

Marc G Chevrette

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🎓 Education & Training

University of Wisconsin-Madison

Madison, WI

DOCTOR OF PHILOSOPHY (PHD) – GENETICS

In progress

MASTER OF SCIENCE (MS) – GENETICS

10/2017

- **Advisor:** Cameron Currie, PhD
- NIH Chemistry-Biology Interface Predoctoral Fellow

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
- **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, 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.

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

Varigen Biosciences Madison, WI

2017–present

LifeMine Therapeutics Manhattan, NY

2016–present

Publications, Talks, & Abstracts

PEER-REVIEWED PUBLICATIONS

*contributed equally

- P7 Adnani, N, **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*, *in press*.
- P6 Sanchez-Larrayoz, AF, 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: j11700877. [Click here](#)
- P5 **Chevrette, MG**, 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 Miller, IJ, **MG Chevrette**, JC Kwan. (2017). "Interpreting Microbial Biosynthesis in the Genomic Age: Biological and Practical Considerations." *Marine Drugs*, 15(6), 165. [Click here](#)
- P3 Blin, K, 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 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*. 70: 235–254. [Click here](#)
- 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. [Click here](#)

INVITED TALKS

- T4 "Insect-associated Microbes as a Source of New Antibiotics." Natural Product Discovery & Development in the Genomic Era, Society for Industrial Microbiology & Biotechnology. Clearwater Beach, FL. Jan 21, 2017.
- 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.

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

GENOME ANNOUNCEMENTS (EDITORIAL REVIEW ONLY)

- G2 Adnani, N, DR Braun, BR McDonald, **MG Chevette**, 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 Adnani, N, DR Braun, BR McDonald, **MG Chevette**, 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 Chevette**, 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 Acharya, D, N Adnani, D Braun, IJ Miller, Q Yu, **MG Chevette**, 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 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 Udway, **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

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|--|---|-----------------|
| Chemistry-Biology Interface Predoctoral Fellowship | National Institutes of Health, NIGMS – UW-Madison | 06/2016–present |
| 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

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|---|--|-----------------|
| 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

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

Professional Societies & Groups

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|--|--------------|
| 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 |