Marc G **Chevrette**

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Education

University of Wisconsin-Madison — *Madison, WI*

Doctor of Philosophy (PhD) – Genetics — *In progress*

- **Advisor:** Cameron Currie, PhD
- 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, PharmD, PhD
- **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

P11 Blin, K, T Wolf, **MG Chevrette**, X Lu, S Kautsar, E de Los Santos, HU Kim, M Nave, E Shelest, R Breitling, E Takano, SY Lee, T Weber, MH Medema. *In preparation*. "antiSMASH 4.0 - New and Improved Features for Biosynthetic Gene Cluster Analysis."

P10 McDonald, BR, **MG Chevrette**, JL Klassen, HA Horn, EJ Caldera, E Wendt-Pienkowski, MJ Cafaro, MG Poulsen, NM Gerardo, AC Ruzzini, EB van Arnam, GM Weinstock, J Clardy, CR Currie. *In preparation*. "Population Genomics of Fungus-growing Ant-associated *Pseudonocardia*."

P9 Miller, IJ, **MG Chevrette**, JC Kwan. *In preparation*. "Whole-genome Approaches for Small Molecule Discovery in Uncultured Symbionts."

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 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."

P5 **Chevrette, MG**, F Aicheler, O Kohlbacher, CR Currie, MH Medema. *Under review*. "SANDPUMA: Ensemble Predictions of Nonribosomal Peptide Chemistry Reveals Biosynthetic Diversity across Actinobacteria."

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. (2016). "Complete Genome Sequence of Rhodococcus sp. Strain WMMA185, a Marine Sponge-Associated Bacterium." *Genome Announcements*, **4**(6), 1–2. DOI: 10.1128/genomeA.01406-16

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. DOI: 10.1146/annurev-micro-102215-095748

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. DOI: 10.1371/journal.pone.0122869

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, **MG Chevrette**, 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

JF Crow Institute for the Study of Evolution – UW-Madison

Evolution Coordinating Committee *01/2017–present*

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 468: General Genetics II (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