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Selected Publications by EVBC Members publications on Pubmed

All

Virus Evolution and Genomic Surveillance

📖 This study models SARS-CoV-2 evolution in response to population immunity, predicting variant dynamics using genomic surveillance data. (Nature: [10.1038/s41586-024-08477-8](https://doi.org/10.1038/s41586-024-08477-8))

📖 This study investigates the factors influencing genome size in nidoviruses, linking translation fidelity, host interactions, and genome organization to RNA genome expansion. (Proc Natl Acad Sci U S A: [10.1073/pnas.2413675122](https://doi.org/10.1073/pnas.2413675122))

📖 This review discusses how protein language models (pLMs) can enhance pathogen genomic surveillance, predicting viral properties and evolution. (J Virol: [10.1128/jvi.01601-24](https://doi.org/10.1128/jvi.01601-24))

📖 This study analyzes early SARS-CoV-2 genomes, concluding that genomes previously thought to be intermediates between lineages A and B are likely derived from either lineage, supporting separate introductions into humans. (Virus Evol: [10.1093/ve/veaf008](https://doi.org/10.1093/ve/veaf008))

Virome and Microbiome Diversity

📖 This study explores ANI patterns in bacterial dsDNA viruses, revealing a distinct genetic gap and extensive mosaicism in temperate phages. (mSystems: [10.1128/mSystems.01661-24](https://doi.org/10.1128/mSystems.01661-24))

📖 This study provides a phylogenetic analysis of rodent adenoviruses, revealing ancient host-switch events and adenoviral diversity. (Mol Phylogenet Evol: [10.1016/j.ympev.2025.108287](https://doi.org/10.1016/j.ympev.2025.108287))

📖 This review examines the concept of a 'healthy' human microbiome, highlighting microbial variability, challenges in defining health, and implications for research and industry. (Nat Rev Microbiol: [10.1038/s41579-024-01107-0](https://doi.org/10.1038/s41579-024-01107-0))

📖 This study characterizes a novel *Klebsiella pneumoniae* phage vBkpUKJ_2 isolated from hospital sewage, providing insights into its potential therapeutic applications against multidrug-resistant strains. (BMC Microbiol: [10.1186/s12866-025-03813-y](https://doi.org/10.1186/s12866-025-03813-y))

Emerging Viral Taxonomy and Host Interactions

📖 This study refines *Bacilladnaviridae* taxonomy and reveals new insights into diatom-infecting DNA viruses, identifying 13 novel viruses and four new genera. (J Gen Virol: [10.1099/jgv.0.002084](https://doi.org/10.1099/jgv.0.002084))

📖 This study characterizes hedgehog arterivirus genomic diversity, suggesting a new genus in the subfamily *Heroarterivirinae*. (Arch Virol: [10.1007/s00705-025-06231-7](https://doi.org/10.1007/s00705-025-06231-7))

Innovative Methods in Virology Research

📖 This review explores organ-on-chip (OoC) technology for studying respiratory viral infections and gut-lung axis interactions, highlighting its role in personalized virology research. (Open Biol: [10.1098/rsob.240231](https://doi.org/10.1098/rsob.240231))

📖 – open access X – preprints 📖 – reviews, meta analyses 🔧 – tools

ViBioM 2025

Register



RDRP Summit 2025

Register

RdRp Summit 2025

Upcoming Events

Subscribe to Calendar

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ISMB/ECCB Conference 2025

20–27 July 2025 | Liverpool, UK

Organized by the International Society for Computational Biology (ISCB), this 33rd annual ISMB meeting, in conjunction with the 24th ECCB, will feature over 500 scientific talks, training workshops, and networking opportunities, available both in-person and virtually. Abstract submission deadline: **17 April 2025.**

1st International Symposium on Ancient Pathogen Genomics

12–13 April 2025 | Querétaro, México


The event aims to unite researchers in the field of ancient pathogen genomics, encompassing both ancient DNA and paleovirology studies. Registration Close: **31 March 2025.**


SIB Course: Virus-Host Interactions in 3D


27 March 2025 | Online: This course by the Swiss Institute of Bioinformatics explores computational approaches for analyzing virus-host interactions in three dimensions. It is designed for virologists and bioinformaticians interested in structural virology.


Tools and Resources

 [Virus tools website](#)

Tools developed by EVBC members are marked .

 **VASIL:** Immunological landscape of SARS-CoV-2 - Variant-resolved - A computational tool for the analysis and identification of viral sequences.

 **MANIAC:** Bioinformatics tool for microbial and viral genome analysis, focusing on automated classification and annotation.

 **detectEVE:** A user-friendly open-source tool designed for the accurate identification of non-retroviral endogenous viral elements (nrVEs) in genomic assemblies, improving genome annotations and helping paleovirological studies.

Announcements

Job Opportunity

Scientist in Computational and Laboratory Infection Research The Department of Translational and Computational Infection Research at Ruhr University Bochum is hiring! We are looking for a scientist to work at the intersection of computational biology and experimental virology, contributing to cutting-edge infection research.

Join our dynamic team and help advance our understanding of viral infections!

[Job Details & Application](#)

Job Opportunity

Viral Evolution and Ecology Researcher

If you work in viral evolution or ecology and are willing to establish yourself in the South of France (Montpellier), we are looking for candidates for a 2-year grant (renewable) for an experienced scientist.

We primarily study the mosquito virome, but related subjects on viruses transmitted by arthropod vectors can also be proposed. Contact: serafin.gutierrez@cirad.fr

[Application Details](#)

ECR Viromics Webinar Series

 [Register](#)

This lecture is organized together with the Center of Microbiome Science at Ohio State University and the NSF EMERGE Biology Integration Institute.

Nextflow pipelines: Connecting Data to Discoveries

9 April 2025 | 04-05 pm CET

[online](#)

Marcel Ribeiro-Dantas, Senior Developer Advocate at Seqera and Professor at Universidade Potiguar, Brazil

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