LUIGUI GALLARDO-BECERRA

BIOINFORMATICIAN | MOLECULAR BIOLOGIST

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CAREER SUMMARY

Experienced Bioinformatician and Molecular Biologist seeking new challenges to apply and expand my expertise in computational biology, data science, and molecular research. Over the past several years, I have contributed to diverse research projects utilizing modern genomic technologies (NGS), advanced data analysis, and data science methodologies to generate novel biological insights that have resulted in high-impact peer-reviewed scientific publications.

RESEARCH EXPERIENCE

Graduate Research Assistant (Bioinformatics & Molecular Biology) | Institute of Biotechnology, UNAM January 2019 - March 2026

Across several interdisciplinary research projects, I contributed to data acquisition, computational analysis, and dissemination of scientific results. My responsibilities included:

- **Project conceptualization:** Assisted in defining research goals, experimental design, analytical workflows, and computational strategies to address multi-omics biological questions.
- **HPC system administration:** Maintained laboratory computational infrastructure, including Linux installation, software configuration, performance optimization, and data security practices.
- **Reproducible workflow engineering:** Built robust, scalable, and reproducible pipelines using Bash, Nextflow, and Snakemake, to automate NGS and metagenomic analyses.
- **Custom tool development:** Implemented specialized algorithms and utilities in Python, R, Bash, and C# to support complex multi-step analyses.
- **Quantitative data visualization:** Designed comprehensive visualizations and figure panels using ggplot2, seaborn, matplotlib, and Jupyter Notebooks.
- **Computational best practices:** Maintained version control through GitHub repositories and incorporated CI/CD testing to ensure workflow reliability.
- **Scientific reporting:** Prepared internal research reports, contributed to manuscript writing, and provided analytical support for high-impact publications.
- **Presentation & outreach:** Delivered oral and poster presentations at national and international conferences and participated in science communication initiatives.

EDUCATION

Ph.D. in Biochemistry| National Autonomous University of Mexico (UNAM) | Mexico — January 2019 – July 2025
Master of Science in Biochemistry | National Autonomous University of Mexico (UNAM) | Mexico — August 2016 - January 2019
Bachelor of Science in Biology | University of Guadalajara (UDG) | Guadalajara, Mexico — August 2012 - January 2016

TEACHING EXPERIENCE

- Organizer and instructor of the "Bioinfo del Norte" bioinformatics and metagenomics training event, CIAD, Hermosillo, Sonora. September 2024.
- Guest lecturer at Universidad de La Sabana (Chia, Colombia). December 2023.
- Microbiota Symposium from Theory to Clinical Practice, Colegio de Profesionales de la Nutrición de Querétaro y el Bajío. June 2021.
- Bioinformatics and Reproducible Research Workshop, Postgraduate Program in Biological Sciences, UNAM. October 2019.
- Guest lecturer at Center of Genomic Sciences, UNAM. August 2018.

DIRECTED THESES

Bachelor's Thesis: Itzel Abigail Hernández Reyna, Bachelor's in Nutrition (Universidad Autónoma del Estado de Morelos), December 2019. "Impact of bacteriophages associated with childhood obesity on the intestinal metagenome."

SOFT SKILLS

- Adaptable and quick to learn new technologies, analytical methods, and computational tools.
- Strong problem-solving skills with the ability to manage multiple complex projects while maintaining high-quality output.
- Effective communicator with experience collaborating in interdisciplinary teams as well as working independently.
- Skilled in technical operations including server maintenance, Git/GitHub workflows, and development of automated scripts for research tasks.

PROGRAMMING LANGUAGES, TOOLS, BIOINFORMATICS & MOLECULAR BIOLOGY SKILLS

Specialized Bioinformatics Skills: Genome and transcriptome assembly & annotation; differential expression analysis; taxonomic profiling; functional & pathway analysis; ETL automation for multi-omics data

Bioinformatics Tools & Methods: Snakemake, Nextflow, QIIME2, Trinity, SPAdes, Bowtie2, BWA, HISAT2, samtools, Spades, Kraken2

NGS & Multi-omics Analysis: RNA-seq, WGS, 16S rRNA profiling, metagenomics, metatranscriptomics, viromics

Molecular Biology Skills: DNA/RNA extraction, PCR/qPCR, gel electrophoresis, sample QC, NGS library preparation, bacterial culture & handling, plasmid preparation, sterile technique (BSL-2), and collaboration with wet-lab teams

Programming Languages: Python, R, Bash, SQL, C#, JavaScript, TypeScript, HTML/CSS

Frameworks & Libraries: React, Django, ASP.NET Core, Shiny

Computing & DevOps: Linux, High-Performance Computing, Docker, Git/GitHub, CI/CD workflows, Conda

Data Science & Visualization: ggplot2, seaborn, matplotlib, Jupyter Notebooks, RStudio

Databases: MySQL, PostgreSQL, MongoDB

LANGUAGES

English – Full professional proficiency

Spanish – Native

PUBLICATIONS

1. Jatuyosporn T, Laohawutthichai P, Cornejo-Granados F, **Gallardo-Becerra L**, Tassanakajon A, Hurtado-Ramírez JM, Ochoa-Leyva A, Krusong K. *De novo* transcriptome assembly and annotation of *Penaeus monodon* hemocytes under WSSV infection and STAT knockdown. Sci Data. 2026.
2. **Gallardo-Becerra L**, Cornejo-Granados F, Bikel S, Arenas I, López-Leal G, Alvarado-Gonzalez C, Sánchez-López F, Manzo R, Corzo G, Espino-Solis GP, Canizales-Quinteros S, Ochoa-Leyva A. Bioactive plasmid- and phage-encoded antimicrobial peptides (AMPs) in the human gut: a metatranscriptome–virome profiling reveals exploratory links to metabolic human diseases. Microb Ecol. 2025 Nov 28.
3. Cornejo-Granados F, **Gallardo-Becerra L**, Romero-Hidalgo S, Lopez-Zavala AA, Cota-Huízar A, Cervantes-Echeverría M, Sotelo-Mundo RR, Ochoa-Leyva A. Host genome drives the microbiota enrichment of beneficial microbes in shrimp: exploring the hologenome perspective. Animal Microbiome. 2025 May 22;7(1):50.
4. Manzo R, **Gallardo-Becerra L**, Díaz de León-Guerrero S, Villaseñor T, Cornejo-Granados F, Salazar-León J, Ochoa-Leyva A, Pedraza-Alva G, Pérez-Martínez L. Environmental Enrichment Prevents Gut Dysbiosis Progression and Enhances Glucose Metabolism in High-Fat Diet-Induced Obese Mice. International Journal of Molecular Sciences. 2024 Jan;25(13):6904.
5. Jatuyosporn T, Laohawutthichai P, Ochoa Romo JP, **Gallardo-Becerra L**, Sánchez Lopez F, Tassanakajon A, Ochoa-Leyva A, Krusong K. White spot syndrome virus impact on the expression of immune genes and gut microbiome of black tiger shrimp Penaeus monodon. Sci Rep. 2023 Jan 18;13(1):996.
6. **Gallardo-Becerra L**, Cervantes-Echeverría M, Cornejo-Granados F, Vazquez-Morado LE, Ochoa-Leyva A. Perspectives in Searching Antimicrobial Peptides (AMPs) Produced by the Microbiota. Microb Ecol. 2023 Dec 1;87(1):8.
7. Chino de la Cruz CM, Cornejo-Granados F, **Gallardo-Becerra L**, Rodríguez-Alegría ME, Ochoa-Leyva A, López Munguía A. Complete genome sequence and characterization of a novel Enterococcus faecium with probiotic potential isolated from the gut of Litopenaeus vannamei. Microbial Genomics. 2023;9(3):000938.
8. Cervantes-Echeverría M, **Gallardo-Becerra L**, Cornejo-Granados F, Ochoa-Leyva A. The Two-Faced Role of crAssphage Subfamilies in Obesity and Metabolic Syndrome: Between Good and Evil. Genes. 2023 Jan;14(1):139.

9. Palomino-Hermosillo YA, Berumen-Varela G, Ochoa-Jiménez VA, Balois-Morales R, Jiménez-Zurita JO, Bautista-Rosales PU, Martínez-González ME, López-Guzmán GG, Cortés-Cruz MA, Guzmán LF, Cornejo-Granados F, **Gallardo-Becerra L**, Ochoa-Leyva A, Alia-Tejacal I. Transcriptome Analysis of Soursop (Annona muricata L.) Fruit under Postharvest Storage Identifies Genes Families Involved in Ripening. Plants (Basel). 2022 Jul 7;11(14):1798.
10. Ochoa-Romo JP, Cornejo-Granados F, Lopez-Zavala AA, Viana MT, Sánchez F, **Gallardo-Becerra L**, Luque-Villegas M, Valdez-López Y, Sotelo-Mundo RR, Cota-Huízar A, López-Munguia A, Ochoa-Leyva A. Agavin induces beneficial microbes in the shrimp microbiota under farming conditions. Sci Rep. 2022 Apr 16;12(1):6392.
11. Bikel S, **Gallardo-Becerra L**, Cornejo-Granados F, Ochoa-Leyva A. Protocol for the isolation, sequencing, and analysis of the gut phageome from human fecal samples. STAR Protocols. 2022 Mar 18;3(1):101170.
12. Bikel S, López-Leal G, Cornejo-Granados F, **Gallardo-Becerra L**, García-López R, Sánchez F, Equihua-Medina E, Ochoa-Romo JP, López-Contreras BE, Canizales-Quinteros S, Hernández-Reyna A, Mendoza-Vargas A, Ochoa-Leyva A. Gut dsDNA virome shows diversity and richness alterations associated with childhood obesity and metabolic syndrome. iScience. 2021 Aug 20;24(8):102900.
13. **Gallardo-Becerra L**, Cornejo-Granados F, García-López R, Valdez-Lara A, Bikel S, Canizales-Quinteros S, López-Contreras BE, Mendoza-Vargas A, Nielsen H, Ochoa-Leyva A. Metatranscriptomic analysis to define the Secrebiome, and 16S rRNA profiling of the gut microbiome in obesity and metabolic syndrome of Mexican children. Microb Cell Fact. 2020 Dec;19(1):61.
14. Cornejo-Granados F, **Gallardo-Becerra L**, Leonardo-Reza M, Ochoa-Romo JP, Ochoa-Leyva A. A meta-analysis reveals the environmental and host factors shaping the structure and function of the shrimp microbiota. PeerJ. 2018 Aug 10;6:e5382.
15. Cornejo-Granados F, Lopez-Zavala AA, **Gallardo-Becerra L**, Mendoza-Vargas A, Sánchez F, Vichido R, Brieba LG, Viana MT, Sotelo-Mundo RR, Ochoa-Leyva A. Microbiome of Pacific Whiteleg shrimp reveals differential bacterial community composition between Wild, Aquacultured and AHPND/EMS outbreak conditions. Sci Rep. 2017 Dec;7(1):11783.