EVBC Newsletter
Volume 106 • October 2026

European VIRUS BIOINFORMATICS Center

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Selected Publications by EVBC Members I
All publications on PubMed

Virology

New study describes two recombinant tick-borne encephalitis viruses carrying eGFP or NanoLuc reporter genes, demonstrating their potential for host-factor screening and antiviral drug testing. It also reveals that reporter stability depends on cell type and experimental duration, with NanoLuc proving more stable than eGFP, and provides guidelines for designing reliable reporter-virus platforms. (Antiviral Res: 10.1016/j.antiviral.2026.106528)

Study identifies homologues of the core membrane-remodelling components ESCRT-III and the ATPase Vps4 in mirusviruses and some members of the phylum Nucleocytoviricota, revealing that certain large eukaryotic DNA viruses encode components of their own ESCRT machinery. This suggests that mirusviruses acquired host ESCRT components early in their evolution and provides new insights into the evolutionary connections between viruses and eukaryotic membrane-remodelling systems. (Nat Microbiol: 10.1038/s41564-026-02470-9)

By screening 818 vertebrate genomes, researchers identified an ancient alpharetrovirus lineage whose envelope genes were independently co-opted on eight occasions in bats between approximately 18.9 and 43.8 million years ago, with evidence of purifying selection and particularly high expression in the endometrium of pregnant bats. Phylogenetic analyses support an ancient cross-class transmission from saurian hosts into mammals and reveal related sequences in several mammalian groups, while the expression patterns suggest a possible reproductive function for these virus genes that requires further investigation. (PLoS Genet: 10.1371/journal.pgen.1012277)

Metagenomic sequencing and targeted PCR identified raccoon dog and fox amdoparvovirus (RFAV) in domestic Dobermann dogs during a severe disease outbreak in Serbia, providing the first evidence of natural infection in this host and revealing virus DNA in multiple tissues and specimen types. Although the findings suggest a potential association between RFAV and the observed multisystemic illness, further studies are needed to establish pathogenicity, clarify transmission routes and assess the virus's distribution in domestic and wild canids. (Animals: 10.3390/ani16162618)

Virus Bioinformatics

χ Researchers used AlphaFold2 and AlphaFold-Multimer to predict virus protein structures and interactions across 2,812 virus proteomes representing 23 virus families relevant to human health, identifying 5,279 high-confidence heterodimers and 2,749 homodimers. Structural clustering revealed 1,598 groups of interaction interfaces, including 471 with no detectable similarity to experimentally characterised interfaces, providing a resource for investigating virus protein function and prioritising potential targets for vaccine and antiviral development. (bioRxiv: 10.64898/2026.09.29.755321)

This review examines genome plasticity in hepatitis E virus (HEV), focusing on insertions of duplicated virus sequences and host-derived fragments within the hypervariable region and their potential effects on virus replication, persistence and pathogenesis. By systematically analysing more than 650 publicly available HEV genotype 3 genome sequences, the authors characterise these insertions, discuss possible mechanisms underlying their emergence and selection, and evaluate their potential relevance to chronic infection, treatment failure and future clinical monitoring. (Commun Biol: 10.1038/s42003-026-11055-5)

– open access χ – preprints – reviews, meta analyses – tools

Selected Publications by EVBC Members II
All publications on Pubmed

Virus Bioinformatics (further)

A new study investigates adaptive mutations and genome formula variation (GFV), reflecting differences in genome segment copy numbers, as potential mechanisms facilitating host alternation in bluetongue virus between ruminants and biting midges. While no host-specific mutations were consistently fixed across the sampled populations, GFV was associated with virus dissemination in midges and displayed reproducible, host-dependent patterns in cell culture, suggesting that genome segment abundance may be shaped by host-specific mechanisms. (J Virol: 10.1128/jvi.00983-26)

Researchers developed HTS-RARE, an optimised high-throughput sequencing library preparation strategy that improves the recovery and accurate determination of virus RNA termini, providing a rapid alternative to conventional RACE methods. Applying the approach to plant viruses revealed a non-templated nucleotide at the 3' end of minus-strand RNA in members of the genus *Ilarvirus* in vivo, suggesting that this feature may be widespread across the family Bromoviridae. (J Gen Virol: 10.1099/jgv.0.002331)

Philosophy/Reviews

This perspective examines why some viruses evolved giant genomes while others retained compact ones, arguing that giant viruses originated from smaller virus ancestors through the accumulation of genes recruited from their cellular hosts. The authors discuss contrasting evolutionary strategies shaped by gene acquisition, host interactions and selection for replication efficiency, concluding that giant viruses remain typical viruses despite their considerable genomic and structural complexity. (Proc Natl Acad Sci USA: 10.1073/pnas.2610442123)

This study evaluates large language models as sources of patient-facing information on bacteriophage therapy, with 12 clinical and research experts assessing responses to 20 patient-relevant questions for accuracy, completeness, clarity and tone or empathy. Although the models received generally favourable ratings, experts recommended improvements to 34–40% of responses and identified incorrect information in 20%, supporting a hybrid approach in which AI-generated educational materials are reviewed and refined by clinical experts. (npj Viruses: 10.1038/s44298-026-00224-2)

This review explores how phage-encoded transcription and sigma factors (TSFs) reprogramme bacterial host gene expression beyond the regulation of virus replication, complementing the better-studied role of auxiliary metabolic genes (AMGs). By synthesising genomic evidence, mechanistic insights and recent experimental and bioinformatic advances, the authors highlight the potential of TSFs to influence cellular physiology, microbial ecosystems and future biotechnological applications. (Trends Microbiol: 10.1016/j.tim.2026.05.019)

This review examines nonstandard virus genomes (nsVGs), including deletion, duplication, copy-back and recombinant forms, as evolving components of RNA virus populations that influence virus fitness, immune activation and within-host infection dynamics. By integrating experimental evidence, bioinformatic methods and mathematical modelling, the authors explain how nsVG–virus interactions generate complex population dynamics and discuss their implications for predicting infection outcomes and developing strategies to interfere with wild-type virus replication. (Curr Opin Virol: 10.1016/j.coviro.2026.101567)

Drawing on experience from the EuCARE project, this paper examines challenges encountered during multinational infectious disease research, including fragmented regulatory and ethics procedures, recruitment constraints, vaccine hesitancy and diagnostic supply chain vulnerabilities. The authors propose six practical recommendations for future pandemic preparedness, emphasising evidence-based science, workforce capacity, data management, specialised professional roles, collaborative networks and effective communication. (J Infect Public Health: 10.1016/j.jiph.2026.103401)

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Selected Publications by EVBC Members III
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Philosophy/Reviews (further)

Using environmental metagenomics, hidden Markov models, protein language models and structural analyses, researchers identify small viruses encoding HK97-fold proteins that share molecular similarities with encapsulins, specialised protein compartments found in prokaryotes. Phylogenetic and structural evidence supports a model of bidirectional evolution between HK97-fold viruses and encapsulins through procapsid-like intermediates, suggesting new evolutionary pathways for protein shells and potential biochemical functions of virus capsids. (Nat Commun: 10.1038/s41467-026-78136-1)

This primer reviews the functions and evolution of virus proteins, covering conserved virus hallmark proteins, the molecular machinery underlying virus replication and virion formation, interactions with host organisms, and the recruitment and repurposing of cellular proteins. It also examines the poorly characterised regions of virus proteomes and highlights how advances in structural biology and computational protein analysis can help uncover previously unrecognised relationships and deepen understanding of virus evolution. (J Virol: 10.1128/jvi.01202-26)

This study investigates the relationship between bacteriophage lifestyle and within-species genetic diversity by analysing 43,171 virus genomes across 12 soil virome datasets, finding that predicted temperate phages exhibit greater microdiversity than virulent phages in eight datasets. These findings suggest that phage lifestyle influences genetic variation within virus populations, with potential implications for understanding phage–host coevolution and environmental adaptability. (ISME Commun: 10.1093/ismeco/ycag265)

This review revisits the life cycle of temperate bacteriophages, examining how emerging insights into phage–host interactions and relationships with other mobile genetic elements extend the traditional focus on excision, replication and particle assembly. The authors propose a more holistic framework in which diverse phage and prophage properties are considered integral to the life cycle, advancing understanding of phage biology, evolution and biotechnological applications. (Nat Rev Microbiol: 10.1038/s41579-026-01318-7)

Methods and Resources

Optical photothermal infrared (OPTIR) imaging and spectroscopy enable label-free monitoring of baculovirus infection in living insect cells by detecting intrinsic biochemical signatures associated with proteins, nucleic acids and lipids. The approach distinguishes infected from uninfected cells with high accuracy and reveals temporal changes and cell-to-cell variability, offering a promising alternative to fluorescence-based reporter systems for studying virus infections. (Anal Bioanal Chem: 10.1007/s00216-026-06801-x)

This study presents a comprehensive data-fusion strategy for nano-FTIR spectral orders to improve the identification of influenza A and SARS-CoV-2 viruses at the single-virus level. By combining surface and subsurface chemical signatures, the approach enables more detailed characterisation of individual virions. (ACS Sens: 10.1021/acssensors.6c02198)

A high-throughput cytopathic-effect area assay quantifies infectious virus in 384-well plates by measuring virus-induced cell lysis and detachment from microscopy images. Automated nnU-Net segmentation closely reproduced manual analysis and enabled scalable, lower-bias virus-titre estimation across multiple viruses. (PLoS Comput Biol: 10.1371/journal.pcbi.1013511)

The ICTV Report chapter on Tospoviridae describes orthotospoviruses, plant-infecting viruses with tripartite RNA genomes that are transmitted by thrips and cause major crop diseases. It summarises their taxonomy, genome organisation, virion structure and species-demotion criteria. (ICTV: https://ictv.global/report/chapter/tospoviridae/tospoviridae)

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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. EVBC members are involved in events marked .

International Virus Bioinformatics Meeting (ViBioM 2027)
9-11 March 2027 | Jena, Germany
SAVE THE DATE for our annual EVBC meeting and celebrate with us the 10th anniversary of the EVBC! Further information will follow soon!

Theo Murphy meeting „Endogenous viral elements“
8-9 February 2027 | Birmingham, UK
Discuss current endogenous viral element (EVE) research, especially endogenous retroviral, RNA viral and DNA viral elements, including their diversity, roles in host biology and impacts on diseases. (Organised by Katy Brown, Emma Harding and Rachael Tarlinton). Requests for an invitation can be made here.

Viral EcoGenomics and Applications (VEGA) 2026 Symposium
18-19 November 2026 | Berkeley, CA, USA
A space for the viral ecogenomics community working in a broad range of environmental and host-associated ecosystems, along with molecular and computational techniques. 3 Sessions: “Functional characterization of novel viral diversity”, “Molecular mechanisms of virus-host interactions”, “Utilizing phages to manipulate microbiomes”.
Poster abstract submission deadline: 30 October 2026

Annual Conference 2027 of the Association for General and Applied Microbiology (VAAM)
14-17 March 2027 | Marburg, Germany
Forum for scientists at all stages of their careers to exchange ideas, discuss recent advances, strengthening existing contacts and establish new collaborations to drive Microbiology forward.
Abstract submission deadline: 6 November 2026
Early bird registration deadline: 10 January 2027

36th Annual Meeting of the Society for Virology (GfV 2027)
1-4 March 2027 | Frankfurt/Main, Germany
The meeting will cover a wide range of topics in basic, translational, and clinical virology. This year, the focus is on key topics including virus evolution, emerging and reemerging viruses, virus-host interactions, structural virology, immunology and vaccinology.
Abstract submission deadline: 6 December 2026
Early bird registration deadline: 1 February 2027

FEMS MICRO 2027
5-8 July 2027 | Ljubljana, Slovenia
Europe's premier Congress and Exhibition for microbial research and collaboration under the theme 'Growing microbial futures'.
Abstract & grant submission deadline: 15 December 2026
Early bird registration: 15 March - 14 April 2027

10th European Congress of Virology (ECV 2027)
7-10 June 2027 | Caglari/Sardinia, Italy
ECV 2027 will cover the full breadth of virology, from emerging and re-emerging human pathogenic viruses to basic, clinical, veterinary, and plant virology. - SAVE THE DATE!

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Tools and Resources — Virus tools website

Tools developed by EVBC members are marked ⚙.

⚙ **Virushunter and Virusgatherer:** Provide a reproducible, two-stage workflow for discovering virus genomes from raw next-generation sequencing data through profile-HMM-based marker detection and targeted genome assembly. Applied to 3348 bat transcriptomes, the workflow revealed extensive RNA-virus diversity and identified likely prototypes of novel virus species, including an alphacoronavirus and a rhabdovirus.

⚙ **Nextstrain:** Automates real-time phylogenetic analysis of open genomic data for 21 viruses and Mycobacterium tuberculosis, providing continually updated surveillance resources. Its modular pipelines integrate data curation, lineage classification, evolutionary inference and interactive visualisation to support public-health responses to endemic and emerging pathogens.

⚙ **Nextstrain and Nextclade resources:** New open-access Nextstrain and Nextclade resources enable live phylogenetic tracking, phylogeographic analysis and rapid lineage assignment for Lassa virus across its L, S and GPC genomes. The tools distinguish Lassa virus from other mammarenaviruses and assign lineages with high accuracy, supporting surveillance, outbreak response and clinical interpretation.

⚙ **InteRRact:** Web server for interactive exploration and comparison of transcriptome-wide human RNA–RNA interactions derived from duplex-probing experiments. It integrates network and genomic visualisations with quantitative confidence filters to support the discovery of biologically relevant cis and trans interactions.

⚙ **Læmple:** Modular, simulation-based Snakemake framework for benchmarking SARS-CoV-2 lineage-deconvolution tools using wastewater sequencing data. Its evaluation of seven tools revealed substantial performance variation, with Freyja showing strong sensitivity and VaQuERo the highest precision.

⚙ **African DSI DataBank:** Proposed federated infrastructure that would enable African organisations to host, govern and share genomic and biodiversity digital sequence information while retaining data custody. It aims to advance African data sovereignty and equitable participation in global genomics research.

Be part of the Newsletter — Email us

We want to know about your **publications**, **tools**, **workshops and other events**, **vacancies** or anything important you would like to share with the EVBC community. Email us here!

Announcements

⚙ **Call for female Humboldt Fellowship nominees**
If you work in the area of phylogenomics/phylodynamics of infectious diseases and want to be considered for nomination for a Humboldt Research Fellowship (6–24-month research stay in Germany) via the Henriette Herz Scouting Programme, then please contact EVBC member Denise Kühnert (RKI Germany, https://denisekuehnert.de/). Beyond scientific excellence and a PhD in a relevant field, the requirement is to not have completed any research stays in Germany and to not have German citizenship. Within the area of phylogenomics/phylodynamics of infectious diseases, the research topic is open. Please find more information about the procedure with the Henriette Herz Scouting Programme here.

ECR Viromics Webinar Series — Register

This lecture series features early career researchers studying viruses in complex communities. It is organized together with the Center of Microbiome Science at Ohio State University and the NSF EMERGE Biology Integration Institute. You can register **here** for the ECR Viromics mailing list and receive the access details for every webinar. You can unsubscribe at any time.

Upcoming talks:

Emma Harding, University of Oxford, UK
9 December 2026 | 4 pm CET online
What makes a "good" virus? Exploring host and viral traits associated with broad host range using endogenous retroviruses

Arthur Kocher, Centre for Anthropobiology and Genomics of Toulouse/France & MPI-EVA, Leipzig/Germany
12 May 2027 | 4 pm CET online

Viruses *in silico* lecture series — Register

This lecture is designed to keep you up to date with the latest developments in virus bioinformatics, especially new tools that might help you in your research. You can register **here** for the viruses in silico mailing list and receive the access details for every lecture. You can unsubscribe at any time.

Upcoming talk:

Alexandros Stamatakis, Institute of Computer Science at the Foundation for Research and Technology Hellas, Heraklion/Crete, Greece
28 January 2027 | 4 pm CET online
Predicting & Propagating Uncertainty in the Bioinformatics Pipeline

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