and society; BIO200 – Undergraduate Research (Kyle Buffin); UROP (Morgan Meade, Amadeus Twu)

**Fall 2015:** UROP (Morgan Meade, Amadeus Twu)

**Winter 2015:** Bio 144 - Life: decoded. Genomics in Society; EEB400 – Undergraduate Research (Edna Chiang); UROP (Seana Florida, Joseph Batdorff)

**Fall 2014:** EEB 446 – Microbial Ecology; EEB400 – Undergraduate Research (Edna Chiang); UROP (Seana Florida, Joseph Batdorff)

**Winter 2014:** Bio 144 - Life: decoded. Genomics in Society; EEB400 – Undergraduate Research (Edna Chiang); EEB300 – Undergraduate Research (Michelle Park, Natalie Imirzian); UROP (Amelia Waters)

**Fall 2013:** EEB 446 – Microbial Ecology, EEB300 – Undergraduate Research (Edna Chiang); UROP (Amelia Waters)

**Winter 2013:** EEB300 – Undergraduate Research (Edna Chiang)

**Fall 2012:** EEB300 – Undergraduate Research (Edna Chiang)

**Winter 2012:** EEB 446 – Microbial Ecology

## Honors

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**2019:** Teaching Excellence Award (University of Michigan Program in Biology).

**2005:** Cum laude (Ph.D.), Department of Bio-engineering, University of Ghent, Belgium.

**2001-2005:** Doctoral fellowship, Flemish Fund for Scientific Research (Belgium)

**2003:** Scholarships, funded by CSHL and the Center for Microbial Ecology, to attend the Advanced Bacterial Genetics Summer Course at Cold Spring Harbor Laboratories (NY, USA).

**2002:** Scholarships, funded by Bernard Davis Scholarship and Howard Hughes Medical Institute and The Center for Microbial Ecology, to attend the 2002 Microbial Diversity Summer Course at the Marine Biological Laboratories (Woods Hole, MA, USA).

**2001:** Magna cum laude (M.S.), Department of Bio-engineering, University of Leuven, Belgium.

**1999:** Magna cum laude (B.S.), Department of Bio-engineering, University of Leuven, Belgium.

## Other scientific activities (since 2012)

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**Mentoring:** Mentor or committee member for 13 PhD and Masters students in Ecology and Evolutionary Biology (6), Earth and Environmental Sciences (3), School for Environment and Sustainability (1), Civil and Environmental Engineering (2), University of Ghent Center for Microbial Ecology and Technology (1). Mentor for 2 postdoctoral researchers, 8 research associates, and 18 undergraduate researchers.

**Scientific service:** Ad hoc reviewer for Science, Proceedings of the National Academy of Sciences USA, Genome Research, Genome Biology and Evolution, The ISME Journal, Environmental Microbiology, Applied and Environmental Microbiology, Nature Microbiology, PLoS Computational Biology, Journal Of Bacteriology, mBio, FEMS Microbiology Letters, and Archives of Microbiology; Editorial Board member for Scientific Reports (2011-2015) and Frontiers in Microbiology (2013 – present); Review panel member for U.S. Department of Energy's Office of Biological & Environmental Research (DOE-BER) and ad hoc reviewer for NSF DEB, NSF GEO, Canadian NSERC, and the Belgian Science Foundation (FWO).

**Diversity, Equity, and Inclusion activities:** Teaching team member for the interdisciplinary biology M-Sci class on Lake Erie environmental issues (2016-2019). The M-Sci program at UM is an intensive summer residential program aimed at increasing retention and diversity in STEM majors. Member and Chair of the UM EEB Diversity committee (2017-current). Faculty panel member for Transfer Days, aimed at recruiting students transferring to U-M from junior and community colleges (2019).

**Educational outreach:** Speaker at Ann Arbor Science Café (Cyanobacteria: Toxic tide or treasure?), a monthly public outreach event organized by the University of Michigan Museum of Natural History. (November 14, 2018). Presentation on invasive species impacts on the Great Lakes at Pattengill Elementary school, Ann Arbor, MI (March 5, 2019) and at the UM LSA Opportunity Hub Social Impact Fair (January 29, 2020).

**Conference/seminar organization:** Chair of session "Microbial Symbionts Driving Diversity and Composition of their Host Communities", American Society for Microbiology Microbe meeting (Chicago, IL; June 2020); Chair of session "Microbial Ecology of the Great Lakes, from Genomes to Geochemistry", International Association for Great Lakes Research Annual Meeting (Guelph, ON; 2016); Chair of session "Relevance of bacterial, archaeal, and viral dynamics to Great Lakes ecosystem processes", International Association for Great Lakes Research Annual Meeting (Detroit, MI; 2017); co-organizer of the 3-day Michigan meeting on "Unseen Partners: Manipulating Microbial Communities that Support Life on Earth" (Ann Arbor, MI; 2016) and 1-day EEB Early Career Scientist Symposium on "Humans as a force of ecological and evolutionary change" (Ann Arbor, MI; 2014); Organizer of monthly cross-departmental Microbial Ecology Seminar Series at the University of Michigan (2012-2015).