

# Marc G Chevrette

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## 🎓 Education & Training

### University of Wisconsin-Madison

DOCTOR OF PHILOSOPHY (PHD) – GENETICS

Madison, WI

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 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.

## Publications, Talks, & Abstracts

### PEER-REVIEWED PUBLICATIONS

\*contributed equally

- P8 N Liu,\* H Li,\* **MG Chevette**, 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 Chevette**, 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 Chevette**, 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 Chevette**, 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 Chevette**, 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 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*, 45(1), 1019–1037. [Click here](#)
- P2 GR Lewin, 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. [Click here](#)
- P1 SS Johnson, **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. [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](#)]

“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 Chevrete**, 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 Chevrete**, 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 Chevrete**, 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 Chevrete**, 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 Chevrete**, 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 - Bioanalytical & Omics Science, Wrocław, Poland; Nov 18, 2017.
- A20 D Acharya, N Adnani, D Braun, IJ Miller, Q Yu, **MG Chevrete**, 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 Chevrete**, 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 Chevrete**, 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 Chevrete**, 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 Chevrete**, 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 Chevrete**, 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 Chevrete**, 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 Gempertine, **MG Chevrete**, 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 Chevrete**, 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 Chevrete**, 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 Chevrete**, 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 Chevrete**, 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 Chevrete**, DW Udway, 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 Chevrete**, 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 Chevrete**, 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 Udway**, K Robison, **MG Chevrete**, 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 Udway, **MG Chevrete**, 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 Chevrete**, 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 Chevrete**, 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 Chevrete**, 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

<b>Chemistry-Biology Interface Predoctoral Fellowship</b>	National Institutes of Health, NIGMS – UW-Madison	06/2016–03/2018
<b>Passed with Distinction</b>	Preliminary Examination A - Dept. of Genetics - UW-Madison	07/2017
<b>Issue Cover</b>	Marine Drugs 15(6): Connecting Marine Microbial Natural Products to Biosynthetic Pathways	06/2017
<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

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

## Teaching Experience

<b>Genetics 468: General Genetics II</b>	UW-Madison	Sp 2016
<b>Microbiology 450: Diversity, Ecology, &amp; Evolution of Microorganisms</b>	UW-Madison	Fa 2016

## Professional Societies & Groups

<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