

Drew T. Doering

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EDUCATION

2013 – present **Doctor of Philosophy, Cellular and Molecular Biology**

University of Wisconsin-Madison
Mentor: Chris Todd Hittinger, PhD
Expected completion: August 2019

2009 –2012 **Bachelor of Science, Biology**

University of Wisconsin-Madison
Certificates in Environmental Studies and Leadership
Mentors: Cameron R. Currie, Jon S. Odorico

RESEARCH EXPERIENCE

2013–present **Graduate Research Assistant**

University of Wisconsin-Madison, Cellular & Molecular Biology Program
Mentor: Chris Todd Hittinger, PhD

- Using genome editing and high-throughput sequencing, I study the functional consequences of sequence divergence and use this information to shed light on the mechanisms used by evolution to influence phenotype via genotype.
- Used mRNA sequencing, 5' and 3' RNA ligase-mediate Rapid Amplification of cDNA Ends (RLM-RACE), HPLC-MS/MS, and chemical indicator-based assays to study the expression of a secondary metabolite operon that was horizontally transferred from an Enterobacteriales lineage into an early member of a clade of budding yeasts from the *Wickerhamiella* and *Starmerella* genera.
- Current work focuses on using long-read RNA sequencing technologies to study how transcript isoform diversity varies among *Wickerhamiella/Starmerella* clade yeasts, which are known to harbor a relatively high number of genes that were horizontally transferred from bacteria.

2012–2013 **Undergraduate Research Assistant**

University of Wisconsin-Madison, Dept. of Bacteriology
Mentor: Cameron R. Currie, PhD

- Studied cellulose degradation of insect-associated and free-living bacteria. Determined the cellulolytic capacity of insect-associated and free-living bacteria in qualitative and quantitative screens of over 300 strains of *Streptomyces* and other bacteria.

Drew T. Doering

- Isolated wild microbes from environmental soil samples, selecting for ability to degrade lignin-derived toxins. Identified several strains with potential use in biofuel generation processes.
- Isolated and identified bacteria associated with orchid bees and prepared insect samples for microscopy.

2010-2011 **Undergraduate Research Assistant**
University of Wisconsin-Madison, Dept. of Surgery
Mentor: Jon S. Odorico, MD

- Used fluorescence microscopy and flow cytometry to evaluate the expression of histocompatibility complexes and costimulatory molecules in human embryonic stem cell lines and pancreatic progenitors upon IFN γ stimulation.

PUBLICATIONS

Kominek J*, **Doering DT***, Oplente DA, Shen X-X, Zhou X, DeVirgilio J, Hulfachor AB, Groenewald M, Mcgee MA, Karlen SD, Kurtzman CP, Rokas A, and Hittinger CT. (2019) Eukaryotic acquisition of a bacterial operon. *Cell* 176(6): 1356-1366. *Contributed equally

Shen X-X, Oplente DA, Kominek J, Zhou X, Steenwyk JL, Buh KV, Haase MAB, Wisecaver JH, Wang M, **Doering DT**, Boudouris JT, Schneider RM, Langdon QK, Ohkuma M, Endoh R, Takashima M, Manabe R, Cadez N, Libkind D, Rosa CA, DeVirgilio J, Hulfachor A, Goenewald M, Kurtzman CP, Hittinger CT, and Rokas A (2018) Tempo and mode of genome evolution in the budding yeast subphylum. *Cell* 175(6): 1533-1545.

Book AJ, Lewin GR, McDonald BR, Takasuka TE, Wendt-Pienkowski E, **Doering DT**, et al. (2016) Evolution of High Cellulolytic Activity in Symbiotic Streptomyces through Selection of Expanded Gene Content and Coordinated Gene Expression. *PLoS Biology* 14(6): e1002475. doi:10.1371/journal.pbio.1002475.

Alexander WG, **Doering DT**, and Hittinger CT. (2014) High-Efficiency Genome Editing and Allele Replacement in Prototrophic and Wild Strains of Saccharomyces. *Genetics* 198(3): 859-866.

Book AJ, Lewin GR, McDonald BR, Takasuka TE, **Doering DT**, Adams AS, Blodgett JAV, Clardy J, Raffa KF, Fox BG, and Currie CR. (2014) Cellulolytic Streptomyces Strains Associated with Herbivorous Insects Share a Phylogenetically Linked Capacity to Degrade Lignocellulose. *Appl. Environ. Microbiol.* 80(15): 4692-4701.

PRESENTATIONS

2018 “Eukaryotic acquisition of a bacterial operon” J.F. Crow Society for the Study of Evolution Seminar Series, Madison, WI. (Talk)

Drew T. Doering

- 2018 **Doering DT**, Kominek J, Opulente DA, Shen X-X, Zhou X, DeVirgilio J, Hulfachor AB, Kurtzman CP, Rokas A, and Hittinger CT. Eukaryotic acquisition of a bacterial operon. Yeast Genetics Meeting, Palo Alto, CA. (Poster + Talk)
- 2018 **Doering DT** and Hittinger CT. A high-throughput approach for investigating the cost of genetic mutations at multiple timescales. Population, Evolutionary, and Quantitative Genetics Conference, Madison, WI. (Poster)
- 2018 Kominek J, **Doering DT**, Opulente DA, Shen X-X, Zhou X, DeVirgilio J, Hulfachor AB, Kurtzman CP, Rokas A, and Hittinger CT. Eukaryotic acquisition of a bacterial operon. Population, Evolutionary, and Quantitative Genetics Conference, Madison, WI. (Poster)
- 2017 **Doering DT** and Hittinger CT. A high-throughput approach for investigating the cost of genetic mutations at multiple timescales. NHGRI Research Training and Career Development Annual Meeting, St. Louis, MO. (Poster)
- 2017 “An approach to track and predict evolutionary paths through fitness landscapes” Genomic Sciences Training Program Seminar Series, Madison, WI. (Talk)
- 2016 **Doering DT** and Hittinger CT. High-throughput investigation into the evolutionary forces underlying sequence divergence. Genetics Departmental Retreat, Madison, WI (Poster).
- 2016 **Doering DT** and Hittinger CT. High-throughput investigation into the evolutionary forces underlying sequence divergence. The Allied Genetics Conference, Orlando, FL. (Poster)
- 2016 **Doering DT** and Hittinger CT. A high-throughput approach for illuminating protein fitness landscapes. NHGRI Research Training and Career Development Annual Meeting, Bethesda, MD. (Poster)
- 2016 “High-throughput approaches for measuring and predicting phenotype from genotype” Genomic Sciences Training Program Seminar Series, Madison, WI. (Talk)
- 2015 **Doering DT** and Hittinger CT. Insights into the consequences of sequence divergence using high-throughput pooled allele replacements. Biology of Genomes Meeting, Cold Spring Harbor, NY. (Poster)
- 2015 “To what extent does sequence divergence matter?” Genomic Sciences Training Program Seminar Series, Madison, WI. (Talk)
- 2014 **Doering DT**, Alexander WG, and Hittinger CT. High-throughput mapping of sequence to function in eukaryotes. Midwest Yeast Meeting, Evanston, IL. (Poster)
- 2014 **Doering DT**, Alexander WG, and Hittinger CT. High-throughput mapping of sequence to function in eukaryotes. Yeast Genetics Meeting, Seattle, WA. (Poster)

Drew T. Doering

- 2014 “To what extent does sequence divergence matter? (A high-throughput approach)”
Cellular & Molecular Biology Program Retreat, Green Lake, WI. (Talk)
- 2014 **Doering DT**, Alexander WG, and Hittinger CT. High-throughput mapping of sequence to function in eukaryotes. UW-Madison Metabolism Symposium, Madison, WI (Poster).
- 2014 **Doering DT**, Alexander WG, and Hittinger CT. High-throughput mapping of sequence to function in eukaryotes. Genomic Sciences Training Program Retreat, Madison, WI (Poster).
- 2013 Lewin GR, Book AJ, McDonald BR, **Doering DT**, Wagar M, Fox BG, and Currie CR. A Phylogenetic-Based, Systems-Analysis of Biomass Degradation by *Streptomyces*. Great Lakes Bioenergy Research Center Annual Retreat, South Bend, IN (Poster).
- 2013 **Doering DT**, Lewin GR, Book AJ, and Currie CR. Isolation of Lignotoxin-Metabolizing Microbes from Leaf-cutter Ant Refuse Dumps. Great Lakes Bioenergy Research Center Annual Retreat, South Bend, IN (Poster).
- 2011 **Doering DT**, Baiu DC, and Odorico JS. A Potential Treatment for Type I Diabetes Using Stem Cells and Pancreatic Precursors. Biology 152 Undergraduate Poster Symposium, Madison, WI (Poster).

AWARDS

Fall 2018	Cellular and Molecular Biology Program Travel Award
2017	Nominee for the Richard M. Heins Wisconsin Distinguished Graduate Fellowship
2013 – 2017	Genomic Sciences Training Program Predoctoral Fellowship
2015, 2016	Best poster award, Annual Genetics Retreat
2016	Best poster award, Cellular & Molecular Biology Program Retreat
Fall 2014, Spring 2016	Cellular and Molecular Biology Program Travel Award

MENTORING

Undergraduate: Ellie Austin, Bowen Jia (former)

PROFESSIONAL MEMBERSHIP AND SERVICE

Member: Genetics Society of America, J.F. Crow Institute for the Study of Evolution

Reviewer: *Yeast* (Co-reviewed with mentor Chris Todd Hittinger)

RELEVANT GRADUATE COURSEWORK

2015: Cellular and Molecular Pathology
2014: Genomic and Proteomic Analysis
2014: Introduction to Bioinformatics
2014: Genome Science
2014: Eukaryotic Molecular Biology

Drew T. Doering

2013: Prokaryotic Molecular Biology

SKILLS

Lab techniques: DNA sequencing (Illumina amplicon, Sanger), mRNA sequencing, 3' and 5' RLM-RACE, genomic DNA extraction, RNA extraction, reverse transcription, yeast genome engineering, micromanipulation (SporePlay), tetrad dissection, TOPO cloning, Gibson assembly, PCR and primer design, gel electrophoresis, cell culture, sterile technique, spectroscopy, flow cytometry, immunofluorescence microscopy, media preparation, equipment maintenance and basic repair

Technical: Scripting (R, Bash, Python), R package development, version control systems (git), reproducible workflows, preparing reports, creating and revising protocols

Bioinformatics: Sequence data analysis (Illumina amplicon, Sanger), BLAST, sequence alignment, GO Term enrichment, hierarchical clustering, read mapping, genome assembly, genome annotation, motif analysis, network analysis (cytoscape)

Languages: English (native), Spanish (conversational)