



KNVM Virology News

Dear fellow virologist,

We would like to draw your attention to the first **Dutch Young Virologists Seminar (DYVS)** on Wednesday May 19th! This online monthly seminar series will allow PhD candidates to showcase their work and connect with others in the virology community. The first presenters will be Shirley Braspenning (Erasmus MC) and Julia Eder (Amsterdam UMC). The presentations can be attended by anyone interested in virology, including other PhD candidates, students, and professors. Register [here](#) to receive the Zoom link to attend the seminar, as well as updates on future seminars.

The interviews in this edition are with two Beijerinck laureates: Sebastian Lequime (2021) and Marit van Gils (2017).

The board of the Virology division of the KNVM

(Emmanuel Wiertz, Jolanda Smit, Jeroen Kortekaas, Ronald van Rij, Bart Haagmans, Katja Wolthers, Martijn Langereis, and Puck van Kasteren)

Virology events

May 19, 2021

PhD defense: Aurora Signorazzi, UMCG ([info](#))

July 5, 2021

PhD defense: Alberto Briseno, UMCG ([info](#))

July 6, 2021

PhD defense: Ellen Bouma, UMCG ([info](#))

June 7-8, 2021

[Nidomeeting](#) - Online



Virology Double-Interview

Sebastian Lequime

Assistant Professor
GELIFES
Groningen University

Marit van Gils

Associate Professor
Medical Microbiology
Amsterdam UMC (AMC)



What is your main research focus?

My research aims to characterize evolutionary pressures and dynamics that impact the evolution of viruses across scales, from within- to between-hosts, from small transmission chains to epidemics and from deep to recent evolutionary processes. Because viral evolution takes place at the same time scale as viral ecological processes, its study can uncover some insights into virus ecology: How do they spread? Where do they come from? What is their host range? To explore these questions, I use an integrated combination of "wet" (controlled experiments, field work, high-throughput sequencing) and "dry" (bioinformatics, phylodynamics, modeling and simulations) approaches.

How do you engage with the lay public?

I have been initiating an outreach video project with two very talented people, Dr. Tania Louis, a science communicator, and Pierre-Baptiste Harrivelle, graphic and motion designer. Together, we created [VirEvo](#), a series of three videos on YouTube which explains how the study of pathogen evolution coupled with a strong analytical framework can help us better understand epidemics. VirEvo is available in French and English, with subtitles in multiple languages, including Dutch, German or Spanish.

Why is your research important?

Characterizing and understanding viral evolution is not only a fundamental question, but can have direct implication in predicting or mitigating novel emergences, epidemics, drug or vaccine escape. Evolutionary thinking is also central to some of the tools we use to understand epidemics, a subfield called "molecular epidemiology". All of these are critical pieces of information to understand and manage viruses' impact on us, on our domesticated animals and plants, on our ecosystems and even on our whole biosphere.

What is your main research focus?

The co-evolution of HIV-1 and the maturing B cell repertoire after HIV-infection has been the main focus of my research already since the start of my PhD project. I set up novel methodologies for single memory B cell sorting using soluble antigens for the isolation of monoclonal antibodies, to better understand the antibody response and as tools for HIV-1 treatment. Currently, my research group focuses on the humoral immune response after natural infection and vaccination of several viral pathogens, including HIV, Influenza virus, Hepatitis C virus and SARS-CoV-2 to better understand pathogenesis and guide vaccine design.

What is your favorite virus?

Even though I study quite a few viruses, I find HIV-1 the most fascinating virus even after so many years of studying it. HIV-1 has almost all the tricks in the book to evade immune responses, making the development of a vaccine extremely challenging. Which is highlighted even more with the rapid development of the SARS-CoV-2 vaccines, many of them based on years of HIV-1 research.

Of which accomplishment are you most proud?

In early 2020, we were able to rapidly isolate monoclonal antibodies from one of the first SARS-CoV-2 patients in the Netherlands and these antibodies have substantially contributed to dozens of studies in understanding the role of antibodies in COVID-19. I am extremely proud of the team that worked very hard as a collective to get this work done in record time.

Recent publications

Fedry J, Hurdiss DL, Wang C, Li W, Obal G, Drulyte I, Du W, Howes SC, van Kuppeveld FJM, Förster F, Bosch BJ. 2021. Structural insights into the cross-neutralization of SARS-CoV and SARS-CoV-2 by the human monoclonal antibody 47D11. *Sci Adv*. doi: [10.1126/sciadv.abf5632](https://doi.org/10.1126/sciadv.abf5632).

Sooksawasdi Na Ayudhya S, Meijer A, Bauer L, Oude Munnink B, Embregts C, Leijten L, Siegers JY, Laksono BM, van Kuppeveld F, Kuiken T, Geurts-van Kessel C, van Riel D. 2020. Enhanced Enterovirus D68 Replication in Neuroblastoma Cells Is Associated with a Cell Culture-Adaptive Amino Acid Substitution in VP1. *mSphere*. doi: [10.1128/mSphere.00941-20](https://doi.org/10.1128/mSphere.00941-20).

Fros JJ, Visser I, Tang B, Yan K, Nakayama E, Visser TM, Koenraad CJM, van Oers MM, Pijlman GP, Suhrbier A, Simmonds P. 2021. The dinucleotide composition of the Zika virus genome is shaped by conflicting evolutionary pressures in mammalian hosts and mosquito vectors. *PLoS Biol*. doi: [10.1371/journal.pbio.3001201](https://doi.org/10.1371/journal.pbio.3001201).

