**Elizabeth McDaniel**

Microbiology PhD Student

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**Education**

**University of Wisconsin – Madison** *Aug. 2016-present*

Ph.D. student in the Microbiology Doctoral Training Program

* Laboratory of Dr. Katherine McMahon, Departments of Bacteriology and Civil and Environmental Engineering

**University of Arkansas – Fayetteville** *Aug. 2012-May 2016*

Bachelor of Science in Biology with Statistics Minor, Cum Laude Honors

* GPA: 3.71/4.0
* Honors Thesis: Natural Variation of the Ena1p Sodium Pump in *S. cerevisiae*

**Research Experience**

**McMahon Lab – University of Wisconsin – Madison** *Jan. 2017 - present*

Graduate research assistant in the laboratory of Dr. Katherine McMahon investigating bacterial communities of engineered wastewater systems. I use a combination of genome-resolved metagenomics approaches and enrichment culture techniques to probe the diversity, functional activity, and population dynamics of microorganisms that perform phosphorus removal.

**Lewis Lab – University of Arkansas – Fayetteville** *Aug. 2013-Aug. 2016*

Undergraduate research assistant in the laboratory of Dr. Jeffrey Lewis studying the natural variation of stress defense mechanisms in the budding yeast *Saccharomyces cerevisiae.*

**Broach Lab – Penn State Hershey College of Medicine** *May-Aug. 2014*

Intern in the Summer Undergraduate Research Internship Program in the laboratory of Dr. James Broach studying the interactions and movements of chromosomes during quiescence in the budding yeast *S. cerevisiae.*

**Peer-Reviewed Publications**

**1.** **McDaniel E.A.,** Stuecker T.N., Veluvolu M., Gasch A.P., Lewis J.A. **Independent Mechanisms for Acquired Salt Tolerance versus Growth Resumption Induced by Mild Ethanol Pretreatment in *Saccharomyces cerevisiae****.* mSphere. *Editor’s Pick.* Nov 2018, 3 (6) e00574-18; **DOI:** 10.1128/mSphere.00574-18

**Preprints and Submissions**

**2. McDaniel E.A.,** Peterson B., Stevens S.L.R., Tran P.Q., Anantharaman K., McMahon K.D.. **Expanded Phylogenetic Diversity and Metabolic Flexibility of Microbial Mercury Methylation.** Jan. 2020. *bioRxiv.*

**1.** **McDaniel E.A.,** Anantharaman, K., McMahon K.D. **metabolisHMM: Phylogenomic analysis for exploration of microbial phylogenies and metabolic pathways.** Dec. 2019. *bioRxiv.* **DOI:** 10.1101/2019.12.20.884627

**Oral Presentations**

***Invited Talks and Plenary Sessions***

**5.** McDaniel, E.A.,Moya, F.M., van Steenbrugge, J., Oyserman, B.O., McMahon, K.D. Examining Long-Term Microbial Population Dynamics At Multiple Scales Using Enrichment Bioreactors As Model Ecosystems. **Microbial Ecology and Water Engineering (MEWE) conference**. Hiroshima, Japan. *Nov. 2019.*

**4.** McDaniel, E.A.,Peterson, B., Tran, P., Anantharaman, K., Krabbenhofft, D., McMahon, K.D. Expanded Phylogenetic Diversity and Metabolic Flexibility of Microbial Mercury Methylation. Evolution Series Seminar. **University of Wisconsin – Madison JF Crow Institute for the Study of Evolution**. *Sept. 2019.*

**3.** McDaniel, E.A.,Moya, F., Camejo, P., He, S., McMahon, K.D. Integrating Anvi’o Tools into your Workflow: Insights from a Biological Nutrient Removal (BNR) System. **Resolving Microbial Communities at Strain-Level Symposium**. Penryn, UK. *Aug. 2018.*

**2.** McDaniel, E.A.,Stuecker, T.N., Elkon, I.M., Gasch, A.P., Lewis, J.A. Natural Variation in Yeast Uncovers Novel Regulation of the Ena1p Sodium Pump. **Southeastern Regional Yeast Meeting**. Tuscaloosa, AL. *March 2016.*

**1.** McDaniel, E.A.Stuecker, T.N., Elkon, I.M., Gasch, A.P., Lewis, J.A. Natural Variation in Yeast Uncovers Novel Regulation of the Ena1p Sodium Pump. **Southeastern Regional Yeast Meeting**. Little Rock, AR. *March 2015.*

***Internal Seminars***

**3.** McDaniel, E.A.“Best” Practices in Metagenomic Binning and Annotation. **Computational Biology, Ecology, and Evolution (ComBEE) ‘Omics Study Group session**. University of Wisconsin – Madison. *Dec. 2019.*

**2.** McDaniel, E.A.,van Steenbrugge, J., Oyserman, B.O, Moya, F., McMahon K.D. Eco-systems biology of a Microbial Community Performing Enhanced Biological Phosphorus Removal. **Microbiology Doctoral Training Program Seminar**. University of Wisconsin – Madison. *Nov. 2018.*

**1.** McDaniel, E.A.,McMahon, K.D. Bacterial Communities of Lab-Scale Wastewater Enrichments. **UW-Madison Bioscience Opportunities Preview Weekend Lightning Talk**. *Sept. 2018.*

**Poster Presentations**

**11.** McDaniel, E.A. ComBEE: Computational Biology, Ecology, and Evolution: Enhancing computational literacy in the life sciences through peer-led study groups. UW-Madison Data Science Hub Data Science Research Bazaar and Wisconsin Institute for Discovery “Illuminating Discovery” event. *Jan. & Feb. 2020*. (Poster constructed and presented on behalf of ComBEE Team)

**10.** McMahon Lab. Microbiomes of Freshwater Lakes and Engineered Wastewater Systems. Water@UW Syposium. Madison, WI. *Oct. 2018.* (Poster constructed and presented on behalf of McMahon Lab)

**9.** McDaniel, E.A.,Peterson, B. Stevens, S.L.R., Krabbenhoft, D., McMahon, K.D. Expanded Phylogenetic and Metabolic Diversity of Microbial Mercury Methylation. Department of Bacteriology Raper Symposium. Madison, WI. *Sept. 2018.*

**8.** McDaniel, E.A.**,** Peterson, B. Stevens, S.L.R., Krabbenhoft, D., McMahon, K.D. Comparative Genomics of Microbial Mercury Methylation. International Society of Microbial Ecology Meeting. Leipzig, Germany. *Aug. 2018.*

**7.** McDaniel, E.A.,Moya, F. Camejo, P. He, S. McMahon, K.D. Long-Term Population Dynamics of ‘*Candidatus* Accumulibacter phosphatis’ in Enhanced Biological Phosphorus Removal Sequencing-Batch Reactors. Population, Evolutionary, Quantitative Genetics Conference. Madison, WI. *May 2018.*

**6.** McDaniel, E.A.,Peterson, B. Stevens, S.L.R., Krabbenhoft, D., McMahon, K.D. Comparative Genomics of Microbial Methylmercury Production. Madison Microbiome Meeting. Madison, WI. *April 2018.*

**5.** McDaniel, E.A.,Peterson, B. Stevens, S.L.R., Krabbenhoft, D., McMahon, K.D. Comparative Genomics of Microbial Methylmercury Production. Joint Genome Institute User Meeting: Genomics of Energy and Environment. San Francisco, CA. *Mar. 2018*

**4.** McDaniel, E.A.,Stuecker, T.N., Elkon, I.M., Gasch, A.P., Lewis, J.A. Natural Variation in Yeast Uncovers Novel Regulation of the Ena1p Sodium Pump. Arkansas IDeA Network of Biomedical Research Excellence Meeting. Fayetteville, AR. *Nov. 2015*

**3.** McDaniel, E.A.**,** Stuecker, T.N., Elkon, I.M., Gasch, A.P., Lewis, J.A. Natural Variation in Yeast Uncovers Novel Regulation of the Ena1p Sodium Pump. 27th International Conference on Yeast Genetics and Molecular Biology. Levico, Terme, Trentino, Italy. *Sept. 2015*

**2.** McDaniel, E.A**.,** Stuecker, T.N., Elkon, I.M., Gasch, A.P., Lewis, J.A. Natural Variation in Yeast Uncovers Novel Regulation of the Ena1p Sodium Pump. South Central Branch of the American Society for Microbiology Joint Meeting. Fayetteville, AR. *Sept. 2014*

**1.** McDaniel, E.A. Rutledge, M.T., Broach, J.R. Chromosome Interactions in Quiescent Yeast. Penn State Hershey Summer Undergraduate Research Internship Programs Symposium. Hershey, PA. *Aug. 2014.*

**Honors and Awards**

**Civil and Environmental Engineering Becker Travel Supplement Award** - $500 *November 2019*

**O.N. Allen Soil and Environmental Microbiology Small Grants Award -** $3,290 *August 2019*

**Department of Bacteriology Betley-Allen Fellowship Award** *May 2019*

**University of Wisconsin-Madison Student Travel Grant -** $600 *April 2019*

**Microbiology Doctoral Training Program Travel Award -** $1000 *May 2018*

**Department of Bacteriology Travel Award -** $1000 *May 2018*

**Southeastern Regional Yeast Meeting Travel Award -** $250 *Mar. 2016*

**University of Arkansas Honors College Research Grant -** $1200 *Jan. 2016*

**University of Arkansas Honors College Travel Grant -** $1200 *Aug. 2015*

**Southeastern Regional Yeast Meeting Travel Award -** $250 *Mar. 2015*

**University of Arkansas Honors College Research Grant -** $2500 *Jan. 2015*

**University of Arkansas Academic Scholarship -** $2500  *2014-2015*

**ASM South Central Branch Meeting 2nd Place Poster Award**  *Sept. 2014*

**University of Arkansas Academic Scholarship -** $1000 *2013-2014*

**University of Arkansas Symphony Orchestra Scholarship -** $1000 *2012-2016*

**University of Arkansas New Arkansan Non-Resident Tuition Award - $**39,040 *2012-2016*

**Teaching, Mentoring, and Service**

**Bioinformatics Workshops (Teaching Assistant/Instructor/Course Development)**

***Certified Carpentries Instructor as of June 2019***

Genome-Resolved Metagenomics Binning Workshop Instructor and Developer *April 2020*

Introduction to Github Pages Carpentries Workshop Instructor and Developer *April 2020*

Research Bazaar Software Carpentry Workshop Helper *Jan. 2020*

Carpentries Genomics Introduction to R Instructor *Aug. 2019*

Data Carpentry Workshop Introduction to R Instructor *June 2019*

Software Carpentry Workshop Helper *June 2019*

Microbiome & Data Science Hubs Git/Github Pages Workshop Instructor and Developer *March 2019*

Resolving Microbial Communities at Strain-Level Resolution Symposium Teaching Assistant *Aug. 2018*

ComBEE Git/Github Pages Workshop Instructor and Developer *Sept. 2017*

ComBEE Anvi’o Workshop Teaching Assistant *May 2017*

ComBEE Git Workshop Teaching Assistant *March 2017*

ComBEE R Study Group Instructor and Developer *Spring 2017*

**Computational Biology, Ecology, and Evolution (ComBEE) Study Group Co-Chair** *Jan. 2017-present*

ComBEE is a peer-led group for computational biology researchers on the UW-Madison campus. We hold study groups on the R and python programming languages, current topics in genomics, and host seminars from graduate students, postdocs, and professors on topics broadly ranging in ecology and evolution. Website at combee-uw-madison.github.io

**McMahon Lab Mentoring** *2017-present*

*Graduate Student Mentor for Summer REUs and Undergraduate Research Students*

*- Kaela Amundson:* Characterization and Enrichment of Microorganisms Capable of External Electron Transfer. *Fa. 2017-Sp. 2018. Currently pursuing a Ph.D. in Microbiology at Colorado State University*

*- Matthew Wollf:* Metagenomics of Freshwater Lake and Engineered Wastewater Microbial Communities. *Fa, Sp. 2018*

*- Kali Denis:*Time-Series Analysis of Under-Ice Freshwater Bacterial Communities. *Sp. 2018.*

*- EBPR Reactor Maintenance Team:*Oversaw **6** undergraduate students and **2** masters students for maintenance of lab-scale wastewater bioreactors. *Fall 2018-current.*

**UW-Madison Metagenomics Workshop Development Team** *Sp. 2019 - present*

**Topics in Biotechnology Guest Lecturer** *Sp. 2020*

**Microbiology 551 Guest Lecturer on 16S Workflows and Bioinformatics** *Sp. 2020*

**MEWE Multi-Omics Methods for Water Engineering Workshop Developer and Assistant** *Nov. 2019*

**Microbiology Doctoral Training Program Admissions Committee** *Fall 2019*

**Data Science Hub Research Bazaar Planning Committee** *Fall 2019*

**Microbiology 304: Biology of Microorganisms Laboratory TA** *Spring 2018*

**BIOL 2323: General Genetics Drill Instructor** *Spring 2015*

**University of Arkansas Office of Admissions Ambassador** *Aug. 2013-Dec. 2015*

***Ad-hoc* Journal Reviewer: *Nature Microbiology, ISMEJ, mSystems*** *Fa. 2017-present*

**Professional Development**

**DELTA Research Mentor Training** *Summer 2019*

**Carpentries Instructor Training** *April 2019*

**Microbial Genomics and Metagenomics Workshop, FISABIO** *June 2017*

**Anvi’o Workshop, University of Chicago**  *April 2017*

**Data Carpentry Workshop, University of Wisconsin-Madison**  *Jan. 2017*

**Technical Skills**

**Laboratory Skills:**

DNA Extraction, PCR Amplification, qPCR, RNA Extraction, Primer Construction, Cloning, HPLC Chemical Analysis, Enrichment Lab-Scale Bioreactor Operation

**Computational Skills:**

*Languages and Platforms*: R/RStudio, python, bash, Unix, High-Throughput Computing (HT-Condor), Docker

*Reproducible Research Skills:*  Command-line pipelines/packages in R and python, workflow managers, git/Github

*Bioinformatics and (Meta)Genomics:* Genome Assembly (short Illumina reads, long PacBio reads, and hybrid approaches), Functional Annotation and Metabolic Reconstruction, Mapping and Alignment, Variant Calling and Filtering, Metagenomic Binning and Quality Filtering, Genome-Resolved Metatranscriptomics, Comparative Genomics and Phylogenomics Platforms (KBase, anvi’o, iTOL, etc.), 16S Amplicon Analysis