

Luigui Gallardo-Becerra

BIOINFORMATICIAN & MOLECULAR BIOLOGIST

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Bioinformatician and Molecular Biologist looking for new challenges to apply and expand my skills. In recent years, I participated in different projects using modern Genomic technologies (NGS), Data Analysis, and Data Science, to obtain novel biological information that culminated in high-impact peer-reviewed scientific publications

Research experience

Graduate Research Assistant (Computational Biology)

Institute of Biotechnology, UNAM

January 2019 - Current

I was part of different research projects with a focus on molecular biology and bioinformatics, managing projects from sample preparation and data generation through final reports and publications. Key tasks included:

- Molecular Biology Lab Techniques: DNA/RNA extractions, PCR, gel electrophoresis, cloning, NGS libraries preparation, etc.
- Research Project Management: Participated in defining research objectives, designing experiments, and contributing to the generation of novel biological insights.
- Computational Biology: Managed the laboratory's server (Linux systems), developed pipelines in Bash, Python, and Nextflow for reproducible analysis, and created visualizations using R, Jupyter Notebooks, and other tools.
- Software Development: Built custom software tools in Bash, Python, Perl, and R to solve research challenges and streamline analysis.
- Scientific Communication: Co-authored peer-reviewed publications, prepared reports, and presented findings at seminars and conferences.

Education

National Autonomous University of Mexico

PH.D. (COMPUTATIONAL BIOLOGY)

Mexico City, Mexico

January 2019 - Current

National Autonomous University of Mexico

MASTER OF SCIENCE (COMPUTATIONAL BIOLOGY)

Mexico City, Mexico

August 2016 - January 2019

University of Guadalajara

BACHELOR OF SCIENCE (MOLECULAR BIOLOGY)

Guadalajara, Mexico

August 2012 - January 2016

Soft skills

- Team player who can also work independently with excellent communication skills
- Fast learner and could quickly adapt to new technologies.
- Excellent problem-solving capabilities.
- Can manage a significant workload or several projects from different areas without losing track of them.

Skills:

- Bioinformatic skills: 16S rRNA profiling, Genome/Transcriptome assembly, and annotation, Metagenomics, Metatranscriptomics, Viromics
- Molecular Biology Techniques: DNA/RNA Extraction & Quantification, PCR techniques, Cloning, NGS libraries, RNA-seq
- Programming Languages & Tools: Python, C#, R, SQL, Bash, HTML & CSS, "Python", Jupyter Notebooks, Nextflow

Languages

- English – Full professional proficiency
- Spanish – Native

Publications

1. Gallardo-Becerra, L., Cervantes-Echeverría, M., Cornejo-Granados, F., Vazquez-Morado, L. E., & Ochoa-Leyva, A. (2023). Perspectives in Searching Antimicrobial Peptides (AMPs) Produced by the Microbiota. *Microbial Ecology*, 87(1), 8. <https://doi.org/10.1007/s00248-023-02313-8>
2. Gallardo-Becerra, L., Cornejo-Granados, F., García-López, R., Valdez-Lara, A., Bikel, S., Canizales-Quinteros, S., López-Contreras, B. E., Mendoza-Vargas, A., Nielsen, H., & Ochoa-Leyva, A. (2020). Metatranscriptomic analysis to define the Secrebiome, and 16S rRNA profiling of the gut microbiome in obesity and metabolic syndrome of Mexican children. *Microbial Cell Factories*, 19(1), 61. <https://doi.org/10.1186/s12934-020-01319-y>
3. Bikel, S., Gallardo-Becerra, L., Cornejo-Granados, F., & Ochoa-Leyva, A. (2022). Protocol for the isolation, sequencing, and analysis of the gut phageome from human fecal samples. *STAR Protocols*, 3(1), 101170. <https://doi.org/10.1016/j.xpro.2022.101170>
4. Bikel, S., López-Leal, G., Cornejo-Granados, F., Gallardo-Becerra, L., García-López, R., Sánchez, F., Equihua-Medina, E., Ochoa-Romo, J. P., López-Contreras, B. E., Canizales-Quinteros, S., Hernández-Reyna, A., Mendoza-Vargas, A., & Ochoa-Leyva, A. (2021). Gut dsDNA virome shows diversity and richness alterations associated with childhood obesity and metabolic syndrome. *iScience*, 24(8), 102900. <https://doi.org/10.1016/j.isci.2021.102900>
5. Cervantes-Echeverría, M., Gallardo-Becerra, L., Cornejo-Granados, F., & Ochoa-Leyva, A. (2023). The Two-Faced Role of crAssphage Subfamilies in Obesity and Metabolic Syndrome: Between Good and Evil. *Genes*, 14(1), Article 1. <https://doi.org/10.3390/genes14010139>
6. Chino de la Cruz, C. M., Cornejo-Granados, F., Gallardo-Becerra, L., Rodríguez-Alegría, M. E., Ochoa-Leyva, A., & López Munguía, A. (2023). Complete genome sequence and characterization of a novel *Enterococcus faecium* with probiotic potential isolated from the gut of *Litopenaeus vannamei*. *Microbial Genomics*, 9(3), 000938. <https://doi.org/10.1099/mgen.0.000938>
7. Cornejo-Granados, F., Gallardo-Becerra, L., Leonardo-Reza, M., Ochoa-Romo, J. P., & Ochoa-Leyva, A. (2018). A meta-analysis reveals the environmental and host factors shaping the structure and function of the shrimp microbiota. *PeerJ*, 6, e5382. <https://doi.org/10.7717/peerj.5382>
8. Cornejo-Granados, F., Lopez-Zavala, A. A., Gallardo-Becerra, L., Mendoza-Vargas, A., Sánchez, F., Vichido, R., Brieba, L. G., Viana, M. T., Sotelo-Mundo, R. R., & Ochoa-Leyva, A. (2017). Microbiome of Pacific Whiteleg shrimp reveals differential bacterial community composition between Wild, Aquacultured and AHPND/EMS outbreak conditions. *Scientific Reports*, 7(1), 11783. <https://doi.org/10.1038/s41598-017-11805-w>
9. Jatuyosporn, T., Laohawutthichai, P., Romo, J. P. O., Gallardo-Becerra, L., Lopez, F. S., Tassanakajon, A., Ochoa-Leyva, A., & Krusong, K. (2023). White spot syndrome virus impact on the expression of immune genes and gut microbiome of black tiger shrimp *Penaeus monodon*. *Scientific Reports*, 13(1), Article 1. <https://doi.org/10.1038/s41598-023-27906-8>
10. Ochoa-Romo, J. P., Cornejo-Granados, F., Lopez-Zavala, A. A., Viana, M. T., Sánchez, F., Gallardo-Becerra, L., Luque-Villegas, M., Valdez-López, Y., Sotelo-Mundo, R. R., Cota-Huizar, A., López-Munguía, A., & Ochoa-Leyva, A. (2022). Agavin induces beneficial microbes in the shrimp microbiota under farming conditions. *Scientific Reports*, 12(1), Article 1. <https://doi.org/10.1038/s41598-022-10442-2>
11. Palomino-Hermosillo, Y. A., Berumen-Varela, G., Ochoa-Jiménez, V. A., Balois-Morales, R., Jiménez-Zurita, J. O., Bautista-Rosales, P. U., Martínez-González, M. E., López-Guzmán, G. G., Cortés-Cruz, M. A., Guzmán, L. F., Cornejo-Granados, F., Gallardo-Becerra, L., Ochoa-Leyva, A., & Alia-Tejacal, I. (2022). Transcriptome Analysis of Soursop (*Annona muricata* L.) Fruit under Postharvest Storage Identifies Genes Families Involved in Ripening. *Plants*, 11(14), 1798. <https://doi.org/10.3390/plants11141798>