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Assistant Professor

Emerging Pathogens Institute

Department of Pathology

College of Medicine

University of Florida (UF)

**EDUCATION**

2008-2013 **Doctor of Philosophy** **in Molecular Biology**

 Autonomous University of Madrid, Spain

2004-2007 **Master of Industrial Biotechnology** **(Immunology Major)**

 University of Padova, Italy

2001-2004 **Bachelor of Biotechnology**

 University of Padova, Italy

**PROFESSIONAL POSITIONS**

2023-current **Assistant Professor**

Department of Pathology, College of Medicine, UF, FL, USA

2023-current **Visiting Faculty**

Stellenbosch University, Cape Town, South Africa.

2022-current **Bioinformatics** **Contractor**

Pandemic Prevention Institute, Rockefeller Foundation, DC, USA

2022-current **Visiting Faculty**

Department for Innovation in Biological, Agrofood and Forest systems, University of Tuscia, Viterbo, Italy

2020-current **Member**

UF Biodiversity Institute, UF, FL, USA

2019-2023 **Research Assistant Scientist**

Department of Pathology, College of Medicine, UF, FL, USA

2016-2019 **Postdoctoral Associate**

Dr. M. Salemi Laboratory, Department of Pathology, College of Medicine, UF, FL, USA

2014-2016 **Postdoctoral Associate**

Dr. M. Goodenow Laboratory, Department of Pathology, College of Medicine, UF, FL, USA

2008-2013 **Doctoral Student**

Dr. A. Alcamí laboratory, Severo Ochoa Molecular Biology Center, Autonomous University of Madrid, Spain

2006-2007 **Master Student**

Dr. J. A. López de Castro laboratory, Severo Ochoa Molecular Biology Center, Autonomous University of Madrid, Spain

**RESEARCH** **SUPPORT**

2022-2027 R01AI170187-01.A Phylodynamic Artificial Intelligence framework to predict evolution of SARS-CoV-2 variants of concern in immunocompromised persons with HIV, Role: Co-Inv (Cal:1.2), NIH ($3,556,267)

2022-2027 1R01DK131533*.* Defining a role for liver and kidney macrophages in viral persistence under ART, Role: Co-Inv (Cal:4.80), NIH ($98,443)

2022-2023 Microbiome-based explainable AI for coronavirus prediction in bats from museum samples. Role: PI, University of Florida Biodiversity Institute, University of Florida SEED grant ($25,000)

2022-2023 Microbiome-based explainable AI for pathogen prediction. Role: PI, Informatics Institute, University of Florida SEED grant ($20,500)

2019-2024 R01AI145552: Forecasting trajectories of HIV transmission networks with a novel phylodynamic and deep learning framework, Role: Co-Inv (Cal:5.40), NIH ($3,629,768)

**PREVIOUS RESEARCH** **SUPPORT**

2021-2022 CBD-induced biomarkers of inflammation reduction in people living with HIV at the single cell level. Role: Co-PI (Cal:0.6), Consortium for Medical Marijuana Clinical Outcomes Research ($67,309)

2021-2022 Characterization of Floridan bat gut microbiota biodiversity using museum collection specimens. Role: PI, Department of Pathology EPIG RAS SEED grant University of Florida ($5,000)

2020-2021 RAPID-2028221: Dynamic Identification of SARS-COV-2 Transmission Epicenters in Presence of Spatial Heterogeneity, Role: Co-Inv (Cal:2.0), NSF ($166,530)

2020-2021 RAPID-330205-01: Epidemiological and phylogenetic models for contact - based control of COVID-19, Role: Co-Inv (Cal:3.0), NSF $199,009)

2017-2019 Salivary microRNA as novel biomarkers of HIV/AIDS disease progression in people living with HIV, Role: PI (Cal:3.0), UF Thomas H. Maren Award ($50,000)

2014-2015 Deep sequencing of the light chain of broadly-neutralizing anti-HIV antibodies, Role: PI (Cal:1.20), UF Experimental Pathology Intramural Grant ($10,000)

**SERVICE**

2023 Editor Peerj

2022 Mentor for ASTMH 8th Annual Speed-Networking with the Experts Session

2022 Reviewer for Swiss National Science Foundation (SNSF) for SNSF Starting Grants

2022-2025 ASTMH Scientific Program Committee, Virology Subcommittee, Chair Dr. Greg Ebel

2022 VEME Scientific organizing committee

2022 Reviewer for the NIH HIV Molecular Virology, Cell Biology and Drug Development (HVCD) review panel

2022 Invited panelist for ASM COVID-19 Registry Virtual Journal Club, “The emergence and ongoing convergent evolution of the SARS-CoV-2 N501Y lineages” by Sergei Pond.

2021 Department of Pathology Review Day (Research leadership team)

2021 Reviewer UF Experimental Pathology Intramural Grant

2021 Chair and Reviewer. Genetic Sequencing & Bioinformatics session at International Dynamics & Evolution of Human Viruses

2020 Department of Pathology Faculty Committee (Research Assistant Scientist hiring committee)

2019-current National Science Foundation Reviewer Graduate Research Fellowships Program (NSF GRFP), Evolutionary Biology & Systematics Panel

2019-current Volunteer at Vertebrate Paleontology at Florida Museum of Natural History

2018-current Certified Data Carpentry Instructor

2017-current Chair and Organization. Next Generation Sequencing module at International Bioinformatics Workshop on Virus Evolution and Molecular Epidemiology (VEME), KU Leuven.

2018 Reviewer UF Experimental Pathology Intramural Grant

2018 Reviewer Thomas H. Maren Postdoctoral Award 2019

**FELLOWSHIPS, HONORS** **AND** **AWARDS**

2023 Second best abstract at the Cannabis Clinical Outcomes Research Conference (CCORC), FL, USA.

2022 Faculty Enhancement Opportunity grant to visit CERI in South Africa, and NIH in Colombia in 2023 (*$17,000*).

2022 Travel Award, UF Partner Travel Fund *($2,000)*

2019 Travel Award, Cold Spring Harbor Laboratory (CSHL), Cold Spring Harbor, NY, USA *($1,350)*

2019 Travel Award, American Society of Microbiology, San Francisco, CA, USA *($500)*

2018 10th Summer Institute in Statistics and Modeling in Infectious Diseases Scholarship, University of Washington, Department Biostatistics, Seattle, WA *($1,950)*

2017 Young Investigator Award, American Society of Tropical Medicine and Hygiene (ASTMH), Baltimore, MD, USA *($750)*

2017 Travel Award American Committee on Arthropod-Borne Viruses (ACAV), Baltimore, MD, USA *($700)*

2017 Travel Award from Ministry of Science, Technology and Productive Innovation of Argentina *($3,500)*

2017 Experimental Pathology Innovative Grants Travel Award, UF, FL, USA *($3,000)*

2017 Fellowship to attend 9th Summer Institute in Statistics and Modeling in Infectious Diseases, University of Washington, Department Biostatistics, Seattle, WA, USA *($1,250)*

2015 Young Investigator Award, Conference of Retrovirology and Opportunistic Infections, Boston, MA, USA *($1,500)*

2013 Cum Laude Ph.D. Mention

2008 Ph.D. Fellowship, Spanish Ministry of Science and Education, Spain *($69,000)*

2004 European Union Erasmus Program Fellowship, University of Padova, Italy *($2,125)*

**NEWS COVERAGE**

2022 https://www.healio.com/news/infectious-disease/20221111/invasive-species-urbanization-raise-risk-for-everglades-virus-spillover-in-florida

2022 WUSF Public Media “All Things Considered” interview on Everglades virus evolution: Genome sequence analysis of the envelope protein reveals recent mutation and divergence in south Florida wetlands

**MENTORING**

2022-current Juan Perez Jimenez. Mechanism: UF Graduate Genetics and IDP Program. *Project:* evolution of cholera epidemics in Goma, DRC.

2022-2023 Jakob Beardsley, Biological scientist, UF Department of Pathology. *Project:* DNA/RNA extractions, NGS metagenomics and 16S library preparation, metagenomics and 16S analyses.

2022-2023 Olivia Gayle. Major: UF Health Science. Mechanism: University Multicultural Mentor Program (UMMP)

2022-2023 Kaidyn Jordan. Major: UF Agricultural and Life Sciences. Mechanism: UMMP

2021-2022 Maria Maneses. Major: UF Microbiology and Cell Science. Mechanism: Honor Thesis Advisor

2021-2022 Melanie Gonzalez. Major: UF Biology Pre-Professional. Mechanism: UMMP

2021-current Maclean Basset. Mechanism: UF Graduate Program Biomedical Sciences. *Project:* intra-host coronavirus evolution.

2020-2021 Malena Diez. Major: UF Biomedical engineering. Mechanism: UMMP

2019-current Shannan Rich, Ph.D. student, Department of Epidemiology. *Project:* Tracking of HIV in Florida.

2019-2020 Shaun Jensen, Biological scientist, UF Department of Pathology. *Project:* NGS library preparation, exosome purification, biomarker discovery.

2018-2020 Andrea Ramirez Mata, Biological scientist, UF Department of Pathology. *Project:* transcriptomics, biomarker discovery.

2017-2021 Taylor K. Paisie. Mechanism: UF Graduate Program Genetics and Genomics. *Project:* Evolution of *vibrio cholera*e in Haiti.

2016-2019 Yaser Alsahafi. Mechanism: UF Graduate Program Environmental and Global health. *Project:* Oral microbiome genomics and database.

2016-2017 Marta Fogolari, MD resident, UF Department of Pathology. *Project:* evolution of Shigella and their phages in Hispaniola.

2015-2016Andrea Ramirez Mata, UF Master student. *Project:* Characterization of the diversity of IgG-IgM light chain among SLE patients.

**TEACHING**

2023 Teaching CERI ACDC Fellows Workshop, Stellenbosch University, Cape Town, South Africa. 21 April 2023.

2022 Organization and teaching. Next Generation Sequencing module at 24th International Bioinformatics Workshop on Virus Evolution and Molecular Epidemiology (VEME) (36 hrs). Ciudad del Saber, Panama City, Panama.

2022 Tracing Outbreaks. PHC 7083: Computational Epidemiology in Population Science course by Dr. Mattia Prosperi, Department of Epidemiology, UF.

2022 Intro to phylodynamics. PHC 6937, Analytic Methods for Infectious Diseases course by Dr. Ira Longini, College of Public Health and Health Professions, UF.

2022 Principles of phylodynamics and case studies. PHC 6937, Analytic Methods for Infectious Diseases course by Dr. Ira Longini, College of Public Health and Health Professions, UF.

2022 Teaching assistant at Programming for Biology - CSHL Course, Cold Spring Harbor, NY, USA

2021 One-Health, vector-borne diseases and emerging arboviruses in the Caribbean area, zoom synchronous discussions (PHC 6446, Systems Thinking in One Health course, Dr. Ilaria Capua), Department of Epidemiology, UF.

2021 Organization. Online Webinar (COVEME): Next-generation Sequencing Day https://rega.kuleuven.be/cev/veme-workshop/2021/

2021 Molecular epidemiology of SARS-CoV-2: VOCs and intra-host evolution. ALS4932, sec. 19163-19164 COV2 Summer A 2021, Living the experiment the circular nature of the 2020 COVID-19 pandemic, course by Dr. Ilaria Capua

2020 Molecular epidemiology of SARS-CoV-2. ALS 4932- COV1/18644; HSC 4930-COVD/18837, The Circular Nature of the 2020 COVID-19 Pandemic, course by Dr. Ilaria Capua (https://youtu.be/\_CJC0bSQ1Ik)

2020 One-Health, vector-borne diseases and emerging arboviruses in the Caribbean area, zoom synchronous discussions (PHC 6446, Systems Thinking in One Health course, Dr. Ilaria Capua), Department of Epidemiology, UF.

2020 Intro to phylodynamics. PHC 6937, Analytic Methods for Infectious Diseases course by Dr. Ira Longini, College of Public Health and Health Professions, UF.

2020 Principles of phylodynamics and case studies. PHC 6937, Analytic Methods for Infectious Diseases course by Dr. Ira Longini, College of Public Health and Health Professions, UF.

2020 Organization and teaching.Data Carpentry Genomics Workshop, Summer 2020, UF (16 hrs). *Teaching objectives:* introduction to the command line, scripts writing, cloud computing, data wrangling and processing, trimming and filtering, variant calling, automating workflow, SLURM jobs submission, reference-based mapping.

2019 Molecular epidemiology of V. Cholera in Haiti: a phylodynamic approach (PHC 6517, Public Health Concepts in Infectious Diseases course, Dr. Chen Xinguang), Department of Epidemiology, UF.

2019 One-Health, vector-borne diseases and emerging arboviruses in the Caribbean area (PHC 6446, Systems Thinking in One Health course, Dr. Ilaria Capua), Department of Epidemiology, UF. Recording: <https://mediasite.video.ufl.edu/Mediasite/Play/ee8896ba54f447cd8f515e5c777c6fd51d>

2019 Organization and teaching. Data Carpentry Genomics Workshop, Fall 2019, UF (16 hrs). *Teaching objectives:* introduction to the command line, scripts writing, cloud computing, data wrangling and processing, trimming and filtering, variant calling, automating workflow, SLURM jobs submission, reference-based mapping.

2019 Organization and teaching. Next Generation Sequencing module at 24th International Bioinformatics Workshop on Virus Evolution and Molecular Epidemiology (VEME) (36 hrs). The University of Hong Kong, Hong Kong. *Teaching objectives:* trimming and filtering, variant calling, *de novo* assembly, reference-based mapping and metagenomics.

2019 Organization and teaching.Data Carpentry Genomics Workshop, Spring 2019, UF, 16 hrs). *Teaching objectives:* introduction to the command line, scripts writing, cloud computing, data wrangling and processing, trimming and filtering, variant calling, automating workflow, SLURM jobs submission, reference-based mapping.

2018 Organization and teaching. Next Generation Sequencing module at 23rd International Bioinformatics Workshop on Virus Evolution and Molecular Epidemiology (VEME) (36 hrs). Robert Koch-Institut, Berlin, Germany. *Teaching objectives:* *de novo* assembly, reference-based mapping and metagenomics.

2017 Zika virus: a pandemic in progress (PHC 4101 course, Dr. Linda Cottler). Department of Epidemiology, UF.

2017 Organization and teaching. Next Generation Sequencing module at 22nd International Bioinformatics Workshop on Virus Evolution and Molecular Epidemiology (VEME) (36 hrs). Lisbon, Portugal. *Teaching objectives:* trimming and filtering, variant calling, *de novo* assembly, reference-based mapping.

2017 Introduction to Phylodynamics - A Practical Approach to Molecular Phylogenetics of Pathogens, GMS 6234, UF (16 hrs). *Teaching objectives:* Molecular evolution, tree-building algorithms (distance, maximum likelihood and Bayesian based methods), molecular clocks theory, coalescence theory, phylogeography.

2017 Phylodynamics and bioinformatics course: evolution, origin and spread of viral pathogens. Pediatric Hospital Garrahan and University of Buenos Aires, Buenos Aires, Argentina (40 hrs). *Teaching objectives:* Molecular evolution, tree-building algorithms (distance, maximum likelihood and Bayesian based methods), molecular clocks theory, coalescence theory, phylogeography, adaptation and natural selection, recombination, Next Generation Sequencing (NGS).

2017 Introduction to Phylodynamics - A Practical Approach to Molecular Phylogenetics of Pathogens, GMS 6234, Spring 2017, UF (16 hrs). *Teaching objectives:* Molecular evolution, tree-building algorithms (distance, maximum likelihood and Bayesian based methods), molecular clocks theory, coalescence theory, phylogeography.

**PEER** **REVIEWED** **MANUSCRIPTS**

1. **Mavian C**, Tagliamonte MS, AlamMT, S. SakibN, CashMN, MoirM, Perez JimenezJ, RivaA, NelsonEJ, CatoET, AjayakumarJ, LouisR, CurtisA, Beau De RocharsVM, RouzierV, PapeJW, de OliveiraT, Morris JGJ, SalemiM, AliA. Ancestral origin and dissemination dynamic of toxigenic V. cholerae re-emergence in Haiti, EID, *in press*
2. Patel AR, Dulcey M, Abid N, Cash MN, Dailey J, Salemi M, **Mavian C#**, Vittor AY**#**. Infectivity of three Mayaro Virus geographic isolates in human cell lines. Acta Trop . 2023 Mar 23;242:106894. doi: 10.1016/j.actatropica.2023.106894. **#=corresponding author].**
3. ValenteMC, PrakosoD, Vittor AY, BlosserEM, AbidN, PuR, BeachboardSE, LongMT#, Burkett-CadenaND, **MavianC#,** Everglades virus evolution: Genome sequence analysis of the envelope protein reveals recent mutation and divergence in south Florida wetlands, *Virus Evolution* **[#=corresponding author].**
4. Paisie TK, Cash MN, Tagliamonte MS, Ali A, Morris, JGJ, Salemi M, **Mavian C#**. Molecular basis of the toxigenic Vibrio cholerae O1 serotype switch from Ogawa to Inaba in Haiti.*Microbiology Spectrum* **[#=corresponding author].**
5. RichS, ProsperiM, DellicourS, VranckenB, CookR, SpencerE, Salemi M#, **Mavian C#**. Phylodynamic characterization of HIV-1 subtype B transmission across Florida reveals few large superclusters with Metropolitan origin. *Microbiology* *Spectrum 2022 Oct 12;e0188922. doi: 10.1128/spectrum.01889-22.* **[#=corresponding author].**
6. AlamMT\*, **Mavian C\*#**., PaisieTK, Tagliamonte MS, Cash MN, AngermeyerA, SeedKD, CamilliA, Masanga MaishaF, Kakongo SengaRK, Salemi M, J Morris JG., Ali A#. Emergence and Evolutionary Response of Vibrio cholerae to Novel Bacteriophage, Democratic Republic of the Congo. *Emerging Infectious Disease October 2022 in press.* **[#=corresponding author, \*=equally contributed].**
7. Lohse ZMM, Shapiro JJ, Lednicky LA, Cash MN, Jun I, **Mavian C**, Tagliamonte MS, Saleem C, Yang Y, Nelson EI, Salemi M, Ryan KA, Morris JG. Persistence of SARS-CoV-2 omicron variant in children and utility of rapid antigen testing as an indicator of culturable virus, 2022 Aug 27;ciac693.doi: 10.1093/cid/ciac693.
8. Prandi IG, **Mavian C**, Giombini E, Cesare E, Gruber M, Pietrucci D, Borocci S, Abid N, Beccari AR, Talarico C, Giovanni Chillemi G. Structural Evolution of Delta (B.1.617.2) and Omicron (BA.1) Spike Glycoproteins *IMJS 2022 Aug; 23(15): 8680.doi: 10.3390/ijms23158680*
9. Alam M, Elbadry M, Loeb J, Stephenson C, Louis R, **Mavian C**, Charrel R, Rahman S, Morris JG, Jr, Lednicky J, Genotype 1A Hepatovirus A isolated from plasma from a Haitian child, Microbiology Resource Announcements; *2022 Sep 15;11(9):e0044922. doi: 10.1128/mra.00449-22. Epub 2022 Aug 11.*
10. Alam M, **Mavian C\***, Okech B, White S, Stephenson C, Elbadry M, Blohm G, Loeb J, Louis R, Saleem C, Beau de Rochars V, Salemi M, Lednicky J, Morris JG, Analysis of Zika virus sequence data associated with a school cohort in Haiti, ASTMH 2022 Sep 12;107(4):873-880. doi: 10.4269/ajtmh.22-0204. Print 2022 Oct 12. **[\*corresponding author]**
11. Hendricks C, Cash M, Tagliamonte M, Riva A, Brander C, Llano A, Salemi M, Stevenson M, **Mavian C\*** Discordance between HIV-1 population in plasma at rebound after structured treatment interruption and archived provirus population in peripheral blood mononuclear cells, ASM Microbiology Spectrum, *2022 Jun 14;e0135322. doi: 10.1128/spectrum.01353-22.* **[\*corresponding author]**
12. Rife Magalis B, **Mavian C\***, Tagliamonte MS, Rich S, Cash MN, Riva A, Marini S, Moraga Amador D, Zhang Y, Shapiro J, Horine A, Starostik P, Pieretti M, Vega S, Lacombe AP, Salinas J, Stevenson M, Myers P, Morris JG, Lauzardo M, Prosperi M, Salemi M. Low-frequency variants in mildly symptomatic vaccine breakthrough infections presents a doubled-edged sword. Journal of Medical Virology. 2022 Jul;94(7):3192-3202. doi: 10.1002/jmv.27726. Epub 2022 Apr 13. **[\*=equally contributed]**
13. Rife Magalis B, Rich S, Tagliamonte MS, **Mavian C**, Cash MN, Riva A, Marini S, Moraga Amador D, Zhang Y, Shapiro J, Horine A, Starostik P, Pieretti M, Vega S, Lacombe AP, Salinas J, Stevenson M, Myers P, Morris JG, Lauzardo M, Prosperi M, Salemi M. SARS-CoV-2 Delta vaccine breakthrough transmissibility in Alachua County, Florida. Clin Infect Dis. 2022 Mar 10:ciac197 PMID: 35271704.
14. Lednicky JA, Tagliamonte MS, White SK, Elbadry MA, Alam MM, Stephenson CJ, Bonny TS, Loeb JC, Telisma T, Chavannes S, Ostrov DA, **Mavian C**, Beau De Rochars VM, Salemi M, Morris JGJ. Independent infections of porcine deltacoronavirus among Haitian hildren. **Nature** (2021). 021 Dec;600(7887):133-137. doi: 10.1038/s41586-021-04111-z. Epub 2021 Nov 17.
15. Alexiev I, **Mavian C**, PaisieT, CiccozziM, DimitrovaR, GanchevaA, KostadinovaA, Seguin-DevauxC, SalemiM. Analysis of the Origin and Dissemination of HIV-1 Subtype C in Bulgaria, Viruses, *2022 Jan 27;14(2):263. doi: 10.3390/v14020263.*
16. Benedetti F\*, Silvestri G\*, **Mavian C\***, Munawwar A, Weichseldorfer M, Cash MN, Dulcey M, Vittor AY, Ciccozzi M, Latinovic OS, Salemi M, Zella D. Comparison of SARS-CoV-2 receptors expression in primary endothelial cells and retinoic acid-differentiated human neuronal cells. **[\*=equally contributed]** Viruses, *2021 Oct 30;13(11):2193*
17. Lednicky JA, Tagliamonte MS, White SK, Blohm GM, Alam MM, Iovine NM, Salemi M, **Mavian C\***, Morris JGJ**\***. Isolation of a Novel Recombinant Canine Coronavirus from a Visitor to Haiti: Further Evidence of Transmission of Coronaviruses of Zoonotic Origin to Humans, Clin Infect Dis .,*2022 Aug 24;75(1):e1184-e1187. doi: 10.1093/cid/ciab924.* **[\*=corresponding author]**
18. Marini S, **Mavian C**, Riva A,Salemi M, Rife Magalis B. Optimizing viral genome subsampling by genetic diversity and temporal distribution (TARDiS) for Phylogenetics. Bioinformatics, 21 October 2021
19. M. Vignoles, V. Andrade, M. Noguera, C. Brander, **C. Mavian**, M. Salemi, R. Paredes, M. Sharkey, M. Stevenson. Persistent HIV-1 transcription in CD4+ T cells from ART-suppressed individuals can originate from biologically competent proviruses. Journal of Virus Eradication, *https://doi.org/10.1016/j.jve.2021.100053*
20. Zecchin B., Fusaro A., Milani A., Schivo A., Ravagnan S., Ormelli S., **Mavian C.**, Michelutti A., Toniolo F., Barzon L., Monne I, Capelli G. The central role of Italy in the spatial spread of USUTU virus in Europe. Virus Evolution. Volume 7, Issue 1, 31 August 2021, veab048, https://doi.org/10.1093/ve/veab048
21. Tagliamonte MS**\***, **Mavian C\***, Zainabadi K, Cash MN, Lednicky JA, Rife Magalis B, Riva A, Deschamps MM, Liautaud B, Rouzier V, Fitzgerald DW, Pape JW, Morris JGJ, Salemi M. Rapid emergence and spread of SARS-CoV-2 gamma (P.1) variant in Haiti. CLIN INFECT DIS 02 September 2021 **[\*=equally contributed]**
22. **Mavian C**, López-Bueno A, Martin R, Nitsche A. Alcami A. Comparative pathogenesis, genomics and phylogeography of mousepox. Viruses 2021 Jun 15;13(6):1146.
23. Tariq K, Akhtar ZR; **Mavian C**, Ali A., Ullah F, Zang LS; Ali F, Nazir T; Ali S. Trophic transfer and toxicity of heavy metals from dengue mosquito Aedes aegypti to predator dragonfly Tramea cophysa. *Ecotoxicology. 2021 Aug;30(6):1108-1115. doi: 10.1007/s10646-021-02448-9. Epub 2021 Jun 24.PMID: 34165678*
24. **Mavian C**, Coman RM, Zhang X, Pomeroy S, Ostrov DA, Dunn BM, Sleasman JW, Goodenow MM, Molecular Docking-Based Screening for Novel Inhibitors of the Human Immunodeficiency Virus Type 1 Protease that Effectively Reduce the Viral Replication in Human Cells; Journal of AIDS & Clinical Research; Volume 12:5, 2021.
25. **Mavian C#,** Ramirez-Mata A, Dollar JJ, Nolan DJ, Rich S, White K, Rife-Magalis B, Cash M, Marini S, Prosperi M., Moraga DA, Riva A, Williams KC, Salemi M**#** Brain tissue transcriptomic analysis of SIV-infected macaques identifies Poly (ADP-ribose) polymerases (PARPs) as potential biomarkers for neuropathogenesis, J. Neurovirol. (2021). https://doi.org/10.1007/s13365-020-00927-z **[#=corresponding author].**
26. Tagliamonte MS, Abid N, Borocci S, Sangiovanni E, Ostrov DA, Kosakovsky Pond SL, Salemi M#, Chillemi G#, **Mavian** **C#**. Multiple recombination events and strong purifying selection at the origin of SARS-CoV-2 spike glycoprotein increased correlated dynamic movements. IJMS 2020 doi: https://doi.org/10.1101/2020.03.30.015685 **[#=corresponding].**
27. Rich S, Poschman K, Hu H, **Mavian C**, Cook R, Spencer E, Salemi M, Prosperi M.Socioecological and spatiotemporal factors associated with HIV drug resistance in Florida: a retrospective analysis. *The Journal of Infectious Diseases,* jiaa413, https://doi.org/10.1093/infdis/jiaa413
28. Rich S, Richards V, **Mavian C**, Bill Switzer, Rife Magalis B, Poschman K, Geary S, Broadway S, Bennett S, Blanton J, Leitner T, Boatwrtight L, Stetten N, Cook R, Spencer E, Salemi M, Prosperi M.Employing Molecular Phylodynamic Methods to Identify and Forecast HIV Transmission Clusters in Public Health Settings: A Qualitative Study. Viruses 2020, 12(9), 921; https://doi.org/10.3390/v12090921
29. **Mavian C#**, Kosakovsky Pond SL, *[….]*, Prosperi M**#**, Salemi M**#**. Letter to the Editor. Sampling bias and incorrect rooting make phylogenetic network tracing of SARS-COV-2 infections unreliable. 2020 Proc Natl Acad Sci USAMay 2020, 202007295; DOI: 10.1073/pnas.2007295117 **[#=corresponding author].**
30. **Mavian C#**, Simone Marini, Prosperi M, Salemi M**#**. A snapshot of SARS-CoV-2 genome availability up to April 2020 and its implications. *JMIR Public Health Surveill*. 2020;6(2):e19170. Published 2020 Jun 1. doi:10.2196/19170 **[#=corresponding].**
31. Boyles M.S. **\***, **Mavian C\***, Finol E. **\***, Ukhanova M., Stephenson C. J., Hamerlinck G., Kang S., Baumgartner C., Geesey M., Stinton I., Williams K., Mathias D. K., Prosperi M, Mai V., Salemi M., Buckner E. A., Lednicky J. A., Rivers A. R., Dinglasan. R.R.. Under-the-radar dengue virus infections in natural populations of *Aedes aegypti* mosquitoes. mSphere Apr 2020, 5 (2) e00316-20; DOI: 10.1128/mSphere.00316-20 **[\*=equally contributed].**
32. **Mavian C #**, Paisie TK, Alam M.T., Nembrini S, Cash M, Nelson EJ, Browne C, Ali A, Morris JGJ, SalemiM. Toxigenic Vibrio cholerae Evolution and Establishment of Reservoirs in Aquatic Ecosystems, 2020 PNAS March 30, 2020 https://doi.org/10.1073/pnas.1918763117**[#=corresponding author].**
33. Machado Andrade V, **Mavian C**, Babic D, Cordeiro T, Sharkey M, Barrios L, Brander C, Martinez-Picado J, Dalmau J, Li J, Jacobson J, Seaman MS, Lavine CL, Salemi M, Stevenson M.2020. A minor population of macrophage-tropic HIV-1 variants is identified in recrudescing viremia following analytic treatment interruption. 2020 PNAS April 16, 2020 https://doi.org/10.1073/pnas.1917034117
34. Blohm GM, Márquez-Colmenarez MC, Lednicky JA, Bonny TS, **Mavian C**, Salemi M, Delgado-Noguera L, Morris JG, Paniz-Mondolfi AE. Isolation of *Mayaro virus* from a Venezuelan patient with febrile illness, arthralgias, and rash; further evidence of regional strain circulation and possible long-term endemicity. Am J Trop Med Hyg 2019 Dec;101(6):1219-1225. doi: 10.4269/ajtmh.19-0357. PubMed PMID: 31595869.
35. Blohm G, A Elbadry M, **Mavian C**, Stephenson C, Loeb J, White S, Telisma T, Chavannes S, De Rochar VMB, Salemi M, Lednicky JA, Glenn Morris J. Mayaro as a Caribbean traveler: Evidence for multiple introductions and transmission of the virus into Haiti. Int J Infect Dis. 2019 Aug 2; doi: 10.1016/j.ijid.2019.07.031.
36. Lednicky JA, White SK, **Mavian C**,El Badry MA, Telisma T, Salemi M, OKech BA, Beau De Rochars VM, Morris JG Jr. Emergence of Madariaga virus as a cause of acute febrile illness in children, Haiti, 2015-2016. PLoS Negl Trop Dis. 2019 Jan 10;13(1):e0006972. doi: 10.1371/journal.pntd.0006972.
37. **Mavian C#**, Dulcey M, Munoz O, SalemiM, Vittor A.Y., Capua I. Islands as Hotspots for Emerging Mosquito-Borne Viruses: A One-Health Perspective, Viruses. 2018 Dec 25;11(1). pii: E11. doi: 10.3390/v11010011. PMID:30585228 **[#=corresponding author].**
38. Fogolari M**\***, **Mavian C\*,** Angeletti S Lampel K A, Maurelli A T, Salemi M. “Distribution and characterization of Shiga toxin converting temperate phage carried by Shigella flexneri in Hispaniola” Infect Genet Evol. 2018 Jul 31. pii: S1567-1348(18)30558-6. doi: 10.1016/j.meegid.2018.07.038. **[\*=equally contributed].**
39. White SK, **Mavian C**, ElbadryMA, Beau De Rochars VM, Paisie T, Telisma T, SalemiM, LednickyJA,Morris, JGJ. Detection and phylogenetic characterization of arbovirus dual-infections among persons during a Chikungunya Fever outbreak, Haiti 2014, PLoS Negl Trop Dis. 2018 May 31;12(5):e0006505. doi: 10.1371/journal.pntd.0006505.
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46. López-Bueno A**\***, **Mavian C\***, Labella A, Castro D, Borrego JJ, Alcami A, Alejo A. Concurrence of iridovirus, polyomavirus and a unique member of a new group of fish papillomaviruses in lymphocystis disease affected gilthead seabream. J Virol. 2016 Sep 12;90(19):8768-79. doi: 10.1128/JVI.01369-16.**[\*=equally contributed].**
47. Martin V, **Mavian C**, López-Bueno A, de Molina A, Díaz E, Andrés G, Alcamí A, Alejo A. Establishment of a zebrafish infection model for the study of wild type and recombinant European sheatfish virus. J Virol. 2015 Oct;89(20):10702-6. doi: 10.1128/JVI.01580-15.
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52. Gómez P, **Mavian C,** Galocha B, García-Medel N, López de Castro JA. Presentation of cytosolically stable peptides by HLA-B27 is not dependent on the canonic interactions of N-terminal basic residues in the A pocket. J Immunol. 2009 Jan 1;182(1):446-55.

**NCBI** **MyBibliography:** <https://www.ncbi.nlm.nih.gov/myncbi/1XmkXVZo4mxQH/bibliography/public/>

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**UNDER REVIEW** **MANUSCRIPTS**

1. Mabry ME\*, Fanelli A\*, **Mavian C\***, Lorusso A, Manes C, Soltis PS, Capua I.The panzootic potential of SARS-CoV-2, *Under Review,* *BioScience.* **[\*=equally contributed].**
2. Meneses M, Riva A, Salemi M, **Mavian C#**. ARCA: the interactive public database for Arbovirus Reported Cases in the Americas. *Submitted to Bioinformatics, January 2023* **[#=corresponding author].**

**INVITED SEMINARS AND SYMPOSIA**

**Invited** **Talks**

2023 Genomic surveillance for all: from HIV, to cholera and emerging zoonotic coronaviruses. Instituto Nacional de Salud, Bogotá, Colombia, 26 June 2023.

2023 13 years of genomics surveillance of *Vibrio Cholerae* in Haiti. CERI seminars. Stellenbosch University, Cape Town, South Africa. 26 April 2023.

2023 Cholera introduction and spread across the African continent. CLIMADE seminars, Stellenbosch University, Stellenbosch, South Africa. 25 April 2023.

2023 13 years of genomics surveillance of *Vibrio Cholerae* in Haiti. Infectious Disease Research conference, College of Medicine, UF.

2022 Phylogenomic tracking of SARS-CoV-2 and emerging coronavirus zoonoses, Grand Rounds, College of Medicine, UF.

2022 Genomic surveillance of SARS-CoV-2 and emerging zoonotic coronavirus, Dipartimento per la Innovazione nei Sistemi Biologici Agroalimentari e Forestali, Universitá degli Studi della Tuscia, Itlay.

2022 EEB Special Seminar: Phylogenomic tracking of SARS-CoV-2 variants and emerging coronavirus zoonoses, Department of Ecology and Evolutionary Biology, University of Michigan.

2022 Phylodynamics & Genomic Surveillance of Infectious Pathogens: Before, During, and “After” the Pandemic, Department of Plant Pathology, UF.

2022 Phylogenetic surveillance of SARS-CoV-2 variants and emerging coronavirus zoonoses, MIMG seminar series, Department of Microbiology, Immunology & Molecular Genetics, The University of Texas Health Science Center San Antonio.

2021 What we know about Coronaviruses in Florida?, COVID-19 Circular Health Seminar Series, UF.

2021 An eco-evolutionary tale of hosts, pathogens and reservoirs, Biology Department, University of Massachusetts Boston

2021 Mutations and recombination findings of SARS-CoV-2, COVID-19 Lenzes Seminar Series, One Health Center, UF.

2019 An eco-evolutionary tale of hosts, pathogens and environmental reservoirs, Keynote lecture, VEME 2019, The University Hong Kong, Hong Kong.

2019 Social-ecological determinants and phylodynamics of HIV epidemic in Florida, CSQUID meeting, UF.

2019 Evidence of Evolution and Persistence of Vibrio cholerae in Aquatic Reservoirs, Annual Resident/Postdoc Research Weekend, UF.

2019 Social-ecological determinants and temporal trends of HIV drug resistance in Florida and subtypes diversification, Florida Department of Health, Tallahassee, FL, USA

2017 Concurrence of iridovirus, polyomavirus, and a unique member of a new group of fish papillomaviruses in lymphocystis disease-affected gilthead sea bream, Florida Museum of Natural History, UF, FL, USA

2016 Phyloanatomy analysis and brain mRNA sequencing, Surviving and Thriving: AIDS, Politics and Culture, Seminars, HSC Library, UF, USA.

2014 Genome sequencing of natural isolates of poxvirus and iridovirus, Department of Molecular Genetics and Microbiology, UF, USA.

2013 The complete genome sequence of nine ectromelia virus isolates: implications for virulence, Institute of Health Carlos III, Majadahonda, Spain.

2012 The complete genome sequence of poxviral and iridoviral natural isolates, 3rd Next Generation Sequencing Day, Molecular Biology Center, Autonomous University of Madrid, Spain.

**Conference Talks**

2023 Genomic surveillance of the 2022-2023 cholera outbreak in Malawi, LIGHTNING ROUND TALK, NIH CREID Annual Meeting, Rockville, MD, USA

2022 Haiti COVID-19 epidemic: the rise of the Omicron lineages. Lightening talk at Wellcome Trust virus genomics and evolution. Virtual conference.

2021 Multiple introductions of Zika virus in the Americas, ASTMH Annual Meeting, Gaylord National Resort and Convention Center National Harbor, MD, USA.

2020 From genome to structure: how recombination conserves the long-range correlated movements of SARS-CoV-2. Webinar: Les chercheurs Tunisiens face a la pandemie COVID-19. Virtual conference.

2020 Recombination and purifying selection preserve covariant movements between furin-like cleavage site and receptor binding domain of SARS-CoV-2 mosaic spike glycoprotein, The 15th annual Sequencing, Finishing & Analysis (SFAF) Meeting 2020, Zoom conference. Virtual conference.

2020 Optimizing viral genome subsampling by genomic diversity and temporal distribution. 2020-COVIDynamics&Evolution. Virtual conference.

2020 Collection of SARS-CoV-2 Virus from the Air in a University Student Health Care Center and Analyses of its Viral Genomic Sequence. American Association for Aerosol Research 38th Annual Conference. Virtual conference.

2019 Evidence of Environmental Persistence-driven Evolution of Vibrio cholerae in Aquatic Reservoirs, EPIDEMICS7, Charleston, SC, USA.

2019 Evidence of Environmental Persistence-driven Evolution of Vibrio cholerae in Aquatic Reservoirs, ASM Microbe 2019, San Francisco, CA, USA.

2017 Spatiotemporal evolution and recombination of Mayaro Virus Isolates Collected Over 60 years in the Americas: the dawn of a new epidemic? ACAV & ASTMH Annual Meeting, Baltimore, MD, USA.

2017Spatiotemporal evolution and recombination of Mayaro Virus Isolates Collected Over 60 years in the Americas: the dawn of a new epidemic? ASTMH Annual Meeting, Baltimore, MD, USA.

1. The complete genome sequence of the gilthead seabream lymphocystis disease virus identifies a novel virus species in the Mediterranean area, 9th International Congress of Veterinary Virology, Madrid, Spain
2. Genome sequence of two European ranaviruses: the common midwife toad virus and the European sheatfish virus, XIX International Poxvirus, Asfavirus and Iridovirus Conference, Salamanca, Spain.

**Posters**

2023 An anti-inflammatory gene expression signature is associated with CBD treatment in people living with HIV. Cannabis Clinical Outcomes Research Conference (CCORC), Orlando, FL, USA.

2022 An anti-inflammatory gene expression signature is associated with CBD treatment in people living with HIV. HIV PERSISTENCE WORKSHOP 2022, Miami, FL, USA.

2022 Everglades virus evolution: Genome sequence analysis of the envelope protein reveals recent mutation and divergence in south Florida wetlands, ASTMH 2022, Seattle, WA, USA

2022 Haiti COVID-19 epidemic: the rise of the Omicron lineages. Wellcome Trust virus genomics and evolution. Virtual conference.

2022 Molecular epidemiology of the hematophagous bat genetic variant in Colombia and its relationship whit other countries of Latin-America. International Virus Bioinformatics Meeting 2022, 23–25 March 2022 online.

2022 Automated processing of Next-Gen Sequencing data from real-time SARS-CoV-2 surveillance. AGBT, Orlando, June 6th-9th 2022

2021 Spatial spread of USUTU virus in Europe: the central role of Italy, EPIDEMICS8, November 30th – December 3rd online.

2021 Multifaceted adaptive landscape of toxigenic Vibrio cholerae during epidemic waves in the Democratic Republic of Congo associated with a novel and unique ICP1 Bacteriophage, EEID. Virtual conference.

2021 Multifaceted adaptive landscape of toxigenic Vibrio cholerae during epidemic waves in the Democratic Republic of Congo associated with a novel and unique ICP1 Bacteriophage, EPIDEMICS8. Virtual conference.

2021 Isolation of a Novel Recombinant Canine Coronavirus from a Visitor to Haiti: Further Evidence of Transmission of Coronaviruses of Zoonotic Origin to Humans, 5th Workshop on Virus Dynamics. Virtual conference.

2020 Bayesian phyloanatomy identifies a population of macrophage-tropic HIV-1 variants in recrudescing viremia following analytic treatment interruption, 2020-COVIDynamics&Evolution. Virtual conference.

2020 Presence macrophage-tropic HIV-1 variants following analytic treatment interruption, CROI 2020. Virtual conference.

2019 Phylodynamics of the HIV epidemic in Florida in the decade from 2007-2017,EPIDEMICS7, Charleston, SC, USA.

2019 Evidence of Environmental Persistence-driven Evolution of Vibrio cholerae in Aquatic Reservoirs, ASM Microbe 2019, San Francisco, CA, USA.

2019 Phylogeographic characterization of minority non-B HIV-1 subtype strains and circulating recombinant forms in Florida, USA, VEME 2019, Hong Kong, China.

2019 Phylogenetic characterization of HIV transmission in Florida 2007-2017, VEME 2019, Hong Kong, China

2019 Harnessing Data Science to Improve Population Health and Public Health Surveillance. International Society for Disease Surveillance (ISDS), San Diego, CA, USA.

2018 Phylodynamic Analysis of HIV in Florida, VEME 2018, Berlin, Germany.

2018 Identification of macrophage reservoirs through tropism of HIV-1 envelopes, CROI 2018, Boston, MA, USA.

2017Spatiotemporal evolution and recombination of Mayaro Virus Isolates Collected Over 60 years in the Americas: the dawn of a new epidemic?, 22nd International Bioinformatics Workshop on Virus Evolution and Molecular Epidemiology, VEME 2017, Lisbon, Portugal.

2016Immunomodulatory Effects of Recreational Marijuana Use in Youth Living with HIV-1, CROI 2016, Boston, MA, USA.

2015STAT5 Activation Supports HIV-1 Infection and TLR7 Responses in Primary Macrophages, CROI 2015, Seattle, WA, USA.

2015Non-active site protease inhibitors (PI) suppress wild type and PI-resistant HIV-1, 2015 International HIV Drug Resistance Workshop, CROI satellite Workshop, Seattle, WA, USA.

1. Role of naturally occurring polymorphisms in HIV-1 subtype A, B or C protease and gag polyproteins in virion maturation, Southeastern Microbiology Summit-2014, Joint meeting of Southeastern and Florida ASM Branch, Ponte Vedra, FL, USA.
2. The complete genome sequence of nine ectromelia virus isolates: implications for virulence, at XII National Congress of Virology, Burgos, Spain.

**EDITORIAL RESPONSABILITIES**

2022-current Ad hoc Reviewer *Epidemics*

2021-current Ad hoc Reviewer *Molecular Biology and Evolution*

2021-current Ad hoc Reviewer *Cell*

2020-current Ad hoc Reviewer *Nature Medicine*

2020-current Ad hoc Reviewer *Nature Communications*

2020-current Ad hoc Reviewer *eLife*

2020-current Ad hoc Reviewer *Plos Computational Biology*

2020-current Ad hoc reviewer *Plos Pathogens*

2020-current Ad hoc Reviewer *BMC Infectious Diseases*

2020-current Ad hoc reviewer *Emerging Infectious Diseases*

2020-current Ad hoc reviewer *Nucleic Acid Research*

2020-current Ad hoc Reviewer *Tropical Medicine and Infectious Disease*

2020-current Ad hoc Reviewer *Journal of Virology*

2019-current Ad hoc reviewer *Viruses*

2019-current Ad hoc reviewer *Pathogens*

2018-current Ad hoc reviewer *PLoS Negl Trop Dis*.

2018-current Ad hoc reviewer *Acta Tropica*

2016-current Ad hoc reviewer *Scientific Reports*

2016-current Ad hoc reviewer *Infection, Genetics and Evolution*

2015-current Ad hoc reviewer *Current HIV Research Journal*

**Verified reviews** **Publons:** https://publons.com/researcher/425876/carla-mavian/

**PROFESSIONAL** **AFFILIATIONS - MEMBERSHIPS**

2021-current Bat One Health Research Network (BOHRN)

2020-current Modeling of Infectious Disease Agent Study (MIDAS)

2019-2020 UF Carpentries Board Member, UF, FL, USA

2019-current Software & Data Carpentry Certified Instructor, UF, FL, USA

2017-current American Society for Virology

2017-current American Society for Microbiology

2016-current American Society of Tropical Medicine & Hygiene (ASTMH)

2016-current ASTMH Committee on Global Health

2016-current American Committee on Arthropod-Borne Viruses (ACAV)

2016-current Data Intelligence Systems Lab, UF, FL, USA

2016-current OneHealth Center of Excellence, UF, FL, USA

2015-current Southern HIV and Alcohol Research Consortium, UF, FL, USA

2014-2019 National Postdoctoral Association

2011-2013 Spanish Society for Virology