EVBC Newsletter
Volume 94 • June 2025

European
VIRUS BIOINFORMATICS
Center

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Selected Publications by EVBC Members
📖 All publications on PubMed

Challenges
This perspective analyzes key challenges in the clinical development of phage therapy, including regulatory hurdles, trial design complexity, and manufacturing standardization. (Nat Rev Microbiol: **10.1038/s41579-024-01091-5**)

Phage Therapy and Bacteriophages
This study describes isolating a lytic bacteriophage active against multidrug-resistant Klebsiella pneumoniae and shows that combining it with cefotaxime restores antibiotic sensitivity and prevents phage resistance. (J Appl Microbiol: **10.1093/jambio/lxaf131**)

This review delves into the genetics, ecology, and evolutionary strategies of phage satellites—parasite-like mobile elements—highlighting their molecular interactions with helper phages, impacts on bacterial virulence, and roles in microbial evolution. (Nat Rev Microbiol: **10.1038/s41579-025-01156-z**)

This narrative review explores the interaction between the gut virome and bacteriome in gastrointestinal diseases, detailing drivers of virome composition, immune interactions, and emerging clinical applications. (Precis Clin Med: **10.1093/pcmedi/pbaf010**)

Viral Taxonomy and Classification
This study presents the annual International Committee on Taxonomy of Viruses (ICTV) 2024 update for the phylum Negarnaviricota, adding 1 order, 1 family, 6 subfamilies, 34 genera, and 270 species, refining the taxonomy to support viral evolution studies and public health identification efforts. (J Gen Virol: **10.1099/jgv.0.002077**)

This study identifies and characterizes 90 Bartonella isolates from honey bees, proposes two new genera based on phylogenomic and functional analyses, and refines the taxonomy of bee-associated Bartonella. (Syst Appl Microbiol: **10.1016/j.syapm.2025.126625**)

Arboviruses and Vector-borne Diseases
This study analyzes Peste des petits ruminants virus genomes from 2024 outbreaks in Greece, Romania, and Bulgaria, revealing a common Northern African origin and identifying protein changes with potential functional significance. (Infect Genet Evol: **10.1016/j.meegid.2025.105774**)

This study evaluates a multi-antigen serology panel and diagnostic algorithm across seven southeast European countries, enabling detection of CCHFV, TBEV, Toscana, and West Nile viruses in complex clinical contexts. (Lancet Infect Dis: **10.1016/S1473-3099(24)00654-6**)

This study examines hospitalized adults with endemic arbovirus infections across seven southeast European countries, highlighting the need for improved diagnostics and surveillance. (Lancet Infect Dis: **10.1016/S1473-3099(24)00655-8**)

This review examines how phylogenetic approaches elucidate the transmission dynamics of arthropod-borne viruses, highlighting advances in genomic surveillance, evolutionary modeling, and outbreak response. (Nat Rev Genet: **10.1038/s41576-025-00854-x**)

SARS-CoV-2 and Pandemic Surveillance
This study demonstrates that integrating individual whole-genome sequencing and wastewater-based sequencing across >4,000 wastewater and >23,000 individual samples enhances detection, concordance, and spatiotemporal tracking of SARS-CoV-2 variants at a national level. (Water Res: **10.1016/j.watres.2025.123953**)

This study shows that non-stabilized SARS-CoV-2 spike mRNA vaccination in macaques induces broadly neutralizing antibody lineages against diverse sarbecoviruses, including Omicron XBB.1.5, and offers protection even without diproline substitutions. (Sci Transl Med: **10.1126/scitranslmed.adn5651**)

∂ – open access   𝒳 – preprints   ⊞ – reviews, meta analyses   🔧 – tools

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Viral Immunology and Vaccines
This study shows that intranasal administration of Venezuelan equine encephalitis virus replicon particles (VEE VRPs) expressing West Nile virus E protein generates robust mucosal and systemic immunity, protecting mice from lethal West Nile virus challenge. (NPJ Vaccines: **10.1038/s41541-025-00321-8**)

Viral Evolution and Genomics
This population-scale genomic study of 32 000 UK individuals reveals regional prevalence of inherited chromosomally integrated HHV-6, confirms its association with angina (OR 1.91), and identifies a limited number of ancestral viral lineages. (J Virol: **10.1128/jvi.02160-24**)

This study finds that influenza A virus–infected cells form tunnelling nanotube-like structures (TLSs) in vivo and in vitro in an apoptosis-dependent manner, facilitating direct cell-to-cell viral spread and immune evasion. (PLoS Pathog: **10.1371/journal.ppat.1013191**)

Methods and Protocols
This study compares two metatranscriptomic sequencing methods for mammalian tissues and finds that using optimized RNA purification with rRNA depletion improves viral RNA recovery fivefold and enables the assembly of full-length RNA virus genomes that the standard method could not. (PLoS One: **10.1371/journal.pone.0324537**)

This study develops a novel replicon-based assay to evaluate antiviral compounds against Crimean–Congo hemorrhagic fever virus and identifies several inhibitors with potent activity in vitro. (Antiviral Res: **10.1016/j.antiviral.2024.105500**)

This study develops a reverse genetics system for Frog virus 3 (Ranavirus), enabling targeted gene knockouts to investigate viral biology, virulence, and host range. (J Virol: **10.1128/jvi.01852-24**)

This study develops novel IgM/IgG enzyme immunoassays for bufavirus, cutavirus, and tusavirus, screens 1,444 sera from six countries, and finds that acute protoparvovirus infections are mild, rare, geographically localized, or undetected in respiratory or GI illness cohorts. (Virology: **10.1016/j.virol.2025.110529**)

This study characterizes SARS-CoV/CoV-2 macro domain bound to MOPS, screens analogs, and identifies MOPSO and CAPSO as promising scaffolds for developing macro domain-targeted inhibitors. (FEBS J: **10.1111/febs.70039**)

Clinical Virology and Epidemiology
This study analyzes HIV-1 molecular epidemiology among people who inject drugs in Thessaloniki (2019–2023), identifying dense local transmission clusters, increasing effective reproduction numbers, and substantial diagnosis delays. (Sex Transm Infect: **10.1136/sextrans-2024-056452**)

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Martin Beer, Li Deng, Bas E. Dutilh, Philippe Le Mercier, Manja Marz, Volker Thiel

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Upcoming Events   📅 Subscribe to Calendar

We do not endorse any of the listings and do not take any responsibility for the accuracy of the information.

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.

International Symposium on Bioinformatics Research and Applications (ISBRA 2025)
3–5 August 2025 | Helsinki, Finland
ISBRA 2025 brings together academic and industry researchers in bioinformatics, computational biology, systems biology, and related fields to share their latest research and innovations.

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.

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.

Aging and Microbiome Conference 2025
13–15 October 2025 | Jena, Germany
This conference will bring together leading researchers to explore the interactions between aging and the microbiome, highlighting cutting-edge research and opportunities for interdisciplinary collaboration.

Tools and Resources   🔧 Virus tools website

Tools developed by EVBC members are marked ☀.

☀ **Gaia Platform**: An AI-enabled genomic context-aware tool for real-time, precise microbial protein annotation using large language models and 85 million protein clusters.

☀ **PINN SARS-CoV-2 Model**: A physics-informed neural network tool for real-time modeling of Omicron variant spread, linking spike mutations to transmission and immune evasion.

☀ **varVAMP**: An open-source command-line tool for real-time design of degenerate primers in viral genome sequencing and qPCR, optimizing pan-specific primer schemes with minimal mismatches.

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