Marc G. Chevrette

1123 East Dayton Ave., Unit A – Madison, WI 53703

☎ (401) 269 9173   •   ✉ chevrm@gmail.com

Research Overview

Scientist with microbial genomics, secondary metabolite biosynthesis, DNA sequencing, and molecular biology background. Experienced in development of novel applications using computational biology, molecular biology, bioengineering, and genomic sequencing approaches. Specific expertise and interest in microbial natural products biosynthesis, drug discovery, chemical ecology, and molecular engineering.

Education

University of Wisconsin, Madison, WI   **(in progress)**
Doctor of Philosophy (Ph.D.), Genetics
Advisor: Cameron Currie, Ph.D.

Harvard University Extension, Cambridge, MA   **03/2015**
Master of Liberal Arts (ALM), Biotechnology – Bioengineering & Nanotechnology
Advisor: Tomás Maira-Litrán, Pharm.D., Ph.D.
Thesis: Transposon-Directed Insertion Site Sequencing for Determination of Fitness Factors in Pulmonary Infection by Acinetobacter baumannii.

Rensselaer Polytechnic Institute, Troy, NY   **12/2010**
Bachelor of Science, Molecular Biology & Bioinformatics

Research Experience

Warp Drive Bio, Cambridge, MA   **04/2013–08/2015**
Head of Experimental Genomics, (04/2014–08/2015)
Research Associate, Experimental Genomics & Computational Biology, (04/2013–03/2014)

- 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 (1.6×10^5 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.

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Brigham & Women's Hospital, Div. of Infectious Diseases, Boston, MA 03/2013–08/2015
Research Assistant, Microbiology & Computational Biology

- 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.

Harvard University (Society of Fellows), Cambridge, MA 10/2013–07/2015
Computational Biologist

- Performed whole genome sequencing and metagenomic analysis of environmental samples from sulfur-rich, extreme environments with implications in microbial ecology and exobiology.
- Characterized biosynthetic potential of metagenomic data.

Broad Institute of MIT & Harvard, Cambridge, MA 01/2011–03/2013
Research Associate II, Molecular Biology Process Development

- 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.

Rensselaer Polytechnic Institute, Troy, NY 05/2010–12/2010
Research Associate, Molecular Genetics, Rutledge Lab

- 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 (now BCR Diagnostics, Chandler, AZ) 09/2009–12/2009
Research Assistant, Microbiology

- Wrote and optimized protocols and methods for engineering synthetic biosensing functions in *Bacillus* spores.

Publications

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.

Abstracts

Chevrette, MG, DW Udwary, CR Currie, SS Johnson. Functional Classification and Secondary Metabolism of an Extreme Metagenome. Poster at: 29th Annual Kenneth B. Raper Symposium; Madison, WI; Sep 1, 2015.

Chevrette, MG, BL Ehlmann, KC Benison, SS Johnson. Microbial Diversity and Biosynthetic Potential of an Extreme Sediment Metagenome. Poster at: Gordon Applied and Environmental Microbiology; South Hadley, MA; Jul 12-17, 2015.

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Chevrette, MG, M Vinacur, T Maira-Litrán. Transposon-Directed Insertion Site Sequencing Reveals *in vivo* Fitness Factors in *A. baumannii* Lung Infections. Poster at: Boston Bacterial Meeting; Cambridge, MA; Jun 18-19, 2015.

Udwary, DW, K Robison, **MG Chevrette**, GL Verdine. Lessons from Long Read Assembly of 100+ Actinomycete Genomes. Poster at: Gordon Marine Natural Products; Ventura, CA; Mar 2-7, 2014.

Robison, K, DW Udwary, **MG Chevrette**, GL Verdine. Long Read Assembly of >100 Actinomycete Genomes. Poster at: Advances in Genome Biology & Technology; Marco Island, FL; Feb 12-15, 2014.

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. Poster at: Sequencing, Finishing, Analysis in the Future; Santa Fe, NM; May 29-31, 2013.

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. Poster at: Advances in Genome Biology & Technology; Marco Island, FL; Feb 15-18, 2012.

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. Poster at: Broad Institute Retreat; Boston, MA; Nov 7-8, 2011.

Achievements & Awards

Dean's Academic Achievement Award   03/2015
Harvard University Extension

Featured Scientific Researcher – "Who is Broad?"   01/2012
Broad Institute of MIT & Harvard

Rensselaer Alumni Scholarship   2004–2008
Rensselaer Polytechnic Institute

Sal H. Alfiero Scholarship   2004–2008
Rensselaer Polytechnic Institute

Rhode Island State Scholarship   2004–2008
Rensselaer Polytechnic Institute

Service

Open Genomics Advisor   04/2014–03/2015
Long Now Foundation – Revive & Restore

- Advised projects with Revive and Restore and Cofactor Genomics seeking to understand the genomics of the endangered and extremely bottlenecked black footed ferret and the extinct heath hen in an effort to reintroduce genetic diversity and aid in restoration of healthy wild populations.

Environmental, Health, and Safety Representative   01/2011–03/2013
Broad Institute of MIT & Harvard