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

Selected Publications by EVBC Members

[All publications on Pubmed](#)

Ancient DNA traces the history of hepatitis B: ancient human remains with detectable levels of virus suggest a common ancestor between 12,000 and 20,000 years ago. (Science: [10.1126/science.abi5658](https://doi.org/10.1126/science.abi5658))

Systematic single-cell analyses of HCMV infection: host factors modulate the progression of infection; course of viral infection itself is determined by virus genes. (Nat Microbiol: [10.1038/s41564-021-00994-w](https://doi.org/10.1038/s41564-021-00994-w))

Viral genome wide association study identifies novel hepatitis C virus polymorphisms associated with sofosbuvir treatment failure. (Nat Commun: [10.1038/s41467-021-25649-6](https://doi.org/10.1038/s41467-021-25649-6))

Impact of influenza A H1N1 infection on structure and function of the respiratory and gastrointestinal tract microbiome. (Microbiol Spectr: [10.1128/Spectrum.00182-21](https://doi.org/10.1128/Spectrum.00182-21))

Interlaboratory comparison study for plant virus detection: 8 participants using same samples, extraction kit, ribosomal RNA depletion kit, commercial sequencing provider, but own bioinformatics pipeline. (Pathogens: [10.3390/pathogens10091174](https://doi.org/10.3390/pathogens10091174))

Identification of a previously undescribed prevalent phage illustrates the usefulness of developing virome catalogs. (mSystems: [10.1128/mSystems.00382-21](https://doi.org/10.1128/mSystems.00382-21))

An early warning system for the discovery and characterization of unexpected viruses in repurposed sequence datasets. (Virus Evol: [10.1093/ve/veab085](https://doi.org/10.1093/ve/veab085))

Whole genomes and phylogenetic analysis of seven bovine rotavirus strains from South Africa and Mozambique. (Pathogens: [10.3390/pathogens10101308](https://doi.org/10.3390/pathogens10101308))

Phylogenomic characterization of two novel rodent-borne arteriviruses illustrates the existence of multiple rodent-borne arterivirus lineages. (Viruses: [10.3390/v13091842](https://doi.org/10.3390/v13091842))

Differences between PCR and PCR-free methods are important to consider when investigating "rare" members of the gut virome. (Viruses: [10.3390/v13102093](https://doi.org/10.3390/v13102093))

Preliminary evidence that intestinal bacteriome and virome signatures could be linked with clinical outcomes in community-acquired pneumonia. (EClinicalMedicine: [10.1016/j.eclinm.2021.101074](https://doi.org/10.1016/j.eclinm.2021.101074))

Summary of the ICTV virus taxonomy profile for *Herpesviridae* 2021. (J Gen Virol: [10.1099/jgv.0.001673](https://doi.org/10.1099/jgv.0.001673))

Reviews / Commentaries / Editorials

Review summarizing the array of impacts that HSV has on RNA Polymerase (Pol) II, which transcribes all mRNA in infected cells. (Viruses: [10.3390/v13091836](https://doi.org/10.3390/v13091836))

Review summarizing the currently available knowledge on African Swine Fever in wild boar in Europe. (Viruses: [10.3390/v13091717](https://doi.org/10.3390/v13091717))

CRISPR/Cas genome editors can be utilized to generate disease-resistant or resilient livestock, develop vaccines, and further understand virus-host interactions. (Viruses: [10.3390/v13101996](https://doi.org/10.3390/v13101996))

Potential range of applications and likely limitations of archeovirological approaches. (Adv Virus Res: [10.1016/bs.aivir.2021.07.002](https://doi.org/10.1016/bs.aivir.2021.07.002))

Preprints

Evidence that the subfamily Parvovirinae has evolved in broad congruence with the emergence and diversification of major vertebrate groups. (bioRxiv: [10.1101/2021.10.25.465781](https://doi.org/10.1101/2021.10.25.465781))

A message queue that allows for instant sharing and discovery of genomes to coordinate containment efforts in pathogen outbreaks. (F1000 Research: [10.12688/f1000research.54255.1](https://doi.org/10.12688/f1000research.54255.1))

viruses *in silico* | EVBC Lectures

[Register](#)

Deciphering viral RNA structure with ViennaRNA

22. November 2021 | 04–05 pm CET

online

Michael T. Wolfinger, University of Vienna, Austria

A deep understanding of RNA structure formation is crucial for the emerging field of virus bioinformatics. The ViennaRNA Package comes with a rich portfolio of tools to analyze RNA folding and the traits that are associated with particular folds.

ECR Viromics Webinar Series

[Register](#)

The EVBC, together with the Center of Microbiome Science at Ohio State University, and the NSF EMERGE Biology Integration Institute are starting a **webinar series for early career researchers studying viruses in complex communities**. The webinar series will start in January 2022 and take place regularly on the second Wednesday of the month at 4 pm CET. **Registration will open soon**. We invite you to nominate speakers (link on website).


ViBioM 2022

[Register](#)

- One more speaker to finish our exquisite line-up: Esteban Domingo will join us giving a talk about quasispecies.
- We will support a PhD student giving a talk in Valencia: [Apply for PhD Travel Award](#)

Upcoming Events

[Subscribe to Calendar](#)


EVBC does not endorse any of the listings. EVBC members are involved in events marked .

Genomics and Clinical Virology

20–25 February 2022 | Wellcome Genome Campus, UK
Application deadline: 04 November 2021

Ascona Workshop 2022 on "Biological systems: from first principles to data-driven modelling and back"

27 March – 01 April 2022 | Ascona, Switzerland
Re-registration deadline: 30 November 2021

 Richard Neher (speaker) | Niko Beerenwinkel (organizer)

Please see the [back of the newsletter](#) to get to know our members!

Member Profile: Denis Kutnjak



Name: Denis Kutnjak

Position: Head of Microbiology Unit, Department of Biotechnology and Systems Biology, National Institute of Biology, Ljubljana, Slovenia

Research focus: Discovery, diversity and evolution studies of viruses (mostly plant viruses and viruses in environmental samples, such as water)



What do you love about viruses?

Adaptability, dynamics and possibility to observe their evolution in real-time.

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

Plant virus discovery.

What is your favourite way to spend a day off?

A trip to the unspoiled corners of the nature, hiking in the mountains, but also reading a good book.

What is the coolest thing about your research?

Probably the coolest thing of any research: looking into the unknown and elucidating a part of it; specifically this means discovering yet unknown microbes, but also the ways they interact and evolve.

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

Neurology, mental health (natural sciences) and research on different aspects of how we interact in society (sociology).

If you had the option to give advice to a younger version of yourself, what would that be?

Every problem has a solution, it just needs time; and probably: say 'no' more often.

Member Profile: Ben Temperton



Name: Ben Temperton

Position: Senior Lecturer at University of Exeter, United Kingdom

Research focus: How interactions between bacteria and phages influence global biogeochemical cycles, and how we might be able to exploit bacteriophages to treat antibiotic resistant infections.



Who is your favourite scientist and why?

Steve Giovannoni from Oregon State University. He was a hero of mine from my earliest introduction to marine microbiology. He spent about ten years trying to figure out how to culture SAR11 bacteria because it was an important and fascinating organism. It's the most abundant bacteria in the oceans and one of the most important for carbon remineralisation. At a time when single cell genomics and metagenomics was growing, it would have been easy to give up and rely only on 'omics to try and figure it out. Steve had the foresight to realise that experimental models are necessary to test the hypotheses derived from 'omics data. I was lucky enough to work in his lab during my postdoc. He's one of the nicest, most chilled out scientists you'll meet.

Also Cameron Thrash at USC. If you've met him, you'll know why.

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

Marine microbiology or long read sequencing, mostly because I've given

lots of presentations on both.

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

Are we alone in the universe?

What is the coolest thing about your research?

Hunting eureka's in a dark, foreboding forest of goddammits. We study viruses. Pretty much everything about viruses is cool.

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

People think I'm a cat person because I have a cat.

What was your most surprising scientific finding?

That hugely abundant viruses infecting the SAR11 clade might not be quite as important in global biogeochemical cycles as would be assumed by their numbers.

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

The Citizen Phage Library we are creating with Phage Directory needs someone who can implement a blockchain back end that will act as a living record of phages for clinical use in perpetuity.

What was your biggest achievement and your biggest failure?

My biggest achievement has to be managing to raise an amazing little human to twelve years of age. Right behind that is helping my PhD students to grow as scientists and produce some amazing work. Running the COVID genomic surveillance in the SouthWest of the UK as part of COG-UK during the pandemic was also pretty awesome. That work had immediate societal benefit. I've been lucky enough that most of my many failures were not hugely important and served as valuable learning experiences.