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Upcoming Events

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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**.

29th International Bioinformatics Workshop on Virus Evolution and Molecular Epidemiology (VEME)

3–8 August 2025 | Dakar, Senegal

Organized by the VEME, this internationally renowned workshop offers intensive training in virus evolution and molecular epidemiology, featuring hands-on modules tailored for different levels of expertise.

Application and abstract submission deadline: **30 April 2025**

First Symposium of the Danish Viruses of Microbes Network

11–13 June 2025 | Copenhagen, Denmark

This inaugural symposium brings together researchers studying viruses of microbes, including bacteriophages and archaeal viruses, for three days of scientific talks, discussions, and community building.

Abstract submission deadlines: **30 April 2025**

8th Annual Training Course on Viral Bioinformatics and Genomics

16–20 June 2025 | Garscube Campus, University of Glasgow, UK

This course provides hands-on training in viral genome assembly, annotation, and analysis of next-generation sequencing data, designed for researchers studying virus genomics.

Application deadline: **30 April 2025**

Phage Therapy Congress 2025

7–9 October 2025 | Porto, Portugal

A congress dedicated to the latest advancements in phage therapy, featuring global experts discussing therapeutic applications and regulatory frameworks.

Conference details: [Phage Therapy 2025 website](#).

ViBioM 2025

 [Register](#)



Registration is still open!

Register now – the deadline is **28 April 2025!**

Selected Publications by EVBC Members (part 1)

 [All publications on Pubmed](#)

Virome and Microbiome Diversity

📖 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))

📖 This review examines the role of the gut virome in the pathogenesis and potential therapeutics of inflammatory bowel disease, highlighting how viral communities influence host immunity and intestinal health. (*BMC Med*: [10.1186/s12916-025-04016-y](https://doi.org/10.1186/s12916-025-04016-y))

📖 This study shows that prophages in the infant gut are pervasively induced and may influence the functionality of their bacterial hosts, highlighting the dynamic role of the gut virome early in life. (*NPJ Biofilms Microbiomes*: [10.1038/s41522-025-00674-1](https://doi.org/10.1038/s41522-025-00674-1))

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))

📖 This study identifies a conserved high-order RNA structure within the M ORF of arteriviruses that regulates subgenomic RNA accumulation and infectious virus production, revealing a key cis-acting element in nidovirus replication. (*J Virol*: [10.1128/jvi.02167-24](https://doi.org/10.1128/jvi.02167-24))

📖 This study investigates Tunturi virus isolates and metagenome-assembled viral genomes, providing new insights into viruses infecting *Acidobacteriota* in Arctic tundra soils and expanding knowledge of soil virome diversity. (*Microbiome*: [10.1186/s40168-025-02053-6](https://doi.org/10.1186/s40168-025-02053-6))

Virus Discovery and Classification

🔧 EFinder, a new tool for identifying and classifying endogenous viral and bacterial elements in eukaryotic genomes, streamlines analysis with six integrated steps and high sensitivity. (*Comput Struct Biotechnol J*: [10.1016/j.csbj.2024.10.012](https://doi.org/10.1016/j.csbj.2024.10.012))

📖 Researchers identified a divergent RNA virus in *Plasmodium knowlesi*, a zoonotic malaria pathogen, expanding the understanding of ormycovirus diversity and its impact on protozoa. (*Virus Evol*: [10.1093/ve/veae091](https://doi.org/10.1093/ve/veae091))


📖 Researchers screened great ape museum specimens for DNA viruses, uncovering multiple near-complete viral genomes, including hepatitis B virus strains phylogenetically linked to gorillas and chimpanzees. (*Sci Rep*: [10.1038/s41598-024-80780-w](https://doi.org/10.1038/s41598-024-80780-w))

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


Selected Publications by EVBC Members (part 2)


 [All publications on Pubmed](#)


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](#))


 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](#))


 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](#))


 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](#))


 This study applies Bayesian phylodynamic approaches to analyze the evolutionary and epidemic dynamics of COVID-19 in Germany through three case studies, providing detailed insights into viral spread and public health responses. (Bioinform Biol Insights: [10.1177/11779322251321065](#))

Virus-Host Interactions and Vector Studies


 This study explores how phage-phage competition and biofilm formation influence interactions between two virulent bacteriophages and *Pseudomonas aeruginosa*, revealing complex dynamics that impact phage therapy strategies. (ISME J: [10.1093/ismejo/wraf065](#))

 This study examines how acute versus persistent insect-specific flavivirus (ISF) infections affect superinfection exclusion of West Nile, Zika, and chikungunya viruses in RNAi-competent and -deficient mosquito cells, providing insights into vector-virus interactions and potential transmission blocking strategies. (One Health: [10.1016/j.onehlt.2024.100960](#))

 This study reports the first isolation of Sindbis virus in mosquitoes from southwestern Spain, suggesting a recent introduction from Africa and highlighting the importance of entomological surveillance. (One Health: [10.1016/j.onehlt.2024.100947](#))


 This study identifies a small molecule that inhibits coronavirus assembly by targeting the viral membrane (M) protein, providing a promising therapeutic strategy against coronaviruses. (Nature: [10.1038/s41586-025-08773-x](#))

Viral Pathogenesis and Public Health


 This multinational cohort study investigates bacterial and viral co-infections in adult COVID-19 patients throughout the pandemic, revealing important insights into co-infection prevalence and outcomes. (J Infect Dis: [10.1093/infdis/jiaf167](#))

 This retrospective cohort study compares viral, bacterial, and coinfections in community-acquired pneumonia, providing valuable insights into infection patterns and clinical outcomes. (Int J Infect Dis: [10.1016/j.ijid.2025.107841](#))

 This multicenter study in Portugal (2014–2019) investigates determinants of HIV-1 transmission clusters and transmitted drug resistance among men who have sex with men, offering insights to improve public health strategies. (Int J Infect Dis: [10.1016/j.ijid.2025.107888](#))

 This study highlights how innovations in wastewater sequencing can strengthen global pathogen surveillance, calling for standardized procedures, improved enrichment methods, and enhanced bioinformatics tools to optimize public health monitoring. (BMC Glob Public Health: [10.1186/s44263-025-00138-w](#))


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](#))


 - open access  - preprints  - reviews, meta analyses  - tools

Tools and Resources

 [Virus tools website](#)

Tools developed by EVBC members are marked .

 **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 aiding paleovirological studies.

 **VirusWarn:** A mutation-based early warning system combining rule-based filters and machine learning to prioritize concerning SARS-CoV-2 and influenza virus variants from genomic sequencing data.

Announcements

Job Opportunity – PhD in Environmental Virus Surveillance

The newly founded Ludwig Boltzmann Institute for Science Outreach and Pandemic Preparedness (SOAP) Vienna offers a fully funded PhD position for dry and wet lab activities!

The project focuses on developing and applying innovative methods to detect and characterize viruses with zoonotic potential from environmental samples in an urban setting.

[Application Details](#)

RDRP Summit 2025

 [Register](#)

Travel Grant Sponsorship by ISME



LISBON, PORTUGAL
MAY 11-12
RDRP
SUMMIT 2025
A satellite conference of EVBC ViBiom 2025
Venue: IHMT NOVA, Lisbon

REGISTRATION	ABSTRACT
Early bird deadline March 31 2025	Deadline March 31 2025

RdRp.io

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