

# Marc G Chevrette

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## Education

### University of Wisconsin-Madison

Madison, WI

DOCTOR OF PHILOSOPHY (PHD) – GENETICS

In progress

MASTER OF SCIENCE (MS) – 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 (BSC) – MOLECULAR BIOLOGY & BIOINFORMATICS

12/2010

## Experience

### WiSolve Consulting

Madison, WI

CO-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 typhi*, 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

- T2 "Computational Insights into the Diverse Nonribosomal Peptide Chemistry of Actinobacteria." Synthetic Biology for Natural Products Conference. Cancun, Mexico. Mar 6, 2017.
- 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

*\*contributed equally*

- P8 Sanchez-Larrayoz, A, N Elshamy, **MG Chevette**, Y Fu, P Giunta, G Spallanzani, GB Pier, S Lory, T Maira-Litrán. "Complexity of Complement-Resistance Factors Expressed by *Acinetobacter baumannii* Needed for Survival in Human Serum." *In press, Journal of Immunology*.
- P7 **Chevette, MG**, F Aicheler, O Kohlbacher, CR Currie, MH Medema. "SANDPUMA: Ensemble Predictions of Nonribosomal Peptide Chemistry Reveals Biosynthetic Diversity across Actinobacteria." *In press, Bioinformatics*.
- P6 Miller, IJ, **MG Chevette**, JC Kwan. (2017). "Interpreting Microbial Biosynthesis in the Genomic Age: Biological and Practical Considerations." *Marine Drugs*, 15(6), 165. DOI: 10.3390/md15060165
- P5 Blin, K, T Wolf, **MG Chevette**, X Lu, CJ Schwalen, SA Kautsar, HG Suarez Duran, ELC de los Santos, HUK Kim, M Nave, JS Dickschat, DA Mitchell, E Shelest, R Breitling, E Takano, SY Lee, T Weber, MH Medema. (2017). "antiSMASH 4.0 - Improvements in Chemistry Prediction and Gene Cluster Boundary Identification." *Nucleic Acids Research*, 1854(1), 1019–1037. DOI: 10.1093/nar/gkx319
- P4 Adnani, N, DR Braun, BR McDonald, **MG Chevette**, CR Currie, TS Bugni. "Draft Genome of *Micromonospora* sp. WMMB-235, a Marine Ascidian-associated Bacterium." *Genome Announcements*, 5(2), 1-2. DOI: 10.1128/genomeA.01369-16
- P3 Adnani, N, DR Braun, BR McDonald, **MG Chevette**, CR Currie, TS Bugni. (2016). "Complete Genome Sequence of *Rhodococcus* sp. Strain WMA185, a Marine Sponge-Associated Bacterium." *Genome Announcements*, 4(6), 1–2. DOI: 10.1128/genomeA.01406-16
- P2 Lewin, GR, C Carlos, **MG Chevette**, HA Horn, BR McDonald, RJ Stankey, BG Fox, CR Currie. (2016). "Ecology and Evolution of Actinobacteria and their Bioenergy Applications." *Annual Review of Microbiology*. 70: 235–254. DOI: 10.1146/annurev-micro-102215-095748
- P1 Johnson, SS, **MG Chevette**, 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

- A19 A. F. Sanchez-Larrayoz, AF, NM Elhosseiny, **MG Chevette**, Y Fu, P Giunta, G Spallanzani, GB Pier, S Lory, T Maira-Litrán. The Membrane Lipid Asymmetry Transport System Plays a Key Role in Protecting *Acinetobacter baumannii* against Killing by Human Complement Killing via the Alternative Pathway. Presented at: American Society for Microbiology Microbe, New Orleans, LA; Jun 2, 2017.
- A18 **Chevette, MG**, CM Carlson, C Thomas, TS Bugni, DR Andes, CR Currie. Evolutionary Trends in Secondary Metabolism Reveal Insect-Associated *Streptomyces* as an Underexploited Antibiotic Resource. Presented at: Perlman Antibiotic Discovery and Development Symposium; Madison, WI; Mar 31, 2017.
- A17 Caldera, EJ, **MG Chevette**, CR Currie. The Geographic Mosaic of Antibiotic Coevolution in a Bacterial Symbiont of the Fungus-farming Ant *Apterostigma dentigerum*. Presented at: Perlman Antibiotic Discovery and Development Symposium; Madison, WI; Mar 31, 2017.
- A16 Bratburd, J, C Keller, E Vivas, **MG Chevette**, F Rey, L Li, CR Currie. The Human Gut Microbiota Metabolomic Response to Infection. Presented at: Perlman Antibiotic Discovery and Development Symposium; Madison, WI; Mar 31, 2017.
- A15 **Chevette, 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 Chevette**, 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 Chevette**, 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 **Chevette, 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 Chevette**, 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 **Chevette, 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 Chevette**, 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 **Chevette, MG**, DW Udvary, 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 **Chevette, 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 **Chevette, 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 Udvary, DW, K Robison, **MG Chevette**, 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 Udvary, **MG Chevette**, 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 Chevette**, 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 Chevette**, 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 Chevette**, 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

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

## Service & Outreach

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

EVOLUTION COORDINATING COMMITTEE

01/2017–present

### Google Summer of Code – antiSMASH – Open Bioinformatics Foundation

MENTOR

03/2016–present

- 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.

### 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.

### 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

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### UW-Madison

TEACHING ASSISTANT

- Genetics 468: General Genetics II (Sp 2016)
- Microbiology 450: Diversity, Ecology, & Evolution of Microorganisms (Fa 2016)

## Professional Societies & Groups

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