Marc G **Chevrette**

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

Education & Training

University of Wisconsin-Madison — *Madison, WI*

Doctor of Philosophy (PhD) – Genetics — *expected 04/2019*

Master of Science (MS) – Genetics — *10/2017*

- **Advisor:** Cameron Currie, PhD
- **Research Focus:** Evolution of Microbial Metabolic Diversity, Chemically-mediated Microbiome Interactions, & Antibiotic Discovery
- NIH Chemistry-Biology Interface Predoctoral Fellow (2016-2018)

Institut Pasteur — *Annecy, France*

Diploma – International Course on Antibiotics and Resistance — *11/2017*

Harvard University Extension — *Cambridge, MA*

Master of Liberal Arts (ALM) – Biotechnology (Bioengineering & Nanotechnology) — *03/2015*

- **Advisor:** Tomás Maira-Litrán, PharmD, PhD
- **Research Focus:** Genome-wide Experimental & Computational Characterization of *In Vivo* Fitness Factors in Bacterial Infections
- **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, Director of Technology, Senior 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*

PhD Candidate — *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.
- Systems investigated include insects (leaf-cutting ants, honey bees, & insects broadly), marine invertebrates, soil communities, & the human microbiome.

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.

Publications, Talks, & Abstracts

Peer-reviewed Publications

**contributed equally*

P8 N Liu,* H Li,* **MG Chevrette**, L Zhang, L Cao, H Zhou, X Zhou, Z Zhou, PB Pope, CR Currie, Y Huang, Q Wang. "Functional metagenomics reveals polysaccharide-degrading gene clusters and cellobiose utilization pathways in gut microbiota of a wood-feeding termite." *Under review*.

P7 N Adnani, **MG Chevrette**, SN Adibhatla, F Zhang, Q Yu, D Braun, J Nelson, SW Simpkins, BR McDonald, CL Myers, J Piotrowski, C Thompson, CR Currie, L Li, SR Rajski, TS Bugni. "Co-culture of Marine Invertebrate-Associated Bacteria and Interdisciplinary Technologies Enable Biosynthesis and Discovery of a New Antibiotic, Keyicin." ***ACS Chemical Biology***, 12(12), 3093. ***Click here*** **[Highlighted by Nature, *Click here*]**

P6 AF Sanchez-Larrayoz, NM Elshamy, **MG Chevrette**, Y Fu, P Giunta, RG Spallanzani, K Ravi, GB Pier, S Lory, T Maira-Litrán. (2017). "Complexity of Complement-Resistance Factors Expressed by *Acinetobacter baumannii* Needed for Survival in Human Serum." ***Journal of Immunology***, 199: ji1700877. ***Click here***

P5 **MG Chevrette**, F Aicheler, O Kohlbacher, CR Currie, MH Medema. (2017). "SANDPUMA: Ensemble Predictions of Nonribosomal Peptide Chemistry Reveals Biosynthetic Diversity across Actinobacteria." ***Bioinformatics***, 2017, 1–9. ***Click here***

P4 IJ Miller, **MG Chevrette**, JC Kwan. (2017). "Interpreting Microbial Biosynthesis in the Genomic Age: Biological and Practical Considerations." ***Marine Drugs***, 15(6), 165. ***Click here*** **[Cover Image for Issue 6, Volume 15 in June 2017]**

P3 K Blin, T Wolf, **MG Chevrette**, 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. ***Click here***

P2 GR Lewin, 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***. 70: 235 -254. ***Click here***

P1 SS Johnson, **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. ***Click here***

Invited Talks

T4 "Host-associated Microbes as a Source of New Antimicrobials." Natural Product Discovery & Development in the Genomic Era, Society for Industrial Microbiology & Biotechnology. Clearwater Beach, FL. Jan 22, 2018.

T3 "Natural Natural Products: Leveraging Chemical Ecology in the Search for New Drugs." Evolution Seminar Series, JF Crow Institute for the Study of Evolution. Madison, WI. Oct 26, 2017.

T2 "Computational Insights into the Diverse Nonribosomal Peptide Chemistry of Actinobacteria." Synthetic Biology for Natural Products Conference. Cancun, Mexico. Mar 6, 2017. **[Highlighted in ACS Synthetic Biology, *Click here*]**

T1 "Darwinian Drug Discovery: Chemical Ecology at Fine and Coarse Evolutionary Scales." International Chemical Biology Society Annual Conference. Madison, WI. Oct 24, 2016.
[Highlighted in ACS Chemical Biology, *Click here*]

Genome Announcements (Editorial Review only)

G4 DR Braun, **MG Chevrette**, D Acharya, CR Currie, SR Rajski, TS Bugni. (2018). "Draft Genome of *Micromonospora sp. WMMA1996*, a Marine Sponge-associated Bacterium." ***Genome Announcements***, 6(8), e00077-18. ***Click here***

G3 DR Braun, **MG Chevrette**, D Acharya, CR Currie, SR Rajski, K Ritchie, TS Bugni. (2018). "Complete Genome of *Dietzia sp. WMMA184*, a Marine Coral-associated Bacterium." ***Genome Announcements***, 6(5), e01582-17. ***Click here***

G2 N Adnani, DR Braun, BR McDonald, **MG Chevrette**, CR Currie, TS Bugni. (2017). "Draft Genome of *Micromonospora sp. WMMB-235*, a Marine Ascidian-associated Bacterium." ***Genome Announcements***, 5(2), 1-2. ***Click here***

G1 N Adnani, 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. ***Click here***

Abstracts

A21 R Zarnowski, **MG Chevrette**, E Dominguez, DR Andes. "Modeling High-throughput Proteomics into Predictive Metabolomics - A Novel Tool for Studies of Medical Device-associated Candida spp. Biofilm Infections." Presented at: Metabolomics Circle 2017 - Bioanylytical & Omics Science, Wrocław, Poland; Nov 18, 2017.

A20 D Acharya, N Adnani, D Braun, IJ Miller, Q Yu, **MG Chevrette**, M Berres, CR Currie, L Li, JC Kwan, TS Bugni. "Chemical Cross-talk in Bacterial Co-cultures Affects Differential Gene Expression and Antibiotic Production." Presented at: American Society for Pharmacognosy Annual Meeting, Portland, OR; Jul 30, 2017.

A19 AF Sanchez-Larrayoz, NM Elhosseiny, **MG Chevrette**, 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 **MG Chevrette**, 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 EJ Caldera, **MG Chevrette**, 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 J Bratburd, C Keller, E Vivas, **MG Chevrette**, 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 **MG Chevrette**, 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 J Bratburd, 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 HA Horn, 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 **MG Chevrette**, 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 SS Johnson, 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 **MG Chevrette**, 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 N Adnani, 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 **MG Chevrette**, 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 **MG Chevrette**, 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 **MG Chevrette**, 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 DW Udwary, 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 K Robison, 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 S Young, 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 S Steelman, 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 S Steelman, 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 06/2016–03/2018
Passed with Distinction Preliminary Examination A - Dept. of Genetics - UW-Madison 07/2017
Issue Cover Marine Drugs 15(6): Connecting Marine Microbial Natural Products to Biosynthetic Pathways 06/2017
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

Ad hoc Reviewer FEMS Microbiology Letters, Microbial Cell Factories
Evolution Coordinating Committee JF Crow Institute for the Study of Evolution – UW-Madison 01/2017–present
Mentor Google Summer of Code – antiSMASH – Open Bioinformatics Foundation 03/2016–09/2017
Co-chair Computational Biology, Ecology, & Evolution (ComBEE) – UW-Madison 01/2016–present
Co-organizer Discovery Niche – Wisconsin Institutes for Discovery 10/2015–11/2015
Volunteer Wisconsin Science Festival 10/2015
Open Genomics Adviser Revive & Restore – Long Now Foundation 04/2014–10/2015
Environmental, Health, and Safety Representative Broad Institute of MIT & Harvard 01/2011–03/2013

Teaching Experience

Genetics 468: General Genetics II UW-Madison Sp 2016
Microbiology 450: Diversity, Ecology, & Evolution of Microorganisms UW-Madison 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