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Selected Publications by EVBC Members All publications on Pubmed

Clinical diagnostics

🔗 The comparison of three automated multiplex PCR platforms for syndromic testing of respiratory samples reveals similar performance between the platforms, identifying BioFire as having the highest relative sensitivity, thus indicating their suitability for rapid and accurate diagnosis in clinical settings. (Diagn Microbiol Infect Dis: [10.1016/j.diagmicrobio.2024.116308](https://doi.org/10.1016/j.diagmicrobio.2024.116308))

Evolution and viromics

🔗 The study investigates the dynamics of defective viral genomes (DVGs) alongside standard viral genomes during long-term experimental evolution of two betacoronaviruses, revealing their widespread formation, greater diversity, and abundance, influenced by factors such as multiplicity of infection (MOI) and cell- and virus-specific conditions. (Viruses: [10.3390/v16040644](https://doi.org/10.3390/v16040644))

🔗 Analysis of invertebrate DNA and RNA viromes across 31 phyla reveals dominant virus families and showcases the diversity of viromes within each phylum, with host phylum explaining over five times more variance in composition than habitat and highlighting similarities between the viromes of phylogenetically related phyla. (mSystems: [10.1128/msystems.00124-24](https://doi.org/10.1128/msystems.00124-24))

Treatment

🔗 Three known Influenza virus endonuclease inhibitors (DPBA, L-742,001, and baloxavir) are repurposed for the La Crosse virus endonuclease, providing insights into their inhibition mechanisms and offering potential avenues for the development of Bunyavirales endonuclease inhibitors. (IUCrJ: [10.1107/S205225252400304X](https://doi.org/10.1107/S205225252400304X))

🔗 A collection of 21 isolated, virulent phages targeting vancomycin-resistant *Enterococcus faecium* strains were mixed into a cocktail using the Appelmann protocol and iteratively grown on naive strains to significantly enhance lytic activity and isolate phages with extended host ranges. Results suggest that point mutations or recombination events in the tail fiber genetic region drove phage evolution. (Antimicrob Agents Chemother: [10.1128/aac.01439-23](https://doi.org/10.1128/aac.01439-23))

🔗 The review highlights the potential of bacteriophage therapy as a novel approach for treating bronchiectasis, citing successful case reports and series with favorable outcomes in patients, but emphasizes the need for further research, including robust clinical trials, to understand its efficacy, interaction with microbiota, and potential development of bacterial resistance. (Curr Opin Pulm Med: [10.1097/MCP.0000000000001050](https://doi.org/10.1097/MCP.0000000000001050))


Public health

🔗 Screening of over 269,000 sequencing datasets from the Sequence Read Archive, using a data-driven virus discovery approach, results in the identification of 40 nidoviruses from six virus families infecting vertebrate hosts, including 11 coronaviruses with bisegmented genomes, revealing insights into their genetic diversity, genome architecture, and evolutionary dynamics. (PLoS Pathog: [10.1371/journal.ppat.1012163](https://doi.org/10.1371/journal.ppat.1012163))

🔗 The study demonstrates the feasibility of using human intestinal enteroids (HIE) to detect the infectivity of various gastroenteritis viruses in wastewater, achieving comparable replication yields for human noroviruses (HuNoVs), rotavirus (RV), astrovirus (HAstV), and adenoviruses (HAdV) in single and multiple co-infections, and identifying diverse viral genotypes in wastewater samples. (Water Res: [10.1016/j.watres.2024.121481](https://doi.org/10.1016/j.watres.2024.121481))

🔗 The authors investigated the impact of reduced sequencing efforts on surveillance outcomes during the SARS-CoV-2 pandemic in Switzerland, finding that while overall national dynamics could be recapitulated with only 35% of the original sequencing effort, certain outcomes and viral lineages, particularly Omicron and Delta, were more sensitive to reduced sequencing, highlighting the importance of balancing societal benefits and costs in genomic surveillance programs. (Microbiol Spectr: [10.1128/spectrum.03628-23](https://doi.org/10.1128/spectrum.03628-23))

Tools and Resources

Tools that have been added to our [collection](#) this month have been newly released or updated. Tools developed by EVBC members are marked .

VirusHunter & VirusGatherer: Data-driven virus discovery from sequencing data using profile Hidden Markov Models

ViBioM 2024

Live Stream:

Last chance to [register](#) for our live stream of ViBioM 2024. The live stream is free of charge, but is only open to people who do not work in the industry. Please note that we will not be able to offer chat or discussion.

Registration deadline:

24 May 2024

viruses *in silico* lecture series

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.

Computational investigation of phage sequences in MetaSUB data

27. May 2024 | 4 pm CET


online

João Carlos Setubal, University of São Paulo, Brazil

The MetaSUB Consortium studied subway systems in 60 cities over 3 years, using metagenomics to analyze bacteriophage genomes. They identified 1,714 phage genomes, mostly novel, with some exceptionally large ones up to 572 kbp. While most phages were site-specific, 194 were found across all sampled cities. Using vHULK and other methods, they predicted hosts for 48 % of the genomes, showing agreement with bacterial abundance, including drug-resistant pathogens.

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.

Upcoming Events

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 .

Workshop on Algorithms in Bioinformatics (WABI)

02–04 September 2024 | Egham, UK

Conference theme: *algorithmic work in bioinformatics, computational biology and systems biology*

Abstract Submission deadline:

19 May 2024

7th International Viromics Workshop

23–25 October 2024 | Columbus, Ohio, USA