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Recent Selected Publications by EVBC Members

Extensive C->U transition biases in the genomes of a wide range of mammalian RNA viruses; potential associations with transcriptional mutations, damage- or host-mediated editing of viral RNA. *PLoS Pathog* [10.1371/journal.ppat.1009596](https://doi.org/10.1371/journal.ppat.1009596)

efam: an expanded, metaproteome-supported HMM profile database of viral protein families. *Bioinformatics* [10.1093/bioinformatics/btab451](https://doi.org/10.1093/bioinformatics/btab451)

Genetic and antigenic evolution of H1 swine influenza A viruses isolated in Belgium and the Netherlands from 2014 through 2019. *Sci Rep* [10.1038/s41598-021-90512-z](https://doi.org/10.1038/s41598-021-90512-z)

Genomic and Micro-Evolutionary Features of Mammalian 2 orthobornavirus (Variegated Squirrel Bornavirus 1, VSBV-1). *Microorganisms* [10.3390/microorganisms9061141](https://doi.org/10.3390/microorganisms9061141)

Discriminating between pre-migration and post-migration HIV acquisition using surveillance data. *J Acquir Immune Defic Syndr* [10.1097/QAI.0000000000002745](https://doi.org/10.1097/QAI.0000000000002745)

A large-scale comparative study on peptide encodings for biomedical classification. *NAR Genom Bioinform* [10.1093/nargab/lqab039](https://doi.org/10.1093/nargab/lqab039)

Reviews / Commentaries

The enzymes for genome size increase and maintenance of large (+)RNA viruses. *Trends Biochem Sci* [10.1016/j.tibs.2021.05.006](https://doi.org/10.1016/j.tibs.2021.05.006)

Mapping the evolution of bornaviruses across geological timescales. *Proc Natl Acad Sci* [10.1073/pnas.2108123118](https://doi.org/10.1073/pnas.2108123118)

Identification of viral-mediated pathogenic mechanisms in neurodegenerative diseases using network-based approaches. *Brief Bioinf* [10.1093/bib/bbab141](https://doi.org/10.1093/bib/bbab141)

Global overview and major challenges of host prediction methods for uncultivated phages. *Curr Opin Virol* [10.1016/j.coviro.2021.05.003](https://doi.org/10.1016/j.coviro.2021.05.003)

Mathematical modelling and phylodynamics for the study of dog rabies dynamics and control: A scoping review. *PLoS Negl Trop Dis* [10.1371/journal.pntd.0009449](https://doi.org/10.1371/journal.pntd.0009449)

Global Advances in Tomato Virome Research: Current Status and the Impact of High-Throughput Sequencing. *Front Microbiol* [10.3389/fmicb.2021.671925](https://doi.org/10.3389/fmicb.2021.671925)

Preprints

Philympics 2021: Prophage Predictions Perplex Programs. *bioRxiv* [10.1101/2021.06.03.446868](https://doi.org/10.1101/2021.06.03.446868)

Characteristics of genetically diverse Antarctic sea ice bacteriophages allow adaptation to changing environmental conditions. *bioRxiv* [10.1101/2021.05.28.446129](https://doi.org/10.1101/2021.05.28.446129)

Discovery, diversity and functional associations of crAss-like phages in human gut metagenomes from four Dutch cohorts. *bioRxiv* [10.1101/2021.06.01.446427](https://doi.org/10.1101/2021.06.01.446427)

 [EVBC publications website](#)

Tools and Resources

efam: expanded, metaproteome-supported HMM profile database of viral protein families

PEPTIDE REACToR: in-depth comparison and benchmarking of peptide encodings.

 [Virus tools website](#)

viruses *in silico* | EVBC Lectures

Phylogenetic modelling of modern and ancient infectious disease dynamics

20. July 2021 | 03–04pm CEST

[online](#)

Dr. Denise Kühnert, MPI-SHH, Germany

Recent advances in ancient DNA research had a great impact on the study of infectious diseases — we can now recover full genome sequences from pathogenic organisms that caused deadly pandemics hundreds or thousands of years ago. How can Bayesian phylogenetic methods be used for the analysis of modern and ancient pathogens?

 [Register](#)

Requests

EVBC member [G. M. Spyrou](#) is looking for a collaboration to provide them with experimental data from patients' samples on autoantibodies produced during a range of diseases, particularly neurodegenerative diseases, autoimmune diseases and viral infections.

News and Announcements

We are happy to announce the first keynote speakers for **ViBioM 2022** in Valencia, Spain.



Evelien
Adriaenssens



Francois
Balloux



Emma
Hodcroft



Philippe
Lemey

Vacancies

Postdoctoral Researcher in Viral Metagenomics / Viromics (f/m/x) at UFZ in Leipzig, Germany in the AquaDiva subproject “Phages as Vectors and Indicators of Biological Information: Selective transport and consequences for nutrient release and cycling”.

Application deadline:

06 July 2021

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