

RICARDO J. RIVERO

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EDUCATION

WASHINGTON STATE UNIVERSITY Pullman, WA
Ph.D. Biomedical Sciences (MPID) Exp. June 2027
Dissertation: The Ecological and Molecular determinants of reassortment in
Influenzaviruses and Hantaviruses.
Advisor: Dr. Stephanie N. Seifert

I.U COLEGIO MAYOR DE ANTIOQUIA Medellín, Antioquia, Colombia
B.Sc. (5-year program) Biotechnology September 2018
Dissertation: “Molecular detection of Hantavirus in Rodents of the Colombian Caribbean
using a Nested RT-qPCR”
Top 1% National Score in Natural Sciences

AWARDS AND HONORS

Andrés Bello Distinction: Awarded for achieving the best state-level score in
Chemistry. 2013

Best Saber pro Distinction: Recognized among the top 1% nationally in
sciences. 2018

Global Voice Travel Award: Chan-Zuckerberg Initiative recipient. 2022

Verena Lighthouse Scholars Fellowship: Selected by the Viral Emergence
Consortium, 2023

RESEARCH & PROFESSIONAL EXPERIENCE

WASHINGTON STATE UNIVERSITY Pullman, WA
Graduate Research Assistant, Paul G. Allen School for Global Health July 2023 - Present

Implemented a machine learning algorithm to study the contributions of ecological and
molecular variables to the reassortment frequency of hantaviruses.

Studied the effect of correcting for surveillance biases on the evolutionary relationship
between hantaviruses and their host species

Co-led the implementation and curation of a global dataset on the surveillance of
Hantaviruses and Arenaviruses in wildlife reservoirs.

Implemented and applied a framework for assembling hantavirus genomes recovered
through amplicon-sequencing from locally collected rodent samples.

Co-mentored two undergraduate studies in projects related to the genomics of Sin Nombre virus and the evolution of Flaviviruses in multi-host systems.

UNIVERSIDAD DE CÓRDOBA
Research Scientist, College of Veterinary Medicine

Montería, Colombia
July 2017 – July 2023

Led phylogenetic and phylodynamic analyses on dengue virus serotypes 2 and 3, showing repeated introductions into Colombia and onward exportation of multiple lineages across regions.

Developed and applied genomic epidemiology frameworks to reconstruct the introduction, local spread, persistence, and exportation of viral lineages in Colombia using large-scale pathogen genome data.

Directed metagenomic surveillance studies in mosquitoes and bats, contributing to the discovery and characterization novel bacterial and viral species, including Influenza A/H18N12

Characterized the genomic epidemiology of SARS-CoV-2 between 2020-2022 in Colombia, tracking variant emergence, replacement dynamics, and patterns of national circulation.

Contributed to the molecular and epidemiological investigation of cross-species SARS-CoV-2 transmission, including the first documentation of human-to-dog transmission in the Americas.

Led SARS-CoV-2 diagnostic development efforts, including the creation of an in-house multiplex RT-qPCR assay, a phenol-free RNA purification kit and a rapid ELISA for serological detection.

Contributed to the design and preclinical validation of a novel chimeric subunit vaccine candidate against SARS-CoV-2.

CORPORACIÓN UNIVERSIDAD DE LA COSTA
Research Scientist

Barranquilla, Colombia
June 2021 – May 2023

Designed and optimized a lateral flow assay prototype for the detection of anti-SNV antibodies from human sera (patent pending).

Optimized purification protocols to obtain Sin Nombre Virus nucleoprotein at serological grade.

Utilized CRISPR/Cas9 for genetic editing of bacterial strains to optimize the recombinant expression of Sin Nombre Virus nucleoprotein.

UNIVERSIDAD DE CÓRDOBA

Assistant Lecturer, Dept. of Health Sciences

Montería, Colombia

November 2019 – December 2021

Directed undergraduate thesis projects for the B.S. in Pharmacy, providing technical and methodological guidance and evaluating adherence to requirements for graduation.

RESEARCH INTERESTS

Genomic epidemiology and phylodynamic of infectious diseases.

Mathematical and epidemiological modeling of pathogen and vector dynamics.

AI and Machine Learning applications for predicting viral antigenic evolution.

Viral evolution and host-pathogen interactions in emerging diseases.

PUBLICATIONS

Citations: **357**; H-index: **12**; i10 index: **12**.

1. **Rivero R.** & Rickard, G. *et al.* First Sin Nombre virus (Orthohantavirus sinnombreense) genome sequences from the Northwestern United States. 2025.09.10.675434 Preprint at <https://doi.org/10.1101/2025.09.10.675434> (2025). Accepted in *Emerging Infectious Diseases*
2. **Rivero, R.** *et al.* Genomic epidemiology of dengue virus 2 and 3 reveals repeated introductions and exportations of several lineages in Colombia. *Cell Rep.* **45**, (2026).
3. Brown, A. J... **Rivero R.** ... Seifert SN *et al.* Comparative susceptibility of Old World and New World bat cell lines to Zika virus: Insights into viral replication and inflammatory responses. *PLoS Negl. Trop. Dis.* **20**, e0014065 (2026).
4. Simons, D., **Rivero R.** *et al.* Protocol to produce a systematic Arenavirus and Hantavirus host-pathogen database: Project ArHa. *Wellcome Open Res.* **10**, 227 (2025).
5. Gastelbondo-Pastrana, B. *et al.* Phenol-free *in-house* kit for RNA extraction with applicability to SARS-CoV-2 genomic sequencing studies: A contribution to biotechnological sovereignty in Colombia. *J. Virol. Methods* **334**, 115116 (2025).
6. Flórez, L. *et al.* Preclinical evaluation of the RBD-Trimeric vaccine: A novel approach to strengthening biotechnological sovereignty in developing countries against SARS-CoV-2 variants. *Travel Med. Infect. Dis.* **64**, 102820 (2025).
7. Echeverri-De la Hoz, D. *et al.* Genomics of novel influenza A virus (H18N12) in bats, Caribe Colombia. *Sci. Rep.* **15**, 6507 (2025).
8. López, Y. *et al.* Hard ticks (Ixodida: Ixodidae) in the Colombian Caribbean harbor the Jingmen tick virus: an emerging arbovirus of public health concern. *Parasit. Vectors* **17**, 268 (2024).
9. Charon, J. *et al.* Consensus statement from the first RdRp Summit: advancing RNA virus discovery at scale across communities. *Front. Virol.* **4**, (2024).
10. López, Y. *et al.* Borrelia puertoricensis in opossums (Didelphis marsupialis) from Colombia. *Parasit. Vectors* **16**, 448 (2023).

11. Wallau, G. L. *et al.* Arbovirus researchers unite: expanding genomic surveillance for an urgent global need. *Lancet Glob. Health* **11**, e1501–e1502 (2023).
12. **Rivero R.** & Jimenez-Silva, C. *et al.* Genomic epidemiology of SARS-CoV-2 variants during the first two years of the pandemic in Colombia. *Commun. Med.* **3**, 1–12 (2023).
13. Martínez, C. *et al.* SARS-CoV-2 in a tropical area of Colombia, a remarkable conversion of presymptomatic to symptomatic people impacts public health. *BMC Infect. Dis.* **2022 221 22**, 1–5 (2022).
14. Díaz, A. *et al.* Immunogenicity and safety of a RBD vaccine against SARS-CoV-2 in a murine model. *Travel Med. Infect. Dis.* **49**, 102427 (2022).
15. **Rivero, R.** *et al.* Human-to-dog transmission of SARS-CoV-2, Colombia. *Sci. Rep.* **12**, (2022).
16. Garay, E. *et al.* SARS-CoV-2 in eight municipalities of the Colombian tropics: High immunity, clinical and sociodemographic outcomes. *Trans. R. Soc. Trop. Med. Hyg.* **116**, (2022).
17. Serrano-Coll, H. *et al.* Effectiveness of the CoronaVac® vaccine in a region of the Colombian Amazon, was herd immunity achieved? *Trop. Dis. Travel Med. Vaccines* **8**, (2022).
18. Serrano-Coll, H. *et al.* High Prevalence of SARS-CoV-2 in an Indigenous Community of the Colombian Amazon Region. *Trop. Med. Infect. Dis.* **6**, 191 (2021).
19. **Rivero, R. H.**, Gonzalez, M. & Mattar, S. SARS-CoV-2 vaccines: evolution and escape. *Rev. Mvz Cordoba* **26**, 10–12 (2021).
20. Novoa, W. *et al.* A first probable case of SARS-CoV-2 reinfection in Colombia. *Ann. Clin. Microbiol. Antimicrob.* **20**, (2021).
21. Mattar, S. *et al.* Epidemiological and viral features of a cohort of SARS-CoV-2 symptomatic and asymptomatic individuals in an area of the Colombian Caribbean. *Ann. Clin. Microbiol. Antimicrob.* **19**, (2020).
22. Faccini-Martínez, Á. A., **Rivero R.** *et al.* Serological cross-reactivity using a SARS-CoV-2 ELISA test in acute Zika virus infection, Colombia. *Int. J. Infect. Dis.* **101**, (2020).
23. Mattar, S. *et al.* Severe Acute Respiratory Syndrome Coronavirus 2 Seroprevalence among Adults in a Tropical City of the Caribbean Area, Colombia: Are We Much Closer to Herd Immunity Than Developed Countries? *Open Forum Infect. Dis.* **7**, (2020).

BOOK CHAPTERS

Contreras V., Sánchez-Lerma. L., Gastelbondo-Pastrana B., Máttar S., **Rivero-Herrera, R.** Epidemiología de la pandemia por COVID-19. En: Máttar S., Gastelbondo-Pastrana B., editores. Lecciones aprendidas del COVID-19: Una mirada interdisciplinaria. Sincelejo (Colombia): Editorial CECAR, 2023. p. 59-82. DOI: <https://doi.org/10.21892/9786287515376.4>

Serrano-Coll H., **Rivero-Herrera R.** Immunopatogénesis de la Infección por SARS-CoV-2. En: Máttar S., Gastelbondo-Pastrana B., editores. Lecciones aprendidas del COVID-19: Una mirada interdisciplinaria. Sincelejo (Colombia): Editorial CECAR, 2023. p. 28-41. DOI: <https://doi.org/10.21892/9786287515376.2>

PRESENTATIONS

Viral tapestry: Decoding the ecological and molecular threads of hantavirus evolution. **Ricardo Rivero**, David Simons, Lambodhar Damodaran, Alexander J. Brown, Daniel J. Becker, Dan L. Warren, Nicola F. Mueller, And Stephanie N. Seifert. – [22nd Ecology and Evolution of Infectious Diseases Conference, University of Notre Dame](#) (June 2025).

Linking genomic and spatiotemporal surveillance datasets to uncover the evolutionary history of hantaviruses. **Ricardo Rivero**, Lambodhar Damodaran, David Simmons, Daniel J. Becker, Stephanie N. Seifert – [Annual Meeting of the Ecological Society of America](#) (August 2024).

Virus-Host dynamics and re-assortment events shape the evolutionary history of Hantaviruses. **Ricardo Rivero**, Lambodhar Damodaran, David Simmons, Daniel J. Becker, Stephanie N. Seifert. - [21st Ecology and Evolution of Infectious Diseases Conference, Stanford University](#) (June 2024).

Linking genomic and spatiotemporal surveillance datasets to uncover the evolutionary history of Orthohantaviruses. **Ricardo Rivero**, David Simons, Lambodhar Damodaran, Stephanie N Seifert. – [Idaho and Washington Chapter of the Wildlife Society Annual Meeting](#) (March 2024)

LEADERSHIP AND SERVICE

Peer Reviewer for: *BMC Public Health, Scientific Reports, International Journal of Infectious Diseases Regions, Virology Journal, iScience, Society and Medicine, Viruses.*

Senator at large, College of Veterinary Medicine – Graduate and Professional Student Association, Washington State University

EschMentor, EschLEAD program, College of Veterinary Medicine, Washington State University.

PROFESSIONAL AFFILIATIONS

[Ecological Society of America](#) – Disease Ecology Chapter, [Washington Chapter of The Wildlife Society](#), [American Association for the Advancement of Science](#), [Sigma-Xi](#)

(Full), Society for Molecular Biology and Evolution (Full), American Society of Virology (Full).

TECHNICAL SKILLS

PROGRAMMING & DATA ANALYSIS

Advanced: R, Python, Shell, AWK, HTML5, CSS, Javascript.
Intermediate: SQL, Docker, Snakemake

BIOINFORMATICS & COMPUTATIONAL BIOLOGY

Next-Generation Sequencing analysis.
Genome assembly and development of bioinformatic pipelines
Data visualization and statistical analysis
Machine learning: Tree-based models, Neural Networks, Transformers.
Bayesian inference.
Phylogenetic analysis.
Workflow automation using Bash/Unix, Snakemake, and GNU Parallel.

LABORATORY & DIAGNOSTIC TECHNIQUES

Molecular assays: RT-qPCR, PCR.
Serological assays: ELISA, immunochromatography.
Nucleic acid extraction and purification.
Library preparation for Long-read and Short-read sequencing platforms (Nanopore, Illumina, BGI).

ADDITIONAL EDUCATION & CERTIFICATIONS

Universidad de Córdoba: Instrumental analysis for the food industry (2018)
Universidad Nacional Autonoma de Mexico: Intro to Data Science: Statistical Programming in R (2020).
Universidad del Rosario: Sequencing Tools for Characterizing Pathogens of Public Health Importance (2021).
Johns Hopkins Bloomberg School of Public Health: Infectious Disease Transmission Models for Decision-Makers (2022).
University of Idaho: Biology of Vector-Borne Diseases (2024).
TOEFL iBT: 111/120, C1 CEFR (November 2022)