

Joseph H. Vineis

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INTERESTS

I am broadly interested in the interaction between microbial communities and their environment. A large part of my work revolves around the integration of high throughput 'omics and ancillary environmental data to identify microbial mechanisms important to biogeochemical cycling and novel genomic insights relevant to these processes. The methods that I used can be applied to a wide spectrum of microbial life, including bacteria and archaea, viruses, and microeukaryotes inhabiting diverse environments.

EDUCATION

PhD, 2022

Northeastern University, Boston, MA
Ecology Evolution and Marine Biology

M.S. in Molecular Ecology, 2010

State University of New York-Environmental Science and Forestry, Syracuse, NY
Ecology and Evolutionary Biology

B.A. in Biology, 2002

University of Vermont, Burlington, VT

RESEARCH EXPERIENCE

Professional Research Specialist: Ward Lab, Princeton University, 2022 – present
Focus: Parasite-diatom interactions and succession in ocean upwelling zones.

PhD Dissertation Research: Bowen Lab, Northeastern University 2017-2022
Focus: Microbial metabolic potential under nitrate enriched conditions in salt marsh sediments

Senior Research Assistant: Keck Facility, Marine Biological Laboratory, 2010 – present

Focus: 1) Gene conversion events and genomic architecture in *Adineta vaga*. 2) Plasmid like behavior of a conjugative transposon in *Bacteroides fragilis*.

Masters Thesis Research: SUNY-ESF (research advisor: Dr. Tom Horton), 2008-2010

Focus: The influence of nitrogen availability on the community composition and traits of ectomycorrhizal fungi in a temperate forest.

Assistant Research Scientist: Wadsworth Center Genomics Core Facility, 2006-2008

Assistant Research Scientist: Wadsworth Center Vector Biology and Population Genetics, 2003-2006

SKILLS

Bioinformatics

Genomics

**Microbial Cultivation
Ecological Models
Molecular Ecology and Evolution**

TEACHING

Assistant and Invited Speaker, Environmental Microbiology: Princeton University, 2023.

Presentation: Salt Marsh Biogeochemistry

Lead organizer and speaker, Genome resolved metagenomics analysis workshop: Princeton University, 2023

Assistant and Invited Speaker, Microbiomes across environments: University of Chicago-Marine Biological Laboratory, 2021

Presentation: Exploring the microbial niche space using enrichment, genome resolved metagenomics, phylogenomics, and metapangenomics.

Teaching Assistant, Genetics: Northeastern, 2018

Assistant and Invited Speaker, Bioinformatics for clinicians: Marine Biological Laboratory, 2018

Lead organizer and speaker, Amplicon and genome resolved metagenomics analysis workshop: Marine Science Center, Northeastern University, 2017

Assistant and Invited speaker, Strategies and Techniques for analyzing microbial population structure: Marine Biological Laboratory, 2006

SELECT PRESENTATIONS

Microbiome, Cold Spring Harbor, 2022

Invited oral presentation

Title: Networks and genome resolved metagenomics shed light on the importance of biotic interactions in a diatom bloom.

NeLLi Symposium on New Lineages of Life, The role of novel lineages on biogeochemical cycles. Joint Genome Institute, 2021

Invited oral presentation

Title: An important niche filled by candidate phylum TA06 – Inhabiting a diverse nutrient space among functionally diverse microbial neighbors.

Annual Ecological Society of America Meeting (ESA), 2021

Invited oral presentation

Title: Nitrate enrichment reveals a niche space for functionally and phylogenetically diverse populations of chemolithoautotrophs in salt marshes.

Plum Island Ecosystem LTER annual meeting, 2020

Invited oral presentation

Title: From survey to genome reconstruction: Understanding microbial contributions to biogeochemistry of salt marsh sediments.

AWARDS

Best presentation, Northeastern Graduate Student Symposium, 2018

Title: Recovery of microbial genomes from salt marsh sediments.

PUBLICATIONS

1. S D Matthews, L J Meehan, D Y Onyabe, J H Vineis, I Nock, I Ndams, J E Conn. Evidence for late Pleistocene population expansion of the malarial mosquitoes, *Anopheles arabiensis* and *Anopheles gambiae* in Nigeria. *Medical and Veterinary Entomology* 01/2008; 21(4):358-69.
2. Lisa Mirabello, Joseph H Vineis, Stephen P Yanoviak, Vera M Scarpassa, Marinete M Póvoa, Norma Padilla, Nicole L Achee, Jan E Conn. Microsatellite data suggest significant population structure and differentiation within the malaria vector *Anopheles darlingi* in Central and South America. *BMC Ecology* 01/2008; 8:3
3. Ling Zhou, Gena G Lawrence, Joseph H Vineis, Janet C McAllister, Robert A Wirtz, William G Brogdon. Detection of broadly distributed sodium channel alleles characteristic of insect pyrethroid resistance in West Nile virus vector *Culex pipiens* complex mosquitoes in the United States. *Journal of Medical Entomology* 03/2009; 46(2):321-7.
4. A.Murat Eren, Joseph H. Vineis, Hilary G. Morrison, Mitchell L. Sogin. A filtering method to generate high quality short reads using Illumina paired-end technology. *PLoS One*, 8(6), e66643.
5. Vincent B Young, Laura H Raffals, Susan M Huse, Marius Vital, Dongjuan Dai, Patrick D Schloss, Jennifer M Brulc, Dionysios A Antonopoulos, Rose L Arrieta, John H Kwon, K Gautham Reddy, Nathaniel A Hubert, Sharon L Grim, Joseph H Vineis, Sushila Dalal, Hilary G Morrison, A Murat Eren, Folker Meyer, Thomas M Schmidt, James M Tiedje, Eugene B Chang, Mitchell L Sogin. Multiphasic analysis of the temporal development of the distal gut microbiota in patients following ileal pouch anal anastomosis. *Microbiome* 2013, 1:9
6. Susan M Huse, Vincent B Young, Hilary G Morrison, Dionysios A Antonopoulos, John Kwon, Sushila Dalal, Rose Arrieta, Nathaniel A Hubert, Lici Shen, Joseph H Vineis, Jason C Koval, Mitchell L Sogin, Eugene B Chang, Laura E Raffals. Comparison of brush and biopsy sampling methods of the ileal pouch for assessment of mucosa-associated microbiota of human subjects. *Microbiome* 2014, 2:5
7. A Murat Eren, Hilary G Morrison, Pamela J Lescault, Julie Reveillaud, Joseph H Vineis, Mitchell L Sogin. Minimum entropy decomposition: Unsupervised oligotyping for sensitive partitioning of high-throughput marker gene sequences. *ISME Journal* 2015, 9:968-979.
8. Ryan J Newton, Sandra L McLellan, Deborah K Dila, Joseph H Vineis, Hilary G Morrison, A Murat Eren, Mitchell L Sogin. Sewage reflects the microbiomes of human populations. *mBio* 2015, 6(2).
9. A Murat Eren, Mitchell L Sogin, Hilary G Morrison, Joseph H Vineis, Jenny C Fisher, Ryan J Newton, Sandra McLellan. A single genus in the gut microbiome reflects host preference and specificity. *ISME Journal* 2015, 9:90-100.
10. A Murat Eren, Özcan C Esen, Christopher Quince, Joseph H Vineis, Mitchell L Sogin, Tom O Delmont. Anvi'o: An advanced analysis and visualization platform for 'omics data. 2016, *PeerJ* 3:e1319 10.7717/peerj.1319

11. Joseph H Vineis, Diana Ringus, Hilary G Morrison, Tom Delmont, Sushila Dalal, Laura H Raffals, A. Murat Eren, Eugene B. Chang, Mitchell L Sogin. Patient-Specific *Bacteroides* Genome Variants in Pouchitis. 2016, *mBio* 7(6):e01713-16. doi:10.1128/mBio.01713-16.
12. Poynton, H.C. et al.. The Toxicogenome of *Hyaella azteca*: a model for sediment ecotoxicology and evolutionary toxicology. 2018, *Environmental Science & Technology*, p.acs.est.8b00837.
<http://pubs.acs.org/doi/10.1021/acs.est.8b00837>
13. Ashley N. Bulseco, Joseph H. Vineis, Anna E. Murphy, Amanda C. Spivak, Anne E. Giblin, Jane Tucker, Jennifer L. Bowen. Metagenomics coupled with biogeochemical rates measurements provide evidence that nitrate addition stimulates respiration in salt marsh sediments. 2019, *Limnology and Oceanography*, <https://doi.org/10.1002/lno.11326>
14. Anna E. Murphy, Ashley N. Bulseco, Ross Ackerman, Joseph H. Vineis, Jennifer L. Bowen. Sulphide addition favours respiratory ammonification (DNRA) over complete denitrification and alters the active microbial community in salt marsh sediments. 2020, *Environmental Microbiology*, <https://doi.org/10.1111/1462-2920.14969>.
15. Christopher A. Lynam, Ashley N. Bulseco, Courtney M. Dunphy, Sean M. Osborne, Joseph H. Vineis, Jennifer L. Bowen. Microbial Community Response to a Passive Salt Marsh Restoration. 2020, *Estuaries and Coasts*.
<https://doi.org/10.1007/s12237-020-00719-y>.
16. Joseph H. Vineis, Ashley N. Bulseco, Jennifer L. Bowen. Microbial chemolithoautotrophs are abundant in salt marsh sediment following long-term experimental nitrate enrichment. 2023, *FEMS Microbiology Letters*.
<https://doi.org/10.1093/femsle/fnad082>.
17. Sherlynette S. Castro, Elena L. Peredo, Olivia U. Mason, Joseph H. Vineis, Jennifer L. Bowen, Behzad Mortazavi, Anakha Ganesh, Emil S. Ruff, Blair G. Paul, Anne E. Giblin, Zoe G. Cardon. Diversity at single nucleotide to pangenome scale among sulfur cycling bacteria in salt marshes. 2023, *Applied Environmental Microbiology*. <https://doi.org/10.1128/aem.00988-23>.
18. Joseph H. Vineis, William S. Reznikoff, Dionysios A. Antonopoulos, Bailey Fallon, Hilary G. Morrison, Mitchell L. Sogin. A novel conjugative transposon carrying and autonomously amplified plasmid. 2023, *mBio*. <https://doi.org/10.1128/mbio.02787-23>.