

Ikaia Leleiwi, PhD
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National Laboratory
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EDUCATION

Doctorate of Philosophy of Science: Cell and Molecular Biology Colorado State University, Fort Collins CO	August 2023
Graduate certificate in Data Analysis Colorado State University, Fort Collins CO	December 2022
Master of Science Degree: Microbiology/Immunology Colorado State University, Fort Collins CO	May 2019
Bachelor of Science Degree: Biology University of Hawai'i at Manoa, Honolulu HI	May 2012

SKILLS AND COMPETENCIES

- **Illumina WGS Library Prep**
- **Multi-omics integration**
 - **Metagenomics**
 - NGS processing (FastQC, BBtools, Bowtie2, Samtools)
 - Comprehensive assembly techniques (co-assembly, subtractive assembly, megahit, IDBA-UD)
 - MAG binning (metabat2)
 - Genome annotation (DRAM, DRAM2)
 - Gene clustering and database creation/query (Prodigal, MMseqs2, HMMER)
 - **Metatranscriptomics**
 - Limma and DESeq2
 - Integration with metagenomics
 - **Metabolomics**
- **Amplicon sequencing** (Qiime2)
- **Multivariate statistics** (PCA, NMDS, LDA)
- **Linux Proficiency**
- **Scripting/Statistical software/Computing**
 - Bash, R, Python
 - HPC environments (SLURM workload manager)
 - Predictive modeling, applied machine learning (caret, glmnet, Knn)
 - Command line tool development
 - Data cleaning and analysis in the Tidyverse (dplyr, purrr)
 - Data visualization expert (ggplot2, Adobe Illustrator)
 - AWS Cloud Practitioner Essentials
- **Bioinformatics**
 - Bowtie2, Samtools, BBtools, Bioconda, CoverM, ht-seq, FeatureCounts, DRAM, HMMER, Qiime2, MMseqs2, Vegan R package
 - Working knowledge of gene/genome databases – GTDB, SILVA, KEGG, dbcan/CAZY, HMDB
- **Bioinformatics pipeline development**
 - Snakemake
- **Multidisciplinary team member**
- **Experimental design**
- **Data organization and management**

EXPERIENCE

Postdoctoral Researcher

September 2023 – current

Lawrence Livermore National Laboratory, Livermore CA

Bioinformatics and Computational Microbial Ecologist for Microbes Persist SFA

Full-time: 40+ Hours/Week

Dr. Jennifer Pett-Ridge

- Analyze qSIP and multi-omic microbiome datasets to quantify biogeochemical elemental cycling; deliver summary reports and documentation to cross-disciplinary teams.
- Develop and implement bioinformatics pipelines for isotope-enabled microbiome analysis; run on HPC (SLURM), keep pipelines current, and test at large scale to harden performance/QC.
- Processed >1,200 metagenomic FASTQ files and integrated community RNA-seq across 3 datasets; modeled microbial activity with logistic regression to identify drivers under anoxic conditions. Analyzed >27,000 genomes/bins (post-assembly/MAG candidates) across studies.
- Communicated results through posters/talks at national/international (ASM Microbe, International Soil Virus Conference).

Graduate Assistant

September 2019 – August 2023

Colorado State University, Fort Collins CO

PhD Candidate, The Microbial Ecosystems Lab, Colorado State University

Full-Time: 40+ Hours/Week

Dr. Kelly Wrighton 970-491-3227

- **Developed CBAJ-DB: the first metagenomic study and genome database of bacteria from healthy and inflamed CBA/J mice.**

The goal of this project was to provide a genome resource to microbiome researchers who use the CBA/J mouse model and those who work in the murine gut microbiome space more broadly. Through iterative assembly and binning of high-depth metagenomic sequencing of both *Salmonella*-infected and uninfected CBA/J mice we recovered more than 2000 metagenomically assembled MAGs displaying taxonomic relevance to CBA mice, other mouse strains, and humans. This resource is made available to the public and can facilitate genome resolved multi-omic mapping of metatranscriptomic, metabolomic, and proteomic data to examine the murine gut microbiome comprehensively and holistically during pathogen challenge and inflammation. (Results accepted for publication in journal Microbiome)

- **Developed a bioinformatic pipeline for streamlined robust genome resolved metagenomic and metatranscriptomic feature mapping.**

The goal of this project was to incorporate the Microbial Ecosystems Lab's best practices into a flexible read-mapping and genome binning pipeline with HPC integration. I worked closely with our lab software developer to adapt bash scripting and command line bioinformatics tools to a Snakemake workflow that utilized FastQC, Sickle, rqcfilter2, Samtools, Bowtie2, CoverM, FeatureCounts, Megahit, IDBA-UD, and Metabat2 to flexibly map metatranscriptomic or metagenomic reads to a MAG database or to assemble and bin metagenomic reads. Pipeline development was an iterative process involving multiple team members. Ultimately, I provided metagenomic expertise, post hoc QC and tool validation, and bioinformatic tool scripts and individual Snakemake workflows which were integrated into the final product. A truncated example of the binning workflow was published in *Exposing New Taxonomic Variation with Inflammation – A Murine Model-Specific Genome Database for Gut Microbiome Researchers* and on Github (https://github.com/ileleiwi/metaG_pipeline).

- **Multi-omics analysis of the murine *Salmonella* pathobiome metabolic framework for sulfur metabolism in the inflamed gut.**

The goal of this research project was to integrate metabolomic, metatranscriptomic, and whole community genomic sequencing of the inflamed *Salmonella*-included murine gut microbiome to expound pathogen/commensal interactions during enteric infection. I used machine learning techniques (association rule mining, logistic regression, and random forest) to predict *Salmonella* association of individual MAGs from DRAM gene annotations. Important features of each model were examined as potential points of interaction between *Salmonella* and commensal bacteria during infection. Metabolomic and metatranscriptomic data from the inflamed mouse guts were interrogated for a system-level depiction of the microbiome during *Salmonella* infection. These data were integral in determining key microbiota membership that persists during inflammation and are involved in sulfur turnover and ultimately inorganic sulfur oxidation to tetrathionate in support of *Salmonella* anaerobic respiration and proliferation in the gut. In the course of this work, I wrote an R based command line tool to perform multi-threaded association rule mining, found here https://github.com/ilelewi/ARM_analysis.

- **Preliminary PhD exam involved substantial research into bacteriocin produced by lactic acid bacteria and recombinant plasmid transformation of bacteria for probiotic bacteriocin production and *Salmonella* amelioration.**

The preliminary exam for PhD candidacy in the Cell and Molecular Biology program consisted of a written grant proposal and an oral section. My successful defense and progression to doctoral candidate required communicating with my program director, advisor, and committee members to produce an NIH grant proposal on the isolation of a probiotic *Lactobacillus* strain from a complex community and further examination of *Lactobacillus* derived antimicrobial peptides for direct antagonism of *Salmonella*. An extensive literature review on the topic of lactic acid bacteriocin and *in silico* analysis of multiple *Lactobacillus* genomes led me to hypothesize that the persistent *Lactobacillus* sp. we observe in highly inflamed mice following *Salmonella* infection produced an antimicrobial peptide antagonistic to *Salmonella*. The grant involved three aims: 1) Identify *Lactobacillus* strains most antagonistic to *Salmonella in vitro*, 2) Identify potential antimicrobial peptides and/or bacteriocin from *Lactobacillus* cell-free supernatant (CFS), and 3) Confirm *Lactobacillus* bacteriocin growth inhibition of *Salmonella*. *Lactobacillus* isolates and purchased strains were to be grown in broth. I planned next to test *Lactobacillus* CFS on plated *Salmonella* cultures. Identification of antimicrobial molecules in the most potent CFS would then be performed with a combination of enzyme digestions to determine the macromolecular class and then with nanoLC-MS/MS. Next, I proposed to confirm antimicrobial inhibition of *Salmonella* with a *Lactobacillus* knockout mutant and an overexpression mutant. The proposal addressed a need for alternative antimicrobial treatments to *Salmonella* infection considering multi-drug resistant *Salmonella* strains and the impact of *Salmonella*-induced enteritis globally.

Laboratory Scientist at Western Health and Safety

May 2017 – July 2019

Greeley, CO

Full-Time: 40+ Hours/Week

Patrick Thomas, Director of Operations (970)776-3190

(promoted from clinical operations)

- Ran and maintained Indiko Plus analyzers for initial ELISA urine drug screen ~100 samples/day
- Ran and maintained Agilent LC/MS QQQ analyzers
- Troubleshoot and fixed mechanical and software problems with instruments
- Created SOPs and accuracy and precision plates integral to instrument validation and lab certification by CLIA/COLA

Lead Specimen Collector at Western Health and Safety

August 2015 – May 2017

Front Range, CO

Full-Time: 40+ Hours/Week

Dr. Kate McNerny and Dr. Stephanie Schittone, Director of Operations (970)776-3190

- Managed specimen collectors at 7 clinic locations
- Responsible for hiring, training, and disciplinary action
- Competent in urine, saliva, and cheek cell specimen collection
- Responsible for inventory of collection supplies at 7 pain clinic locations

Seasonal Field Biologist at Ottertail Environmental

May 2015 – August 2015

Boulder County, CO

Part-Time: 30 Hours/Week

Heidi Gerstrung, Supervisor (303) 858-8350 ext. 102

- Collected data and treated for mosquito larva in Boulder County
- Calculated acreage and lbs/acre of appropriate treatment

Graduate Assistant/Lab Tech in the Tropical Plant Pathology

May 2012 – September 2013

University of Hawaii at Manoa Honolulu, HI

Full-Time: 40+ Hours/Week

Dr. Koon-Hui Wang (808) 956-2455

- Performed agricultural research in plant disease and soil borne parasites, primarily nematodes
- Performed statistical analysis of result using SAS
- Maintained one-acre experimental plot and greenhouse, harvested and sorted produce by marketability for pest impact analysis

ACADEMIC PRESENTATIONS/AWARDS

Leleiwi, Ikaia; Trubl, Gareth; Campbell, Ashley; Kimbrel, Jeffrey A.; Bhattacharyya, Amrita; Riley, Robert; Malmstrom, Rex R.; Blazewicz, Steven J.; Pett-Ridge, Jennifer. 2025. Fluctuating Redox in tropical Rainforest Soils Impacts Microbial Community Structure and genetic Potential. **Rapid Fire Talk at 2025 American Society for Microbiology ASM Microbe, Los Angeles, CA.**

Leleiwi, Ikaia; Trubl, Gareth; Campbell, Ashley; Kimbrel, Jeffrey A.; Bhattacharyya, Amrita; Riley, Robert; Malmstrom, Rex R.; Blazewicz, Steven J.; Pett-Ridge, Jennifer. 2025. Fluctuating Redox in tropical Rainforest Soils Impacts Microbial Community Structure and genetic Potential. **Poster presentation at 2025 Lawrence Livermore National Laboratory Postdoc Poster Symposium, Livermore, CA.**

Leleiwi, Ikaia; Trubl, Gareth; Campbell, Ashley; Kimbrel, Jeffrey A.; Bhattacharyya, Amrita; Riley, Robert; Malmstrom, Rex R.; Blazewicz, Steven J.; Pett-Ridge, Jennifer. 2025. Fluctuating Redox in tropical Rainforest Soils Impacts Microbial Community Structure and genetic Potential. **Poster presentation at 2025 American Society for Microbiology ASM Microbe, Los Angeles, CA.**

Leleiwi, Ikaia; 2025 GRE results and new methods. **Contributing talk at 2025 Soil Microbiome SFA All Hands Meeting, Hopland, CA**

Leleiwi, Ikaia; Kokkinias, Katherine; Kim, Yongseok; Baniasad, Maryam; Shaffer, Michael; Sabag-Daigle, Anice; Daly, Rebecca A.; Flynn, Rory M.; Wysocki, VickiH.; Ahmer, Brian M. M.; Borton, Mikayla A.; Wrighton, Kelly C. 2024 Gut microbiome carbon and sulfur metabolisms support *Salmonella* during pathogen infection. **Poster presentation at 2024 International Society of Microbial Ecologists Symposium, Cape Town, South Africa.**

Leleiwi, Ikaia; Trubl, Gareth; Campbell, Ashley; Kimbrel, Jeffrey A.; Bhattacharyya, Amrita; Riley, Robert;

Malstrom, Rex; Blazewicz, Steven J.; Pett-Ridge, Jennifer. 2024 Tropical soil redox conditions influence viral community structure and virus-host interactions. **Contributing talk (remote) at 2024 International Soil Virus Conference, Livermore, CA**

Leleiwi, Ikaia; Kim, Yongseok; Kokkinias, Katherine; Baniasad, Maryam; Shaffer, Michael; Sabag-Daigle, Anice; Daly, Rebecca A; Flynn, Rory; Wysocki, Vicki H; Ahmer, Brian M M; Borton, Mikayla A; Wrighton, Kelly C. 2023 Multi-omics exposes persistent bacteria and infers new metabolism in the inflamed *Salmonella*-included gut. **Contributing talk at 2023 *Salmonella* Biology and Pathogenesis Gordon Research Seminar, Lucca (Barga), LU, Italy**

Leleiwi, Ikaia; Kim, Yongseok; Kokkinias, Katherine; Baniasad, Maryam; Shaffer, Michael; Sabag-Daigle, Anice; Daly, Rebecca A; Flynn, Rory; Wysocki, Vicki H; Ahmer, Brian M M; Borton, Mikayla A; Wrighton, Kelly C. 2023 Multi-omics exposes persistent bacteria and infers new metabolism in the inflamed *Salmonella*-included gut. **Poster presentation at 2023 *Salmonella* Biology and Pathogenesis Gordon Research Conference, Lucca (Barga), LU, Italy**

GRC Carl Storm Underrepresented Minority Fellowship. \$1000 fellowship to support participation in the 2023 Gordon Research Conference on Salmonella Biology and Pathogenesis.

Leleiwi, Ikaia; Kim, Yongseok; Kokkinias, Katherine; Baniasad, Maryam; Shaffer, Michael; Sabag-Daigle, Anice; Daly, Rebecca A; Flynn, Rory; Wysocki, Vicki H; Ahmer, Brian M M; Borton, Mikayla A; Wrighton, Kelly C. 2023 Multi-omics exposes persistent bacteria and infers new metabolism in the inflamed *Salmonella*-included gut. **Poster presentation at 2023 Computational & Systems Biology Annual Symposium in Fort Collins, CO**

Leleiwi, Ikaia; Shaffer, Michael; Borton, Mikayla A.; Sabag-Daigle, Anice; Rodriguez-Ramos, Josue; Daly, Rebecca A.; Flynn, Rory; Kop, Linnea; Wysocki, Vicki; Ahmer, Brian; Wrighton, Kelly C. 2022. Creation of a gut Microbial and Viral Genome Catalog Exposes Gene Content and Taxonomic Variation in Inflamed and Non-Inflamed Mice. **Award recipient for 3rd place poster at 2022 Front Range Computational & Systems Biology Symposium in Fort Collins, CO**

Leleiwi, Ikaia; Shaffer, Michael; Borton, Mikayla A.; Sabag-Daigle, Anice; Rodriguez-Ramos, Josue; Daly, Rebecca A.; Flynn, Rory; Kop, Linnea; Wysocki, Vicki; Ahmer, Brian; Wrighton, Kelly C. 2022. Creation of a gut Microbial and Viral Genome Catalog Exposes Gene Content and Taxonomic Variation in Inflamed and Non-Inflamed Mice. **Award recipient for 1st place poster at 2022 Front Range Microbiome Symposium in Fort Collins, CO**

Leleiwi, Ikaia; Healthy and Inflamed CBA/J Gut Microbiota Database. **Contributing talk at 2022 Congress on Gastrointestinal Function remote**

Leleiwi, Ikaia; Shaffer, Michael; Borton, Mikayla A.; Sabag-Daigle, Anice; Daly, Rebecca A.; Kop, Linnea; Wysocki, Vicki; Ahmer, Brian; Wrighton, Kelly C. 2021. Friend, foe, or indifferent? Untangling the relationship between *Salmonella* and *Lactobacillus* in the inflamed gut. **Poster presented at 2021 Front Range Computational & Systems Biology Symposium in Fort Collins, CO**

qCMB T32 Fellowship. Quantitative biology training grant award focused on career development and computational biology training. Full tuition, fees, and stipend provided. Fall 2020/Spring 2022

Cell and Molecular Biology CSU 2020 Travel Award. \$500 for travel to ASM Microbe conference.

Leleiwi, Ikaia; K.-H., Wang; B. S., Sipes. 2013. Reniform nematode management using sunn hemp cover cropping and post-plant soil surfactant application. **Poster presented at 2013 Society of Nematologists 52nd annual meeting in Knoxville, TN.**

Leleiwi, Ikaia; Lingenfelser, David; Wang, Koon-Hui. 2013. Marigold planting date for plant-parasitic nematode management on banana. CTAHR Symposium. **Award recipient for best Masters student poster in Plant and Environmental Protection Sciences.**

Lingenfelser, David; Leleiwi, Ikaia; Wang, Koon-Hui. 2012. Using cover crops to manage plant-parasitic nematodes on Banana. CTAHR Symposium. **Award recipient for best undergraduate poster in Tropical Plant and Soil Sciences.**

RESEARCH SUPPORT

- EMSL Exploratory Research Award: CO-PI, **61520 Honeker**: *Using meta-omics and machine learning to predict soil organic carbon transformations following seasonal moisture changes in a Mediterranean grassland 2025-2026*
- NIH T32: Quantitative Cell and Molecular Biology T32 Fellowship Program: Career planning and internship preparation. Curriculum focused on quantitative approaches used to analyze biological data. Ethics, Reproducible Research, Collaboration, communication and networking. Kelly Wrighton, Advisor. 2020-2022.

CONTINUING TRAINING

- PL8000-V: Impact Players, How to step up, take the lead and build a team of difference makers “Multiply Your Impact”
- ED7739-V: Powerful Communication: The Blueprint to a Successful Career for Young Professionals
- ED8361-V: Powerful Technical Presentations

MANUSCRIPTS IN PROGRESS

- (In Prep) **Ikaia Leleiwi**, Gareth Trubl, Ashley Campbell, Jeffrey A. Kimbrel, Amrita Bhattacharyya, Robert Riley, Rex T. Malstrom, Steven J. Blazewicz, Jennifer Pett-Ridge. Fluctuating redox in tropical rainforest soils impacts bacteria community structure and genetic potential. Target journal Microbiome.
- (In Prep) Gareth Trubl, **Ikaia Leleiwi**, Ashley Campbell, Jeffrey A. Kimbrel, Amrita Bhattacharyya, Robert Riley, Rex T. Malstrom, Steven J. Blazewicz, Jennifer Pett-Ridge. Soil redox drives virus-host community dynamics and plant biomass degradation in tropical rainforest soils. Target journal Microbiome bioRxiv preprint <https://www.biorxiv.org/content/10.1101/2024.09.13.612973v1>.
- (In Review) Maryam Baniasad; Michael Shaffer; Yongseok Kim; Anice Sabag-Diagle; **Ikaia Leleiwi**; Mikayla A. Borton; Brian M. M. Ahmer; Kelly C. Wrighton; Vicki H. Wysocki. Proteomics Characterization of CBA/J Mouse Feces During *Salmonella* Infection. Journal of Proteome Research

PUBLICATIONS

- Mikayla A Borton, Bridget B McGivern, Kathryn R Willi, Ben J Woodcroft, Annika C Mosier, Derick M Singleton, Ted Bambakidis, Aaron Pelly, Filipe Liu, Janaka N Edirisinghe, José P Faria, **Ikaia Leleiwi**, Rebecca A Daly, Amy E Goldman, Michael J Wilkins, Ed K Hall, Christa Pennacchio, Simon Roux, Emiley A Eloie-Fadrosch, Stephen P Good, Matthew B Sullivan, Christopher S Henry, Elisha M Wood-Charlson, Matthew RV Ross, Christopher S Miller, Byron C Crump, James C Stegen, Kelly C Wrighton. A functional microbiome catalog crowdsourced from North American rivers. Nature. <https://doi.org/10.1038/s41586-024-08240-z>

- **Ikaia Leleiwi**, Katherine Kokkinias, Yongseok Kim, Maryam Baniasad, Michael Shaffer, Anice Sabag-Daigle, Rebecca A. Daly, Rory M. Flynn, Vicki H. Wysocki, Brian M. M. Ahmer, Mikayla A. Borton, Kelly C. Wrighton. Gut microbiota carbon and sulfur metabolisms support *Salmonella* infections. ISMEJ <https://doi.org/10.1093/ismejo/wrae187>
- Katherine Kokkinias, Anice Sabag-Daigle, Yongseok Kim, **Ikaia Leleiwi**, Michael Shaffer, Richard Keverkian, Rebecca A. Daly, Vicki H. Wysocki, Mikayla A. Borton, Brian M. M. Ahmer, Kelly C. Wrighton. Time resolved multi-omics reveals diverse metabolic strategies of *Salmonella* during diet-induced inflammation. mSphere <https://doi.org/10.1128/msphere.00534-24>
- Yongseok Kim, Katherine Kokkinias, Anice Sabag-Daigle, **Ikaia Leleiwi**, Mikayla Borton, Michael Shaffer, Maryam Baniasad, Rebecca Daly, Brian MM Ahmer, Kelly C Wrighton, Vicki H Wysocki. Time-Resolved Multiomics Illustrates Host and Gut Microbe Interactions during *Salmonella* Infection. Journal of Proteome Research <https://doi.org/10.1021/acs.jproteome.4c00172>
- **Ikaia Leleiwi**; Josue Rodriguez-Ramos; Michael Shaffer; Anice Sabag-Daigle; Katherine Kokkinias; Rory M Flynn; Rebecca A Daly; Linnea FM Kop; Lindsey M Solden; Brian M. M. Ahmer; Mikayla A Borton; Kelly C Wrighton. Exposing New Taxonomic Variation with Inflammation – A Murine Model-Specific Genome Database for Gut Microbiome Researchers. Microbiome Journal <https://doi.org/10.1186/s40168-023-01529-7>
- Maryam Baniasad, Yongseok Kim; Michael Shaffer; Anice Sabag-Daigle; **Ikaia Leleiwi**; Rebecca A. Daly; Brian M. M. Ahmer; Kelly C. Wrighton & Vicki H. Wysocki. Optimization of proteomics sample preparation for identification of host and bacterial proteins in mouse feces. Journal of Analytical and Bioanalytical Chemistry. <https://doi.org/10.1007/s00216-022-03885-z>

REFERENCES

- Dr. Gary Trubl – Lawrence Livermore National Laboratory – Staff Scientist – Bioscience and Biotechnology Division
 - Postdoctoral Mentor
 - 602-317-8208
 - Trubl1@llnl.gov
- Dr. Jeffrey Kimbrell – Lawrence Livermore National Laboratory – Staff Scientist – Bioscience and Biotechnology Division
 - Bioinformatics Mentor
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 - Kimbrell1@llnl.gov
- Dr. Kelly Wrighton - Colorado State University – Associate Professor – Soil and Crop Sciences
 - Doctoral advisor
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- Dr. Carol Wilusz – Colorado State University – Cell and Molecular Biology Program Director – MIP
 - Program director
 - 970-491-4919
 - carol.wilusz@colostate.edu
- Dr. Michael Shaffer – Bill & Melinda Gates Medical Research Institute – Bioinformatics Scientist
 - Bioinformatics researcher and biological data scientist
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