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Selected Publications by EVBC Members

 [All publications on Pubmed](#)

Expansion of the global RNA virome reveals diverse clades of bacteriophages: subsets of picobirnaviruses and partitiviruses, previously associated with eukaryotes, infect prokaryotic hosts. (Cell: [10.1016/j.cell.2022.08.023](https://doi.org/10.1016/j.cell.2022.08.023))

Unprecedented spatial and temporal diversity in viral community composition and activity across root, rhizosphere soil, and bulk soil compartments: roles of soil viruses need greater consideration to exploit the rhizosphere microbiome for food security, food safety, and environmental sustainability. (Microbiome: [10.1186/s40168-022-01371-3](https://doi.org/10.1186/s40168-022-01371-3))

Marine DNA methylation patterns are associated with microbial community composition and inform virus-host dynamics. (Microbiome: [10.1186/s40168-022-01340-w](https://doi.org/10.1186/s40168-022-01340-w))

By analysing geotagged viral genomes using spatially-explicit phylogeography and simulating virus dispersal, we find that in the event of Lassa virus being introduced into a new suitable region, its spread might remain spatially limited over the first decades. (Nat Commun: [10.1038/s41467-022-33112-3](https://doi.org/10.1038/s41467-022-33112-3))

Examination of the viral content of diverse human-pathogenic fungi in a clinical biobank identified numerous viral genomes, including one lineage previously not known to infect fungi. (Microbiol Spectr: [10.1128/spectrum.01610-22](https://doi.org/10.1128/spectrum.01610-22))

Endogenous viral elements in shrew genomes expand the current known Pestivirus host range and provide novel insight into the ancient evolutionary history of pestiviruses and the Flaviviridae family in general. (Mol Biol Evol: [10.1093/molbev/msac190](https://doi.org/10.1093/molbev/msac190))

Emergence of Compensatory Mutations Reveals the Importance of Electrostatic Interactions between HIV-1 Integrase and Genomic RNA. (mBio: [10.1128/mbio.00431-22](https://doi.org/10.1128/mbio.00431-22))

Surface water in small shallow water bodies may play an important role as a mediator of AIV infection of aquatic wild birds. (Emerg Microbes Infect: [10.1080/22221751.2022.2065937](https://doi.org/10.1080/22221751.2022.2065937))

Coupling between stable isotope probing and complementary shotgun metagenomic analyses to identify viruses of methanogens involved in the bioconversion of formate. (Environ Microbiol: [10.1111/1462-2920.16120](https://doi.org/10.1111/1462-2920.16120))

Systems Bioinformatics Reveals Possible Relationship between COVID-19 and the Development of Neurological Diseases and Neuropsychiatric Disorders. (Viruses: [10.3390/v14102270](https://doi.org/10.3390/v14102270))

Set of prudently chosen viral contigs, which should help not only better understanding of freshwater viruses but also be a valuable resource for future virome studies. (Front Microbiol: [10.3389/fmicb.2022.953500](https://doi.org/10.3389/fmicb.2022.953500))

HSV-1 and influenza infection induce linear and circular splicing of the long NEAT1 isoform. (PLoS One: [10.1371/journal.pone.0276467](https://doi.org/10.1371/journal.pone.0276467))

An Evolved 5' Untranslated Region of Alfalfa Mosaic Virus Allows the RNA Transport of Movement-Defective Variants. (J Virol: [10.1128/jvi.00988-22](https://doi.org/10.1128/jvi.00988-22))

Reviews / Commentaries / Editorials

As long suspected, poxviruses capture host genes through a reverse-transcription process now shown to be mediated by retrotransposons. (eLife: [10.7554/eLife.83488](https://doi.org/10.7554/eLife.83488))

A community effort is needed to establish a 'global soil virosphere atlas' that can be used to address the roles of viruses in soil microbiomes and terrestrial biogeochemical cycles across spatiotemporal scales. (Trends Microbiol: [10.1016/j.tim.2022.05.003](https://doi.org/10.1016/j.tim.2022.05.003))

An introduction to the Marburg virus vaccine "MARVAC" consortium representing leaders in the field of vaccine research and development aiming to facilitate a rapid response to this infectious disease threat. (PLoS Pathog: [10.1371/journal.ppat.1010805](https://doi.org/10.1371/journal.ppat.1010805))

Current knowledge of viral and host determinants that may affect the evolutionary trajectories of Hepatitis E virus. (Curr Opin Virol: [10.1016/j.coviro.2022.101274](https://doi.org/10.1016/j.coviro.2022.101274))

Preprints

Impact of the COVID-19 pandemic on the circulation of other pathogens in England. (medRxiv: [10.1101/2022.10.21.22281366](https://doi.org/10.1101/2022.10.21.22281366))

Global landscape of the host response to SARS-CoV-2 variants reveals viral evolutionary trajectories. (bioRxiv: [10.1101/2022.10.19.512927](https://doi.org/10.1101/2022.10.19.512927))

Distinct phenotype of SARS-CoV-2 Omicron BA.1 in human primary cells but no increased host range in cell lines of putative mammalian reservoir species. (bioRxiv: [10.1101/2022.10.04.510352](https://doi.org/10.1101/2022.10.04.510352))

A pseudovirus system enables deep mutational scanning of the full SARS-CoV-2 spike. (bioRxiv: [10.1101/2022.10.13.512056](https://doi.org/10.1101/2022.10.13.512056))

Possible adaption of the 2022 Monkeypox virus to the human host through gene duplication and loss. (bioRxiv: [10.1101/2022.10.21.512875](https://doi.org/10.1101/2022.10.21.512875))

Identification of RNA virus-derived RdRp sequences in publicly available transcriptomic datasets. (bioRxiv: [10.1101/2022.10.18.512700](https://doi.org/10.1101/2022.10.18.512700))

Community types of the human gut virome are associated with endoscopic outcome in ulcerative colitis. (Preprints: [10.21203/rs.3.rs-2166222/v1](https://doi.org/10.21203/rs.3.rs-2166222/v1))

Publication shortcuts: If you would like us to add a shortcut to a specific virus (family) or topic, drop us an [email](mailto:evbc@uni-jena.de).

SARS-CoV-2

influenza

HIV

monkeypox

EVBC Special Issues

 [Special issue list](#)

For our special issue **Virus Bioinformatics 2023** running alongside ViBioM 2023, we have vouchers available for EVBC members. Get in contact if you are interested!

ViBioM 2023

 [Save the date](#)

We are happy to announce further keynote speakers:



Simon Dellicour
Université libre de Bruxelles and
Evolutionary and Computational
Virology lab, KU Leuven, BE



Gülsah Gabriel
Viral Zoonoses - One Health,
Leibniz Institute of Virology, DE

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 ✨.

jGfV virtual virology lecture series

10 November 2022 | 05 pm CET

West Nile viruses (Pietro Scaturro, ✨ Jonas Schmidt-Chanasit)

ISCB Rocky 2022

08-10 December 2022 | Snowmass Village, Colorado, US and online

Early Registration Deadline: **15 November 2022**

3. Symposium of the Geneva Centre for Emerging Viral Diseases: Covid-19 and beyond: Emerging viral diseases and their public health impact

07-09 December 2022 | Geneva, Switzerland and online

✨ I. Eckerle (Scientific Committee), E. Hodcroft, R. Neher, V. Thiel (speakers)

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.

Computational Tools for Deeper Mining of Viromes and Bacteriophage Genomes

28 November 2022 | 06 pm CET / 09 am PST

Anca Segall, San Diego State University, USA

Please be aware of the deviating time!

online

Given the numerical dominance of bacteriophages, their central roles in all microbiomes, and their diversity, we clearly need a better understanding of the genetic and functional potential of viruses. In recent years, the resurgence and greater spread of phage therapy has raised the stakes even higher: the better we know our phages, the more safely we can use them as surrogate antibiotics. I will describe our most recently developed, machine learning-based tools for more thorough annotation of bacteriophage genomes.

ECR Viromics Webinar Series

 [Register](#)

This lecture for early career researchers studying viruses in complex communities is organized together with the [Center of Microbiome Science](#) at Ohio State University and the [NSF EMERGE Biology Integration Institute](#).

"Introduction to MuDoGeR - a pipeline to automatically recover and analyse (viral) genomes from metagenomes

09 November 2022 | 04-05 pm CET

online

René Kallies, Helmholtz-Zentrum für Umweltforschung GmbH UFZ, Germany

Vacancies

 [Find a job](#)

Joint PostDoc position at FSU Jena, Germany, and EMBL/EBI, Hinxton, UK. This project is about virus alignments with secondary structures and covariance models for Rfam. The position will be 1 year in Jena and 2 years in Hinxton. If you are interested, you will have to apply for an EIPOD-LinC fellowship together with Manja Marz (FSU Jena) and Blake Sweeney (EMBL-EBI). Please contact [Manja](#) to learn how to proceed.

Call deadline:

18 January 2023

Bioinformatics Core Manager at RKI, Germany. The Robert Koch Institute (the German Public Health Institute) is looking for a team leader and coordinator of the Bioinformatics Core Facility.

Application deadline:

27 November 2022

Two PostDoc positions at Artem Babaian's Laboratory for RNA-Based Lifeforms at University of Toronto. Join the Laboratory for RNA-Based Lifeforms as a [Computational Virologist](#) or [Bioinformatician](#) to develop state of the art for the detection and sequence analysis of RNA viruses and virus-like agents.

Application deadline:

as soon as vacancies are filled

Member Profile: David L Robertson



Name: David L Robertson
Position: MRC Investigator and Head of CVR Bioinformatics, University of Glasgow, UK
Research focus: Viral origins, evolution, and host-interactions; mostly SARS-CoV-2 since the 2020



[Full interview online](#)

What do you love about viruses?

That despite their relatively simple genomes viruses contain the information to usurp host cells for their own replication and on top of this counteract host responses. Their dependency on host systems makes them interesting to study, eg, this tells us about both virus and host biology, and as viruses evolve very quickly this yields plenty of signal for evolutionary questions to be addressed.

On what topic could you give a 30-min talk without preparation?

SARS-CoV-2 origins and evolution has been my favourite topic to talk about in the last few years. It's been incredible to watch a new human virus evolve, eg, how few changes there were in most of 2020, the extent of convergent mutation and the emergence of VOCs, to have had so much genomic data available for analysis, characterisation of antigenic properties etc., and to compare it to the first SARS virus and broader set of SARS-related viruses circulating in bats. There's clear similarity in their spillover associated with animal markets and this risk should have been better understood prior to the COVID-19 pandemic.

What is your favourite way to spend a day off?

I'm a keen cyclist and enjoy long hilly rides, whatever the weather.

If you could create a new invention, what would it be?

We need help, an invention, for digesting the high volume of data and information that now exists and delivering connected and pertinent information from disparate sources. Datasets are ever larger and more complex, preprints and the published literature is enormous, our collaborative networks global and communication systems such as email overwhelming, we're reaching the limits of what individual humans can keep on top of.

What is the coolest thing about your research?

That there's sufficient data in the public domain to be able to do meaningful computational research without the need for experiments. It's great of course to work with experimentalists and help with data analysis but there's also something very satisfying and rewarding about getting new knowledge and value from previously published datasets.

Member Profile: Isabella Eckerle



Name: Isabella Eckerle
Position: Associate Professor, Hôpitaux universitaires de Genève, Switzerland
Research focus: Emerging viruses



[Full interview online](#)

What do you love about viruses?

That they are simple in terms of their composition, and at the same time so complicated! And that we can still discover so many new characteristics and there is so much knowledge still to be gained!

On what topic could you give a 30-min talk without preparation?

Emerging viral diseases and how anthropogenic changes increase the risk of viral spillovers

What is your favourite way to spend a day off?

Hiking in the French Alps, then spending the evening with a good book and a glass of wine on the sofa

What is the coolest thing about your research?

Working in emerging viruses means that we have to be ready to study a new virus at any time, adapt our research & public health questions to quickly evolving knowledge. Also to know that new viruses will never stop to surprise us - which means that often established paradigms need to be revised! Of course the same aspect is also a challenge - but it also ensures that we constantly have to stay flexible and alert, and be ready to start new collaborations with researchers outside of our field. Working in emerging viruses is very interdisciplinary, which I enjoy a lot!

What was your most surprising scientific finding?

One of my most exciting projects was the isolation of a new coronavirus from camels, which we found to be the ancestor of one of our common cold coronaviruses. Although it is genetically close to the human virus, it is not capable of replicating in human airway cells anymore - for me it highlights how little we know even about endemic human viruses, and how important it is that we translate genomic findings into a phenotypic assessment!

Which scientific topic (outside of your field of research) do you think should have more scientific attention?

How climate change will impact human disease (not only infectious diseases but also non-communicable diseases) - and how important diagnostics are!

Is there anything you would like to share with the EVBC members?

Do not miss our symposium on emerging viruses from December 7-9, 2022 in Geneva and online: "Covid-19 and beyond: Emerging viral diseases and their public health impact"