
DIEGO RIVERA GELSINGER

Department of Biology • Johns Hopkins University • Baltimore, MD 21218

dgelsin1@jhu.edu • (323) 314-4077

📧 <https://github.com/dgelsin> 🏠 <https://dgelsin.github.io>

PROFESSIONAL STATUS

Johns Hopkins University - Baltimore, MD

2015–2020

PhD Research Assistant, Department of Biology, Program in Cellular, Molecular, Developmental, and Biophysics

Advisor: Dr. Jocelyne DiRuggiero

Research thesis: Mechanistic insight into small non-coding RNA (sRNA)-mediated regulation of stress response in halophilic archaea from desiccated environments and metatranscriptomic discovery of sRNAs in halophilic microbial communities from the Atacama Desert. High throughput profiling of translation and ribosomes in Archaea. Saul Roseman award winner for exceptional thesis research.

San Francisco State University - San Francisco, CA

2012–2014

Undergraduate Research Fellow, Department of Biology

Advisor: Dr. José de la Torre.

Research thesis: Physiology and ecological interactions of thermophilic archaea and bacteria in geothermal hot springs across the globe.

EDUCATION

Johns Hopkins University - Baltimore, MD

Completed Spring 2020

Ph.D. Molecular biology and Microbiology

San Francisco State University - San Francisco, CA

Completed Spring 2014

B.Sc. Microbiology, minor in French

PUBLICATIONS

- **Gelsinger, D.R.**, Dallon, E., Reddy, R., Mohammed, F., Green, R., Buskirk, A., and DiRuggiero, J. **2020**. “*Ribosome profiling in Archaea reveals leaderless translation, novel translation initiation sites, and ribosome pausing at single codon resolution*”. *Nucleic Acids Res.*
 - Selected as a NAR **Breakthrough Article**.
- Urtskiy, G., Tisza, M.T., **Gelsinger, D.R.**, Munn, A., Taylor, J., and DiRuggiero, J. **2020**. “*Cellular life from the three domains and viruses are transcriptionally active in a hypersaline desert community*”. *Environ Microbiol.*
- **Gelsinger, D.R.***, Urtskiy, G.*, Reddy, R., Munn, A., Farney, S.K., and DiRuggiero, J. **2020**. “*Regulatory non-coding RNAs are diverse and abundant in an extremophilic microbial community*”. *mSystems*.
- **Gelsinger, D.R.** and J. DiRuggiero. **2018**. “*The non-coding regulatory RNA revolution in Archaea*”. *Genes*; 9(3), 141 <https://doi.org/10.3390/genes9030141>
- **Gelsinger, D.R.** and J. DiRuggiero. **2018**. “*Transcriptional landscape and regulatory roles of small non-coding RNAs in the oxidative stress response of the haloarchaeon Haloferax volcanii*”. *J Bacteriol*; 200:e00779-17 doi: 10.1128/JB.00779-17
- Crits-Christoph, A., **Gelsinger, D.R.**, Ma, B., Wierzechos, J., Ravel, J., Davila, A.F., Casero, M.C., and DiRuggiero, J. **2016**. “*Functional interactions of archaea, bacteria and viruses in a hypersaline endolithic community*”. *Env Microbiol*; 18:2064 PMID: 26914534
- Davila, A.F., Hawes, I., Araya, J.G., **Gelsinger, D.R.**, DiRuggiero, J., Ascaso, C., Osano, A., and Wierzechos, J. **2015**. “*In situ metabolism in halite endolithic microbial communities of the hyperarid Atacama Desert*”. *Front. Microbiol*; 6:1035 PMID: 26500612

- Trujillo, G., Aguinaldo, P., Anderson, C., Bustamante, J., **Gelsinger, D.R.**, Pastor, M.J, Wright, J., Marquez-Magaña, L., and Riggs, B. **2015** “*Near-peer STEM Mentoring Offers unexpected benefits for mentors from traditionally underrepresented backgrounds*”. *PURM*.

In preparation

- **Gelsinger, D.R.**, Reddy, R., Whittington, K., and DiRuggiero, J. **2020**. “*Post-transcriptional regulation of redox homeostasis during oxidative stress in haloarchaea by the small RNA SHOxi*”.

AWARDS AND FELLOWSHIPS

2020	JHU Saul Roseman award for exceptional thesis research, selection committee: Dr. Carl Wu (chair), Dr. Yumi Kim, Dr. Tatjana Trcek, Dr. Nichole Broderick
2019	Travel award for invited speakers to the International Workshop on Geo-Omics of Archaea (IWGOA)
2019	Invited Discussion Leader for the Gordon Research Seminar Archaea, RNA biology section
2017	Best poster award, Gordon Research Conference Archaea
2017	Trends in Microbiology best presentation award, Gordon Research Conference Archaea
2015	1 st place award for JHU CMDB Annual Retreat Poster Competition, The Johns Hopkins University
2015	Institution Nominee for HHMI Gilliam Fellowship, The Johns Hopkins University
2014	Wyche Fellowship, The Johns Hopkins University
2013	Instructional Related Activities (IRA) Grant, San Francisco State University
2013	CSU Louis Stokes Alliance for Minority Participation (LSAMP), San Francisco State University
2013	NIH Minority Access to Research Careers (MARC), San Francisco State University
2013 & 2014	NSF University of Nevada, Las Vegas-China PIRE Undergraduate Research Experience
2012	Institutional Nominee for HHMI Exceptional Research Opportunities Program (EXROP), San Francisco State University
2012	NIH MBRS Research Initiative for Scientific Enhancement (RISE), San Francisco State University

PRESENTATIONS

May 2020	<i>25th Annual Meeting of the RNA Society, online</i> Ribosome Profiling in Archaea Reveals Leaderless Translation, Novel Translational Initiation Sites, and Ribosome Pausing at Single Codon Resolution (poster)
September 2019	<i>International Workshop on Geo-Omics of Archaea (IWGOA), SUSTech University, Shenzhen, China</i> Ribosome profiling reveals translation dynamics and alternative reading frame usage in Archaea (Invited speaker)
September 2019	<i>JHU CMDB Annual Research Retreat, Liberty Mountain, PN</i> Ribosome profiling in Archaea reveals leaderless translation, novel translation initiation sites, and ribosome pausing at single codon resolution (poster)
July 2019	<i>Gordon Research Conferences Archaea: Ecology, Metabolism & Molecular Biology, Les Diablerets, Switzerland</i> SHOxi: a small RNA post-transcriptional regulator in the oxidative stress response of <i>Haloferax volcanii</i> (Poster)
January 2019	<i>Mid-Atlantic Microbiome Meetup (M³), Baltimore, Maryland</i> Novel insight in identifying and monitoring regulatory small non-coding RNAs in halophilic microbial communities from the Atacama Desert (Poster)
October 2018	<i>JHU CMDB Annual Research Retreat, Rocky Gap, MD</i> Profiling global translational effects and translation regulation in an oxidative stress-resistant haloarchaea (Talk)
March 2018	<i>5th Meeting of Regulating with RNA in Bacteria & Archaea, Seville, Barcelona</i>

August 2017	Intergenic sRNA277.2: a post-transcriptional regulator of the oxidative stress response of the haloarchaeon <i>Haloferax volcanii</i> (Poster) <i>Gordon Research Conferences Archaea: Ecology, Metabolism & Molecular Biology, Waterville valley, New Hampshire</i>
October 2015	Transcriptional landscape and regulatory roles of small non-coding RNAs in the oxidative stress response of the haloarchaeon <i>Haloferax volcanii</i> (Poster) <i>JHU CMDDB Annual Research Retreat, Saint Michaels, Maryland</i>
July 2015	Surviving in Extreme Environments by Regulating the Oxidative Stress Response in Haloarchaea (Poster) <i>Gordon Research Conferences Archaea: Ecology, Metabolism & Molecular Biology, Sunday River, Maine</i>
April 2014	Small RNA-mediated Regulation of Stress Response in Haloarchaea (Invited Talk) <i>ASBMB Annual Meeting, San Diego, California</i>
January 2014	Chemical inhibition of ammonia oxidation in the thermophilic nitrifying archaeon <i>Nitrosocaldus yellowstonii</i> (Poster) <i>CSUPERB Annual Meeting, Santa Clara, California</i>
June 2013	Chemical inhibition of ammonia oxidation in the thermophilic nitrifying archaeon <i>Nitrosocaldus yellowstonii</i> (Poster) <i>Symposium: China-US Collaborative Research on Life in Terrestrial Geothermal Springs, Yunnan University, Kunming, China</i>
May 2013	Inhibition of Ammonia Oxidation in the Thermophilic Ammonia-Oxidizing Archaeon <i>Nitrosocaldus yellowstonii</i> (Poster) <i>15th Annual COSE Student Project Showcase, San Francisco State University</i>
August 2012	Inhibition of Ammonia Oxidation in the Thermophilic Ammonia-Oxidizing Archaeon <i>Nitrosocaldus yellowstonii</i> (Poster) <i>SFSU Undergraduate Summer Research Symposium, San Francisco State University</i>
	<i>Nitrosocaldus yellowstonii</i> : Ammonia Oxidation at Low NH ₃ Concentrations (Talk)

RELEVANT EXPERIENCE

PhD Research Assistant – Johns Hopkins U. RNA biology, molecular biology, & genomics 2015–2020

I used high throughput sequencing techniques (metagenomics/transcriptomics/ribosome profiling) to probe microbial dynamics of hypersaline endolithic communities in the Atacama Desert, Chile. I used bioinformatic approaches to identify novel small non-coding RNAs that regulate stress response in haloarchaea found in these endolithic communities to confer adaptation to such extreme environments. This was done using a two-pronged approach: (1) studying the regulation of the oxidative stress response of a cultured representative of the endolithic communities, *Haloferax volcanii*, in order to use genetics to elucidate mechanistic actions of sRNAs, and (2) development of a bioinformatic program, SnapT (<https://github.com/ursky/SnapT>), to identify and track sRNAs *in situ* over temporal scales in endolithic microbial communities. After *in silico* analysis, results were validated with *in vivo* experiments such as qPCR, northern blots, genetic manipulations (knockout, overexpression), and mRNA-sequencing. The majority of this work focused on the most up-regulated sRNA during oxidative stress in *H. volcanii*. I found that this sRNA, SHOxi, is highly specific to oxidative stress conditions, that it is required for increased survival, and that its mechanistic function is to post-transcriptionally degrade a messenger RNA involved in redox homeostasis through RNA-RNA interactions, effectively reducing the amount of damage during oxidative stress. This work culminated into three publications (see PUBLICATIONS), and one more in preparation. Future work to be done includes establishing the direct mechanistic action of SHOxi in *Haloferax volcanii* on all its potential targets and whether RNA-binding proteins are involved.

A second project I worked on was to elucidate the first highly resolved view of translation in Archaea. This involved the adaptation and development of ribosome profiling for an extremophilic Archaea with 2-3M intracellular salt concentrations. This work determined the major ribosome footprint of Archaea to be comparable in size to that of Eukarya

and captured high resolution periodicity and reading frame in sequenced footprints. Ribosome activity was manipulated with translation inhibitors to reveal ribosome pausing at specific codons and to assign footprint lengths to the various stages of translation in a primarily leaderless transcriptome. Coupling ribosome profiling with inhibitors and stress conditions I found evidence that many genes not only initiate on alternative translation start sites (aTSS) around and within open reading frames (ORFs) but that these aTSS may be regulated translationally during oxidative stress. This work demonstrates how a microbe with a gene dense genome can potentially produce proteins with distinct functions (isoforms) using the same gene. This work culminated into a publication (see PUBLICATIONS).

All of this work was awarded the Johns Hopkins University, program in Cellular, Molecular, Developmental, and Biophysical Chemistry Saul Roseman award for exceptional thesis research in 2020.

Undergraduate Research Scholar – San Francisco State U. Microbial ecology

2012–2014

I employed molecular, microbiological, and bioinformatic techniques to investigate the physiology and microbial interactions of nitrifying thermophilic archaea in geothermal springs. Major projects included: 1) transcriptional response to low and high substrate (NH₃) concentrations in AOA, 2) chemical inhibition of thermophilic AOA ammonia oxidation activity, and 3) exploring the physiology, genomics, and evolutionary relationship between novel thermophilic AOA from Chinese hot springs.

Summer Research Scholar – Tongji U. Shanghai, China, Biogeochemistry

August 2013 & 2014

I employed organic chemistry and isotopic techniques to investigate carbon metabolism of AOA. Used a variety of ¹³C-labeled carbon compounds in hot spring microcosms and extracted lipid biomarkers to use in conjunction with Liquid Chromatography-Mass Spectrometry and Gas Chromatography-Infrared-Mass Spectrometry.

TECHNIQUES AND SKILLS

Bench

- PCR
- (RT-)qPCR
- Gel electrophoresis (agarose, polyacrylamide)
- Restriction digest
- Cloning (Traditional/Gibson)
- Overexpression of genes/ncRNAs
- DNA/RNA extraction
- Protein extraction
- Western Blotting
- Northern Blotting
- CRISPR Interference
- Illumina Sequencing
- Nanopore Sequencing
- NGS Library Construction and Optimization
 - (Meta)genomics
 - (Meta)transcriptomics
 - Ribosome profiling
- Colorimetric assays
- Light and Confocal Microscopy
- Immunostaining
- Gradients and fractionation (sucrose, percoll)
- Lipid Extractions (Bligh & Dyer)
- Metabolic radio-labeling
- Mass spectrometry
- Cell culture (microbial, eukaryotic) and plating (microbial)

Computational

- Languages:
 - Bash/Unix
 - Python
 - R
 - html
 - markup
- Cloud computing (AWS and others)
- Analysis:
 - Gene expression (RNA-seq/ribosome profiling)
 - Gene ontology enrichment
 - Genome and transcriptome assembly
 - Gene annotation
 - Homology (BLAST, DIAMOND, rfam, etc.)
 - Sequence motif finding
 - Variant calling from genomic data
 - RNA structure
- Software development:
 - Co-lead developer of SnapT - Small NcRNA Annotation Pipeline for (meta)Transcriptomic data
<https://github.com/ursky/SnapT>
 - Lead developer of mRibo - Microbial Ribosome Profiling Analysis (mRibo)
<https://github.com/dgelsin/mRibo>

FIELD WORK

Atacama Desert, Chile (2 trips)

January 2016 & February 2017

In collaboration with the NASA ARADS team we tested the capabilities of new rover technology to drill and collect deep subsurface samples for microbial phylogenetic and functional analysis. In addition, I did independent research on the dynamic metabolic capabilities of the endolithic microbial communities occupying halite nodules using *in situ* RNA acquisition and sequencing approaches.

Tengchong, Yunnan, China

July 2013

Participated in a collaborative NSF research project, Partnerships in International Research and Education (PIRE), to assess the ammonia oxidizing archaeal (AOA) diversity and investigate their metabolism and physiology in high temperature hydrothermal environments.

PROFESSIONAL DEVELOPMENT WORKSHOPS

CMDB Bioinformatics Bootcamp, Johns Hopkins University

Fall 2014

Week intensive course on big data analysis, Python scripting, and biostatistics taught by Galaxy founder Dr. James Taylor.

Bioinformatics Programming Group, San Francisco State University

Fall 2013

Learned Unix and became familiar with regular expressions, scripting, Python, and R.

SYNERGISTIC ACTIVITIES (EDUCATIONAL AND OUTREACH)

- | | |
|-----------|--|
| 2017 | Designed and taught lectures on microbial genomics and bioinformatics to undergraduates in the Microbiology course at the Johns Hopkins University Homewood Biology Department |
| 2017 | Laboratory Sustainability Representative of a pilot sustainability project at JHU to make laboratories greener and more sustainable |
| 2016–2019 | Lead member of the graduate student group Teachers and Researchers United (TRU) in order to promote better conditions for graduate students at JHU |

2016	Invited and taught a bioinformatics lecture at the Halophiles 2016 meeting
2016	Invited and taught Quantitative Biology Bootcamp to Master Students at the University of Puerto Rico Mayaguez Campus
2016	Mentor for an undergraduate (Aldo Salazar Morales) recipient of the NSF REU
2016	Teacher's Assistant in Cell Biology
2015–2018	Executive lead position of the Mentoring to Inspire Diversity in Science (MInDS) group at the Department of Biology, the Johns Hopkins University. MInDS is a peer-mentorship and outreach group for graduate students the in the CMDB program at JHU
2015	Mentor in STEM Achievement in Baltimore Elementary Schools (SABES)
2015	Teacher's Assistant in Biochemistry
2012–2014	Mentor in Biology Undergraduate Mentoring Program (BUMP) which partners successful upper division biology majors with entering biology majors to provide them with guidance and advice. Influential in shaping the direction of the program and bringing other students into research

STUDENT MENTORSHIP

Rahul Reddy	Undergraduate student	09/2014 – 05/2019
Kevin Maciuba	CMDB PhD rotation student	Fall 2015
Gherman Uritskiy	CMDB PhD rotation student	Spring 2016
Aldo Morales	REU undergraduate student	Summer 2016
Ariel Parker	CMDB PhD rotation student	Fall 2016
Neta Shwartz	CMDB PhD rotation student	Winter 2016
Katherine Huffer	CMDB PhD rotation student	Fall 2017
Michelle Biederman	CMDB PhD rotation student	Winter 2017
Anthony Mclean	CMDB PhD rotation student	Spring 2018
Kathleen Whittington	Undergraduate student	03/2018 – 05/2019
Diego Tanton	Undergraduate student	03/2018 – 08/2018
Emma Dallan	CMDB PhD rotation student	Fall 2018
Grace Tamofolau	CMDB PhD rotation student	Fall 2018
Sara Debic	CMDB PhD rotation student	Fall 2019
Dylan Taylor	CMDB PhD rotation student	Winter 2020
Rima Sakhawala	CMDB PhD rotation student	Winter 2020

LANGUAGES

Fluency in Spanish (mother tongue), English, and French (intermediate to advanced).