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Selected Publications by EVBC Members

[All publications on Pubmed](#)

Diversity and ecological footprint of Global Ocean RNA viruses: The influence of RNA viruses on ecosystems appears to be large, as predicted hosts are ecologically important. (Science: [10.1126/science.abn6358](https://doi.org/10.1126/science.abn6358))

Computational identification of HCV neutralizing antibodies with a common HCDR3 disulfide bond motif in the antibody repertoires of infected individuals. (Nat Commun: [10.1038/s41467-022-30865-9](https://doi.org/10.1038/s41467-022-30865-9))

Gut virome profiling identifies a widespread bacteriophage family associated with metabolic syndrome. (Nat Commun: [10.1038/s41467-022-31390-5](https://doi.org/10.1038/s41467-022-31390-5))

Has Epizootic Become Enzootic? Evidence for a Fundamental Change in the Infection Dynamics of Highly Pathogenic Avian Influenza in Europe, 2021. (mBio: [10.1128/mbio.00609-22](https://doi.org/10.1128/mbio.00609-22))

Enterovirus D68's rapid evolution of surface proteins, extensive diversity, and high rate of geographic mixing could hypothetically be explained by substantial reinfection of adults. (PLoS Pathog: [10.1371/journal.ppat.1010515](https://doi.org/10.1371/journal.ppat.1010515))

Identification of Phage Receptor-Binding Protein Sequences with Hidden Markov Models and an Extreme Gradient Boosting Classifier. (Viruses: [10.3390/v14061329](https://doi.org/10.3390/v14061329))

Redesign and Validation of a Real-Time RT-PCR to Improve Surveillance for Avian Influenza Viruses of the H9 Subtype. (Viruses: [10.3390/v14061263](https://doi.org/10.3390/v14061263))

PIMGAVir and Vir-MinION: Two Viral Metagenomic Pipelines for Complete Base-Line Analysis of 2nd and 3rd Generation Data. (Viruses: [10.3390/v14061260](https://doi.org/10.3390/v14061260))

Functional Analysis of a Frontal miRNA Cluster Located in the Large Latency Transcript of Pseudorabies Virus. (Viruses: [10.3390/v14061147](https://doi.org/10.3390/v14061147))

Co-infections of respiratory viruses are frequent; data obtained from multiplex testing is fundamental for analysis of respiratory viruses dynamics in mono-infection and co-infection for prevention, diagnostic, treatment, and development of new therapeutics. (BMC Public Health: [10.1186/s12889-022-13555-3](https://doi.org/10.1186/s12889-022-13555-3))

Reviews / Commentaries / Editorials

Antibodies to combat viral infections: development strategies and progress. (Nat Rev Drug Discov: [10.1038/s41573-022-00495-3](https://doi.org/10.1038/s41573-022-00495-3))

Changes in the gut virome through life, health, and disease; interactions between the virome, the microbiome, and the human host; overview of their contribution to

gut disease and disease of distant organs. (FEMS Microbiol Rev: [10.1093/fems-re/fuac027](https://doi.org/10.1093/fems-re/fuac027))

Emerging viruses: Cross-species transmission of coronaviruses, filoviruses, henipaviruses, and rotaviruses from bats. (Cell Rep: [10.1016/j.celrep.2022.110969](https://doi.org/10.1016/j.celrep.2022.110969))

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))

Reconstruction of the origin and dispersal of the worldwide dominant Hepatitis B Virus subgenotype D1. (Virus Evol: [10.1093/ve/veac028](https://doi.org/10.1093/ve/veac028))

One Health: A new definition for a sustainable and healthy future. (PLoS Pathog: [10.1371/journal.ppat.1010537](https://doi.org/10.1371/journal.ppat.1010537))

Emerging technologies in the study of the virome. (Curr Opin Virol: [10.1016/j.coviro.2022.101231](https://doi.org/10.1016/j.coviro.2022.101231))

Past and ongoing studies on ancient pathogenic and non-pathogenic viruses and usage of ancient viral genomes to understand their long-term viral evolution. (Viruses: [10.3390/v14061336](https://doi.org/10.3390/v14061336))

When an appropriate sample and library preparation are selected, nanopore MinION sequencing could be used for the detection of plant viruses and viroids with similar performance as Illumina sequencing. (Front Microbiol: [10.3389/fmicb.2022.883921](https://doi.org/10.3389/fmicb.2022.883921))

A Tale of Three Recent Pandemics (Influenza, HIV and SARS-CoV-2): main determinants of the emergence, epidemic response and available countermeasures to prepare for the next pandemic. (Front Microbiol: [10.3389/fmicb.2022.889643](https://doi.org/10.3389/fmicb.2022.889643))

Preprints

Mystery of fatal 'Staggering disease' unravelled: Novel rustrela virus causes severe encephalomyelitis in domestic cats. (bioRxiv: [10.1101/2022.06.01.494454](https://doi.org/10.1101/2022.06.01.494454))

Even in a relatively well studied agroecosystem, a large part of plant viromes can still be unknown: In-depth study of tomato and weed viromes reveals undiscovered plant virus diversity in an agroecosystem. (bioRxiv: [10.1101/2022.06.30.498278](https://doi.org/10.1101/2022.06.30.498278))

New Members

[EVBC members website](#)

We are happy to welcome our new members:

- **Artem Babaian**, University of Cambridge, UK
- **Dimitri Boeckeaerts**, Ghent University, BE
- **Liam Brierley**, University of Liverpool, UK
- **Lander De Coninck**, KU Leuven, BE
- **Fernando González-Candelas**, University of Valencia, ES
- **Jiarong Guo**, Ohio State University, US
- **Naushad Khan**, University of California Irvine, US
- **Kunaphas Kongkitimanon**, Robert Koch Institute, DE
- **Anuj Kumar**, Dalhousie University, CA
- **Andrew Millard**, University of Leicester, UK
- **Luca Nishimura**, The Graduate University for Advanced Studies, JP
- **Ari Aditya Parikesit**, Indonesia International Inst. for Life Sciences, ID
- **Mark Paul Selda Rivarez**, National Institute of Biology, SI
- **Shahram Saghaei**, Friedrich Schiller University Jena, DE
- **Anca M. Segall**, San Diego State University, US
- **Alexandru Tomazatos**, Bernhard Nocht Inst. for Tropical Medicine, DE
- **Alex Veglia**, Rice University, US

viruses *in silico* lecture series

[Register](#)

SARS-CoV-2 Lineages: Lessons Learned and Perspectives for Future Epidemic Tracking

25 July 2022 | 04–05 pm CEST

Áine O'Toole, University of Edinburgh, UK

online

ECR Viromics Webinar Series

[Register](#)

Dwelling in the ocean's skin: lessons learned from studying viruses at the air-sea boundary

13 Jul 2022 | 04-05 pm CEST

Janina Rahlff, Linneaus University, Sweden

online

Member Profile: Spyros Lytras



Name: Spyros Lytras

Position: PhD Researcher at the MRC - University of Glasgow Centre for Virus Research

Research focus: arms-race evolution between viruses and their hosts, genomic signatures in viral genomes, recombination in coronaviruses.



What do you love about viruses?

For me, viruses are the perfect model system for studying evolution! Their genomes change very fast and are under all sorts of interesting selective pressures. They really give us a sped up view of how all life has come to be.

What is your favourite way to spend a day off?

Read a good book at the park or have wine with friends.

What are you currently learning?

Started learning Japanese on duolingo during the first lockdown, 550 days so far and going strong!

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

A virtual reality software for exploring sequence data (walking into chromosomes/segments and looking at the sequence would be so much cooler than scrolling).

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

How did all life begin!

What is the coolest thing about your research?

I primarily work on sequence data made available by other scientists, so I find really cool how many scientific insights one can get by analysing the knowledge already available out there.

What was your most surprising scientific finding?

Finding an endogenous viral element shared between lizards and birds that must have integrated >300 million years ago (probably in a dinosaur!)

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

Using social media data to better understand and predict human behaviour.

Member Profile: Jelle Matthijssens



Name: Jelle Matthijssens

Position: Associate professor at the Rega Institute at the University of Leuven in Belgium

Research focus: Vviral metagenomics applied to a wide range of systems, ranging from the healthy and diseased human gut over insects viromes (mosquitoes and honeybees) to detection of novel plant viruses.



What do you love about viruses?

They keep surprising us over and over again, and the majority of viruses out there have not yet even been discovered. And for the viruses which have been "discovered" a very large fraction of proteins they encode have no known function to date. The amount of things to be learned here is endless.

On what topic could you give a 30-minute presentation without any preparation?

Rotavirus genetic diversity

What is your favourite way to spend a day off?

Sleeping a bit longer, brunching, doing some sports (preferentially with my 3 boys), play some board games, and enjoy an nice summer evening with friends and a "kriek" (Cherry-beer).

What are you currently learning?

The majority of my research career I have been researching eukaryotic viruses. However, more recently I also have become fascinated by the world of bacteriophages. Outside my day-job as a researcher, I spend a considerable amount of time learning about cryptocurrencies/blockchains and their (future) applications.

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

Would it not be awesome to have a microscope with the resolution of an electron microscope able to visualize living systems on a microscopic level in real-time?

What is the coolest thing about your research?

The coolest thing about my research is that I have the freedom to investigate anything I find interesting. For example in my "virome research" we have many small side projects investigating viromes of seaweed, amoeba, caves, etc. These always give fun results!

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

I would have spend more time on learning various (bio-)informatics skills. I do encourage my PhD students to gain as much experience as possible. The result is that they know much more bioinformatics, then I do.