Marc G **Chevrette**

2001 Monroe Street, Madison, WI, 53711

401.269.9173 | chevrm@gmail.com | chevrm.github.io | chevrette | @wildtypeMC

Education

University of Wisconsin-Madison
Madison, WI

DOCTOR OF PHILOSOPHY (PH.D.) – GENETICS
In progress

- **Advisor:** Cameron Currie, Ph.D.
- NIH Chemistry-Biology Interface Predoctoral Fellow

Harvard University Extension
Cambridge, MA

MASTER OF LIBERAL ARTS (ALM) – BIOTECHNOLOGY (BIOENGINEERING & NANOTECHNOLOGY)
03/2015

- **Advisor:** Tomás Maira-Litrán, Pharm.D., Ph.D.
- **Thesis:** Transposon-Directed Insertion Site Sequencing for Determination of Fitness Factors in Pulmonary Infection by *A. baumannii*.

Rensselaer Polytechnic Institute
Troy, NY

BACHELOR OF SCIENCE – MOLECULAR BIOLOGY & BIOINFORMATICS
12/2010

Experience

WiSolve Consulting
Madison, WI

FOUNDER, PROJECT CONSULTANT
03/2016–present

- Provided business services (including market research analysis, business plan development, competitive landscape analysis, SBIR grant writing, and others) to early-stage companies in the biotech and pharmaceutical industries.

Currie Lab, University of Wisconsin-Madison
Madison, WI

GRADUATE RESEARCH ASSISTANT
08/2015–present

- Built genomics-driven computational and analytic pipelines to uncover novel therapeutics and study the evolution of biosynthesis in free-living and host-associated microbes.

Johnson Biosignatures Lab, Harvard & Georgetown Universities
Cambridge, MA

LEAD COMPUTATIONAL BIOLOGIST
10/2013–10/2015

- Performed whole genome sequencing and metagenomic analysis of environmental samples from sulfur-rich, extreme environments with implications in microbial ecology, biogeochemistry, and exobiology.
- Characterized biosynthetic potential of metagenomic data.

Warp Drive Bio
Cambridge, MA

HEAD OF EXPERIMENTAL GENOMICS
04/2013–08/2015

- Executed genomic-directed natural products drug discovery, high throughput Next Generation Sequencing (htNGS), computational biology, and molecular biology of actinomycetes and fungi.
- Designed and implemented genomic natural products searches over various scaffolds of business development and internal interest.
- Developed and curated computational pipelines and databases for assembly, annotation, and custom analysis of public and internal htNGS data (160,000 bacterial genomes, >150 closed and complete genomes) for analysis of novel polyketide, non-ribosomal peptide, and other natural product classes.
- Handled processing and management of sequence data, predictions, and analyses supporting multiple projects across discovery, molecular biology, engineering, and synthetic biology.
- Executed elucidation and prediction of novel chemical products of bacterial biosynthetic gene clusters and metabolic pathways (e.g. beta-lactams, aminoglycosides, rapamycin analogues, etc.).
- Developed internal pipelines for applied phylogenomic annotations and prioritizations of multiple data types to inform discovery and engineering efforts.
- Oversaw all lab and experimental support of actinomycete and fungal sequencing efforts for Illumina, Pacific Biosciences, and Oxford-Nanopore platforms.
- Bioinformatics software development to support molecular and synthetic biology efforts.
- Direct written and verbal communication of findings to senior leadership and business partners.
- Database management and delivery of sequence information to molecular biology, microbiology, and chemistry groups to aid drug discovery, strain engineering, and generation of expression constructs.

Maira-Litrán Infectious Disease Lab, Brigham & Women's Hospital
Boston, MA

RESEARCH ASSISTANT, MICROBIOLOGY & COMPUTATIONAL BIOLOGY
03/2013–08/2015

- Investigated *in vivo* fitness, horizontal gene transmission, and pathogenesis of *Acinetobacter baumannii*, *Staphylococcus aureus*, *Salmonella typhii*, and other virulent pathogens through microbiology, computational, and genomic techniques.
- Developed and optimized genetic tools to enable novel examinations of pathogen fitness, invasion, and virulence using high-throughput transposon-directed insertion site sequencing of infections in murine models.

Broad Institute of MIT & Harvard *Cambridge, MA*

RESEARCH ASSOCIATE II, MOLECULAR BIOLOGY PROCESS DEVELOPMENT *01/2011–03/2013*

- Independently designed development initiatives including supporting htNGS, microfluidics, and automation goals.
- Oversaw production and up-scaling of microbial mate-pair library construction (LC), integrated internal development with vendor technologies, and managed sample-tracking via real-time messaging to internal LIMS.
- Increased throughput of microbial LC Platform 4-fold by automation and protocol development.
- Worked extensively with mate-pair NGS LC, sequence analysis tools, genomic databases, statistical software, and programming/operating lab robotics.

Rutledge Molecular Genetics Lab, Rensselaer Polytechnic Institute *Troy, NY*

RESEARCH ASSOCIATE, MOLECULAR GENETICS *05/2010–12/2010*

- Designed and developed protocols and operating procedures for transgenic *Caenorhabditis elegans* cultures to model stress-induced neural degeneration and Parkinson's Disease.

BCR Biotech *Jamestown, RI*

RESEARCH ASSISTANT, MICROBIOLOGY *09/2009–12/2009*

- Wrote and optimized protocols and methods for engineering synthetic biosensing functions in *Bacillus* spores.

Consulting

LifeMine Therapeutics Manhattan, NY 2016–present

Talks, Publications, & Abstracts

INVITED TALKS & SEMINARS

T1 "Darwinian Drug Discovery: Chemical Ecology at Fine and Coarse Evolutionary Scales." International Chemical Biology Society Annual Conference. Madison, WI. Oct 24, 2016.

PEER-REVIEWED PUBLICATIONS

P8 Lui, N, H Li, **MG Chevrette**, L Cao, L Zhang, M Zhang, Y Huang, S Wang, Q Wang, Z Zhou. *In preparation*. "Discovery of Diverse Hydrolase Gene Clusters and Cellobiose Utilization Pathways in the Gut Metagenome of a Wood-feeding Higher Termite."

P7 Lewin, GR, M Davis, BR McDonald, E Glasgow, AJ Book, **MG Chevrette**, S Suh, A Boll, BG Fox, CR Currie. *In preparation*. "Long-term Cellulose Enrichment Selects for Highly Cellulytic Taxa and Competition for Public Goods."

P6 **Chevrette, MG**, F Aicheler, O Kohlbacher, CR Currie, MH Medema. *In preparation*. "Ensemble Computational Predictions of NRPS Adenylation Domain Substrate Specificities."

P5 Horn, HA, E Gemperline, **MG Chevrette**, E Mevers, J Clardy, L Li, CR Currie. *In preparation*. "Mass Spectrometry Imaging Reveals Differential Chemical Response to Pathogens in an Ancient Ant-Microbe Symbiosis."

P4 Adnani, N, DR Braun, BR McDonald, **MG Chevrette**, CR Currie, TS Bugni. *In press*. "Draft Genome of *Micromonospora sp. WMMB-235*, a Marine Ascidian-associated Bacterium." *Genome Announcements*.

P3 Adnani, N, DR Braun, BR McDonald, **MG Chevrette**, CR Currie, TS Bugni. *In press*. "Complete Genome of *Rhodococcus sp. strain WMMA-185*, a Marine Sponge-associated Bacterium." *Genome Announcements*.

P2 Lewin, GR, C Carlos, **MG Chevrette**, HA Horn, BR McDonald, RJ Stankey, BG Fox, CR Currie.2016. "Ecology and Evolution of Actinobacteria and their Bioenergy Applications." *Annual Review of Microbiology*. 2016 Sep; **70**: 235 -254.

P1 Johnson, SS, **MG Chevrette**, BL Ehlmann, KC Benison. 2015. "Insights from the Metagenome of an Acid Salt Lake: the Role of Biology in an Extreme Depositional Environment." *PLOS ONE*. 2015 Apr; **10**(4):e0122869.

ABSTRACTS

A15 **Chevrette, MG**, CR Currie, MH Medema. prediCAT: An Accurate Predictive Method for Substrate Specificity of Nonribosomal Peptide Synthetase Adenylation Domains. Presented at: 30th Annual Kenneth B. Raper Symposium on Microbial Research; Madison, WI; Sep 2, 2016.

A14 Bratburd, J, BR McDonald, **Chevrette, MG**, JL Klassen, HA Horn, CR Currie. Comparative Genomics of Fungus-growing Ant-associated Pseudonocardia. Presented at: 30th Annual Kenneth B. Raper Symposium on Microbial Research; Madison, WI; Sep 2, 2016.

A13 Horn, HA, E Gemperline, **MG Chevrette**, BR Mcdonald, J Bratburd, E Mevers, J Clardy, L Li, CR Currie. Mass Spectrometry Imaging Reveals Differential Chemical Response to Pathogens in an Ancient Ant-Microbe Symbiosis. Presented at: ISME International Symposium on Microbial Ecology; Montreal, QC, Canada; Aug 21-26, 2016.

A12 **Chevrette, MG**, CR Currie, MH Medema. Computational Predictions of Substrate Specificity in Nonribosomal Peptide Synthetases through Comparative Adenylation Domain Trees. Presented at: American Society for Microbiology Microbe; Boston, MA; Jun 16-20, 2016.

A11	Johnson, SS, ML Soni, DJ Collins, KC Benison, MR Mormile, **MG Chevrette**, BL Ehlmann. Biosignatures in Mars Analog Acid Salt Lakes. Presented at: USRA Biosignature, Preservation and Detection in Mars Analog Environments; Lake Tahoe, Nevada; May 16-19, 2016.
A10	**Chevrette, MG**, C Carlson, C Thomas, TS Bugni, CR Currie. Multifaceted Antibiotic Profiling across Actinomycete Chemical Ecology. Presented at: Perlman Antibiotic Discovery and Development Symposium; Madison, WI; Apr 29, 2016.
A9	Adnani, N, S Adibhatla, E Vazquez-Rivera, GA Ellis, D Braun, **MG Chevrette**, BR McDonald, C Thompson, JS Piotrowski, Q Yu, L Li, CR Currie, TS Bugni. Driving Production of Novel Natural Products through Marine Microbial Interspecies Interactions. Presented at: Gordon Marine Natural Products; Ventura, CA; Mar 6-11, 2016.
A8	**Chevrette, MG**, DW Udwary, CR Currie, SS Johnson. Functional Classification and Secondary Metabolism of an Extreme Metagenome. Presented at: 29th Annual Kenneth B. Raper Symposium on Microbial Research; Madison, WI; Sep 1, 2015.
A7	**Chevrette, MG**, BL Ehlmann, KC Benison, SS Johnson. Microbial Diversity and Biosynthetic Potential of an Extreme Sediment Metagenome. Presented at: Gordon Applied and Environmental Microbiology; South Hadley, MA; Jul 12-17, 2015.
A6	**Chevrette, MG**, M Vinacur, T Maira-Litrán. Transposon-Directed Insertion Site Sequencing Reveals *in vivo* Fitness Factors in *A. baumannii* Lung Infections. Presented at: Boston Bacterial Meeting; Cambridge, MA; Jun 18-19, 2015.
A5	Udwary, DW, K Robison, **MG Chevrette**, GL Verdine. Lessons from Long Read Assembly of 100+ Actinomycete Genomes. Presented at: Gordon Marine Natural Products; Ventura, CA; Mar 2-7, 2014.
A4	Robison, K, DW Udwary, **MG Chevrette**, GL Verdine. Long Read Assembly of >100 Actinomycete Genomes. Presented at: Advances in Genome Biology & Technology; Marco Island, FL; Feb 12-15, 2014.
A3	Young, S, S Steelman, R Daza, **MG Chevrette**, R Lintner, S Gnerre, A Berlin, B Walker, C Nusbaum, R Nicol. Generation of High-quality Draft Assemblies with a Single Sequencing Library. Presented at: Sequencing, Finishing, Analysis in the Future; Santa Fe, NM; May 29-31, 2013.
A2	Steelman, S, R Daza, **MG Chevrette**, P Kompella, P Trang, T Surabian, R Lintner, CZ Zhang, J Jung, M Meyerson, C Nusbaum, R Nicol. Automated Low Input Mate-Pair Library Construction for Illumina Sequencing. Presented at: Advances in Genome Biology & Technology; Marco Island, FL; Feb 15-18, 2012.
A1	Steelman, S, R Daza, **MG Chevrette**, P Kompella, P Trang, T Surabian, R Lintner, R Nicol. Microbial Mate-Pair Library Construction for De Novo Detection of Structural Rearrangements. Presented at: Broad Institute Symposium; Boston, MA; Nov 7-8, 2011.

Honors & Awards

Chemistry-Biology Interface Predoctoral Fellowship National Institutes of Health, NIGMS – UW-Madison	06/2016–present
Bacteriology Departmental Travel Grant University of Wisconsin-Madison	2016
Vilas Travel Grant University of Wisconsin-Madison	2016
Dean's Academic Achievement Award Harvard University Extension	03/2015
Finalist, Core Value Award: *"Courageous: Uncompromising Science"* Warp Drive Bio	2014
Finalist, Core Value Award: *"Unbounded: Reimagining the Possible"* Warp Drive Bio	2014
Featured Scientific Researcher – *"Who is Broad?"* Broad Institute of MIT & Harvard	01/2012
Rensselaer Alumni Scholarship Rensselaer Polytechnic Institute	2004–2008
Sal H. Alfiero Scholarship Rensselaer Polytechnic Institute	2004–2008
Rhode Island State Scholarship Rensselaer Polytechnic Institute	2004–2008

Service & Outreach

Computational Biology, Ecology, & Evolution (ComBEE) – UW-Madison

CO-CHAIR   *01/2016–present*

- Coordinated and scheduled speakers, discussions, workshops, and meetings focused on molecular microbial ecology and evolution, computational biology, and data science.

Google Summer of Code – antiSMASH – Open Bioinformatics Foundation

MENTOR   *03/2016–08/2016*

- Provided both scientific and technical mentorship in the development of predictive models for ribosomally synthesised and post-translationally modified peptide (RiPP) biosynthesis in the widely-used genome-mining software suite, antiSMASH.

Discovery Niche – Wisconsin Institutes for Discovery

CO-ORGANIZER   *10/2015–11/2015*

- Planned, built, and maintained interactive public exhibits showcasing natural products drug discovery and bioenergy research for local Madison, Wisconsin community.

Wisconsin Science Festival

VOLUNTEER   *10/2015*

Revive & Restore – Long Now Foundation

Open Genomics Adviser   *04/2014–10/2015*

- Advised projects with Revive & Restore and Cofactor Genomics seeking to understand and engineer the genomics of the endangered black-footed ferret and the extinct heath hen in an effort to restore genetic diversity in wild populations.

Broad Institute of MIT & Harvard

Environmental, Health, and Safety Representative   *01/2011–03/2013*

Teaching Experience

UW-Madison

Teaching Assistant

- Genetics 466: General Genetics (Sp 2016)
- Microbiology 450: Diversity, Ecology, & Evolution of Microorganisms (Fa 2016)

Professional Societies & Groups

International Chemical Biology Society	2016–present
Natural Products Discovery and Bioengineering Network	2016–present
American Society for Microbiology	2015–present
Computational Biology, Ecology, & Evolution (ComBEE) – UW-Madison	2015–present
JF Crow Institute for the Study of Evolution	2015–present
Society for Industrial Microbiology and Biotechnology	2014–present
Laboratory Robotics Interest Group – New England Chapter	2011–2015