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Selected Publications by EVBC Members

 [All publications on Pubmed](#)

Using arrayed expression screening, human BTN3A3 was identified as a potent inhibitor of avian influenza A viruses (IAVs), highlighting its role in limiting avian IAV transmission to humans and suggesting that sensitivity or resistance to BTN3A3 is an additional factor to consider in assessing the zoonotic potential of avian influenza viruses. (Nature: [10.1038/s41586-023-06261-8](#))

During a pilot trial treating chronically hepatitis E virus (HEV)-infected patients with sofosbuvir, high population diversity led to the emergence of variants, particularly A1343V, which displayed lower sensitivity to the drug, highlighting a new mechanism of resistance-associated variants during sofosbuvir treatment. (Hepatology: [10.1097/HEP.0000000000000514](#))

Long- and short-read viromics and metatranscriptomics to examine viruses in Arctic cryopeg brine, sea ice brine, and seawater, reveals novel viral diversity in these extreme environments, indicates distinct virus-host interactions, and showcases differing evolutionary pressures between stable cryopeg and fluctuating sea ice ecosystems. (Microbiome: [10.1186/s40168-023-01619-6](#))

GrandR is a comprehensive package for analyzing and visualizing RNA metabolic labeling data, demonstrating its usefulness for quality control, differential gene expression analysis, kinetic modeling, and studying the temporal dynamics of RNA using snapshot experiments. (Nature Communications: [10.1038/s41467-023-39163-4](#))

The study investigates host-virus interactions in subsurface fractured shales, demonstrating the widespread presence of CRISPR-Cas defense systems in host genomes and revealing complex dynamics of host-virus co-existence and the development of viral strategies to evade host CRISPR-Cas systems over time. (Current Biology: [10.1016/j.cub.2023.06.033](#))

Impact of influenza virus infections on the development of premature cellular senescence and macrophage-mediated inflammation, finding that influenza A virus infection leads to early cellular aging in a murine model, characterized by senescent cells in the lungs, and these senescent cells influence subsequent viral infections by exhibiting higher viral loads and affecting viral replication through altered signaling pathways and cellular conditions. (Aging Dis: [10.14336/AD.2023.0310](#))

The authors reveal that the core structural domain of the 30K superfamily of movement proteins (MPs) found in diverse plant viruses is homologous to the jelly-roll domain of the capsid proteins (CPs) of small RNA and DNA (plant) viruses, suggesting their evolutionary origin through duplication or horizontal acquisition of the CP gene, followed by neofunctionalization, contributing to the expansion of host ranges of emergent plant viruses. (PLOS Biology: [10.1371/journal.pbio.3002157](#))

Metatranscriptomic analysis unveils 763 new virus sequences of the family Mitoviridae, identifying novel mitovirus clades and a potential new viral class, annotates mitovirus-specific protein motifs, and highlights that mitochondrial viruses co-opt mitochondrial biology for their survival, shedding light on the

complex interplay between RNA viruses and host organelles. (mSystems: [10.1128/msystems.01002-22](#))

The African swine fever virus (ASFV), responsible for a severe haemorrhagic disease in pigs, has recently exhibited unexpected genetic diversity during its incursion into Germany in 2020, with newly identified variants sharing a frameshift mutation in a DNA polymerase gene, suggesting a significant impact on the virus's evolution and potential outcomes of the pandemic. (Emerg Microbes Infect: [10.1080/22221751.2022.2146537](#))

Avian viral pathogens in Germany, highlighting an overlap of infections across nine avian genera, particularly raptors, suggesting their suitability for combined surveillance efforts to improve understanding and control of these zoonotic viruses. (Emerg Microbes Infect: [10.1080/22221751.2023.2231561](#))

Tool to investigate the genetic diversity of anelloviruses through metagenomic next-generation sequencing data, using an up-to-date database of anellovirus reference sequences. (Viruses: [10.3390/v15071575](#))

Two-step nested PCR protocol to analyze near full-length proviral HIV-1 DNA from PBMC specimens, successfully detecting drug resistance mutations in individuals with low or undetectable viremia, highlighting the prevalence of these mutations and the importance of considering computational tools for accurate mutation reporting. (J Antimicrob Chemother: [10.1093/jac/dkad240](#))

The introduced HIV-1 "Gag and Envelope reactivation co-detection assay" (GERDA) enables sensitive detection of Gag+/Env+ protein-expressing cells using flow cytometry, revealing the presence and functionality of HIV-1 in critical body compartments, particularly lymph-node-homing cells with central memory T cells (TCMs), highlighting their importance for HIV-1 reservoir eradication. (Cell Reports Methods: [10.1016/j.crmeth.2023.100485](#))

A new viral metagenomic Next-Generation Sequencing (mNGS) protocol based on Nanopore Flongle sequencing, significantly reducing sample-to-result times and costs while maintaining sensitive virus detection, making it suitable for clinical diagnostics in cases of unclear symptoms. (J Virol Methods: [10.1016/j.jviromet.2023.114784](#))

Reviews / Commentaries / Editorials / ...

The evolutionary advantages of RNA viruses due to high mutation rates and adaptability are contrasted with the risks of deleterious mutations, focusing on the overlooked role of indels in shaping viral populations; CirSeq and MultiMatch pipeline to accurately identify and quantify indels, emphasizing their significant impact on viral evolution and potential for new antiviral strategies. (PNAS: [10.1073/pnas.231078512](#))

With the example of SARS-CoV-2, this comment emphasizes the importance of distinguishing between a virus itself, the resulting disease, and the societal impact in understanding and addressing pandemics effectively. (PLOS Biology: [journal.pbio.3002130](#))

Publication shortcuts: If you would like us to add a shortcut to a specific virus (family) or topic, drop us an [email](#).

SARS-CoV-2


influenza


HIV


monkeypox

Tools and Resources

 [Virus tools website](#)

Tools that have been added to our [collection](#) this month, or have now been published. Tools developed by EVBC members are marked .

 **BacteriophageHostPrediction**: Predicting bacteriophage hosts based on sequences of annotated receptor-binding proteins


 **CoVigator**: A monitoring system for SARS-CoV-2, integrating a NGS variant calling pipeline, a database that stores all relevant information about mutations in SARS-CoV-2 and a dashboard to enable visual analytics.

CrisprOpenDB: Predicting large numbers of phage genomes with a more customized host prediction process

MultiMatch: detection of indels in CirSeq data sets.

PHERI: Prediction of suitable bacterial host genus for purification of individual viruses from different samples

Prokaryotic virus Host Predictor (PHP): Host prediction of prokaryotic viruses based on Gaussian Model (GM), taking the complete or partial genomic sequences of prokaryotic viruses as inputs

 **SCANellome**: Genomic diversity of anelloviruses.

EVBC Special Issues

 [Special issue list](#)

Submission deadline for our special issue **Virus Bioinformatics 2023** has been closed.

New papers published:

CoVigator—A Knowledge Base for Navigating SARS-CoV-2 Genomic Variants [10.3390/v15061391](#)

Genomic Characterization of a Halovirus Representing a Novel Siphoviral Cluster [10.3390/v15061392](#)

Novel Approach for Identification of Basic and Effective Reproduction Numbers Illustrated with COVID-19 [10.3390/v15061352](#)

viruses *in silico* lecture series

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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 already [register](#) for our upcoming lectures:

- | | |
|--------------------------------|---|
| 23. October 2023 | Gabriel da Luz Wallau, Bernhard Nocht
Institute for Tropical Medicine,
Germany |
| 20. November 2023
postponed | Anton Petrov, Riboscope Ltd., UK
Dominik Heider, University of Marburg,
Germany |

If you are attending the "viruses in silico" lecture regularly and do not want to register every month, you can choose to be permanently registered. You will be added to the mailing list and receive the access details every month. You can unsubscribe at any time.

Vacancies

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PhD Position in biomedical data sciences and bioinformatics for studying TP53 mutants. The Gruber Lab has an open PhD position in biomedical datasciences. You will be developing data science approaches to analyze TP53 mutants. By analysing and integrating multi-omics data you will enable a panoramic view on the gene activity programs impacted by specific TP53 mutants.

Application deadline:

21 August 2023