

Send us your news to evbc@uni-jena.de.

For more frequent updates, please follow us on Twitter  [EVirusBioinfC](https://twitter.com/EVirusBioinfC).

Selected Publications by EVBC Members

 [All publications on Pubmed](#)

Influenza A Virus Infection Reactivates Human Endogenous Retroviruses Associated with Modulation of Antiviral Immunity. (Viruses: [10.3390/v14071591](#))

Evolutionary analysis showed that HCV GT-3a worldwide might have been transmitted from the Indian subcontinent to South Asia, Europe, North America and then become endemic in China. (Viruses: [10.3390/v14071514](#))

SMEAGOL: study specific ssRNA virus-host cell interactions and support identifying antiviral drug targets. (Viruses: [10.3390/v14071436](#))

Deep origination of modern HERVs in pan-primates. (Viruses: [10.3390/v14071370](#))

Towards reliable whole genome sequencing for outbreak preparedness and response. (BMC Genomics: [10.1186/s12864-022-08749-5](#))

TreeKnit: a method that infers ancestral reassortment graphs of influenza viruses from two segment trees. (PLoS Comput Biol: [10.1371/journal.pcbi.1010394](#))

Reviews / Commentaries / Editorials

Respiratory syncytial virus prevention within reach: the vaccine and monoclonal antibody landscape. (Lancet Infect Dis: [10.1016/S1473-3099\(22\)00291-2](#))

Current knowledge on the structure, assembly, and transport of filovirus nucleocapsids. (PLoS Pathog: [10.1371/journal.ppat.1010616](#))

HIV and SARS-CoV-2: the interplay of two wicked problems. (BMJ Glob Health: [10.1136/bmjgh-2022-009105](#))

Potential endogenous viral elements and the range of novel aquatic flaviviruses discovered thus shed light on virus origins and evolutionary history. (J Virol: [10.1128/jvi.00439-22](#))

Preprints

Genetic variability, including gene duplication and deletion, in early sequences from the 2022 European monkeypox outbreak. (bioRxiv: [10.1101/2022.07.23.501239](#))

Deep evolutionary history between modern RNA viruses and sub-viral elements and new perspectives on the evolution of primordial infectious agents and RNA life. (bioRxiv: [10.1101/2022.08.21.504695](#))

Mathematical modeling of plus-strand RNA virus replication to identify broad-spectrum antiviral treatment strategies. (bioRxiv: [10.1101/2022.07.25.501353](#))

SARS-CoV-2

 [Pubmed](#)

Context-specific emergence and growth of the SARS-CoV-2 Delta variant. (Nature: [10.1038/s41586-022-05200-3](#))

The emergence of SARS-CoV-2 occurred via the live wildlife trade in China, and the Huanan market was the epicenter of the COVID-19 pandemic. (Science: [10.1126/science.abp8715](#))

SARS-CoV-2 emergence likely resulted from multiple zoonotic events. (Science: [10.1126/science.abp8337](#))

Monoclonal antibody from a previously infected vaccinated donor has potential as an anti-Omicron drug. (Nat Microbiol: [10.1038/s41564-022-01198-6](#))

Distinct evolutionary trajectories of SARS-CoV-2-interacting proteins in bats and primates identify important host determinants of COVID-19. (PNAS: [10.1073/pnas.2206610119](#))

Estimation and worldwide monitoring of the effective reproductive number of SARS-CoV-2. (eLife: [10.7554/eLife.71345](#))

Structural Evolution of Delta (B.1.617.2) and Omicron (BA.1) Spike Glycoproteins. (Int J Mol Sci: [10.3390/ijms23158680](#))

A Comparison of Bioinformatics Pipelines for Enrichment Illumina Next Generation Sequencing Systems in Detecting SARS-CoV-2 Virus Strains. (Genes: [10.3390/genes13081330](#))

The past, current and future epidemiological dynamic of SARS-CoV-2. (Oxf Open Immunol: [10.1093/oxfimm/iqac003](#))

EVBC Special Issues

 [Special issue list](#)

Special issues edited by EVBC members:

Bioinformatics for Plant Health in *Life* (edited by **L. Miozzi** | G. Bubi | S. Ghignone)

Deadline: **30 September 2022**

Drivers of Evolution of Animal RNA Viruses, Volume II in *Viruses* (edited by **A. Fusaro**)

Deadline: **31 October 2022**


Virus Bioinformatics 2023 in *Viruses* (edited by **F. Hufsky** | **A. Pérez-Cataluña** | **F. González-Candelas** | **M. Marz**)


Deadline: **30 June 2023**

We have waivers to distribute among submissions to this special issue. Get in contact if you are interested!


Tools and Resources


 [Virus tools website](#)


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

 **INPHARED**: INfrastructure for a PHAge REference Database.

MicrobeTrace: The Visualization Multitool for Molecular Epidemiology and Bioinformatics.


 **SMEAGOL**: identify and visualize enrichment (or depletion) of sequence motifs in DNA/RNA sequences.

 **TreeKnit**: inference of Ancestral Reassortment Graph for segmented genomes (typically, human influenza).

 **vAMPirus**: Automated virus amplicon sequencing analysis program integrated with Nextflow pipeline manager.

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 .

European Conference on Computational Biology

12–21 September 2022 | Barcelona, Spain


Registration deadline: **09 September 2022**

 M. Wass, S. Böcker, D. Frishman (Programme Committee)

European Seminar in Virology: Next Gen Virology – New Frontiers and Methodologies in Research and Diagnostics

21–23 October 2022 | Bertinoro, Italy


Submission deadline: **12 September 2022**

 Noam Stern-Ginossar (keynote speaker)

Virus Genomics and Evolution

09–11 November 2022 | Wellcome Genome Campus, UK / Virtual


Abstract and bursary deadline: **13 September 2022**

 Emma Thomson (programme committee)

International dsRNA Virus Symposium

10–14 October 2022 | Banff, Canada

Registration deadline: **01 October 2022**

 Jelle Matthijnsens (session chair, committee)

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.

Title and abstract tba

26 September 2022 | 04–05 pm CEST

Ana Abecasis, Universidade Nova de Lisboa, Portugal

[online](#)

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](#).

Community typing as a way to explore virome compositional changes in IBD patients

22 September 2022 | 04–05 pm CEST

Daan Jansen, Catholic University of Leuven, Belgium

[online](#)

ViBioM 2023

 [Save the date](#)



We have waited patiently, and now we're crossing our fingers that we'll finally meet you in person again at ViBioM 2023 in **Valencia, Spain, May 24–26, 2023**. ViBioM 2023 is again jointly organized by EVBC, IATA-CSIC, and the University of Valencia.

Key dates:

Submission and registration opens: **09 January 2023**

Submission deadline for oral presentations: **15 March 2023**

Notifications for oral presentations: **05 April 2023**

We are happy to announce the first keynote speakers:



Bernhard Renard

Data Analytics and Computational Statistics, Hasso Plattner Institute, Germany



Santiago F. Elena

Institute for Integrative Systems Biology, University of Valencia, Spain

Vacancies

 [Find a job](#)

Doctoral researcher 'Genomics of Bacteriophage-Host Interactions' at the Viral Ecology and Omics Group of Bas E. Dutilh at FSU Jena. Using cutting-edge experimental and computational tools, you will characterize the genes involved in bacteriophage-rhizobium and rhizobium-legume interactions.

Application deadline: **4 September 2022**

Post-Doctoral Fellows and/or Graduate Students in RNA Virus Discovery. Artem Babaian is starting a laboratory at the University of Toronto (Canada) and is looking to hire Post-Doctoral Fellows and/or Graduate Students. [Reach out to him.](#)

Member Profile: Simon Roux



Name: Simon Roux

Position: Research Scientist at the DOE JGI

Research focus: "Viral EcoGenomics"
i.e. understanding the impact of viruses on environmental microbiomes



What do you love about viruses?

I love the diversity of the viral world, and the many solutions that evolved in the virosphere in response to all the challenges and hurdles viruses are facing to replicate.

What is the coolest thing about your research?

I would argue the coolest thing right now about our research is that we have known (or at least suspected) for a while that viruses of microbes are important for microbiome processes (ecological, evolutionary, and metabolic), and it feels like we are finally starting to get the right tools to characterize these viruses and their impacts.

What was your most surprising scientific finding?

When we identified what looked like a "filamentous phage" (in-ovirus) in some archaeal genomes. I am still puzzled by these filamentous archaeoviruses and how they came to be, especially whether they originated from a relatively recent "host switch" from a bacterial host to an archaeal host (and if so, how did they manage that !)

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

Phage-like microbial (mobile) elements. There is a seemingly large collection of genomic elements in bacterial and archaeal genomes that appears to be "repurposed phages/viruses", such as Gene Transfer Agents (GTA), tailocins, type VI secretion systems, or phage-like-protein-translocation structures (PLTSs). They perform important functions for these microbes, yet so far it seems like they are only studied for specific hosts and separately from each other.

If you were completely free to choose a scientific topic to work on, which would it be?

Understanding how microbiomes (and their viruses) can be used for terraforming other planets.

Member Profile: Mark Paul Selda Rivarez



Name: Mark Paul Selda Rivarez

Position: Researcher, National Institute of Biology Slovenia

Research focus: virus evolution and ecology



[Full interview online](#)

What do you love about viruses?

Their unexpectedly vast diversity, surprising ecological and biogeochemical functions, fascinating evolution and co-evolution with their hosts.

Who is your favourite scientist and why?

Currently, I am inspired by many scientists in diverse fields not because of their achievements but on how they triumph over certain difficulties. Nobel laureate Barbara McClintock stands out. I really liked how she overcame the difficulties of being a woman scientist during her era and used it to instead focus on her science even if people did not believe her. Her story resonates so much with me.

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

Shoes, cap, eye glasses, wrist watches or any wearable tech that is capable of aerosolized or particulated pathogen detection in the air or surfaces.

What is the most interesting question or challenge in science that is still unanswered?

Are viruses alive, and are we yet to discover non-obligate viruses? If no, then our definitions of life stay the same. If yes, then how do we now draw the line between life and non-life in biology?

What is the coolest thing about your research?

That there is always a new virus species anywhere you look.

What do people think about you that isn't true?

That I am smart, although I am just really passionately curious and highly driven by people that inspire me.

For which project idea are you looking for a cooperation partner?

We have a very raw idea, with a few young researchers, to estimate global risks associated with the emergence of plant viruses in crops / wild flora / etc. and how it will impact global food supply in the next decades. There is a lot of computational, machine learning and modeling work involved, so we for sure would be glad to involve people who are experts on this.

What was your biggest achievement / your biggest failure?

My biggest achievement is finishing my PhD within 3 years, during the COVID-19 pandemic, and away from home. My biggest failure is doing a PhD in the middle of a pandemic, away from home. It's ironic, but I could've been with my family and friends during this extremely difficult period.