UNIVERSITY OF BERN
MCID
MULTIDISCIPLINARY CENTER FOR INFECTIOUS DISEASES

THE SPREAD

A NEWSLETTER FROM THE MCID

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ARTICLES ON:

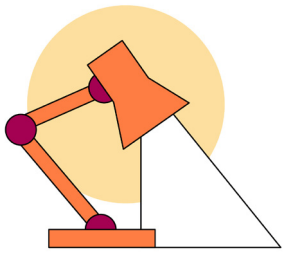
News from the Center

Dear readers,

we are pleased to bring you the latest issue of The SPREAD. With many infectious diseases, including Ebola, hantavirus, measles and diptheria all in the news in recent weeks, the importance of research linked to infectious diseases is more apparent than ever- as is the critical need for this research to cover all disciplines. As always in this issue, we bring you articles on a range of topics, including morbilliviruses, school student well-being during the covid-19 pandemic, and a guest article by Christian Frei, director of the film BLAME.

This issue also marks the launch of a new The SPREAD interview series: Coffee with the MCID. Each upcoming issue will feature an interview with an MCID group leader- and their team, aiming to showcase MCID researchers and infectious disease-linked research happening at the University of Bern. Would you like your research team to be featured? We would love to hear from you — please contact the MCID Management Team.

Yours sincerely,
Rebecca Limenitakis (MCID Managing Director)
Anita Hochuli (MCID Teaching and Outreach Coordinator)
Lisa Thomann (MCID Communications Officer)



Bats, Politics, and a Planet Out of Balance

Article by Christian Frei, Swiss filmmaker, Christian Frei Filmproductions, Zürich

Reflections on the challenges of making the award-winning documentary BLAME[1] about the origins of COVID-19.

Next to my Oscar nomination certificate hangs a quote by Ernest Hemingway: "This is what the artist must do. He must capture the thing so truly that its magnification will endure." For many years, the quote hung in my editing room. It reminded me, again and again, to search for depth and truthfulness within the complexity — and sometimes the sheer chaos — of reality. I am certainly proud of the many awards my documentaries have received over the years. But what truly fills me with pride is the fact that my films age well. They stand the test of time. Even decades later, they remain relevant.

I remember the moment, in the spring of 2020, when I first had the idea for a film about the origins of COVID-19. My mother, already over ninety years old, was staying with me in my loft during lockdown, and I suddenly had time to read extensively. Then came the epiphany — that moment when I simply know: this will be my next film. I had been reading a landmark 2005 paper on SARS-like coronaviruses in bats, published in Science. What captivated me was the story of three researchers: Zhengli Shi, Linfa Wang, and Peter Daszak. Their work helped trace the 2003 SARS outbreak to horseshoe bats in China. After years of field research and international collaboration, they warned that another coronavirus could eventually spill over into humans. The world paid little attention.

Then COVID-19 erupted. Almost overnight, these same scientists were catapulted onto the center stage of an unprecedented media frenzy and geopolitical blame game. Suddenly, scientific uncertainty became political ammunition. Complex research was compressed into headlines, accusations, and simplistic narratives about laboratories, cover-ups, and global conspiracies.

My decision to dedicate a film to these three scientists — and to give them a voice — took only seconds. As a filmmaker, I was fascinated by the cinematic contrast: the darkness of bat caves; the cultural fear and mythology surrounding bats; our ignorance of the complexity of nature; the patience and precision of scientific research and field expeditions — versus the geopolitical storm that was to erupt now, fifteen years later around the same scientists and the same questions. But almost immediately, doubt set in. My heart was pounding. Do I really want to do this? This story is too big for me, I thought. I had to sit down and take a deep breath. It was as if I could already sense the countless hyperventilating media voices that would cover the same subject. As if I could already glimpse the sheer scale and complexity of what lay ahead: feverish debates, speculation, outrage — and, of course, geopolitics.

I have a reputation for finding my subjects in some of the most inaccessible and dangerous places on the planet: war zones, Afghanistan, even outer space. I have also tried to enter the fragile world of the heartbroken and explore the science of lovesickness — which, at the time, felt just as intimidating and emotionally demanding. I am drawn to challenges and seemingly impossible subjects, partly because there is less competition, but mainly because such stories often reveal something essential about the human condition. When I embarked on BLAME, I did what I always do: I began to read. Books, hundreds of articles, scientific papers. I spoke with authors such as David Quammen, who later became a scientific advisor to the film.

I write, direct, and produce my own films, and I spend years working on them. Patience and stubbornness are among my advantages. So is the fact that I am an independent filmmaker. Thanks to Switzerland's public funding system for cinema, I do not have to focus primarily on sales or box office expectations. Of course, I want my films to succeed and to reach audiences. But I also have the freedom to make radical decisions.

One of those decisions was to avoid the familiar trap of a "both sides" approach. I did not approach Zhengli Shi, Peter Daszak, and Linfa Wang by saying: "I want to give you the opportunity to present your side of the story." Instead, I asked them to trust me and to embark with me on an attempt to tell the story from their perspective. Why? Because after years of public suspicion, media frenzy and political instrumentalization, a global audience has the right to hear directly from the three scientists at the very center of the storm. This is what I did. And I never regretted this decision.

The process of scientific discovery is a complicated story, and the universe and complexity of scientific debate are a huge challenge for a filmmaker. The strength of a theatrically released documentary lies in emotion and suspense — and in allowing the audience to come to their own conclusions. Inviting a large audience to dive into fact-driven storytelling and detailed accuracy is not easy at all.

We began with something deceptively simple. I remember how much fun my assistant and I had when we edited one of the first short sequences in the film, dedicated to the global blame game that erupted at the very beginning of the pandemic. Iran's Supreme Leader Ali Khamenei suggested that "the Americans" may have created the virus. Saudi Arabia accused Israel. Singapore pointed to migrant workers. In India, some voices blamed Pakistan. Donald Trump repeatedly referred to COVID-19 as the "Chinese virus". Meanwhile, China responded with its own counterclaims, with some officials suggesting that the virus may have originated outside China and could have been brought to Wuhan by the U.S. military.

In the film, my three protagonists recall that they initially reacted to these accusations with a certain calm detachment. Rumors and finger-pointing, they told me, accompany almost every pandemic. In the age of social media, shrill claims and outright nonsense can rapidly escalate into a global storm. What Zhengli, Linfa, and Peter probably could not foresee was the sheer magnitude of this storm. BLAME shows, step by step, how the three scientists became entangled in it, starting with the decision of the Trump administration to cut funding for EcoHealth Alliance, which had been researching bat coronaviruses in collaboration with the Wuhan Institute of Virology. That was how the politicization of pandemic science began. The pandemic hit us like a bat out of hell.

BLAME (official press photo): Adam Dean for CF Filmproductions

A lot of questions were raised, and journalists feverishly tried to give us answers. More and more of them insinuated that the virus could have come from Zhengli Shi's lab. Lacking hard evidence, they could only speculate and keep raising questions. Many traded almost entirely in suspicion and innuendo. We have a natural tendency to think that big events must have big causes — a tendency to assume that events with a significant impact are the result of deliberate acts by intentional and powerful agents. Seduced by the sheer scale of the story, many journalists, bloggers and influencers forgot a basic rule: you need strong evidence for drastic accusations.

Due to the political polarization and geopolitical blame games surrounding the pandemic, the filming of BLAME had to take place largely under the radar of the authorities. Locations and participants had to be protected. In northern Thailand, in the Pang Mapha region, where we shot a large part of the film, we found a kind of substitute for China: the same dramatic karst landscapes and bat caves as in China's Yunnan province. BLAME has been praised by audiences and critics alike for its powerful visual language. We filmed field research on fruit bats and the Nipah virus, and we developed a special drone technique to celebrate our flying protagonists — the bats. Eventually, I invited my protagonists to a retreat that we called the Silent Lab. There, we encountered a forest monk meditating in the darkness of a cave. We spoke about science and spirituality, logical thinking and serenity. He told me: "If you want insight into the true nature of reality, you have to get rid of the noise."

BLAME suggests that complexity loses against conspiracy because the human brain tends to favor simplicity over nuance. The scientific process, with its uncertainty, investigation, and evolving evidence, often feels unsatisfactory to a public hungry for definitive and bold answers. Conspiracy theories and speculative stories, on the other hand, offer neat and easily digestible narratives, even when they lack evidence. The slow, iterative nature of science is less emotionally satisfying than the instant certainty that conspiracy theories appear to provide.

Through the work of Austrian-Swiss science blogger Philipp Markolin[2], the film reflects on how the human brain is wired for pattern recognition, leading us to see connections where none exist. In times of uncertainty, this cognitive bias makes conspiracy theories and simple narratives more appealing than the complex reality of scientific research. The film also critiques the commercialization of suspicion, showing how political figures, media outlets, and social platforms profit from promoting rumors and doubt, ultimately undermining efforts by the scientific community to address the real causes of pandemics. Evidence-free narratives are not just psychological phenomena; they have become profitable industries. Sensational stories about the virus being engineered in a Chinese lab were more likely to capture attention and generate clicks than nuanced scientific discussions of zoonotic spillover. The clickbait culture of modern media thrives on suspicion, as suspicion drives engagement and advertising revenue. In this sense, suspicion is commodified, and conspiracy theories become a business model. The film demonstrates that while science seeks the truth, conspiracy often wins the battle for public attention because it is easier to consume, profitable, and emotionally satisfying.

At its core, BLAME delivers a crucial message: we need global cooperation to prevent future pandemics. The film emphasizes the importance of understanding the true origins of diseases like COVID-19 through evidence-based research rather than speculation and conspiracy. It highlights how human encroachment on wildlife habitats and the exploitation of nature are central drivers of zoonotic spillover, urging audiences around the world to recognize that environmental sustainability and public health are deeply interconnected. For a worldwide audience, BLAME serves as a call to action — encouraging viewers to be more critical of sensational media narratives and to seek out scientific truth in an age of misinformation. By exposing the dangers of misinformation and the politicization of science, BLAME aims to restore public trust in scientific expertise, demonstrating that addressing the root causes of pandemics requires a collective, fact-based effort.

Christian Frei (courtesy of Nina Dick)

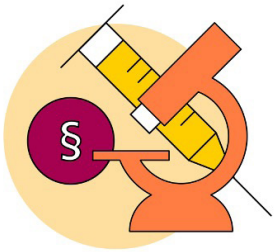
[1] BLAME, documentary by Christian Frei

After years exploring remote bat caves, three scientists are catapulted into the harsh spotlight of politics and serious accusations. Once ignored, these early warners must now defend themselves. A visually striking film journey about the role of science in increasingly dark times. With calm, factual clarity, the film reveals how the deliberate fueling and amplification of fears and feverish myths are driving our world out of balance. **www.blame-documentary.com**

Christian Frei kindly offers to provide a Vimeo link to the film. Please contact him by email if you are interested: christianfrei@gmx.ch

[2] LAB LEAK FEVER, book by Philipp Markolin

Lab Leak Fever exposes how the search for COVID-19's origins was derailed by disinformation campaign, media manipulators and political agendas. Blending science, storytelling, and investigative analysis, Markolin weaves unheard testimony from frontline scientists and unique access to insider information into a revealing account of how lab leak speculation hardened into a widely believed narrative, distorting public understanding and deepening the divide between science and society. **www.lab-leak-fever.com**



Student well-being and the COVID-19 pandemic

Article by: Prof. Dr. Tina Hascher, Dr. Jakob Schnell, Dr. Tanja Held, Institute of Education Science (IES), Prof. Dr. Lukas Fenner, Dr. Nicolas Banholzer, Dr. Kathrin Zürcher, Institute of Social and Preventive Medicine (ISPM), PD Dr. med. Philipp Jent, University Hospital Bern, Dr. Pascal Bittel, Institute for Infectious Diseases (IFIK)

In the MCID- funded project "AirChecker", we combined perspectives from medical science and psycho-educational research. In addition to examining the transmission of infectious diseases in classrooms, we investigated student well-being in school. In this brief report, we outline several key findings on student well-being during and in the aftermath of the COVID-19 pandemic[1].

The COVID-19 pandemic and resulting changes in the educational system became a major source of stress for teachers, students, and families alike. Once it became clear that schools were key settings for the transmission of infectious diseases, schools in Switzerland – as well as around the world - were closed. Following their reopening, various infection control measures were introduced, including facial masks, social distancing, and split-class instruction.

Research has shown that school closure adversely affected students' academic trajectories and educational outcomes in Switzerland and as well as internationally. It is therefore of paramount importance to understand how school closure might be prevented in the event of future pandemics.

Alongside improved ventilation, facial masks and air cleaners represent important infection control measures. At the same time, however, such interventions may have unintended negative consequences for student well-being in school. For instance, wearing facial masks can hinder student-teacher interaction and communication, and previous studies have documented students' negative perception of mask-wearing in educational settings. Similarly, portable air cleaners introduce additional noise in the classroom, potentially impairing learning conditions and reducing acceptance among both students and teachers. Overall, the impact of infection control measures such as facial masks and air cleaners on student well-being has received little scholarly attention.

Across two studies, we investigated the impact of two infection control measures – facial masks and portable air cleaners – implemented in selected classrooms at two Swiss secondary schools. The measures were introduced during, and in the aftermath of the COVID-19 pandemic, specifically during the winters of 2021/2022 (Study 1) and 2022/2023 (Study 2), periods characterized by exceptionally high infection rates.

Student self-reported well-being was measured prior to and following the implementation of the measures, based on a six-dimensional framework which we usually apply to measure student well-being in school (Figure 1). The questionnaire comprised three positive dimensions (positive attitudes toward school, enjoyment in school, and positive academic self-concept) and three negative dimensions (worries in school, physical complaints in school, social problems in school).

In addition, we assessed student state well-being over seven-week study periods through the collection of daily self-reported data of student well-being and emotional experiences.

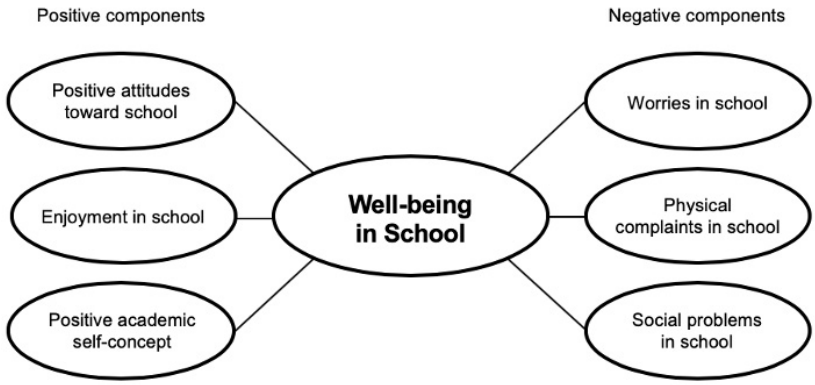


Figure 1: Six-dimensional well-being framework

The assessment of student self-reported daily well-being and emotions was grounded on the circumplex model of affective states, which distinguishes among three affective dimensions: positive activation (e.g, "relaxed"), negative activation (e.g., "stressed"), and valence, reflecting either a positive hedonic tone (e.g. "satisfied") or a negative hedonic tone ("unsatified"). In addition, students self-rated their level of concentration on a continuum ranging from "unconcentrated" to "concentrated".

In both studies, we employed a quasi-experimental design. Study 1 comprised a sample of N = 115 students from five lower secondary classes (Grades 8 and 9). The design was largely determined by local infection control policies implemented during the COVID-19 pandemic. We compared students' six dimensional well-being before and after the intervention and their daily emotional experiences across three conditions: (1) compulsory face-mask use in all five classes, (2) a standard condition without infection control measures following the lifting of school-wide mask mandates, likewise involving all five classes, and (3) the installation of two portable air cleaners with HEPA filters (Xiaomi Mi Air Pro 70m2, China) in two classrooms, with one device positioned at the front and the other at the back of each classroom (2x 600 m3/h cleaning power).

At the outset of Study 1, student well-being scores in the positive dimension were satisfactory, although not particularly high, averaging approximately 4 on a scale from 1-6. School-related worries in school were likewise rated around 4, indicating an unfavorable tendency. Physical complaints were reported at a moderate level (around 3), whereas social problem were low (below 2).

A comparison of the well-being dimensions assessed at the start of Study 1 (January 2022) and at its conclusion (March 2022) revealed a significant decline of enjoyment in school, alongside a significant increase in physical complaints experienced in the school context. All other well-being dimensions remained stable over time. During periods in which face masks were mandatory, students reported on average significantly higher levels of negative activation and lower levels of concentration compared with periods without infection-control measure. Similarly, when air cleaners were installed in the classrooms, students reported a significantly higher negative activation and lower valence than without such measures.

During the winter of 2022/2023, face mask use was neither mandatory nor commonly practiced in schools. Consequently, Study 2 compared two quasi-experimental conditions: (1) the installation of portable air cleaners with HEPA filters (Xiaomi Mi Air Pro 70m2, China), and (2) the standard condition without infection control measures. A sample of N = 62 students from two classes participated in a 7-week cross-over design, alternating between periods with and without air cleaners.

At the outset of Study 2, student well-being scores in the positive dimension were satisfactory, though not elevated, averaging around 4 on a scale from 1-6. In contrast, worries in school were rated between 4 and 4.5, indicating a comparatively unfavourable tendency. Physical complaints were somewhat lower, with mean scores 3, while social problems remained low, scoring below 2.

A comparison of the well-being dimensions before Study 2 (January 2023) and at the end (March 2023) revealed that students' well-being remained largely stable over time. Notably, however, worries in school significantly decreased.

With regard to students' daily well-being and emotional experiences, lower levels of positive activation and concentration were reported on average during periods in which air cleaners were installed in the classroom compared with periods without such measures. No significant differences between the two conditions were observed for negative activation or valence.

Prof. Dr. Tina Hascher

Overall, these findings suggest that infection-control measures may exert a modest negative influence on student well-being, although the observed effects were not pronounced. At the same time, the analyses revealed potentially beneficial developments within specific phases of the implemented measures. For instance, in Study 1, time-sampling analyses demonstrated that during the period of mandatory mask wearing, students' self-reported negative activation decreased significantly over time, possibly reflecting a gradual process of adaptation to the prevailing circumstances. Interestingly, following the lifting of the mask mandate, students' self-reported negative activation significantly increased while their self-reported valence declined. This pattern may indicate that the removal of the protective measure itself constitutes a new and potentially unsettling situation, in which students experienced heightened feelings of insecurity and reduced protection.

With regard to Study 2, it is important to note that no significant increase over time in students' self-reported negative activation was observed in either of the air cleaner group. This finding suggests that the presence of air cleaners in the classroom was not perceived by students as burdensome or distressing. On the contrary, the results even point to the possibility that air cleaners may contribute to an improvement in students' positive affect. Indeed, when comparing students' self-reported state well-being during the first two weeks of the study, a comparable increase in positive activation was found in both conditions (with and without air cleaners), indicating that students' positive activation increased over time irrespective of the implemented measures.

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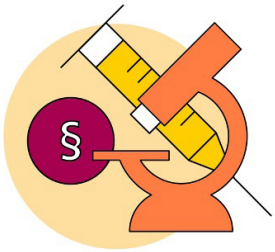

Broad-spectrum morbillivirus antivirals targeting the fusion protein for human and animal health

Article by: Prof. Dr. Philippe Plattet, Clinical Neuroscience Bern, Vetsuisse faculty and Prof. Dr. Dimitrios Fotiadis, Institute of Biochemistry and Molecular Medicine (IBMM), Medical faculty

Morbilliviruses are highly contagious pathogens that infect a wide range of mammalian species and cause severe systemic disease[1]. This genus includes well-known viruses such as measles virus (MeV) and canine distemper virus (CDV). Despite the availability of vaccines against only a limited number of morbilliviruses, members of this genus continue to pose a major threat to both human and animal health. Measles virus still causes substantial mortality in humans worldwide, while canine distemper virus infects a broad range of domestic and wild carnivores, complicating eradication efforts. Moreover, newly identified morbilliviruses have highlighted the ongoing emergence and diversification of this viral family[2]. Little is currently known about the molecular determinants of host range, receptor usage and pathogenicity induced by newly emerging morbilliviruses. Understanding how such viruses enter host cells and spread between hosts is therefore essential for evaluating their zoonotic potential and for developing future antiviral strategies.

Prof. Dr. Philippe Plattet

Up to now, all morbilliviruses possess a single-stranded negative-sense RNA genome encoding six structural proteins as well as accessory proteins[3,4]. Viral entry into host cells is mediated by two interacting envelope glycoproteins: the receptor-binding hemagglutinin (H) protein and the fusion (F) protein[5]. The H protein binds to cellular receptors such as signalling lymphocyte activation molecule (CD150/SLAM)[6,7] on immune cells and nectin-4[8,9] on epithelial cells. Upon receptor engagement, H will activate the F protein.

Prof. Dr. Dimitrios Fotiadis

Consequently, F undergoes major conformational changes, transitioning from a metastable prefusion state[10-12] to a stable postfusion state[12]. Such modifications are assumed to be associated with the merging of the viral envelope with the host cell membrane, thereby enabling viral entry[5]. Interestingly, the amino acid sequence identity of the F protein of various morbilliviral members is much better conserved as compared to their H proteins, which highlights the F protein as a potential target for the development of antivirals with broad-spectrum activity.

The aim of our MCID-funded project is to obtain functional and structural insights into the F protein of poorly characterized and newly emerging morbilliviruses, allowing us to define their relationship to F proteins from other circulating morbilliviral members. Furthermore, a functional cell-cell fusion assay, relying on the co-expression of both glycoproteins as well as a host cell receptor (CD150/SLAM), will be established. We will also initiate a campaign to discover camelids-derived neutralizing variable heavy domain of heavy chain-only antibodies (VHHs) targeting the prefusion conformation of selected F proteins (Figure 1). Candidate VHHs will be tested for their ability to inhibit membrane fusion, as well as for their cross-reactivity with other morbilliviruses.

Finally, structural studies of F proteins of various morbilliviruses in complex with selected neutralizing VHHs will be determined to potentially (i) improve their neutralizing potency and (ii) enhance their broad-spectrum activity.

Overall, this project will provide important insights into the biology, receptor usage and host range of newly emerging morbilliviral members, while simultaneously advancing the development of VHH-based antivirals with, broad, or even pan-morbilliviral activity. Therefore, by targeting conserved regions of the membrane fusion machinery, this work may contribute to the development of broadly reactive therapeutic strategies with relevance for both animal and human health.

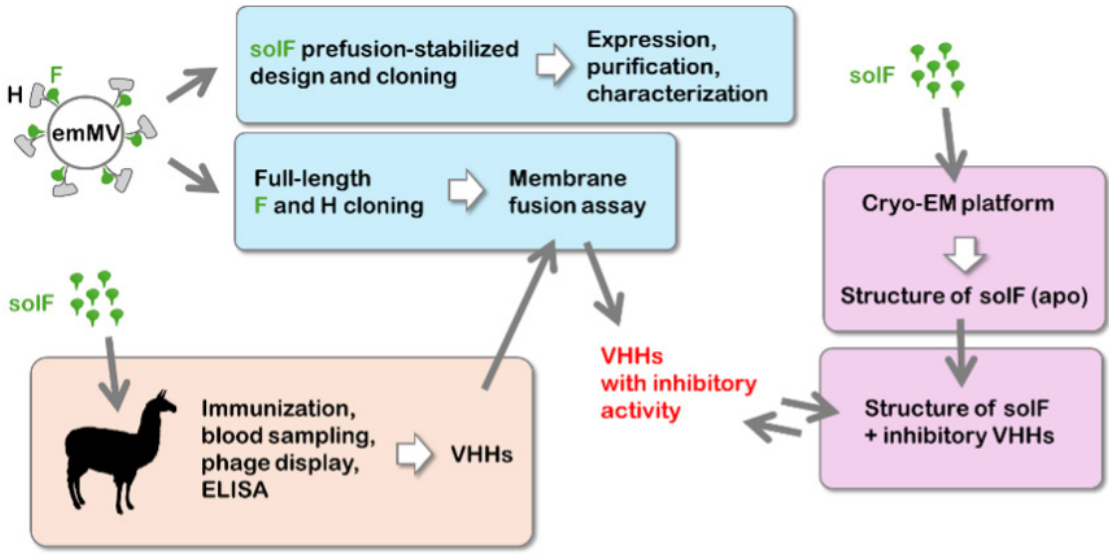

Figure 1. Schematic representation of the project goals. The steps planned to achieve the design of the prefusion-stabilized solF-ectodomain, as well as the establishment of a functional membrane fusion assay are highlighted in blue. Steps towards the identification of VHHs are shown in pale orange. The cryo-EM platform to determine structures of solF is color-coded in purple. emMV: newly emerging morbillivirus member.

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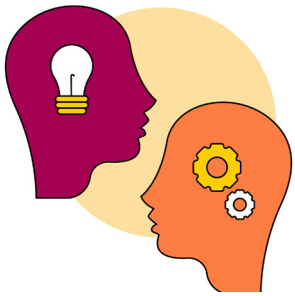

Coffee with the MCID: meet the Ramette Team

Dr. Lisa Thomann interviews Prof. Dr. Alban Ramette and his team at the Institue for Infectious Diseases (IFIK)

From Sequencing to Clinical Insight: How Bioinformatics Is Transforming Infectious Disease Research

To kick off the new "Coffee with the MCID" interview series, Lisa Thomann visited Prof. Ramette's group to discuss how bioinformatics, sequencing technologies, and interdisciplinary collaboration are transforming infectious disease research and clinical diagnostics. Modern infectious disease research is increasingly defined by the convergence of clinical medicine, molecular biology, genomics, and data science — precisely the interdisciplinary space in which the Bioinformatics and Biostatistics Group, Institute for Infectious Diseases of the University of Bern, operates. Led by Prof. Alban Ramette, the team exemplifies the mission of the MCID by translating cutting-edge sequencing technologies into clinically actionable insights while simultaneously advancing fundamental understanding of pathogen biology and disease dynamics. Their work spans the full spectrum of infectious disease investigation, from routine diagnostics and translational assay development to large-scale genomic surveillance and collaborative sequencing services for academic, clinical, and industrial partners.

Your group brings together diverse expertise from laboratory science to computational analysis—how does this interdisciplinary setup function in practice?

The group operates across four interconnected areas: infectious disease research, routine pathogen diagnostics, development of translational assays, and external sequencing services for academic and industrial partners. Our work spans bacteria, viruses, fungi, parasites, and even environmental samples, using genomic, metagenomic, and transcriptomic approaches powered by both Illumina and Oxford Nanopore sequencing technologies. A defining feature of the group is its ability to manage the complete workflow internally, from wet-lab sample preparation to bioinformatic analysis and clinical reporting. This integration allows rapid communication between laboratory scientists and computational researchers. If unexpected findings appear during sequencing analysis, the same team can immediately revisit sample preparation, laboratory protocols, or computational pipelines to investigate further.

Prof. Ramette describes interdisciplinarity as part of the group's "DNA." Team members frequently combine multiple roles, ranging from laboratory work and bioinformatics to systems administration and project management. However, integrating such diverse expertise also creates communication challenges. Biologists, clinicians, and computational scientists often use very different technical vocabularies and conceptual frameworks. To bridge these gaps, the group organises regular cross-disciplinary meetings where researchers present methods, scientific papers, and ongoing projects. The goal is not for everyone to master every technical detail, but rather to understand the challenges faced by colleagues working in other parts of the pipeline. According to the team, this mutual understanding is essential for translating complex genomic data into clinically meaningful insights.

With rapidly advancing sequencing technologies, how do you ensure that innovation goes hand in hand with rigorous validation and biological interpretation?

The group gained international recognition in 2019 when it became the first laboratory worldwide to receive accreditation for clinical nanopore sequencing. At the time, nanopore sequencing was still viewed skeptically because of relatively high sequencing error rate. The team therefore invested heavily in quality control, validation, and workflow optimisation. Their clinical workflow was capable of identifying bacterial pathogens within approximately six hours, moving from amplicon sequencing to an automatically generated diagnostic report. Early implementation was technically demanding. Small mistakes during library preparation could rapidly compromise expensive sequencing flow cells. Nevertheless, these challenges ultimately helped the group refine robust and reliable protocols that are now routinely used in diagnostics.

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The COVID-19 pandemic dramatically accelerated recognition of sequencing as an essential public health tool. Sequencing allowed researchers and health authorities to monitor viral evolution, identify emerging variants, and track transmission dynamics in real time. According to the group, the pandemic fundamentally changed perceptions of sequencing technologies, shifting them from research-focused tools to critical components of clinical and public health decision-making. Despite this progress, cost remains a major barrier to widespread implementation. Sequencing technologies are powerful, but routine diagnostic integration requires balancing speed, reliability, scalability, and affordability. Maintaining sequencing infrastructure, computational resources, and long-term data storage also represents a substantial investment for healthcare systems.

What does 'big data' actually mean in infectious disease research, and what challenges arise when working with it in practice?

The researchers emphasize that "big data" in infectious disease research is less about raw file size and more about complexity. A single clinical sample can generate enormous amounts of highly detailed genomic information, while the number of available patient cases may remain relatively small. This creates analytical challenges for statistical interpretation and clinical decision-making. Clinical genomics also introduces strict regulatory and ethical requirements. Patient sequencing data cannot simply be uploaded to public repositories. Laboratories must maintain secure long-term storage systems, ensure reproducibility, and comply with quality assurance standards. In parallel, biological interpretation remains inherently difficult because biological systems rarely behave in fully predictable ways.

"In 2019, we became the first laboratory in the world to receive accreditation for clinical nanopore sequencing. We used this technology to identify bacterial pathogens via 16S rRNA gene sequencing…within about six hours we can go from amplicon sequencing to a fully automated diagnostic report. This workflow has been running continuously ever since"-Prof. Ramette

Dr. Aileen Geers and Prof. Dr. Alban Ramette

Bioinformatician Dr. Aileen Geers highlighted an important distinction between diagnostics and research. In diagnostics, the priority is speed and reliability. Clinicians often need rapid answers that can directly guide patient treatment decisions. Research, by contrast, allows deeper exploration of unusual findings and integration of broader biological context. Technological advances frequently reveal additional biological complexity rather than simplifying interpretation. Nanopore sequencing provides a striking example. Early critics often interpreted irregular signal patterns as sequencing errors, but researchers later discovered that some of these "errors" reflected biologically meaningful features such as DNA methylation. As sequencing technologies continue to evolve, scientists must constantly adapt their analytical frameworks and biological understanding.

Beyond clinical diagnostics, the group is also deeply involved in infectious disease surveillance and public health genomics. Increasingly, surveillance systems combine clinical sequencing with environmental monitoring approaches such as wastewater surveillance. During the COVID-19 pandemic, wastewater sequencing in Switzerland and neighbouring countries demonstrated the ability to detect emerging viral variants before large numbers of clinical cases appeared. The researchers stress that surveillance is fundamentally international. New variants are often detected in neighbouring countries before appearing locally. Effective monitoring therefore depends on global data sharing, collaboration, and sustained infrastructure. A major challenge lies in maintaining surveillance systems after acute outbreaks subside. Emergency funding often becomes available during crises, but long-term monitoring programs are politically and economically more difficult to sustain. Yet proactive surveillance depends precisely on maintaining infrastructure before major outbreaks occur.

The group is cautiously optimistic about the ability of public health systems to keep pace with rapidly evolving technologies. Swiss public health institutions have shown increasing support for genomic surveillance and data science capabilities in recent years. There is also a growing drive to integrate human, veterinary, and environmental datasets into unified monitoring frameworks. At the same time, sequencing technologies, automation systems, and artificial intelligence tools are advancing rapidly. Automation already plays a central role in laboratory workflows, particularly for high-throughput diagnostics where reproducibility and quality control are essential. Bioinformatic pipelines increasingly rely on workflow frameworks such as Nextflow and Snakemake to standardise analyses. This trend is progressively lowering barriers to scalable, reproducible genomic surveillance across institutions.

How do you see emerging tools like artificial intelligence and large language models influencing research workflows in infectious disease research, and what challenges do they introduce?

Artificial intelligence and large language models are also beginning to influence research workflows, especially in coding, troubleshooting, and pipeline development. However, Prof. Ramette cautions that growing dependence on automated systems risks creating "black-box" workflows in which scientists receive results without fully understanding the analytical processes that produced them, and especially their limitations. Ensuring transparency and interpretability will therefore remain essential.

How is the relationship between academic research and biotechnology companies evolving in infectious disease research, and what does this mean for students entering the field?

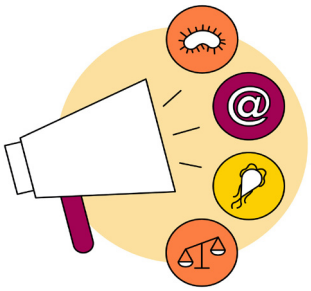
The conversation also touched on the evolving relationship between academia and biotechnology companies. Academic laboratories often pioneer innovative diagnostic approaches, but commercialisation can rapidly reshape the field. Researchers must continuously evaluate whether to maintain internally developed tools or adopt industrial platforms that provide regulatory compliance, certified reagents, and scalable infrastructure. For students entering infectious disease research, both Prof. Ramette and Dr. Geers strongly emphasise interdisciplinarity. Future scientists will need competencies spanning biology, microbiology, statistics, programming, ecology, and data analysis. Equally important is the ability to continuously learn and adapt. Modern infectious disease science is no longer driven by isolated specialisation. The most important innovations emerge when expertise from multiple disciplines is integrated to address complex biological and public health problems.

"For tasks like writing a script, this could be done by AI in the future, but having the knowledge of the biology background is essential for problem solving in cases when an unexpected output is generated….is it coming from the patient or the lab?"-Dr. Geers

What does the future hold?

Looking ahead, the Bioinformatics and Biostatistics Group believe the future of infectious disease research lies in deeper integration, combining genomics, clinical metadata, epidemiology, environmental monitoring, and computational modeling in real time. Yet technology alone will not determine success. Sustained investment, interdisciplinary collaboration, and global scientific solidarity will remain equally critical for preparing for future outbreaks and translating genomic innovation into meaningful clinical impact.

Read more about Prof. Dr. Alban Ramette and his team



News

CoRE-GHA@UniBE hosts seven African fellows working on mpox and Lassa fever- part of an Africa-Europe programme
Organised by MCID CoRE Scientific Officer, Dr. Phaedra Simitsek, CoRE-GHA hosted fellows from Uganda, Nigeria & Malawi for a 4-day workshop, part of the Europe-Africa Fellowship Programme on Translational Research for Priority Diseases

Congratulations to MCID-funded PhD students who have recently been awarded their doctorate!

Dr. Jonas Steiner, May 2026:
"Influenza A viruses circulating in Swiss pig herds and farmers„

Dr. Isabel Schultz-Pernice, May 2026:
"Brain Teasers: Deciphering the Riddles of Viral Neuropathologies Using Human Neural Organoids„

Congratulations to MCID Members who have recently habilitated!
Dr. phil. Eva Maria Hodel, Epidemiology and Public Health and **Dr. med. Philipp Jent,** Infectious Diseases, March 2026

Events

Webinar series, Cluster of Research Excellence-Genomics for Health in Africa (CoRE-GHA), 8th June
On 8th June, CoRE-GHA will host its latest monthly webinar, featuring Dr. Gerald Mboowa (Broad Institute of MIT and Harvard). Talk entitled "Genomic Surveillance for Antimicrobial Resistance in Africa: From Data to Public Health Action„

The Tiger Mosquito and its Dangers, a BEready Cohort information event, 16th June
On 16th June, the BEready Cohort team will hold an information event on the tiger mosquito, vector of a range of human viruses. The event will feature expert insight on the mosquito and control mechanisms. To be held in person and online

EPIZONE Annual Meeting 2026, 2nd-4th September
The Annual Meeting of EPIZONE (an international network of veterinary research institutes working on epizootic- and potentially zoonotic- animal diseases), holds its 2026 annual meeting in Bern, hosted by Institute for Virology and Immunology

Highlighted publications

Christian Althaus and project team on forecasting of Covid-19 hospital admissions using machine learning
MCID project team, led by Christian Althaus, evaluated and compared the ability of different machine learning tools to predict hospital admissions due to Covid-19, revealing the power of electronic health record data for forecasting

Llorenç Grau-Roma and team on use of digital histopathology to study Wesselsbron virus (WSLV)-induced pathology
MCID project team, led by Charaf Benarafa & Obdulio García-Nicolás, used machine learning-driven, pathologist-led digital histopathology to study WSLV-induced liver pathology in sheep, revealing novel findings on cell type involvement

Franziska Suter-Riniker and co-authors on detection of a Swiss parvovirus outbreak via blood donor surveillance
A team including Franziska Suter-Riniker analysed routine surveillance data for parvovirus detection in donated blood, revealing a massive outbreak of the virus in 2023/2024, a situation similar to that in other European countries

Volker Heussler and team on the role of host SNARE proteins in malaria parasite liver stage development
Volker Heussler and team studied the role of host cell SNARE proteins in the intrcellular development of the malaria liver stage parasite, revealing that the parasite hijacks SNARE-mediated lysosomal trafficking to aid its own resource supply

Susanne Hadorn and co-authors on the role of blame-avoidance & credit-claiming on how governance a crises
Susanne Hadorn and colleagues study how officeholders use blame-avoidance and credit-claiming when governing crises, revealing distinct patterns separating cases of governing during a crisis, governing the crisis and governing by the crisis

IMPRINT

THE SPREAD
A NEWSLETTER FROM THE MCID

The Multidisciplinary Center for Infectious Diseases (MCID) is a strategic center of the University of Bern, Switzerland, founded through the generous support of the Vinetum Foundation

Register here to receive future copies of the newsletter by email and visit the MCID website to read more about MCID activities and news

Image (front and back cover) Courtesy of Kamran Aydinov via Magnific

CONTACT

University of Bern
Hallerstrasse 6
Multidisciplinary Center for Infectious Diseases
3012 Bern
Switzerland

Website: www.mcid.unibe.ch
Email: info.mcid@unibe.ch
Bluesky: @mcid-unibe
Linkedin: mcidbern

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