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MCID
MULTIDISCIPLINARY CENTER FOR INFECTIOUS DISEASES

THE SPREAD

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ARTICLES ON:

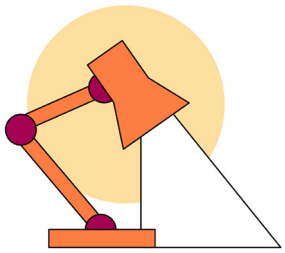
News from the Center

Dear readers,

welcome to another issue of the MCID newsletter, The SPREAD. This issue comes out as many of us are returning from time away over the summer, and gearing up for the start of a new semester. At the MCID we are also looking forward to the start of a new chapter with the announcement of the outcome of the MCID Project Funding Call 2024; after a thorough reviewing process, involving close to 70 peer reviewers, eight projects have been selected for funding and new projects will begin by January 2026. Congratulations to all successful applicants and thank you to all who applied. See here for a list of funded projects:

As we put together this issue of The SPREAD, final preparations are underway for the University of Bern's "Nacht der Forschung" (Night of Research) on 6th September. After the success of the MCID's involvement at the Vetsuisse Open Day, with this event we are looking forward to another opportunity to engage with the public, with a range of activities for guest of all ages. We are very grateful to all who have offered their help for the two events!

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



Theileria annulata: A Veterinary Parasite that Rewires Immune Cells for Clonal Proliferation

Article by: Dr. Kerry Woods, Lab of Prof. Dr. Sven Rottenberg, Institute of Animal Pathology, Vetsuisse

Theileria annulata, a tick-borne apicomplexan protozoan parasite, infects cattle and buffalo and causes tropical theileriosis, a severe lymphoproliferative disease with profound implications for animal health and agriculture. Transmitted primarily by *Hyalomma* ticks, this pathogen drives uncontrolled proliferation of host immune cells, mimicking cancer-like phenotypes. Its unique ability to reversibly transform leukocytes into immortalized, tumor-like cells distinguishes it as the only known eukaryote capable of transforming another eukaryote.

Geographically, *T. annulata* is prevalent in subtropical and tropical regions, including southern Europe, North Africa, the Middle East, Central Asia, and parts of East Asia, such as India and China. An estimated 250 million cattle are at risk, particularly in regions with intensive livestock farming[1]. The disease is absent in the Americas and Australia, but global trade increases the risk of introduction. Tropical theileriosis imposes a significant economic burden due to high mortality (40–90% in susceptible exotic breeds), morbidity, reduced milk and meat production, weight loss, and costs of control measures like acaricides, vaccines, and veterinary care. Indigenous cattle often exhibit milder or subclinical infections, but the disease still impacts productivity. Live attenuated vaccines, such as cell culture-derived schizont vaccines, offer partial protection but are limited by efficacy issues and cold chain requirements. Buparvaquone, the primary treatment, is effective early in infection but faces challenges with cost and emerging resistance[2].

The *T. annulata* life cycle begins with tick-mediated transmission of sporozoites, which invade host mononuclear leukocytes, such as macrophages and B-lymphocytes. Unlike many intracellular pathogens that reside in a parasitophorous vacuole, *T. annulata* differentiates into schizonts that reside freely in the host cell cytoplasm. This allows the direct manipulation of host cell dynamics, enabling the parasite to rewire signaling pathways and drive clonal proliferation. The schizonts associate with host mitotic machinery, including microtubules and kinases like Plk1, ensuring their segregation into daughter cells during division[3]. This co-opting of mitotic processes allows infected cells to divide clonally, each daughter cell retaining the parasite, thus perpetuating the infection (Figure 1).

Dr. Kerry Woods

The uncontrolled clonal proliferation and systemic dissemination of infected cells resembles lymphoma. Clinical signs include high fever (up to 42°C), lymphadenopathy, anemia, jaundice, respiratory distress, and, in severe cases, multi-organ failure, often resulting in death within weeks. Later stages involve piroplasm infection of erythrocytes, causing hemolytic anemia. The immunopathology is complex, with transformed cells evading immune clearance while triggering systemic inflammation and vascular damage through pro-inflammatory cytokines.

***Theileria annulata*'s ability to immortalize host leukocytes is a hallmark of its pathogenicity**. The parasite induces a cancer-like phenotype characterized by infinite replication, invasiveness, and metastasis-like dissemination. Unlike oncogenic viruses, *T. annulata* achieves transformation without genomic integration, relying on the presence of the cytoplasmic schizont (reviewed in[4,5]). This transformation is reversible: eliminating the parasite with buparvaquone halts proliferation and induces apoptosis, highlighting the parasite's direct role.

At the molecular level, *T. annulata* hijacks key host signaling pathways. Constitutive activation of NF-κB, AP-1, JNK, and PI3K-Akt pathways promotes anti-apoptotic mechanisms, metabolic reprogramming, and uncontrolled proliferation. NF-κB activation suppresses apoptosis by upregulating anti-apoptotic genes like Bcl-2, while PI3K-Akt enhances cell survival and metabolism. JNK and AP-1 drive proliferative gene expression, including proto-oncogenes like c-Myc. The parasite also enhances host cell motility through kinase induction, facilitating dissemination. RNA sequencing and differential gene expression analysis performed in our lab revealed the altered expression of thousands of host genes. Despite this, very little is known about precisely how the parasite drives these phenotypic changes in the host.

Figure 1: (A) *T. annulata* infected cow (Sri Lanka). (B) *T. annulata* infected bovine macrophage during cell division. The schizont is labelled green (anti-TaSP), the host cytoskeleton is labelled red (anti-alpha tubulin), host and parasite DNA is blue (DAPI)

Recent advances have elucidated the role of *T. annulata*'s exportome, comprising secreted proteins translocated into host cell compartments. Using TurboID-based proximity labeling, we have identified intrinsically disordered parasite proteins that interact with host proteins[6]. Several of these effectors are enriched in the host nucleus, where they bind transcription factors and DNA-binding proteins. These interactions likely modulate host DNA replication and repair pathways, contributing to the cancer-like phenotype. By targeting nuclear processes, *T. annulata* effectively reprograms the host cell's transcriptional landscape, ensuring sustained division and immune evasion. Investigating the function of these effectors, and understanding their interaction with the host cell, is a central theme in our research group at the Institute of Animal Pathology.

Within the framework of our recently funded MCID project, we will, in collaboration with the Reymond lab at the Department of Chemistry, Biochemistry and Pharmaceutical Sciences, explore targeted protein degradation (TPD) to combat *T. annulata*. TPD employs bifunctional molecules, such as proteolysis-targeting chimeras (PROTACs), to recruit host E3 ubiquitin ligases to degrade specific parasite effectors. By selectively eliminating exported proteins critical for transformation, TPD could disrupt the parasite's ability to maintain immortalized cells. This approach offers a novel strategy to unravel the molecular mechanisms of theileriosis and to develop therapeutics. Unlike buparvaquone, which targets the parasite directly and faces resistance, TPD focuses on host-parasite interactions, potentially bypassing resistance mechanisms.

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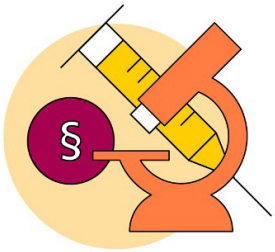

Syndromic Surveillance in Swiss Wild Birds – From Research to Implementation

Article by: Dr. med. vet. Saskia Keller, med. vet. Isabelle Wethli, Dr. med. vet. Mirjam Pewsner, Institute for Fish and Wildlife Health (FIWI), Vetsuisse

Why wildlife health surveillance matters

Wildlife health is an essential pillar of conservation, ecosystem sustainability, and important to understand within the One Health approach[1]. As humans, domestic animals and wildlife share the same environments, pathogens can circulate among them. Wildlife health surveillance (WHS) enables the rapid detection of unusual disease events in wildlife. This, in turn, helps to supports targeted control measures, prevent disease spread, and mitigate risks for all members of the shared ecosystem[2, 3, 4].

In Switzerland, WHS is well established[5, 6]. The Institute for Fish and Wildlife Health (FIWI) conducts General WHS through opportunistic pathological examinations of sick or dead wildlife. Additional health data are collected by cantonal authorities and via annual federal hunting statistics. Targeted surveillance programs, such as for Avian influenza or African swine fever, are conducted by other partners. However, a recent evaluation by the FIWI revealed several challenges , including opportunities for improvement in the harmonization and collection of field data, so-called syndromic surveillance[6]. To address these gaps, the **WildGuARDS project** explored a novel approach: a participatory syndromic surveillance system for sick and dead wild birds, implemented through an online reporting system (ORS).

Retrospective analysis of bird mortalities

We analysed over 20 years (2000-2022) of bird necropsy reports generated at FIWI, covering 1,252 birds from 88 species. Songbirds (42%) and raptors (30%) dominated, followed by pigeons (10%) and waterfowl (9%), reflecting their frequency in occurrence in urban and peri-urban landscapes.

A total of 79 different causes of mortality or morbidity were identified. Non-infectious causes were most frequent (48%), mainly trauma (25%) due to collisions or predation. Accidental or deliberate intoxications accounted for 9%, caused by substances including rodenticides, barbiturates, and heavy metals. Infectious diseases comprised 30% of cases, notably Usutu virus in blackbirds, trichomoniasis in finches, and salmonellosis in finches and sparrows. 22% of cases remained undiagnosed. Spatiotemporal patterns were evident, including epidemic peaks (e.g., 2018 Usutu virus outbreak in blackbirds) and seasonal trends, with trauma dominating migrations periods and infectious diseases more frequent in winter and summer.

Dr. med. vet. Saskia Keller

Defining a syndrome catalogue

Syndromes are defined as non-specific pre-diagnostic health indicators. We established a catalogue of 30 syndromes based on the necropsy reports and literature research, focusing on external visible signs observable in the field. These syndromes were grouped into:

- Behavioural syndromes such as weakness, inability to fly, or neurological signs etc.
- Physical syndromes such as external injuries, feather abnormalities, beak adhesions, or emaciation etc.

Syndrome linked to diagnoses showed varying specificity

Some signs were nonspecific, like emaciation, while others clearly indicated causes (e.g., trauma, trichomoniasis, avipoxvirus). Species context refined patterns further, such as neurological signs indicating intoxication in raptors but usutuvirosis in blackbirds.

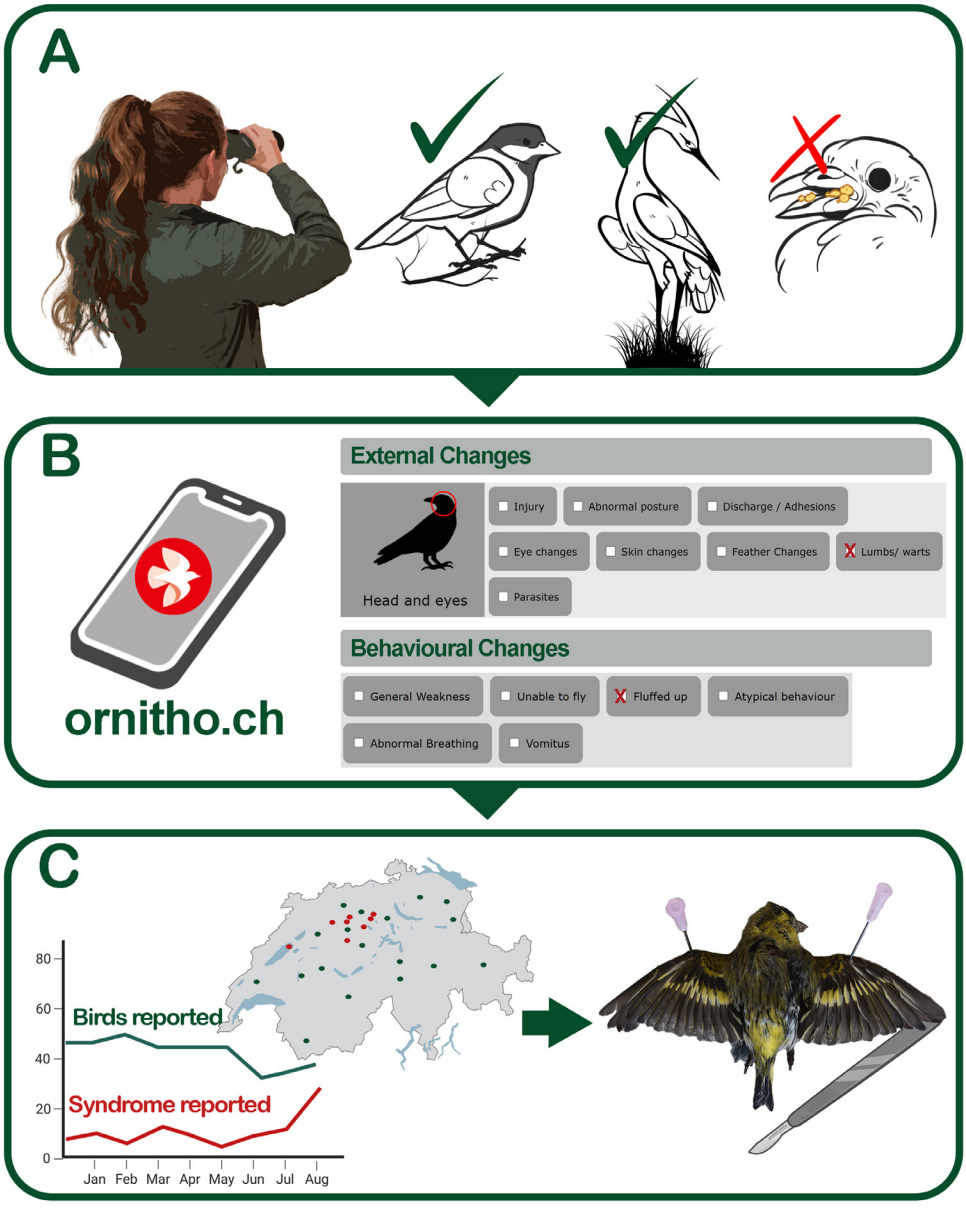

Figure 1: Workflow of a participatory syndromic surveillance system for sick and dead wild birds, implemented through an online reporting system (ORS). (A) Observation of health or sick birds in the field. (B) Reporting of both healthy and sick birds on ornitho.ch. Possible observed clinical signs can be selected from a syndrome catalogue. (C) Analysis of syndrome reports allows detection of spatial and temporal clusters. Animals from such cluster may then be examined within the framework of the general wildlife surveillance program to determine the cause of sickness or death.

Prototype development and stakeholder workshop

Together with the Swiss Data Science Center (SDSC), we developed a prototype for a citizen-based ORS. Users could report sick or dead birds via an intuitive interface, upload images, select affected body parts, and choose from the syndrome catalogue. To evaluate the prototype, a workshop with 14 representatives from federal agencies, cantonal authorities, NGOs, and the Swiss Ornithological Institute (SOI) was held.

The following key requirements were identified:

- User-friendliness: entries should be intuitive and efficient (around five minutes).
- The used terminology should reflect demands and expertise of the ORS-target audience.
- Feedback loops: users expect guidance on what to do after reporting, or confirmation of the likely cause.

The prototype was appreciated for its intuitive design, the photo function and syndrome selection. However, participants highlighted that true added value lies in harmonized terminology and integration with existing systems.

Integration Switzerland's largest citizen-science platform for bird observations

Following this recommendation and collaboration with the SOI, the syndromic approach has now been integrated into the mortality tool of ornitho.ch. The syndrome catalogue was adapted for the *ornitho.ch* audience, translated into German, French, Italian, and English, and, moreover, made available at the European level. This integration ensures that morbidity and mortality data are collected alongside population observations, building the basis for integrated wildlife monitoring[7]. With *ornitho.ch*'s large, active user community, the approach has a strong foundation for long-term sustainability. Currently, the module is available on the web platform, with plans for future inclusion in the mobile app.

Isabelle Wethli, med. vet doctoral student

Dr. med. vet. Mirjam Pewsner

Conclusion and outlook

The WildGuARDS project has demonstrated that syndromic surveillance is both feasible and welcomed by stakeholders. By combining retrospective analysis, syndrome definition, prototype development, and stakeholder engagement, we established a foundation for national implementation. Ongoing evaluation and adaptation will be needed to ensure success. We hope that such data collection could guide case selection for laboratory confirmation in the General WHS and allow both experts and citizens to describe observations in a shared language. Most importantly, the system enables earlier detection of unusual disease events, contributing to a clearer national overview of wildlife health. We hope this model will inspire further expansion of syndromic surveillance to other taxa and expert levels, strengthening the integration of population and health monitoring in Switzerland and beyond.

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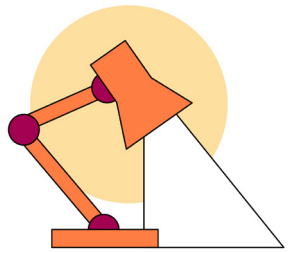

Discovery of antimicrobial peptides

Article by: Linus Rechsteiner, PhD student in the lab of Prof. Dr. Lucy Hathaway, Institute for Infectious Diseases (IFIK)

There is an alarming lack of innovation when it comes to the discovery and development of novel antibiotics. The limited number of candidates in the drug pipeline are mostly derivatives of compounds currently in clinical use, raising concerns regarding their ability to effectively counter the development of antimicrobial resistance. Yet, there is hope; the extensive diversity of specificity and activity profiles found in antimicrobial peptides might hold the key to combat multidrug-resistant pathogens. In addition, tools based on artificial intelligence could help overcome the current stagnation in antibiotic research.

Antimicrobial resistance (AMR) is a growing global health crisis and a leading cause of death worldwide. If current trends persist, AMR is projected to account for more than eight million deaths annually by 2050. Despite these worrying prospects, there remains a serious lack of novel antibacterial compounds in both preclinical and clinical development. In recent years, the responsibility for advancing antibacterial research has shifted largely to academic institutions and small companies, which often struggle to sustain the substantial financial demands of drug discovery, development, and clinical trials[1].

Linus Rechsteiner, PhD student

The mid-20th century „Golden Age of Antibiotic Development“ was mainly driven by discovery of compounds from natural sources and led to the introduction of most antibiotic classes used in clinical practice today. By the 1970s, the pace of antibiotic discovery had slowed considerably, and the general approach shifted towards chemical modification of existing antibiotic classes to improve stability and bioavailability or overcome resistance that had emerged. However, given that all generational variants of a class retain the same target specificity and molecular binding site, cross-resistance developed rapidly, stressing the urgent need for truly novel antibiotic classes. In recent years, antimicrobial peptides have gained increasing attention as alternative therapeutic agents due to their abundant natural sources, structural diversity, broad range of activity profiles and relatively straightforward production[3,4].

Antimicrobial peptides (AMPs) are produced across all domains of life as an ancient form of host defense against various pathogens, including bacteria, fungi and viruses. **Bacteriocins** are a subset of bacterially produced, ribosomally synthesized AMPs, generally targeting phylogenetically related bacterial strains. These peptides typically consist of 10 to 50 amino-acid residues, possess a net positive charge and contain both hydrophobic and hydrophilic regions. Due to this amphiphilic structure, bacteriocins primarily target the bacterial cell wall and disrupt membrane integrity, leading to cell death. In addition, some bacteriocins can penetrate the cell envelope and interfere with central cellular processes, such as DNA and protein synthesis, enzyme activity and cell wall synthesis.

In pathogens with pronounced AMR, combining AMPs with conventional antibiotics offers a promising therapeutic strategy. AMPs can dirupt bacterial membrane integrity or biofilms, thereby enhancing the efficacy of classical antibiotics through synergistic interactions (Figure 1). Additionally, their ability to target multiple cellular processes further increases the effectiveness of combination therapies and substantially reduces the risk of further resistance development. In the same context, the generally narrow-spectrum activity of bacteriocins allows for more targeted interventions, limiting selective pressure on commensal bystanders and preserving the overall integrity of the host microbiota.

Regarding resistance development against AMPs, evidence suggests that resistance arises infrequently, and when it does, genetic changes typically confer only modest levels of resistance. Moreover, no cross-resistance between AMPs and antibiotic-resistant bacteria has yet been observed. Nonetheless, the development of resistance to AMPs appears to depend strongly on the physicochemical properties of individual peptides and remains, in general, an underexplored area[5].

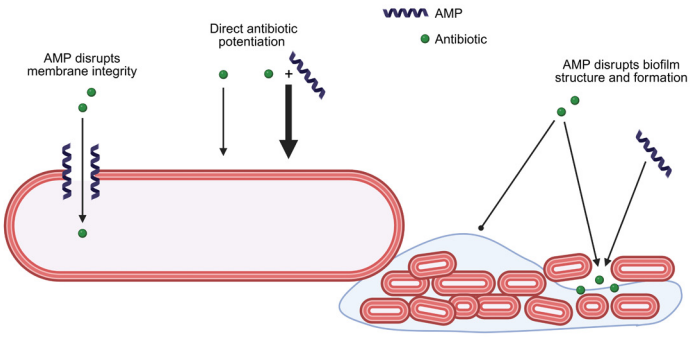

Figure 1: Mechanisms of AMP-antibiotic synergy, adapted from Taheri-Araghi S (2024)[2].

Despite these promising attributes, the clinical translation of AMPs is limited by several challenges, including poor bioavailability, short half-lives and cytotoxicity. Of particular concern are non-specific interactions arising from their amphiphilic nature, which can lead to dose-dependent toxicity in eukaryotic cells. Additionally, natural peptides are generally prone to rapid proteolytic degradation, necessitating chemical modifications - such as incorporation of D-amino acids, cyclization, acetylation - or delivery via sophisticated nanocarrier systems to improve stability and therapeutic efficacy[6].

Over the past several decades, novel AMPs have been identified across a wide range of organisms, including plants, animals, humans and microorganisms. Traditionally, AMP and bacteriocin discovery relied on laborious workflows involving column-based isolation, purification and subsequent characterization through methods like Edman degradation, SDS-PAGE, or mass spectrometry. More recently, the availability of extensive genomic datasets and the development of specialized bioinformatic pipelines have shifted bacteriocin research into the metaomics era. These advances now allow *in silico* genome screening and large-scale metagenomic mining for the presence of novel bacteriocin gene clusters. With ongoing advances in computational power and artificial intelligence, the discovery of new AMPs, and potentially even novel classes of bacteriocins, is likely to further accelerate in the near future[7].

In the **Pneumococcal Biology Group**, led by Prof. Dr. Lucy Hathaway at the IFIK, we focus on the human pathogen *Streptococcus pneumoniae*, a Gram-positive bacterium responsible for severe diseases including bacterial meningitis and pneumonia. Despite its pathogenic potential, *S. pneumoniae* commonly colonizes the human nasopharynx asymptomatically as part of the microbiota. Our research focuses on interspecies communication within the nasopharyngeal niche, which is frequently mediated by signaling peptides and bacteriocins.

In a study on interactions between bacteria of the respiratory tract, we identified a peptide within the secretome of *Klebsiella pneumoniae*, capable of selectively entering *Streptococcus pneumoniae* via the AmiA-AliA/AliB permease system. Once internalized, the peptide disrupts pneumococcal physiology by inhibiting growth, reducing transformation efficiency, and inducing irregular cell morphology. In addition, it significantly reduces pneumococcal adherence to primary human airway epithelial cultures and decreases colonization of the rat nasopharynx. Notably, this peptide retains activity against antibiotic-resistant *S. pneumoniae* strains and shows no detectable cytotoxicity, thus, highlighting it as a promising therapeutic candidate for pneumococcal infections[8].

In my PhD I study if commensal bacteria colonizing the human nasopharynx may provide colonization resistance against invading pathogens through bacteriocin production. We are currently investigating *Haemophilus paraphrohaemolyticus*, an underrecognized bacterial commensal of the respiratory and oral tract. Co-culture experiments with isolates from a healthy respiratory microbiota revealed that the secretome of *H. paraphrohaemolyticus* exhibits potent antimicrobial activity against bacterial pathogens. Subsequent analyses revealed that this activity is mediated by peptides. Interestingly, these antimicrobial peptides display strong genus specificity, targeting selectively members of the genus *Streptococcus*. Current experiments aim at investigating the determinants of this specificity, seeking to elucidate the precise molecular mode of action.

In a separate project, I assessed a publicly available machine learning tool for its ability to predict antimicrobial activity of peptides[9]. Candidate peptides were selected based on their origin (commensal bacteria of the human respiratory tract), physicochemical properties, stability and net charge. In our *in vitro* screening, nearly half of the peptides exhibited antimicrobial activity against at least one tested bacterial pathogen, with diverse specificity and potency profiles. The majority of active peptides exerted fast bactericidal effects via membrane pore formation in both Gram-positive and Gram-negative bacteria (Figure 2). Cytotoxicity, however, remained a significant concern as some active peptides lacked prokaryotic selectivity. On the other hand, we did discover a subset of bacteriocins with more favorable toxicity profiles, higher specificity and bacteriostatic modes of action.

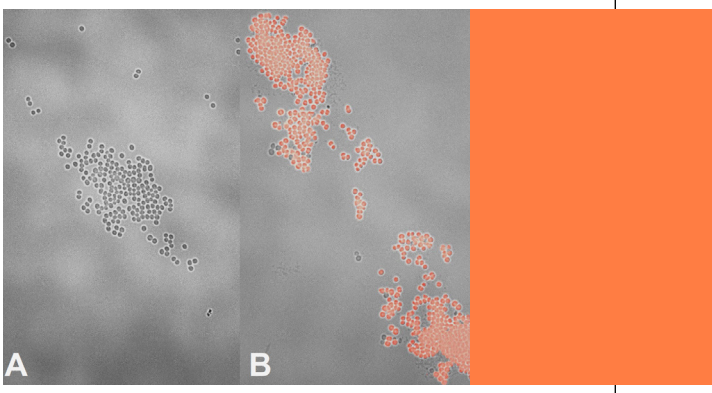

Figure 2: Bacteriocin induced membrane disruption in *Staphylococcus aureus*. *S. aureus* incubated in chemically defined medium without (A) or with (B) antimicrobial peptide AMP_3. Stained red with propidium iodide to visualize membrane disruption and cell death.

Overall, the use of machine learning enabled the discovery of antimicrobial peptides from multiple sources, showing diverse mechanisms of action while considerably reducing experimental workload and time. Nonetheless, current machine learning tools are trained on datasets of previously characterized AMPs, thus, they are inherently biased toward established mechanisms of action and entirely novel antimicrobial pathways may be overlooked.

With antimicrobial resistance rising and few novel antibiotics in the pipeline, bacteriocins and other antimicrobial peptides offer promising approaches for the development of alternative therapies. We identified novel peptides with antimicrobial properties that may mediate interspecies communication in the human respiratory tract and demonstrated that implementation of artificial intelligence might accelerate the discovery of such compounds.

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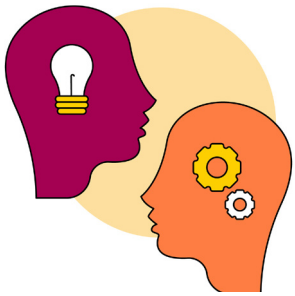


Bright and earlier: meet two young MCID researchers

Interview with:
Mike Mwanga, Institute for Infectious Diseases (IFIK) and Institute of Virology and Immunology (IVI) and
Martin Wohlfender, Institute of Social and Preventive Medicine (ISPM)

Can you describe briefly the MCID-funded project you are working on and what you aim to achieve?

Martin: During the COVID-19 pandemic, a larger amount of data, e.g., daily number of new cases or viral genome sequences, has been collected than during any previous major infectious disease outbreak. In the MCID-funded project "Early detection for early action: integrating multiple data sources for monitoring the SARS-CoV-2 epidemic in near real-time" we aim to develop the bases of new digital tools relying on large datasets from different sources, e.g., hospital patient electronic health records, to improve the monitoring of epidemic trends and to obtain more precise short-term forecasts of COVID-19-related hospital admissions.

Mike: My PhD project is part of the Integrated One Health Network to monitor and characterize Influenza A Viruses (IAV) circulating in Pig and Human Populations, funded by the MCID. The project focuses on understanding how IAVs evolve and circulate between pigs and humans in Switzerland. I analyze virus genetic data to map the diversity of IAVs found in Swiss pigs and compare this data with sequences of similar strains circulating across Europe. In parallel, I study IAV detected in humans through routine diagnostics, looking at how their genetic makeup may be linked to the severity of illness in patients. By combining these approaches, the project aims to provide insights into how IAVs spread, how they might jump from animals to humans, and what risks they pose to human and animal health. Ultimately, this knowledge will help to inform and strengthen prevention and control strategies for influenza.

Mike Mwanga, PhD student

How does your project contribute to preparedness for infectious disease threats?

Mike: IAVs are a global health concern and remain among the top candidates to cause the next pandemic. These viruses infect a wide range of species including pigs and humans. Pigs are considered ‚mixing vessels' since they can be simultaneously infected with diverse IAVs strains from different hosts. This co-infection phenomenon creates an environment for exchange of genetic material between viruses and possible emergence of novel hybrid strains. Studying IAVs at the pig-human interface is a valuable opportunity to gain insights into the virus's epidemiology and evolution, directly informing assessment of spillover risk. This allows for identification of strains with ability to cross species barriers, to evade treatments and to cause wide-spread outbreaks. Findings of the project will inform veterinary and public health intervention measures thereby strengthening pandemic preparedness.

Martin: Our work on new digital tools for epidemic monitoring and forecasting is directly linked to preparedness for infectious disease threats. While we focus on the SARS-CoV-2 pandemic, due to the large amount of available data, our models could also be applied to other pathogens. Reliable information on the current transmission dynamics or well-founded short-term forecasts that are based on a broad data foundation are very valuable during an infectious disease outbreak and can support decision-makers in determining good strategies to control the epidemic.

What excites you about multidisciplinary research?

Martin: This is a great opportunity to look at a certain question from multiple perspectives and to work with experts from different fields. For example, in the MCID-funded project I am involved in, the team includes not only people from the ISPM, but also researchers from the Insel hospital and the IFIK. Both from them and from talks and discussions at conferences, I have been able to greatly improve my knowledge on a variety of topics such as infectious diseases.

Mike: It is really exciting to work closely and interact with research experts from diverse fields. This study has enabled my collaboration with veterinarians, physicians, clinicians, virologists and fellow bioinformaticians. I have learned a lot from them and gained ideas that I would never have had on my own. You also get a clear view of how everyone's project is connected and contributes to the bigger vision of the initiative.

Martin Wohlfender, PhD student

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

Martin: When working on a multidisciplinary research project, it is almost impossible to be an expert on all relevant topics. At least for me, it took some time to gain an overview of important aspects outside my area of expertise. One example of such an aspect is the process of data collection in a hospital and the resulting limitations, e.g. delays in data collection, which prevent the real-time use of a tool based on this data. It is also important to find a common language and approach. Depending on the discipline, different terms are used for the same concepts, or some things are approached differently.

How did your education lead you to choose a multidisciplinary project for your PhD thesis?

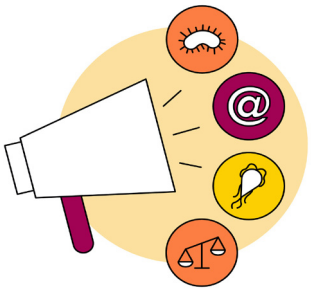
Mike: My path towards this PhD project started with my early work after completing my bachelor's and master's degrees. During these early days, I focused on virus epidemiology and evolution, which built the foundation for my interest in how viruses spread and change. That experience shaped my fascination with studying viruses across species and contexts. This project builds on that foundation but also pushes me into new territory. While it aligns with my core interests, it involves a different virus type and broader research questions. The multidisciplinary nature makes it both challenging and exciting, and it allows me to expand beyond what I had earlier on envisioned.

Martin: Although I focused on rather theory-heavy mathematics courses during my studies, I also attended some lectures covering applications of mathematics in political sciences, e.g., the analysis of different election systems. This sparked my interest of applying mathematics within a different scientific field. When I was looking for a PhD position, I was explicitly looking for a project, involving mathematics, but also another discipline.

Short biography of the two young researchers:

Martin Wohlfender started his PhD at the Institute of Social and Preventive Medicine (ISPM) in June 2022 supervised by Dr. Julien Riou and PD Dr. Christian Althaus. The focus of his research is leveraging large datasets from different sources to improve epidemic surveillance. In the context of the MCID-funded project "Early detection for early action: integrating multiple data sources for monitoring the SARS-CoV-2 epidemic in near real-time", Martin developed a statistical framework to estimate parameters describing the transmission dynamics of SARS-CoV-2 from viral genome sequences (shared first author publication) and applied different machine learning models to forecast COVID-19 related hospital admissions a few weeks ahead (first author, preprint). He obtained his Bachelor's and Master's degrees in mathematics from ETH Zurich. Before starting the PhD, he worked for one year as an academic intern in the IT security domain at the Federal Office of Information Technology, Systems and Telecommunication FOITT.

Mike Mwanga is currently a PhD student at the Institute for Infectious Disease (IFIK) and Institute for Virology and Immunology (IVI) under the supervision of PD Dr. Ronald Dijkman and Dr. Jenna Kelly. His thesis is focused on undertaking a comprehensive genomic analysis of IAVs to understand virus evolution and transmission dynamics in pigs and humans in Switzerland. Mike holds a Bachelor's degree in biochemistry and a Master's in Bioinformatics from Pwani University, Kenya. He previously undertook research work in virus epidemiology and evolution at the Kenya Medical Research Institute - Wellcome Trust in Kenya. Mike contributed to two publication on the topic of "Optimized workflow for high-throughput whole genome surveillance of influenza A virus" (preprint) and "Concurrent detection of swine Influenza A Virus H1N1 in a pig herd and a farmer in Switzerland" by Steiner J et al. (submitted for publication).



News

New MCID-funded projects to begin by January 2026: result of the MCID project funding call 2024
In response to the MCID project funding call 2024, 27 project funding applications were received. Following a thorough peer review process, eight projects have been selected for funding and will begin by January 2026. See here for details:

Habilitation of MCID Members Stephanie Ganal-Vonarburg and Caroline Brall
MCID Members, Stephanie Ganal-Vonarburg (Chair, Immunity Cluster) and Caroline Brall (Manager, Ethics @MCID Ethics and Policy Lab) have successfully habilitated at the UniBE Medical Faculty. Congratulations, Stephanie and Caroline!

BEready Cohort: 1‘000 households now enrolled!
In July, the BEready Cohort team enrolled their 1‘000th household! This is a significant milestone in the aim to enrol 1‘500 households within Canton Bern. Do get in touch with the team if you want to enrol or to discuss collaborative projects

Events

MCID Annual Event 2025
On 21st November, the MCID will host its Annual Event 2025. The event will feature presentations of MCID-funded research, as well as external speakers and opportunities for exchange and discussion. Stay tuned for more information

UniBE Talks: “Wo sind die Grenzen der Wissenschaftlichkeit”, 5th November
As part of the UniBE Talks series, on 5th November, a podium discussion will take place to address the topic of the boundaries of scientific integrity lie. MCID Members Eva Glünz, Caroline Schlaufer and Volker Thiel will be part of the panel

Workshop: engaging in policymaking as a researcher
On 25th November, a workshop will be held for PhD students and post-docs keen to explore how their research can have societal impact; hosted by V-R International and Academic Careers, organised by Caroline Schlaufer and the Franxini Project

Highlighted publications

Marco Alves and team on neuronal death caused by monkeypox virus (MPXV)
As part of an MCID-funded project, Marco Alves and team used human neural organoids to study MPXV infection in the context of mpox-linked encephalitis. They show that viral disruption of neuritic transport can drive neuronal degeneration

Silke Adam and team on the contribution of media to the spread of conspiracy theories
In a project part-funded by the MCID, Silke Adam and team investigated the role played by mainstream and alternative media in the spread of Covid-19 conspiracy theories, with insights that have the potential to inform journalistic practice

Jörg Jores and team on host immune responses to bacteriophages
In work part-funded by the MCID, Jörg Jores and team use an *ex vivo* system to study bovine immune responses to bacteriophages, with results that demonstrate the need for characterising potential immune responses prior to phage treatment

Tina Hascher and team on the effect of Covid-19 control measures on school student well-being and emotions
As part of an MCID-funded project on the effect of Covid-19 control measures in secondary school classrooms, Tina Hascher and team studied the effect of measures on student welfare, revelaing both positive and negative impacts

Olivier Guenat and team on organ-on-chip endothelial cell responses to different fluid flow conditions
In a part MCID-funded study, Olivier Guenat and team show that endothelial cells in an organ-on-chip model differ greatly in their gene expression when fluid flow is unidirectional compared to bidirectional, a finding critical for future studies

Caroline Schlaufer and MCID-PhD student, Jule Ksinsik on scientists’ engagement with policy processes
As part of an MCID-funded project, Caroline Schlaufer and Jule Ksinsik studied communication of scientists in Switzerland during the Covid-19 pandemic, revealing a limited use of process narratives and more emphasis on policy substance

MCID-funded PhD students present their work at the 2025 GCB Annual Research Symposium

On 26th June, the Graduate School for Cellular and Biomedical Sciences held its annual research symposium, this time the event also marking the occasion of the School's 20th anniversary. At this event, eight MCID-funded PhD students had the opportunity to showcase their research by giving oral or poster presentations: L to R; Jonas Steiner (Swine Clinic), Melanie Schmid (DBMR), Marta Zimoch (IVI), Mike Mwanga (IFIK), Isabel Schultz-Pernice (IVI / Vetsuisse), Negar Vahdani (sitem-Insel), Simone Leoni (IFIK)

MCID engages with the public at the Vetsuisse Open Doors Event

On 28th June, the Vetsuisse Faculty opened its doors to the public to celebrate 125 years since its founding. The MCID, a strategic center of the faculty, was present to engage with the public on the topic of infectious disease preparedness.

MCID activities at the event included an antibiotic resistance-themed "splat the pathogen" challenge and a pathogen-detective game, both with pathogen-themed prizes. We tested visitor's knowledge with a pathogen quiz, presented posters featuring MCID-funded research and also engaged with younger guests with face-painting and a create-a-pathogen station. The BEready team presented their "tick-talk" station, providing advice on avoiding tick bites and introducing the public to the BEready Cohort.

We are grateful to all our volunteers who helped create the activities and took part on the day and to the organisers for the opportunity to be part of the event !

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 Pixabay

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