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## News from the Center

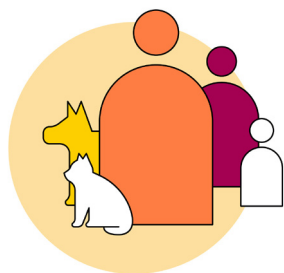
Dear readers, we are happy to publish the second issue of the MCID newsletter, The SPREAD. The months since the release of the first issue have been busy and particularly exciting for the MCID Core Activities:

- The BioPreparedness BioBank has been awarded a VITA label by the Swiss BioBanking Platform, reflecting compliance with legal and ethical standards.
- Ethics and Policy Lab Managers Caroline Schlauffer and Caroline Brall have been awarded SNSF NRP79 funding for an EPL-embedded project on the debate on research with animals in Switzerland.
- The BReady Cohort has received approval from both the Bern Cantonal Ethics Commission for Research (Kantonale Ethikkommission für die Forschung) and Bern Veterinary Services Office (Amt für Veterinärwesen) for its pilot study to begin in May. Read more about the BReady Cohort [here](#).

Make sure you keep up-to-date on MCID news and activities by visiting our [website](#) and [signing up](#) to receive future copies of The SPREAD as well as following us on twitter ([@MCIDBern](#)) and [LinkedIn](#).

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





## Bern, get ready!

Article by: Dr. phil. Eva Maria Hodel (Manager, MCID BEREADY Cohort / Institute of Social and Preventive Medicine) on behalf of the BEREADY Cohort Team

The next pandemic could start tomorrow and we don't know which pathogen will cause it. Epidemic preparedness programmes were planned and discussed in most high-income countries after the 2009 H1N1 influenza pandemic, but many plans were never implemented. The experience from the first months of the coronavirus disease 2019 (COVID-19) pandemic showed how unprepared we actually were<sup>1</sup>.

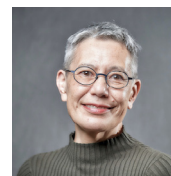
### A platform that can adapt rapidly to launch studies about newly emerging infections

This article introduces the BEREADY (short for "Bern, get ready") cohort, one of three MCID core activities, the team and its progress in 2023. The aims of BEREADY are:

1. to understand how the population of the canton of Bern has been and will be affected by COVID-19
2. to understand the epidemiology and transmission of pathogens, particularly respiratory viruses
3. to establish and maintain a platform for the investigation of infectious diseases

**Prof. Dr. med. Nicola Low**  
Lead, BEREADY

"Research studies take a long time to set up from scratch. When the next pandemic starts, BEREADY and its study participants will be in place to start work quickly on the emerging pathogen."



We plan to initiate research studies on infectious diseases and how they affect people in the canton of Bern. BEREADY will be a household cohort study, meaning that we will collect data from adults, children and pets in the same households over a long period of time. We are a multidisciplinary team of researchers with expertise in clinical epidemiology, infectious diseases, veterinary medicine, and community engagement.

**Prof. Dr. med. Gilles Wandeler**  
Co-Lead, BEREADY

"Our results have the potential to be generalizable to the population of Switzerland because the demographic characteristics of the Canton of Bern are very similar to those nation-wide."



By 2024, BEREADY plans to enrol approximately 1,500 households into a population-based cohort. Participants will be characterised according to demographic, socio-economic, behavioural and health-related factors and through collection of biological samples for phenotypic and genotypic studies, with ongoing surveillance for circulating infections. This research platform will use innovative decentralised data collection methods, a flexible and novel bioinformatics infrastructure, and a biobank including human and pet samples. BEREADY provides a unique opportunity to collect data on transmission patterns of circulating infectious diseases both between individuals and at the human-animal interface (the concept known as 'One Health').

**Prof. Dr. med. vet. Simone Schuller**  
BEREADY Study Veterinarian

"Including pets in the BEREADY cohort as part of a 'One Health' approach is crucial in investigating household transmission of infectious diseases."



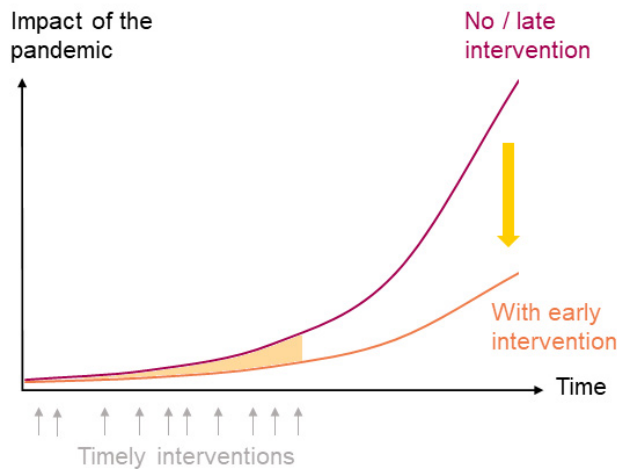


Figure 1: Why it pays to prepare for a pandemic early

## From the people of Bern, for the people of Bern

One of the challenges for BReady is to involve the population in preparing for a future pandemic. This challenge is well known in the field of preventive public health: convincing people to take measures to prevent something that has not happened yet, and from which they might feel no benefit. After all, the success of prevention only becomes apparent in the future, when the effects of the pandemic are not as severe as they would have been without action (Figure 1).

Community engagement is a crucial aspect of BReady. Within BReady, community members will co-develop meaningful and relevant research questions, promote the cohort study in their personal networks and relevant communities, and contribute to the enrolment of households, collection of data, and to making sense of the findings. We will jointly develop recommendations for action at community and policy level. Together with the Franxini Innovation Hub (a participatory support programme of the think tank Reatch), we are currently exploring how we can effectively communicate with people and policy makers to inspire them to support and participate in research that will improve preparedness and responses to future pandemics.

**Prof. Dr. phil. Annika Frahsa**  
BReady Community Engagement Lead

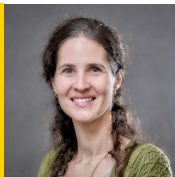
“BReady is a real-life participatory endeavour. We want to sensitise the population to the concept of preparing for and researching future pandemics, and to get them actively involved.”



## Would you be willing to provide blood samples and nasal swabs for research purposes?

In autumn 2022, we conducted an online survey among 15,000 adults in the canton of Bern about their views, attitudes, beliefs, concerns and expectations about their potential participation in a research study about infectious disease. People were given a brief description of BReady and were asked if they would be willing to be a member of a cohort like BReady.

Among the 3,425 people who responded to the survey, 1,667 (49%) said that they would be willing to participate in BReady. The main motivation was the ability to contribute to the health of people around them, followed by the ability to contribute to better preparedness for the next pandemic, and interest in health and research.



**Dr. phil. Eva Maria Hodel**  
Project Manager, BReady

“We have been impressed by the altruism of people in the canton of Bern. Many are willing to do their part if it helps those around them.”



In May 2023, we will start our pilot study to establish the feasibility and logistics of a decentralised cohort with online self-administered questionnaires, self-sampling and telemedicine consultations. The data collected in a small set of 100 households over 12 months will provide invaluable information for the implementation of the full cohort.

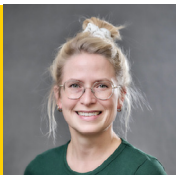
**Dr. med. Karin Grimm**  
BEready Study Physician



“During the one year pilot study, we will investigate which respiratory viruses are circulating in households in Bern during disease events.”

### BEready as an MCID core activity

BEready can be used to investigate transmission patterns as well as the direct and indirect impact of the pandemic on the population's health, e.g. prevalence, immunity, and vaccine effectiveness and the social, economic and policy aspects of a pandemic. As a core activity of the MCID, we are keen to collaborate with researchers from the MCID, the University of Bern, the Inselspital and other research organisations. We are actively engaging with other cohorts nationally and internationally.



**Selina Wegmüller**  
BEready Junior Project Manager

“A key strength of this research platform is its ability to host nested studies on emerging infectious diseases.”

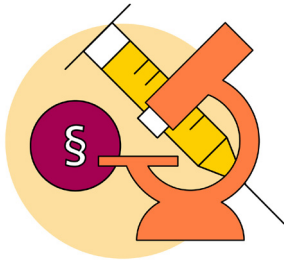
MCID members are already collaborating with the BEready cohort. Their projects cover ethics and policy, neglected zoonotic flavivirus infection, models to monitor epidemics in near real-time, personalised disease management in menopausal women, and political polarisation during pandemics.



We are looking forward to more researchers getting in touch to discuss future collaborations. Send us an email: [BEready.mcid@unibe.ch](mailto:BEready.mcid@unibe.ch).

### Reference

<sup>1</sup>The Independent Panel for Pandemic Preparedness & Response. COVID-19: make it the last pandemic. (2021) [🔗](#)



## Turning sleeping bacteriophages into efficient therapeutics

Article by Dr. Fabien Labroussaa (Institute for Veterinary Bacteriology (IVB), University of Bern) and Prof. Dr. med. Stephen Leib (Institute for Infectious Diseases (IFIK), University of Bern) on behalf of the MCID consortium including also: Jérémy Cherbuin (IVB / Graduate School for Cellular and Biomedical Sciences (GCB), University of Bern), PD. Dr. Alban Ramette, Dr. Peter Keller, Dr. Denis Grandgirard (IFIK)

The recent Covid-19 pandemic caught the world off guard, but another pandemic is silently spreading and is projected to have an even more devastating global impact on our lives and healthcare system, namely the antimicrobial resistance (AMR) crisis.

The AMR crisis refers to the increasing resistance to many if not all existing antimicrobial drugs such as antibiotics, antivirals, antifungals, and antiparasitics. However, this crisis started quite a while ago! As early as in 1945, during his Nobel Prize acceptance speech, Alexander Fleming himself warned the world about the buildup of penicillin-resistant bacteria. Over time, the inappropriate use of antibiotics in different fields such as human- and veterinary medicine, agriculture or in the pharmaceutical sector has fueled the emergence and rapid dissemination of multi-drug resistant (MDR) bacteria. These bacteria, also called “superbugs”, are by definition resistant to all existing antibiotics, even those used as last-resort treatments, as seen with the emergence of vancomycin-resistant *Staphylococcus aureus* (VRSA) species in many countries, including Switzerland.

However, all superbugs have their own Achilles’ heel and the one of MDR bacteria was discovered even before the introduction of antibiotics. Bacteriophages (or phages), characterized for the first time in 1917 by Félix d’Hérelle, are viruses that target bacterial cells and are natural bacterial killers. Like most viruses, phages must infect a bacterial cell to reproduce themselves. Most phages use a so-called lytic cycle in which they first attach to the surface of susceptible bacteria cells, inject their genetic material and then hijack the cellular machinery of its host to produce more virions, ultimately resulting in the lysis of the cell.



Dr. Fabien Labroussaa



Prof. Dr. med. Stephen Leib

As a result, bacteriophages were rapidly seen as potential therapeutics to treat bacterial infections, particularly in Eastern Europe. So far, phage therapy strictly relies on the isolation and purification of natural lytic phages that specifically infect and kill the targeted bacteria. However, the development of phage therapy is still limited and the appearance of phage resistance in bacteria already requires the use of cocktails containing several different phages.

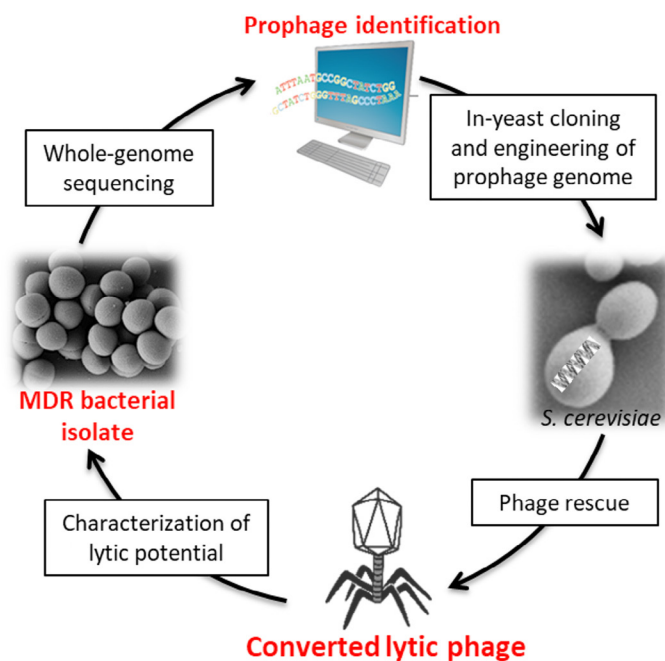
In contrast to lytic phages, temperate phages (or prophages) have the ability to integrate and park their genome at specific sites of bacterial genomes. This capacity is controlled by genes encoded in a so-called lysogeny control region (LCR). Such a lysogenic cycle results in the stable propagation of the prophage genome to every daughter



cell. Even if prophages remain “dormant” once integrated, they often carry other genes such as toxin-encoding or AMR genes, which can make the cells they infect more dangerous. However, under specific stress conditions, such as exposure to UV radiation or certain chemicals, prophages can wake up, excise themselves from the bacterial genome and enter the lytic cycle, leading to the production of new phage particles and the killing of the host cell.

The recent advance of next-generation sequencing technologies facilitated the sequencing of an increasing number of bacterial genomes. Such efforts clearly highlighted the systematic presence of one or more prophage sequences integrated in the genome of many multi-drug resistant (MDR) bacteria. Their sole presence implies that these prophages already possess all the genetic attributes allowing them to invade and lyse their host. These Sleeping Beauties simply need to be “awakened” on demand in order to be used as therapeutics for phage therapy.

An MCID-funded research consortium at the University of Bern led by Dr. Fabien Labroussaa (IVB) and Prof. Dr. Stephen Leib (IFIK) is pursuing this idea, aiming to develop a yeast-based synthetic genomics pipeline to convert temperate phages into tailor-made lytic phages for the treatment of MDR bacterial infections in personalized medicine (Figure 1). First, these tailor-made phages are intended to be used for the treatment of infections caused by clinically relevant strains such as *Staphylococcus aureus* and *Klebsiella pneumoniae*. These bacteria are considered high priority targets by the World Health Organization for the development of new antimicrobials, making them ideal candidates to test this new concept. However, this pipeline has the potential to be extended to other gram-positive and gram-negative MDR bacteria subsequently.



**Figure 1: Overview of MCID-funded project with the aim of producing lytic phages for the treatment of MDR bacterial infections.**

First, a powerful and efficient genetic engineering platform was established for the precise modification of these prophage genomes (Figure 2). This ensures that all the genes responsible for the prophage integration, namely the LCR region, as well as the detrimental genes encoding bacterial virulence factors or toxins, could be accurately removed from the phages’ genome sequences. This is an absolute requirement to prevent these candidate therapeutic phages to re-enter the lysogenic cycle but also to improve their safety profile. In that respect, the consortium uses the Baker’s yeast, *Saccharomyces cerevisiae*, as an engineering platform. In particular, the Transformation-Associated Recombination (TAR) cloning technique, previously implemented and used at the IVB to reassemble and engineer different viral genomes including those of SARS-CoV-2<sup>1</sup>





and African Swine fever virus<sup>2</sup>, has been already adapted to the modification of *S. aureus* prophages. Efforts to boot-up these engineered phages are currently underway and are scientifically challenging especially for gram-positive bacteria.

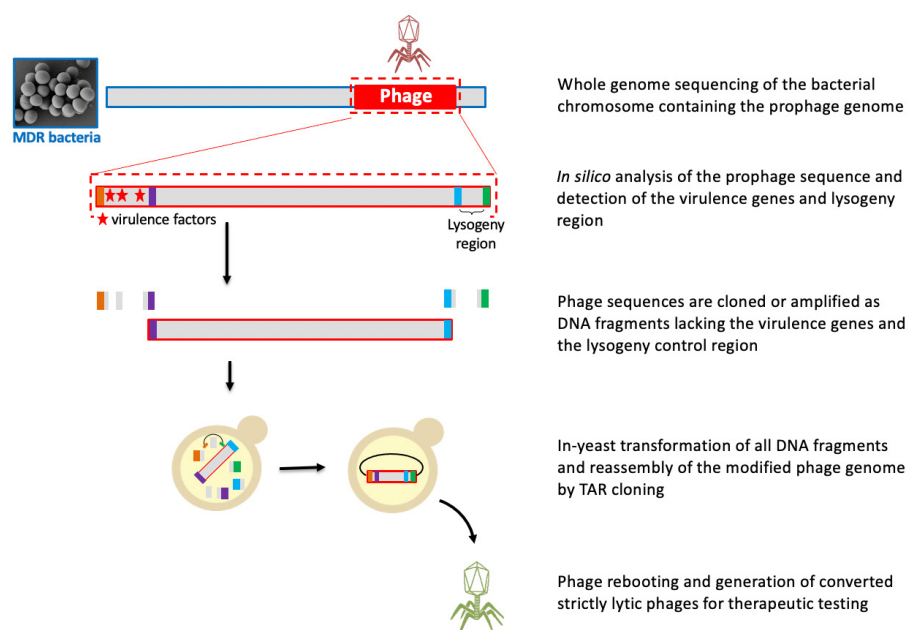


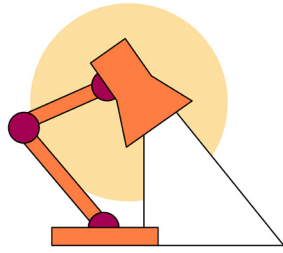
Figure 2: Overview of phage genome modification using yeast synthetic genomics platform

In addition, this project also aims to better apprehend the diversity of temperate phages for the two species considered. When it comes to bacteria belonging to the family of *Staphylococcaceae*, most of the knowledge regarding prophage biology mainly comes from clinical isolates of *S. aureus*. For this concept to be widely applicable, the consortium needs to characterize a wide variety of prophage sequences in order to grasp the true repertoire of genetic attributes they harbor. To do so, they can rely on the two diagnostic center biobanks available at the IVB and the IFIK, which allow them to gain access to a large variety of both veterinary and human isolates. The genomes of more than a hundred selected *Staphylococcaceae* strains isolated from different hosts and continents have been already sequenced<sup>3</sup>. A great diversity of phage sequences was detected and functional prophages are now being characterized in respect to their host-range, genetic content and lytic properties. Sequencing efforts will continue for *K. pneumoniae* isolates and identified prophages will be tentatively engineered using the yeast-based synthetic genomics pipeline.

Overall, this “high risk–high gain” project has great potential for phage therapy in the field of personalized medicine in the mid to long-term. If successful, this project will result in the easy and fast production of novel phages with higher lytic efficacy that might be combined with other antibacterial agents. Therefore, the lytic conversion of temperate phages would greatly increase the pool of phages with therapeutic potential, which will ultimately expand the impact of phage therapy in our fight against MDR bacterial infections.

## References

- <sup>1</sup>Thi Nhu Thao, T., Labroussaa, F., Ebert, N., V’Kovski, P., Stalder, H., *et al.* (2020). Rapid reconstruction of SARS-CoV-2 using a synthetic genomics platform. *Nature*, 582(7813), 561-565 [🔗](#)
- <sup>2</sup>Labroussaa, F., Lebaudy, A., Baby, V., Gourgues, G., Matteau, *et al.* (2016). Impact of donor-recipient phylogenetic distance on bacterial genome transplantation. *Nucleic Acids Res*, 44(17), 8501-8511 [🔗](#)
- <sup>3</sup>Akarsu, H., Liljander, A., Younan, M., Brodard, I., Overesch, G., *et al.* (2022). Genomic Characterization and Antimicrobial Susceptibility of Dromedary-Associated Staphylococcaceae from the Horn of Africa. *Appl. Environ. Microbiol.*, 88(21): e01146-22 [🔗](#)



## The fox tapeworm: a neglected parasite

Article by: Prof. Dr. Britta Lundström-Stadelmann (Co-Director, Institute of Parasitology, Vetsuisse Faculty)

**Have you heard of the fox tapeworm? Do you know how it is transmitted and why we need to learn more? Find out more here, including about ongoing projects at the Bern Vetsuisse Faculty.**

*Echinococcus multilocularis* is a multicellular parasite, a tapeworm, also known as small fox tapeworm, and it causes the disease alveolar echinococcosis (AE). AE is the foodborne parasitic zoonosis of greatest concern in Europe. The parasite is endemic in Central and Eastern Europe, Central and Eastern Asia, and North America, and “emergence” has been reported for all these regions, in particular also for Switzerland. However, human infections are rare in comparison to other infectious diseases with less than 20'000 reported novel cases annually – though this number is probably an underestimation. AE is a life-altering, chronic disease that cannot be cured by medication. It is a neglected zoonosis, even though apart from humans it also affects other mammals (aberrant hosts) like monkeys, dogs, or pigs.

*E. multilocularis* is transmitted by foxes, dogs and other canids, which can be infected by adult worms of few millimeters in size and these worms shed infectious eggs into the environment (see Figure 1). Infection of humans or dogs takes place when *E. multilocularis* eggs are taken up with contaminated food or water. Egg uptake remains unnoticed, as the eggs are not visible by eye, and the parasite does not induce any acute symptoms.

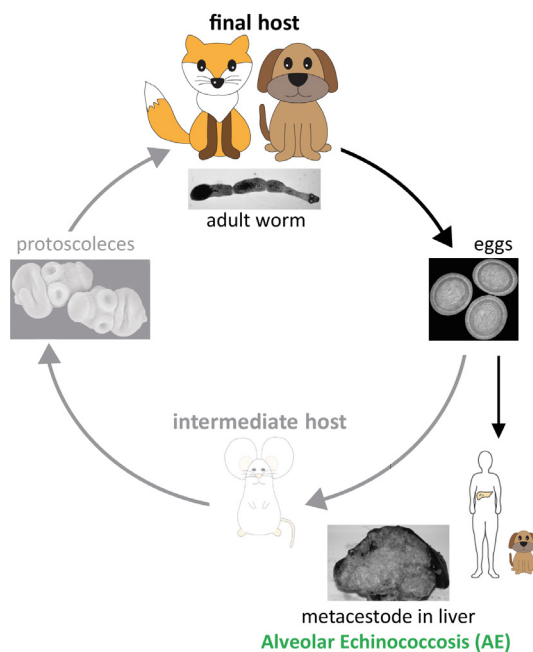


Figure 1: life cycle of *Echinococcus multilocularis* and infection route for aberrant hosts such as humans or dogs.

Each egg releases a larva, which then migrates to the liver, and differentiates into a multivesicular parasitic structure, the metacestode. The metacestode represents the disease-causing stage of the parasite, undergoing potentially unlimited proliferation, and infiltrating the surrounding tissue, similar to a malignant tumor. This process causes severe organ dysfunction, mostly in the liver, but also in other infected organs. Moreover, metacestodes can form metastases and spread to other body locations.

In a natural life cycle, a new generation of cestodes, the so-called protoscolexes, will form within metacestodes in wild rodents. Once ingested by a suitable final host, they will develop into adult worms again. This part of the life-cycle, however, is normally not present in humans or other aberrant hosts.





AE is a chronic disease, which in humans is mostly diagnosed 10-15 years after infection. In the progressive stage of human AE non-specific symptoms appear. At an advanced stage, and if not treated properly or if treatment fails, the disease can be fatal.

The only curative treatment for AE is surgical resection of the whole parasite tissue. However, radical surgery cannot be performed when diagnosed at a late stage of infection with the parasite growing highly invasively, and it relies on the access to good health infrastructure that may be lacking in large parts of endemic regions (i.e. rural areas in Asia). Surgery is combined with temporary chemotherapy and long-term monitoring to treat and follow-up eventual parasite residuals. In cases where complete resection is not possible, AE patients are left with chemotherapeutic treatment based on benzimidazoles. A major drawback is that these drugs are not able to kill the parasite, but at best halt further parasite growth. This is due to parasite stem cells that are not easily treated. Thus, these medications must be taken daily and life-long, which in turn increases the risk of side-effects and poses a heavy psychological and economic burden on patients.

In other aberrant hosts such as dogs or captive monkeys, the parasite follows similar growth characteristics, although in such cases it develops faster, and treatment is more problematic. For this reason also novel treatment options against AE are urgently needed.

In our laboratory at the Institute of Parasitology, we have established *in vitro* culture techniques for *E. multilocularis* metacestodes, stem cells and protoscoleces, and based on these we generated an *in vitro* screening platform for the identification of novel drugs against AE (see Figure 2).



**Figure 2:** *In vitro* culture of *E. multilocularis* metacestodes that each represent a multicellular organism. Each metacestode vesicle grows *in vitro* to a size of up to 15 mm (left). Enlarged metacestode vesicle with budding daughter vesicles (middle). Schematic representation of a metacestode, with thousands of living parasite cells (green), including 20 to 30% stem cells (enlarged nuclei, right).

We perform pharmacodynamic studies *in vitro* and in the mouse model, we investigate the mode of action of active compounds, as well as the structure activity relationship (SAR). We largely focus on repurposing of drugs, which means that we apply compound classes that are on the market or being developed for other indications. This approach is commonly used for neglected diseases. These drugs include anti-cancer compounds, natural compounds like the Peruvian root Maca, and anti-infective compounds like the anti-malarial mefloquine. We also investigate the current drugs in use, the benzimidazoles, and study their molecular modes of action with the aim to further improve their efficacy.

Very recently, we have established respective methods for screening against metacestodes, stem cells and protoscoleces of the closely related *E. granulosus*, the dog tapeworm, causative agent of cystic echinococcosis (CE).



Like AE, CE is also a neglected disease, even though its prevalence is roughly ten times higher than that of AE, and it is found worldwide, being particularly problematic in the global South. Novel therapies are also needed against CE.



**Figure 3: Adult *E. multilocularis* tapeworm from an infected fox (source: Institute of Parasitology)**

In addition to drug testing, investigation and improvement, we are very interested in the basic understanding of the parasite's energy metabolism. Our in vitro culture system offers a perfect model to investigate the mitochondria of *Echinococcus* and to study an exciting alternative pathway the parasite applies to thrive also in low-oxygen conditions: the malate dismutation. This pathway is not found in humans or other mammals. Thus, it represents a perfect target for new and specific treatment options. Another pathway we intensely study is the threonine-metabolism, as the analysis of the metabolic footprint of *E. multilocularis* showed that the parasite highly consumes this amino acid through an enzyme that is not active in humans, and this might offer a new key for treatment.

One puzzling aspect of AE is that it is usually only noticed after a long incubation period, mostly as an incidental finding. At this point, the parasite often has grown to a relatively big mass, albeit not inducing a strong inflammatory response. Thus, the parasite actively modulates the host immune response. For this reason, we also study parasite-mediated immunomodulatory mechanisms.

In a long term study, we address questions that are relevant for the general public regarding food safety. We develop methods that can reliably detect viable, infectious *E. multilocularis* eggs contaminating food or the environment. Even though many people have heard about the parasite and request such tests, there are still no such protocols established anywhere.



**Prof. Dr. Britta Lundström-Stadelmann**

All these studies are carried out within our highly dedicated team at the Vetsuisse Bern. We benefit from many collaborators at the University of Bern and abroad. The interdisciplinary exchange is extremely important on a zoonotic disease like AE and only multidisciplinary approaches will let us advance in this field.

Hopefully, some of your questions regarding the “fox tapeworm” have been answered in this article. More information can be found [here](#).



## Acknowledging one's ignorance: a recipe for responsible decision-making

Article by: Dr. Rowan Iskandar (sitem Center for Translational Medicine and Biomedical Entrepreneurship)

Uncertainty is pervasive and inevitable in all facets of life, from weather forecasts to the gender of a baby or the prognosis of an illness to policymaking. In the context of COVID-19, policymakers were uncertain about the nature of the novel viral disease, the measures for curbing the spread of the virus, the consequences of implementing them in different sectors of life, and the desirability of these consequences. In the early phase of the pandemic, the nature of these uncertainties was markedly different. If one views a state of uncertainty as a degree of incompleteness or imprecision in decision-relevant information, policymakers were faced with severe uncertainty since they had little, if any, information to inform their scientific deliberations about policy options, which typically necessitate a robust evidence base. Do policymakers have the necessary tools to reason about uncertainty characterized by a complete lack of information or prior knowledge?

We first seek some formalisms to fully appreciate this pertinent question's epistemic significance. One could conceptualize different degrees of uncertainty (evidentiary uncertainty) as each point on a continuum representing a different amount of decision-relevant information, from a complete absence of decision-relevant information (ignorance) to full knowledge of all decision-relevant information (probabilistic certainty). Then, one could use either a unique mathematical framework to represent each degree of uncertainty along the continuum or leverage a sufficiently general framework to capture this broad concept of evidentiary uncertainty.

Though rarely articulated explicitly, the predominant paradigm equates evidentiary uncertainty with probability. Within this probabilistic view of uncertainty, the most widely accepted approach, Kolmogorov's axiomatic probability theory, assumes that uncertainty can always be represented quantitatively by a single precise probability function irrespective of how much information one has. This one-theory-to-rule-them-all view of uncertainty underlies many methods in statistics, economics, and many other disciplines, regardless of whether one subscribes to Bayesianism or frequentism.



Dr. Rowan Iskandar

There are at least three shortcomings of probability theory. First, when dealing with ignorance, probability theory tends to assume the existence of more information than one actually has. For example, if we only know the boundary values (say  $L$  and  $U$ ) of a quantity of interest, say a probability of death due to a novel virus ( $p$ ), Bayesianism will assign a uniform distribution to the interval  $[L,U]$  to quantify their ignorance about the value of  $p$ . However, assuming each potential value of  $p$  in the interval  $[L,U]$  is equally likely (Laplace's principle of insufficient reason) is qualitatively and quantitatively different from knowing that the true  $p$  is somewhere between  $L$  and  $U$ .

The second drawback refers to the "illusion of having a precise estimand or prediction" when one can produce a measure of uncertainty for a quantity of interest, i.e., confidence or credible interval, in addition to a point estimate. It is impossible to verify whether such intervals reflect the true uncertainty, specifically when we operate under ignorance.



The well-known Ellsberg's two-urn experiment highlights another problem with probability theory: people prefer bets with precise probabilities to those with unknown probabilities. The observed reversal in preference (Ellsberg paradox) reflects a behavior that cannot be explained if decision-makers quantify uncertainty probabilistically. In sum, the prevailing approach asserting that all kinds of uncertainty can be represented by a single precise probability is too restrictive. The amount of information used for making an uncertainty assessment is not reflected in the assessment itself. On the background of this vacuum of robust uncertainty quantification approaches, how can policymakers decide on an optimal policy in a scientifically credible way and justifiable by existing evidence in the face of severe uncertainty?

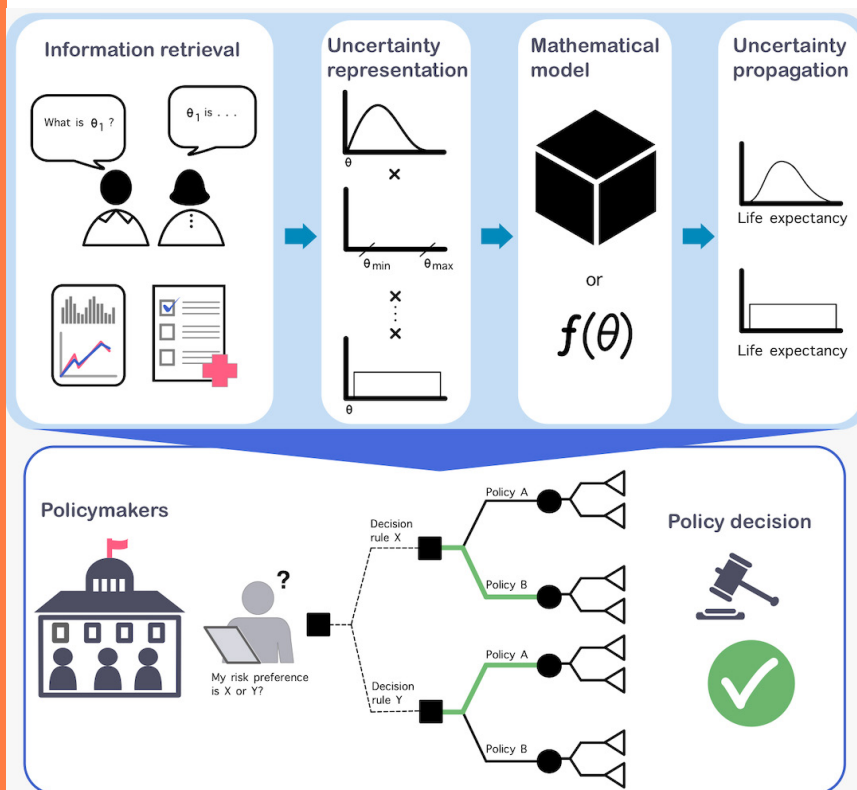
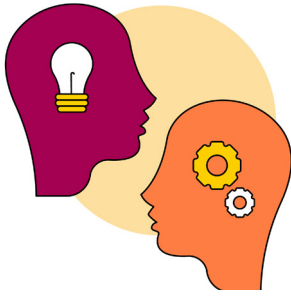


Figure 1: “A decision-making framework under severe uncertainty for optimizing future pandemic responses”

The three-year MCID-funded project titled “A decision-making framework under severe uncertainty for optimizing future pandemic responses” aims to assist policymakers by developing practical tools to aid them in making decisions about the optimal pandemic response, given varying degrees of data availability (Figure 1). To achieve this, we will develop a generalized approach to represent and reason with uncertainty that is sufficiently expressive for representing uncertainty over the continuum of decision-relevant information. Specifically, we seek to systematically explore the nature of these uncertainties, how they should be represented and quantified, and how they should be reflected in choosing the optimal policy. We will demonstrate the utility of our approaches by applying the decision-making framework to public health decision-making during the coronavirus pandemic in Switzerland. We will compare the actual decisions made by the policymakers against the optimal decisions recommended by our decision-making framework, given the level of uncertainty in the data when the decisions were made.

If you want to learn more about the project or explore possible collaborations, please contact Rowan Iskandar ([rowan.iskandar@sitem-insel.ch](mailto:rowan.iskandar@sitem-insel.ch)).



## First in the series: meet MCID early career researchers

Interview with:

Dr. Susanne Hadorn, Recipient of MCID Early Career Research Grant for Women (ECRG-W), KPM Center for Public Management (KPM) and  
Dr. Jenna Kelly, Recipient of Career Development Grant, Institute of Virology and Immunology, Vetsuisse Faculty (IVI)

### Can you describe briefly your MCID-funded project and what you aim to achieve?

**Jenna:** Our MCID-funded project aims to establish a One Health network that will identify and characterize influenza viruses circulating in the human and pig populations within Switzerland. We will develop and implement a new computational and biological workflow to examine influenza samples from pigs and humans and evaluate their zoonotic potential, identifying influenza viruses with zoonotic potential before they become a public health concern. This is critical as pigs play a crucial role in the evolution and cross-species transmission of influenza viruses to humans and other animals. To do this, we have assembled an excellent multidisciplinary team of researchers with diverse skills, including human and veterinary medicine, epidemiology, molecular virology, and computational biology.

**Susanne:** The project “Blame deflection during the Covid-19 crisis” will be conducted by myself and a doctoral student, Céline Honegger, together with a part-time student assistant. The project will examine blame avoidance behavior encompassing “all kinds of integrity-protecting activities by officeholders in the face of potentially blame-attracting events”<sup>1</sup> during the Covid-19 pandemic. We will compare which corresponding strategies the Swiss and German governments used, to whom they shifted blame during the pandemic and with what effect. The project thus provides insights on how to prevent government inaction and blame avoidance that arguably leads to political deadlock instead of pro-active problem solving.

### What excites you about multidisciplinary research?

**Jenna:** Complex and multifaceted problems, such as improving pandemic preparedness, require more than one discipline to be sustainable and effective. For me, what’s most exciting about multidisciplinary research is that it has the potential to tackle some of the world’s most pressing challenges – things like climate change, poverty, and pandemic preparedness. When researchers from different fields work together towards a common goal, they can combine their knowledge and unique perspectives to come up with more innovative and panoptic solutions to achieve this goal.



Dr. Jenna Kelly

**Susanne:** The Covid 19 pandemic has impressively shown that the management of such a far-reaching crisis is only possible with close collaboration between a wide range of disciplines. I believe that the exchange between the natural sciences and researchers from the social sciences in particular can lead to us being better prepared for future pandemics or epidemics. This exchange helps to ensure that in the crisis itself, solutions can be presented that are not only effective, but also accepted and implemented by the political system and the population.

### What do you see as being the main challenges in multidisciplinary research?

**Jenna:** I think communication and coordination are two of the main challenges in multidisciplinary research. It can be difficult for researchers from different disciplines, who may approach a particular research question quite differently and often use field-specific terms and methodologies, to understand each other and communicate





effectively. It can also be challenging to coordinate and integrate the data and knowledge generated by multidisciplinary research to ensure it accurately represents everyone involved. To address these challenges, I think it's crucial for researchers involved in multidisciplinary research to remain as flexible and open-minded as possible and for team members to communicate regularly throughout the project. This can help researchers work together more effectively and find solutions that work for everyone.

### What does pandemic preparedness mean in your field of research?

**Jenna:** My field of research, which is virus genomics and bioinformatics, involves compiling and analyzing genetic material from viruses and using computational tools/methods to examine large amounts of biological data. This includes using advanced genomic sequencing technologies to identify, monitor, and characterize viruses that have the potential to cause epidemics and pandemics. Such so-called “big data” can not only be used to examine how viruses evolve and cause disease, but also to help develop new therapies and vaccines. For example, during the COVID-19 pandemic, genomics and bioinformatics played an essential role in the identification of SARS-CoV-2 as the causative agent of COVID-19, as well as in tracking its evolution and developing effective diagnostics, treatments, and vaccines against the virus.



Dr. Susanne Hadorn

**Susanne:** As a researcher in public administration with a focus on public policy, I would say that pandemic preparedness is a mixture of clearly defined responsibilities and processes as well as a clear idea of feasible policy options. First, as regards responsibilities and procedures, in a federal system such as Switzerland, the clear definition of the division of roles between the federal government and the cantons is a crucial aspect of preparedness. Also, the procedures for interdepartmental coordination and for the integration of scientific expertise (from as broad a range of disciplines as possible) should be clearly defined before a crisis begins. Second, good crisis preparation includes thinking about possible policy options. This is not only a matter of finding the ‘best’ solutions, e.g., from an epidemiological point of view, but also of clarifying the acceptance of these measures - which always entail a restriction of the personal freedom of the addressees - at an early stage.

### How has your career path led to your research as a Member of the MCID?

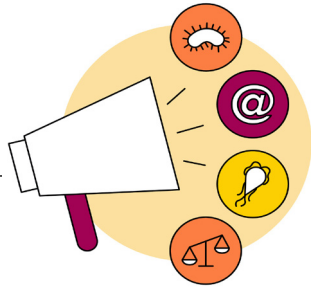
**Susanne:** A substantial part of my research activities to date focus on the analysis of the design and implementation of health policies, particularly in the multi-level context of the Swiss federal system. I have also been involved in a project comparing the Science-Policy-Interface in different countries during Covid-19 and am currently involved in an SNF-project “CoWiNaCo-Complying with National Covid-19 Responses” examining reasons for (non-)compliance with Covid-19 measures at different levels in four countries. My MCID-funded project “Blame deflection during the Covid-19 crisis” is therefore a natural continuation of my research experience to date. Read Susanne’s bio [here](#).

**Jenna:** My area of expertise is virus genomics and bioinformatics, which is an inherently interdisciplinary field. My interest in global health was first sparked by an internship in infectious diseases in India. Later, during my PhD, I developed an interest in genomics and bioinformatics, and ultimately in “big data” analysis and its potential in the context of infectious disease research. During a fellowship at the Viral Special Pathogens Branch at the CDC, U.S.A., I gained invaluable experience in Bioinformatics for Public Health and became fascinated by emerging zoonotic viruses. This is a topic that I have focussed my research on since joining the IVI in 2018 and lead me to apply for MCID funding to continue this research and to help train a new generation of young scientists in this multidisciplinary field. Read Jenna’s bio [here](#).

#### Reference

<sup>1</sup>Hinterleitner, M., & Sager, F. (2017). Anticipatory and reactive forms of blame avoidance: Of foxes and lions. *European political science review*, 9(4), 587-606. [Q](#)





## News

### MCID Member, Evangelos Karousis, awarded Holcim Stiftung Wissen fellowship

MCID Career Development Grant (CDG) recipient, Evangelos Karousis has been awarded a Holcim Stiftung Wissen fellowship, allowing him to establish himself as a junior group leader at the DCBP from January 2023 [🔗](#)

### MCID Member, Tim Rollenske, awarded Emmy Noether fellowship

Tim Rollenske, MCID CDG recipient, has received a prestigious Emmy Noether Fellowship from the German Research Foundation (DFG), moving to the Institute of Molecular Medicine and Experimental Immunology, Bonn as a junior professor [🔗](#)

### MCID Ethics and Policy Lab managers awarded SNSF “Advancing 3R - Animals, research and society” funding

MCID Ethics & Policy Lab managers Dr. Caroline Brall and Dr. Caroline Schlauffer secure SNSF NRP 79 funding for their project entitled “A public policy and ethical analysis of the debate on research with animals in Switzerland” [🔗](#)

### MCID BioPreparedness BioBank awarded VITA label by Swiss Biobanking platform

The MCID BioPreparedness BioBank has been awarded a VITA label by the Swiss Biobanking Platform, recognising the Biobank’s compliance with ethical and legal standards

### MCID BReady Cohort receives ethical and veterinary approval for pilot study

The BReady Cohort has received both ethical and veterinary approval at the governmental level to begin the pilot phase of the cohort activities in the coming weeks.

## Events

### Boot camp on politics for researchers

On 7th and 8th June, a boot camp training course on politics for researchers will be conducted by the Franxini Project, and organised together with the MCID Ethics and Policy Lab and the Oeschger Center for Climate Change Research. Event in German and free of charge [🔗](#)

### MCID Annual Event, 2023

On 6th July the MCID will hold its annual event. On this occasion the annual event will focus on the MCID Core Activities, with interactive workshops designed to inform and to spark potential collaborations [🔗](#)

## Highlighted publications

### Bettina Zimmermann et al. on Covid-19 vaccine decision-making

Bettina Zimmermann, recipient of MCID ECRG-W funding, and co-investigators carry out an in-depth interview analysis over five European countries on the social and socio-political embeddedness of decision-making related to vaccine uptake [🔗](#)

### Carmen Faso et al. on virulence mechanisms of the *Giardia* parasite

Carmen Faso, MCID Co-chair, and team, identify a virulence-associated protein complex associated with unconventional protein secretion at the interface between the intestinal parasite *Giardia lamblia* and its host cell [🔗](#)

### Philipp Plattet et al. on the structure of a virulence-associate protein of canine distemper virus

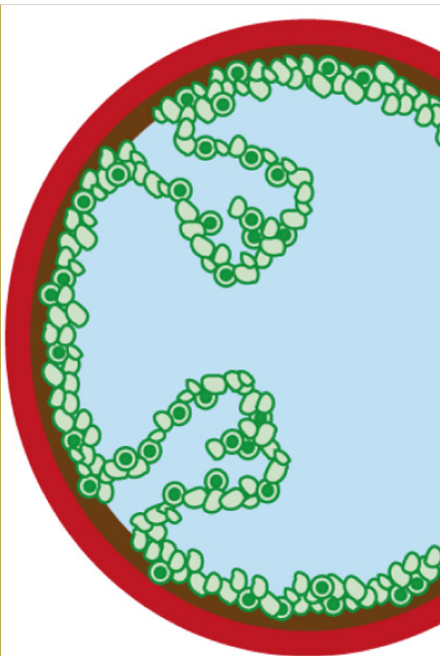
MCID Microbiology cluster member, Philippe Plattet, and collaborators uncover the structure of a protein key for infectivity of the canine distemper virus, closely related to measles virus, unlocking the potential for therapeutic targeting [🔗](#)

### Thomas Sauter et al. on telehealth during the Covid-19 pandemic

Thomas Sauter, Co-chair of the MCID Patient-focused research cluster, and collaborators, investigate telehealth use by emergency department patients in Switzerland, observing an increase in the use of telehealth during the pandemic [🔗](#)

### Guido Beldi et al. on prevention of post-operative infections

MCID Member, Guido Beldi, and colleagues, uncover intestinal bacteria as being the major cause of infections post-visceral surgery and identify specific immune cells (ILC3s) as being key to host protection from such infections [🔗](#)



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

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## CONTACT

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

Website: [www.mcid.unibe.ch](http://www.mcid.unibe.ch)  
Email: [info.mcid@unibe.ch](mailto:info.mcid@unibe.ch)  
Twitter: @MCIDBern