DOCIDOH 2026

Abstract book

3rd Debrecen Online Conference on Infectious Diseases in a One Health context

11-13 May 2026

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Programme at a glance

For detailed program, please see the conference website:

https://e-konferencia.unideb.hu/en/program-3rd-debrecen-online-conference-infectious-diseases-one-health-context-docidoh

Time	Section type	Section
Day 1 - 11 May		
9:00 - 9:30	Opening speech	
9:30 - 10:00	Semi-plenary	Environmental Pathways of AMR and Infection
10:00 - 11:15	Regular talks	
11:15 - 11:45	Break	
11:45 - 12:15	Semi-plenary	Choices, Cultures and Phytochemicals: The Behavioural AMR Interface
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Day 2 - 12 May		
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10:45 - 11:15	Break	
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13:15 - 14:15	Breakout room	CEEPUS - Discover CEEPUS Mobility at DOCIDOH 2026
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11:30 - 12:00	Closing ceremony	

Abstracts

Semi-plenary presentations

Section 1: Environmental Pathways of AMR and Infection

One Health surveillance goes environmental

Ana Maria de Roda Husman[1]

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The One Health concept entails a worldwide strategy for expanding interdisciplinary collaborations and communications in all aspects of health care for humans, animals and the environment. This synergism could advance health care for the 21st century and beyond by accelerating biomedical research discoveries, enhancing public health efficacy, expeditiously expanding the scientific knowledge base, and improving medical education and clinical care. When properly implemented, it will help protect and save untold millions of lives in our present and future generations.

However, the One Health approach is often anthropocentric and focused on infectious diseases. And the representation of the environment in the One Health approach is lagging behind. Actions to enhance environmental surveillance are needed including strategic sampling, omics, interpretation, communication, public health decision-making and proactive governance. Opportunities and challenges will also be discussed.

Section 2: Choices, Cultures and Phytochemicals: The Behavioural AMR Interface

Understanding and shaping behaviour in a One Health context

Aapo Kuusipalo[1]

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The semi-plenary will focus on the application of Behavioural and Cultural Insights (BCI) approaches within a One Health framework. Drawing from recent and ongoing research in Infection Prevention and Control (IPC) practices and analysing the success of vaccination campaigns designed to limit the risk of zoonosis, the talk will highlight the ways in which BCI can be crucial tools in both understanding and shaping health behaviours. The talk will cover some of the more established themes within One Health (antimicrobial resistance and zoonosis) but seeks to provide some fresh perspectives into these phenomena.

In 2023, mass deaths of wild birds in Finland were linked to the highly pathogenic subtype of avian influenza (HPAI H5N1). In response, the following year Finland became the first country to offer the freshly approved H5-vaccine for avian influenza to population groups who, mostly due to their occupation, had an increased risk of infection. The vaccination campaign had limited success, and coverage in the target populations peaked at around 8 %. A rapid qualitative study, conducted to better understand reasons behind this failure, revealed broader societal discussions and tensions as central factors affecting uptake in some target groups (namely fur farmers), alongside reasons more commonly documented in vaccine hesitancy literature.

Antimicrobial resistance remains a key threat to global health, and IPC and hand hygiene practices some of the most critical dimensions of its alleviation. The use of alcohol-based hand rub frequently falls short of target levels in various contexts around the world and has proven to be a persistent challenge. A pilot intervention currently being planned in a Finnish healthcare setting seeks to utilise BCI approaches, namely behaviour change frameworks and sociological theories, to alleviate these shortcomings. Of special interest are broader shifts in patient-professional relations and their possible roles in finding effective and lasting solutions.

Section 3: Bacterial and Viral Spillover Across Taxonomic Orders

Photobacterium damselae subsp. *damselae*: A Potential Emerging Zoonotic Threat at the Animal-Human-Climate Nexus – A Razorbill Case Study

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Climate change is altering marine microbial dynamics, promoting the emergence of zoonotic pathogens like *Photobacterium damselae* subsp. *damselae* (Pdd). This study reports the first isolation of a hyper-virulent Pdd strain in a Razorbill (*Alca torda*) during a recent migratory "wreck event" in the Mediterranean. Molecular characterization confirmed the presence of the pPHDD1 plasmid, encoding the potent cytotoxin Damselysin. Our findings indicate that rising sea temperatures act as a dual driver: triggering host immunosuppression and upregulating pathogen virulence factors. This case underscores the role of seabirds as sentinels for shifting epidemiological risks. Under the One Health paradigm, integrated surveillance is now essential to monitor the environmental dispersal of Pdd and its growing threat to marine biodiversity and global public health.

Section 4: When Clinical AMR Meets the Planetary Crisis

Health implication of the planetary triple crises

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The planetary triple crises of climate change, environmental pollution and the loss of biodiversity lead to unprecedented, interwining impacts on human and animal health and the environment. Direct consequences of climate change on human health include lives lost to heatwaves and extreme weather events. Air pollution lead to 182,000 premature deaths in 2023 in the EU-27 member states alone. The loss of biodiversity leads to reduced ecosystem services, such as natural purification processes of water and wastewater. Implications for infectious diseases are just as severe: the rise in vector-borne, zoonotic and certain waterborne disease incidences as well as their expanding geographical coverage is a direct consequence of rising temperatures. Healthcare facilities need to prepare and respond to new challenges associated with the triple crises, both by recognising the connection between the environment and various health outcomes (such as air pollution and COPD) and by introducing patient care practices aligned to climate adaptation.

Regular talks

Section 1: Environmental Pathways of AMR and Infection

Beyond One Health: One Biosecurity

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Behind the One Health concept is the recognition that human and animal health are interrelated, and they are best treated together. One Health is a limited concept and needs to be extended. The overarching approach should be One Biosecurity. Biosecurity commonly refers to the research, procedures, and policies that cover the exclusion, eradication, or effective management of the risks posed by the introduction of alien plant or animal pests and diseases, zoonoses, the release of genetically modified organisms and their products, and the management of invasive alien species. The key connection among these seemingly disparate phenomena is the appearance of a genotype, or organism, in places or situations where it has not been present before. This may be a "normal" organism arriving to a new location (biotic invasion), one with a natural mutation in host range (an animal pathogen host-jumping, as SARS-CoV-2), or an intentionally generated one (a genetically modified organism with changed tolerance limits, like a herbicide-tolerant crop plant). Yet these are usually handled by different (and too often not cooperating) national and international organisations. If we insist on dealing with such organisms on a sectorial basis, we do the invasive species a favour, but to ourselves a disservice. So, One Biosecurity should take environmental, plant, animal and human health under one umbrella. Without a "healthy" environment, human health may be a wish, but will never become a reality.

I thank Phil Hulme for insightful discussions.

Emerging microbial risks in Hungarian bathing waters

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The majority of Hungarian natural bathing waters are classified as good or excellent quality, based on the level of faecal indicators, but other microbiological agents can also impact the health of bathers. In rivers, the greatest risk is the discharge of treated or untreated wastewater. This is a significant microbiological load on the receiving water body, including resistant organisms from communal, industrial and hospital wastewater. Increased water temperatures and nutrient concentrations due to climate change pose a higher risk in standing waters. The proliferation of indigenous organisms and the emergence of new pathogens can also endanger bathing safety. To respond to these emerging risks, the National Center for Public Health and Pharmacy has been investigating bathing waters in recent years. Antibiotic-resistant bacteria were examined at a Danube river bathing site and suspected sources of pollution. On a wider scale, national survey was conducted to determine the number of non-toxinogenic *Vibrio* species in standing waters. The Danubian beach was confirmed to be suitable for bathing; the main risk being a smaller stream, introducing ESBL-producing coliforms periodically. NT *V. cholerae* was found in 88% of the investigated lakes. Counts generally ranged between 100-1000 CFU/100 ml, but extreme levels were also detected. Beach operators, public health professionals, and general practitioners should be prepared for emerging risks associated with recreational waters.

We would like to thank the samplers and colleagues from the laboratories for their help. This work was supported by UrbanBlueHealth project (Interreg CE0200763).

Investigating the spread of antibiotic resistance using wastewater-based epidemiology

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The National Centre for Public Health and Pharmacy has recently begun detecting various antibiotic resistance genes and gene families in addition to monitoring upper respiratory pathogens within wastewater-based epidemiological studies. This work follows international trends and new guidelines, as wastewater is a key medium for the environmental spread of resistant and multi-resistant microorganisms.

The selected targets encode resistance to antibiotics widely used in human medicine and were chosen for their epidemiological relevance. They are detected from DNA isolated from pellets remaining after centrifugation of raw wastewater samples. Primers and probes for RT-qPCR were selected from the literature, and copy number controls were established using digital PCR. DNA from bacteria with confirmed resistance served as reference material.

Measurements were performed weekly from May 2024 to August 2025, and monthly thereafter, using samples from major city wastewater treatment plants covering 40% of the national population. The parameters can be reliably detected in wastewater, revealing diverse spatial and temporal resistance patterns. Further analysis and comparison with drug-consumption and clinical data may help clarify the dynamics of resistance spread and support effective control measures. A pilot shotgun WGS analysis was also conducted to determine the resistance profile of one major city.

This work was supported by EU-Jamrai2 (No. 101127787).

Microbiological Risks in Hospital Water Systems

Boglárka Pollák[1], Emese Tornainé Kálmán[1], Bernadett Khayer[1], Márta Vargha[1]

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Inadequately designed and operated hospital water distribution systems, water associated with air-conditioning devices, and water used in treatment equipment such as dialysis machines or dental chairs, as well as aqueous solutions and even bottled water, can provide a favourable environment for the growth of opportunistic pathogens and act as potential reservoirs for nosocomial infections.

Legionella species are the most recognized indicators of premise-plumbing-related risk, whereas *Pseudomonas aeruginosa* frequently signals biofilm formation and local colonisation. However, the water microbiology laboratory of the NCPHP has been asked to investigate several unusual hospital infections suspected to originate from water. This presentation reviews the major risk factors associated with hospital water systems, such as stagnation, suboptimal temperatures, biofilm formation, and system complexity and highlights a few cases from recent years involving atypical bacterial infections caused by *Achromobacter*, *Ralstonia*, *Delftia* and non-tuberculous mycobacterial species traced to different water sources.

Understanding how water system characteristics, maintenance practices, and environmental conditions influence microbial proliferation is essential for effective prevention. These findings emphasise the need for periodic risk assessment of assumed “low-risk” water sources in clinical settings and reinforce the importance of robust water safety management.

Emergence and genomic characristics of a mcr-1 *Escherichia coli* in waterfowl in Hungary

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Plasmids carrying high-risk resistance mechanisms in pathogenic *E. coli* have gained particular attention in veterinary medicine, particularly since the identification of the colistin resistance gene, mcr-1. We provide the first evidence of mcr-1 *E. coli* emergence and describe the complete mcr-1 plasmid sequence of a multiresistant (MDR) avian pathogenic *E. coli* (APEC) strain in waterfowl in Hungary. Whole-genome sequencing and core-genome MLST were performed to characterize the genome structure of the mcr-1 plasmid and to reveal the phylogenetic relation of the Hungarian duck strain Ec45-2020 with other mcr-1-positive *E. coli* strains globally. Results showed that plasmid pEc45-2020-33kb shared a high level of genome identity with IncX4 type mcr-1 plasmids widespread among human, animal, and food reservoirs of enteric bacteria of public health concern. The mcr-1-positive *E. coli* strain Ec45-2020 belongs to the ST162 genotype, recognized as a globally disseminated zoonotic genotypes of MDR *E. coli*. These findings underscore the importance of continuous surveillance of enteric bacteria carrying high-risk antimicrobial resistance genotypes, including often-neglected animals, such as waterfowls, as potential reservoirs for colistin resistance genes like mcr-1. This study highlights the critical role of the a One Health approach, integrating human, animal, and environmental health sectors to monitor and control the spread of antimicrobial resistance.

This research was funded by the K 140349 grants of the National Research, Development and Innovation Office and by the SA-27/2021 grant of the Hungarian Research Network. Additional support was provided by the TKP2021-EGA-01 grant of the National Research, Development and Innovation Office.

Section 2: Choices, Cultures and Phytochemicals: The Behavioural AMR Interface

Psychological Barriers and Opportunities for Behavior Change in the One Health Approach: Risk Perception and Cognitive Biases at the Human-Animal-Environment Interface

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The success of the One Health approach depends not only on biological or ecological data but also on understanding and shifting human behavior. While scientific evidence regarding the risks of zoonoses and antimicrobial resistance is clear, societal responses often lag behind. This presentation utilizes psychological frameworks to examine the knowledge-action gap within public and environmental health strategies.

The presentation explores cognitive biases affecting risk perception, such as optimism bias – the illusion of personal invulnerability – and psychological distance, which often hinder the adoption of preventive measures. Special attention is given to the role of affective bonding with animals in hygiene practices, as well as the influence of cultural rites and social norms on antibiotic use.

Furthermore, the talk proposes the application of behavioral science interventions, such as nudging, within the One Health context. The conclusion highlights that effective surveillance and epidemic control must include building psychological resilience and implementing culturally adapted health communication. These strategies should treat individuals not merely as data points, but as active, psychological decision-makers.

Yamo: Folk Taxonomies in Antibiotic Use Among Community Members in Manyatta A Sub-Location, Kisumu, Kenya

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Antimicrobial resistance (AMR) is a pressing global health threat, with inappropriate antibiotic use in communities as a key driver. This paper examines how folk taxonomies shape antibiotic use among caregivers in Manyatta 'A', Kisumu County, Kenya, focusing on the illness category yamo (Dholuo: ""wind""). Using mixed methods (102 pharmacy clients; 31 household interviews; 8 key informants; 3 FGDs), the study reconstructs yamo's symptoms, causes, and treatments. Findings reveal yamo as a multidimensional taxonomy encompassing respiratory, gastrointestinal and dermatological symptoms attributed to weather change or contaminated food. Amoxicillin (38%), co-trimoxazole (18%), and metronidazole (17%) were commonly purchased. Care-seeking bypasses formal clinics for pharmacies, where attendants validate lay diagnoses. Acquisition without prescription (73%) and early treatment discontinuation (34.7%) reflect cultural logic where symptom disappearance signals illness resolution. The yamo taxonomy thus structures a coherent alternative care system, with implications for antimicrobial resistance. Interventions must engage with this emic logic using local categories as entry points for stewardship discourse.

Keywords: Yamo, folk taxonomies, antibiotic use, explanatory model, antimicrobial resistance

The authors gratefully acknowledge the original research conducted by Allan Odhiambo Okeyo, whose thesis data forms the foundation of this analysis. We also extend our thanks to the residents of Manyatta ‘A’, the pharmacy clients, attendants, and pharmacists who participated in the original study.

COVID-related health literacy, information sources, and vaccine acceptance during the COVID-19 era in Hungary

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Understanding how COVID-related health literacy (COVID-HL) affects vaccine acceptance is essential for improving vaccine uptake and preparing for future pandemics.

This study aimed to assess the level of COVID-HL, the used and trusted information sources, and examine the association between COVID-HL and vaccine acceptance in a sample of Hungarian adults.

In 2022, we conducted a survey of 1,200 Hungarian adults aged 18 years and older using a probability sample representative of the adult population. The questionnaire included items on socio-demographics, vaccine acceptance, COVID-HL, and information sources on COVID-19. Weighted percentages and binary logistic regression were used during analyses.

43.6% of the sample demonstrated sufficient, 25.2% had inadequate and 31.3% showed problematic level of COVID-HL. Compared to inadequate COVID-HL, both problematic (OR: 2.55) and sufficient COVID-HL (OR: 2.57) were associated with higher odds of COVID-19 vaccine acceptance. Older age (OR: 1.02) and tertiary education (OR: 1.98) were also positively associated with COVID-19 vaccine acceptance. Regarding information sources, health professionals were the most trusted sources (53.4%), followed by official, government websites or spokespersons (28.4%).

COVID-HL was an important determinant of vaccine acceptance among Hungarian adults. Efforts to improve health literacy, particularly through reliable sources such as health professionals, may increase COVID-19 vaccination uptake.

Antimicrobial and Phytochemical Properties of Greenhouse-Grown Purslane (*Portulaca oleracea* L.) Extracts

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Purslane (*Portulaca oleracea* L.) is widely regarded as a weed, yet it is a nutritionally and medicinally valuable succulent consumed as food worldwide. It's therapeutic potencial attributed bioactive compounds, such as quercetin, gentisic acid and kaempferol. This study aimed to evaluate the antimicrobial activity and phytochemical composition of purslane extracts prepared from leaves and stems grown under greenhouse conditions. Antimicrobial properties were assessed using ethanol and physiological saline extract tested against *Staphylococcus aureus* (ATCC 6538), *Pseudomonas aeruginosa* (ATCC 15442), *Escherichia coli* (ATCC 10536) and *Enterococcus hirae* (ATCC 10541). Ethanolic extracts produced inhibition zones for most tested bacterial strains, while the physiological saline extract yielded an inhibition zone in one case. Additionally, the Klason-Lignin, total polyphenol, flavonoid and glucose contents were determined and compared with the data from an open-field experiment conducted in 2024. Greenhouse-grown purslane showed lower fiber, flavonoid, glucose and polyphenol contents compared to open-field grown plants. These findings highlight the influence of growing conditions on purslane's phytochemical profile and support further research into use in functional foods, dietary supplements and pharmaceutical applications.

Section 3: Bacterial and Viral Spillover Across Taxonomic Orders

Surveillance of swine coronaviruses in Hungary

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Swine coronaviruses (ScoV) are economically significant pathogens that can cause primarily severe gastrointestinal and respiratory diseases. Six main ScoVs are distinguished, but due to the high mutational rate and recombination, new viruses are also expected to emerge. The aim of our recent project is to assess the presence of ScoVs in Hungarian swine herds using broad-spectrum, coronavirus-specific universal RT-PCR system amplifying a fragment of RNA-dependent RNA polymerase. PCR products are extracted from agarose gel and are submitted for sequencing. So far, a total of 121 samples from clinically healthy animals were collected from eleven Hungarian swine farms, and ScoV sequences were detected in 24 samples from five farms. Twelve sequences showed high similarity to porcine respiratory coronavirus and transmissible gastroenteritis virus, while the remaining twelve corresponded to porcine hemagglutinating encephalomyelitis virus. Complete genome sequences of coronaviruses planned to be determined through shotgun sequencing to gain details about genetic variations of SCoVs.

This work was supported by the National Research, Development, and Innovation Office, grant number FK154149. Further support was provided by the National Research, Development, and Innovation Office, project name National Laboratory for Infectious Animal Diseases, Antimicrobial Resistance, Veterinary Public Health, and Food Chain Safety, grant number RRF-2.3.1-21-2022-00001. Project no. 2024-2.1.2-EKÖP-KDP-2024-00013 has been implemented with the support provided by the Ministry of Culture and Innovation of Hungary from the National Research, Development and Innovation Fund, financed under the 2024-2.1.2-EKÖP-KDP funding scheme.

Detection of Circoviruses in Geese and Pigeons in Hungary

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Circoviruses (CVs) are small viruses with circular, single-stranded DNA genomes that infect a wide range of hosts, including birds. Several CVs are known pathogens and may induce immunosuppression, which can predispose affected birds to secondary infections and may lead to mortality. The aim of this study was to assess the presence and occurrence of CVs in geese and pigeons, and to genetically characterize the detected viruses. 70 pooled tissue samples (pool 1: thymus, kidney, liver, spleen; pool 2: bursa of Fabricius, caecal tonsil) were collected from domestic geese (*Anser anser domesticus*, n=28) of different age groups from six farms in Hungary, rock dove (*Columba livia domestica*, n=5) and greylag geese (*Anser anser*, n=2). Targeted molecular screening for CV genomic sequences was performed using a broad-range nested and specific PCR assays from the extracted nucleic acid. CVs were detected in all 70 pools. Goose circovirus genomic fragments were amplified in all 35 (from one or two pool samples), while pigeon circovirus sequences in 34 birds (from one or two pool samples; 27 domestic geese, 2 greylag geese, 5 pigeons). Accordingly, co-infection with both goose and pigeon circoviruses was observed in 34 birds. For further analysis, complete genome sequence of circoviruses will be determined by sequencing. The findings highlight the widespread occurrence of these CVs and suggest frequent cross-species circulation of goose and pigeon circoviruses between geese and pigeons.

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Correlating mortality peaks with respiratory virus emergence: a blueprint for identifying historical pandemics

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Just as SARS-CoV-2 is transforming into a seasonal respiratory pathogen, the causative agents of other seasonal respiratory infections may also have caused pandemics with substantial global mortality when they first entered the human population. The footprint of such historical pandemics may be detectable in historical mortality data.

We extracted historical mortality data from the Human Mortality Database. For broadest possible coverage and due to the uncertainty of causes of death in the historical data, we chose to analyze all-cause mortality in the datasets. We compiled published estimates on the most recent common ancestors (tMRCA) of common respiratory viruses and used expert opinion to select likely best estimates and defined potential pandemic years.

We identified ten common respiratory viruses that had tMRCA estimates overlapping with the range of historical mortality data. We selected coincidence metrics that reliably highlighted known historical influenzavirus pandemics as local peaks of combined mortality. We present a list of potential pandemic years that coincide with the estimated origin of one or more seasonal respiratory viruses. While the uncertainty in the tMRCA estimates precludes the unique association of each peak mortality year with a single pathogen, potential pandemic years could be identified. The potential pandemic years identified in our analysis can motivate targeted validation efforts and contribute to a better understanding its emergence.

We would like to sincerely thank James R. Otieno for providing the tMRCA estimates from his paper Origins and Evolution of Seasonal Human Coronaviruses (2021), which significantly contributed to this research at the Division of International Epidemiology and Population Studies, Fogarty International Center, National Institutes of Health, Bethesda, MD 20892, USA.

Detection and genomic characterization of porcine rotavirus H in diarrheic piglets from Hungary

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Rotaviruses (RVs) belong to the Sedoreoviridae family and are major causative agents of acute gastroenteritis in both animals and humans. The genus comprises nine species (A–I), classified based on the VP6 protein. Rotavirus H (RVH) has been detected in humans, pigs, and bats, and increasing reports from swine farms worldwide highlight its epidemiological relevance. However, genomic data on RVH remain limited. This study aimed to investigate the occurrence and genetic characteristics of RVH in diarrheic piglets in Hungary. A total of 77 fecal swab samples were collected from 15 swine farms and analyzed using Nanopore sequencing. RVH was detected in 5 farms and in 22% (17/77) of the samples. Only two samples contained RVH alone, while most occurred in co-infections with other RV species, indicating that mixed infections are common in diarrheic piglets. Complete genome sequences were obtained for two RVH strains, showing P[10]-G18-I3 and P[12]-G18-I3 genotype constellations based on the VP4, VP7, and VP6 genes, and clustered closely with Italian RVH strains. These findings support the high genetic diversity described for porcine RVH and provide the first genomic data on porcine RVH from Hungary. Our results indicate that RVH circulates in Hungarian swine herds predominantly in co-infections, highlighting the potential role of reassortment in RV evolution and underscoring the importance of genomic surveillance to better understand RV epidemiology in pigs.

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Molecular Tracking of the Origin of Vesicular Stomatitis Outbreaks in Ecuador

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The Vesicular Stomatitis Virus (VSV) is a high-impact arbovirus that poses a significant threat to animal health, rural economies, and potentially public health, fitting perfectly within a One Health framework. This study investigates a major 2018 outbreak in Ecuador involving 399 cases across 18 provinces, caused by both New Jersey (VSNJV) and Indiana (VSIV) serotypes. By sequencing the viral phosphoprotein gene and employing Maximum Likelihood phylogenetic trees and haplotype networks, we identified two distinct evolutionary origins: one lineage persisting from a 2004 outbreak and another emerging from a separate 2018 transmission source. Crucially, the analysis reveals divergent transmission dynamics that intersect with environmental and anthropogenic factors. In the Amazon, small, independent outbreaks suggest a sylvatic cycle driven by insect vectors (mosquitoes and sandflies) and wildlife reservoirs (bats and monkeys). Conversely, in the Andean and Coastal regions, the virus spread was primarily driven by livestock movement. Beyond animal welfare, VSV causes severe declines in milk production and weight, devastating the livelihoods of farming communities. Our findings underscore that managing VSV requires more than veterinary intervention; it demands a transdisciplinary One Health approach that integrates entomological surveillance, wildlife ecology, and strict control of animal transit to mitigate the reemergence of this complex zoonotic pathogen.

We thank field technicians, General Coordination of Animal Health, and General Coordination of Laboratories of the Agencia de Regulación y Control Fito y Zoosanitario (AGROCALIDAD) for responding to case notifications in various Ecuadorian provinces, managing animal health programs to raise animal health standards in the country, and managing resources for the development of diagnostic activities.

Equine Flavivirus Infections in Northeastern Hungary: Clinical Insights and Vector-Based Epidemiological Surveillance of West Nile and Tick-Borne Encephalitis Viruses

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Equine infections caused by flaviviruses, particularly West Nile virus (WNV) and tick-borne encephalitis virus (TBEV), are an increasing veterinary and public health concern in Central and Eastern Europe. In Hungary, WNV has been endemic since 2007, causing recurrent outbreaks in humans and horses, while TBEV persists in natural foci in the northeast. We conducted a combined clinical and epidemiological assessment of equine flavivirus infections in Northeastern Hungary, focusing on suspected and confirmed cases serological and vector surveillance. Mosquitoes were trapped using BG-Sentinel CO2-baited traps nearby horse stables at Kulcsárvölgy, Szuhakálló, and Szirmabesenyő, while ticks were manually collected from horses across the region. Specimens were identified to species level and screened for pathogens via PCR. Among 174 horses, TBEV seroprevalence was 3.40% and WNV 4.59%, with no cross-reaction, indicating local circulation. WNV was not detected in mosquitoes, nor TBEV in ticks. Integrating clinical and entomological data highlights the endemic and evolving nature of flavivirus infections. Continuous monitoring, vector control, vaccination, and coordinated One Health surveillance are essential to mitigate emerging arboviral threats.

Doctoral School of Biology and Sport Biology
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Impact of field conditions and long-term freezing on the detectability of West Nile virus and Usutu virus in mosquito samples

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Under the One Health framework, the OH SURVector project established Slovakia's first national monitoring system for mosquitoes and ticks to safeguard public and animal health. This initiative focuses on the early detection of vector-borne pathogens and the strengthening of intersectoral cooperation.

A primary objective involved mosquito monitoring and the detection of West Nile virus (WNV) and Usutu virus (USUV). Mosquitoes were collected at 16 sites across Slovakia using BG-Sentinel 2 traps from June to mid-October. Site selection was based on environmental (habitat, altitude) and epidemiological criteria (host presence, prior virus detection). Mosquito nets were collected twice weekly and subsequently stored at -20°C for 6–8 weeks prior to analysis.

To verify trapping and storage strategy, field conditions were simulated to test the stability of the virus, including temperature cycling (20°C, 38°C, and 20°C over 24h for 4 days). The model demonstrated that USUV remains detectable via RT-qPCR at a 10-4 dilution (initial dose 1.4×107 PFU/ml), maintaining titers of 7.6×102 PFU/ml before freezing and 3.6×103 PFU/ml after two months of freezing at -20°C. These findings, supported by successful WNV and USUV isolation on C6/36 cell line, confirm that the implemented strategy could be sufficient for the isolation of infectious virus particles from field-captured mosquitoes.

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Molecular Screening and Distribution of West Nile and Usutu Viruses in *Culex* Mosquito Populations in Slovakia (2024–2025)

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West Nile virus (WNV) and Usutu virus (USUV) are mosquito-borne zoonotic flaviviruses circulating in Europe. However, Slovakia has lacked systematic vector-based surveillance of these pathogens. To address this, the OHSURVector project launched the first nationwide mosquito screening for WNV and USUV. Mosquitoes were collected at 14 localities: 34,705 specimens in 2024 and 8,814 in 2025. Samples were pooled by locality, date, sex, and species, with a maximum of 50 mosquitoes per pool, and screened for viral RNA by qPCR. Differences in mosquito abundance between years likely reflected differing climatic conditions, with more favourable temperature and precipitation patterns in 2024 contributing to markedly higher mosquito numbers than in 2025. WNV RNA was detected only in 2024, in seven *Culex pipiens* pools from four sites, indicating a spatially limited occurrence; the minimum infection rate (MIR) was 0.20 per 1,000 mosquitoes. In contrast, USUV was detected in 64 pools from 12 sites, suggesting broader circulation. In 2024, 52 USUV-positive pools were identified—50 *Cx. pipiens* and one *Cx. modestus*—while in 2025, 13 positive pools came solely from *Cx. pipiens*. The USUV MIR was 1.5 per 1,000 mosquitoes in 2024 and 1.48 per 1,000 mosquitoes in 2025, despite the substantially lower mosquito abundance in 2025. These results show broader circulation of USUV than WNV in Slovakia and emphasise the value of integrated mosquito surveillance for understanding flavivirus distribution.

This work was funded by the European Union under the project 101132974 - OH SURVector. Views and opinions expressed are however those of the author(s) only and do not necessarily reflect those of the European Union or European Health and Digital Executive Agency (granting authority). Neither the European Union nor the granting authority can be held responsible for them.

Evaluating the Effects of *Prosopis juliflora* on Tick Oviposition and Survival

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Due to environmental issues and resistance brought on by the extensive use of synthetic acaricides, ticks are now major carriers of diseases that harm both people and animals and have detrimental impacts on both human health and the economy. *Prosopis juliflora* and other plant-based extracts offer a useful and environmentally responsible substitute for tick management and control over the long term. Tick samples were collected from camels at several livestock farms located around Qatar in different localities between February 2024 and January 2025. These samples were then molecularly and morphologically identified at the species level. Female *Hyalomma dromedarii* ticks, both engorged and unfed, were exposed to different doses of *Prosopis juliflora* extract using the adult immersion test (AIT) in order to calculate the oviposition inhibition (%) and mortality rates. The effectiveness of the plant extract and its effect on tick survival were statistically examined using R software and the GLM model. Every tested dosage of *P. juliflora* (0.05 mg/mL to 0.5 mg/mL) was tested for its acaricidal effectiveness against *H. dromedarii*. According to the dose-response study, 50% of the ticks could be killed with an effective dosage of 0.05 mg/ml, and the untreated ticks had a 1.72-fold higher chance of surviving than the treated groups. Future research should look at various dosages, identify key bioactive ingredients, and assess the impact of *P. juliflora* throughout the tick life cycle.

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Section 4: When Clinical AMR Meets the Planetary Crisis

Convergence of carbapenemase and hypervirulence-associated genes among *Klebsiella pneumoniae* high risk clones in Hungary

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The hypervirulence-associated (hva) and carbapenemase genes carrying *Klebsiella pneumoniae* strains (hvaCpKp) represent an emerging global public health threat. Our study aimed to comprehensively characterise the genomics of hvaCpKp isolates in Hungary. We investigated 89 aerobactin-positive (iucA–D, iutA), carbapenemase-producing *K. pneumoniae* isolates collected from 15 Hungarian healthcare institutions between January 2022 and April 2024. After short-read sequencing (Illumina) of all isolates, we performed long-read sequencing (Oxford Nanopore MinION) on 32 representative strains for comparative genomic analysis. Most isolates (79/89) belonged to ST147 high-risk clone. Hva genes (rmpA/rmpA2, peg344, shiF) were consistently present and 59 isolates carried chromosomal yersiniabactin loci. Nearly all isolates (87/89) harboured blaNDM-1 carbapenemase gene. During plasmid analysis, hva genes were predominantly located on IncHI1B/IncFIB(Mar) plasmids. Notably, 13 of 32 strains carried hybrid plasmids co-harbouring hva and blaNDM-1 genes. The blaNDM-1 region was linked to IS26 transposase and conserved cassettes on all plasmids. Our study showed that hva and carbapenemase genes were linked to ST147 clone. Our findings suggest an increasing risk of rapid dissemination of these strains across healthcare and potentially environmental settings, and highlight the need for routine monitoring of hva genes and continuous genomic and plasmid-based surveillance within a One Health framework.

The authors express their gratitude to the staff of the National Center for Public Health and Pharmacy, the One Health Institute and Centre for Metagenomics at the University of Debrecen, and to the laboratories that provided the samples.

Bacteriophages against carbapenem resistant *Klebsiella pneumoniae* strains

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Twenty-four carbapenemase producing *Klebsiella pneumoniae* strains collected from an Eastern-Hungarian clinic in 2025 were chosen for genomic epidemiology analysis, and bacteriophages were isolated against these bacteria. Drop agar test was used for cross activity testing to determine the specificity of phages on non-host strains as well as other important nosocomial pathogens. Their stability after a six month-long storage at 4°C, -20°C and -80°C was also analysed by top agar test. Whole genome sequencing of the hosts' genomes was also performed; it confirmed the presence of carbapenemase gene and defined the sequence types (ST) of host bacteria; ST395 was the most frequent.

Ninety-eight bacteriophage isolates were separated; in cross tests phages were not active against other bacterium species, while cross activity was detected in the case of phages against *K. pneumoniae* strains belonging to ST268, ST307, ST395 and ST2674; and a single isolate showed strict ST specificity. Activity of phages was approved after long-term storage.

In conclusion, bacteriophages isolated for *K. pneumoniae* strains demonstrated strict host species specificity, but some phage isolates showed activity against different sequence types of target bacterium species. To determine whether broad spectrum phages or a phage mixture is responsible for the damage of multiple bacterial strains, ultracentrifugation and top agar method will be performed and sequence analysis of the isolated phages is planned.

I would like to thank the One Health Institute and the bacteriophage research group for their assistance during my research.

Genomic and functional evidence for the convergence of virulence and antimicrobial resistance in uropathogenic *Escherichia coli*

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We aimed to assess the clonality, resistance, and virulence characteristics of third-generation cephalosporin-resistant (3GCR) *Escherichia coli* isolated from urine samples collected in hospitals in Baranya County, Hungary. We performed whole-genome sequencing (WGS) in case of 45 isolates, and 15 strains were further analyzed using in vitro functional assays: biofilm formation, siderophore production and cell adhesion, invasion (RT-112 cells).

The 45 sequenced strains belonged to 22 sequence types (STs) and carried 13 different ESBL or AmpC genes associated with 9 transposons located on plasmids or chromosomes. Eleven plasmid clusters were identified and were shared across different STs and hospitals. All isolates carried multiple virulence factors. Hybrid plasmids encoding blaCTX-M-15 together with two siderophore clusters were identified in three isolates, while plasmids carrying three siderophore gene clusters were detected in eight non-clonal strains. Among the 15 functionally characterized isolates, six produced biofilm, all produced siderophores, and nine showed cell adhesion. Three isolates (two ST131 and one ST301) exhibited all studied virulence traits simultaneously.

Both horizontal and vertical dissemination of resistance and virulence genes were observed. Plasmids are significant drivers of resistance and virulence leading to the accumulation of these phenotypes. The suggested convergence of resistance and virulence was also supported by functional assays.

Whole genome sequencing was performed in the Centre of Metagenomics, University of Debrecen, Debrecen, Hungary and in the Hungarian Centre of Genomics and Bioinformatics, Szentágothai Research Center, University of Pécs, Pécs, Hungary
The in vitro functional studies were performed in the Microbial Genome Plasticity section at the Institute of Hygiene, University of Münster in Münster, Germany.
The project was supported by Pannónia exchange program.

Towards the establishment of a harmonized EARS-Env framework within the EU

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The second chapter of EU-Jamrai2 set out the ambitious goal to assess the problem antimicrobial resistance (AMR) also establishing mitigation strategies with cooperative effort from 30 EU member states including 120 partner institutions. The scope of the project spans over several sectors including human health, animal health and environmental health in the context of One Health. As one of the main objectives of the environmental domain, the establishment of a pilot EARS-Env (European AMR surveillance network in the environment) network is expected to provide complementary information alongside the already operational EARS-Net and EARS-Vet systems in the context of One Health. A pilot study is expected later this year based on preliminary prioritization efforts performed by participating institutions. The exercise arched from the definition of clear objectives of the pilot ES system to ensure that adequate information is captured focusing on AMR circulating in the human populations, impact of sewage treatment and risk assessment for the users of bathing waters. The pilot EARS-Env network will use a combined approach of culture-based and quantitative PCR techniques, supplemented with screening by non-targeted sequencing. This tripartite method will also provide evidence-based data for the implementation of the recast Urban Wastewater Treatment Directive (EU, 2024/3019). This work represents the Hungarian aspect of the project and was supported by EU-Jamrai2 (No. 101127787).

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Section 5: Omics, Genomics and Neglected Interfaces

From Genotype to Host Response: A Multiomics Framework for Understanding Rabies Virus Biology in a One Health Context

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Rabies virus (RABV) a zoonotic and neurotropic virus, which causes rabies, has been known to mankind for >4000 years, yet remains neglected. It is responsible for an estimated 59,000 human deaths annually, with the greatest burden in Asia and Africa. Despite its clinical severity, the molecular determinants of RABV pathogenesis and the clade-specific molecular features of RABV remain poorly explored.

I present findings from my PhD. First, we performed whole-genome sequencing of canine RABV isolates from India. We generated the first complete genomes from this region and found Indian strains belong to the Arctic-like-1a lineage and later identified lineage-specific molecular signatures through a systematic analysis of the mutational landscape across all known RABV clades. To enable scalable surveillance in resource-limited settings, we developed a PCR-based clade-typing assay that does not require genome sequencing.

To investigate the implications of these molecular differences for the host, we performed LC-MS/MS-based proteomic profiling of RABV-infected canine brain tissue, identifying widespread dysregulation of pathways involved in neuroinflammation, synaptic signalling, mitochondrial function, and cytoskeletal integrity. These findings reveal the molecular fingerprint of rabies encephalitis in the natural host.

I would like to thank the organisers and acknowledge my lab

Saccharomyces yeasts in our extended microbiome: domestication, adaptation and human colonization

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The yeast *S. cerevisiae* is a domesticated species central to global food systems and widely used as a probiotic, placing it at the interface of human, environmental, and industrial ecosystems. It can be regarded as part of the extended human microbiome, with the capacity for transient colonization and occasional opportunistic pathogenicity. Other *Saccharomyces* species, less domesticated, persist in environmental and traditional fermentation niches, acting as reservoirs of genetic diversity. Many clades are adapted to anthropogenic environments and shaped by extensive admixture driven by human activity. We investigated macro- and microevolutionary patterns in probiotic and human-associated strains using the "Compendium of Saccharomyces" database (>6000 genomes). Phylogenomic and comparative analyses of genome structure variation and mutational spectra were applied to clades containing human isolates to assess the impact of domestication and breeding on adaptation and pathogenic potential. Our results identify multiple industrial clades capable of transient human colonization, highlighting exchange between food and host environments. Domestication-related genomic features strongly influence in-host microevolution, particularly in baking strains. These findings indicate that human-associated *S. cerevisiae* populations are largely composed of domesticated lineages shaped by industrial processes, underscoring the importance of food-associated microbes in One Health.

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Liver Proteome Alterations during Feed Deprivation in Quail: From Anabolism to Energy Conservation

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This study aimed to identify hepatic proteomic differences between ad libitum fed and feed-deprived quail by conducting differential protein abundance analysis, followed by a protein-protein interaction mapping and functional enrichment analysis using STRING to identify key pathways. The study included two groups of adult male quail (n=6). We performed mass spectrometry analysis on quail liver, and each sample had two technical replicates. The Limma test was used to detect differentially abundant proteins (DAPs) between the groups. Out of 524 filtered proteins, 81 DAPs differentiated between the control and feed-deprived birds, comprising 39 upregulated proteins in the feed-deprived group and 42 downregulated proteins. In the feed-deprived group, upregulated DAPs were enriched for the mitochondrial respiratory chain, metabolism of carboxylic acids, and fatty acid beta oxidation, emphasizing the shift in metabolism in the liver for energy production under nutrient scarcity. In contrast, proteins that were downregulated during starvation (abundant in the ad libitum group) were associated with protein metabolic processes and translation, indicating a suppression of ribosomal activity and protein turnover as a mechanism for energy conservation. Overall, starvation causes the liver to shift from anabolic and broad metabolic functions to mitochondrial optimization, lipid and organic acid utilization, and enhanced detoxification during periods of nutrient deprivation in quail.

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Detection of Canine Circovirus in the Hungarian Red Fox Population

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Canine circovirus (CanineCV) was first identified in 2012 in the United States from canine serum samples. In Europe, it was initially detected in Italy and subsequently reported in several countries. Although its exact pathogenesis remains unclear, it has been associated with severe clinical conditions, including fatal hemorrhagic enteritis, diarrhea, vasculitis, and respiratory disease. Beyond domestic dogs, CanineCV has also been detected in wild canids. Isolates from domestic and wild hosts share approximately 80% genomic identity but cluster into two distinct phylogenetic groups. Foxes may represent a potential source of infection for domestic dogs; thus, their investigation can provide insight into viral transmission dynamics. This study aimed to screen Hungarian red fox populations for CanineCV by SYBR Green-based qPCR, characterize circulating strains by melting curve analysis and sequencing, and perform phylogenetic comparisons with reference sequences from GenBank. DNA extracted from 365 brain samples of wild carnivores provided by NÉBIH was analyzed. The virus was detected in 6.84% (25/365) of samples, including four golden jackals. Four complete genomes were obtained, showing 96.03–97% similarity to Hungarian strains detected in 2025. Our findings confirm the ongoing circulation of CanineCV in Hungarian wild canids and contribute to understanding its genetic diversity and evolution.

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Food safety issues in cheese production: the prevalence and survival of *Escherichia coli*

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Enteropathogenic *E. coli* is one of the bacteria responsible for foodborne illnesses associated with cheese consumption. Several outbreaks have been associated with the presence of *E. coli* in different types of cheese worldwide. *E. coli* is the most relevant hygienic indicator of faecal contamination. The survival of bacteria in the cheese-making environment is affected by various factors, including acidification levels, moisture content, salt content, temperature and time during processing and ripening.

In our recent studies, we examined the prevalence of microorganisms that are important from food safety perspective in different types of artisanal and industrial cheese. The most abundant bacterial species were identified on the basis of 16S rDNA sequences. One of the most common bacteria detected was *E. coli*.

In our region, little information is available on the viability of *E. coli* in artisanal cheese. The detection of these bacteria in some cheese samples provides the necessary and relevant support for public health and food safety to determine viability. The survival of *E. coli* and the change in the total aerobic count of three types of cheese were determined by storing them in the refrigerator at 6°C and at room temperature (21°C). The control cheese and the cheese supplemented with rosemary and sea buckthorn were produced in laboratory conditions using a traditional cheese-making process.

The Impact of Chitosan Treatment on Spinach Nutritional Quality and Bacterial Growth

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Fresh leafy vegetables such as spinach typically possess a short postharvest shelf life due to rapid respiration, bacterial growth, and quality deterioration. The use of natural compounds on vegetables to extend their shelf life is being widely investigated. Chitosan is a polysaccharide that can form a semipermeable coating on the surface of plants to delay their respiratory rate and preserve overall quality.

This study investigated the effect of chitosan treatment on spinach compared to a water-washed control, particularly on nutritional parameters such as chlorophyll and total polyphenol content, as well as changes in freshness and color. Furthermore, we tested its effect on bacterial growth. Assessments were performed immediately post-treatment and after three days.

Chitosan treatment significantly reduced the total bacterial count; however, no significant differences were observed between the various concentrations used. No significant improvements were observed in other parameters.

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Natural Weapons Against *Fusarium*: The Antifungal Potential of Medicinal Plants

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Fusarium species are among the most destructive plant pathogenic fungi, causing significant yield losses worldwide and producing harmful mycotoxins that threaten food safety. The increasing resistance to synthetic fungicides and the demand for sustainable agricultural practices have intensified interest in plant-derived antifungal agents. This study investigates the antifungal potential of selected medicinal plant extracts against *Fusarium* spp., integrating both bioactivity assays and transcriptomic analyses.

In vitro antifungal activity was evaluated through growth inhibition assays, spore germination tests, and minimum inhibitory concentration (MIC) determinations. Several extracts demonstrated significant inhibitory effects on mycelial growth and conidial development, indicating strong bioactive potential.

To elucidate the underlying mechanisms of action, transcriptomic profiling was performed on treated *Fusarium* cultures. Differential gene expression analysis revealed substantial modulation of genes involved in cell wall biosynthesis, membrane integrity, oxidative stress response, and secondary metabolism pathways. Notably, the downregulation of key virulence-associated and mycotoxin biosynthesis genes suggests that medicinal plant-derived compounds may not only inhibit fungal growth but also attenuate pathogenicity.

These findings highlight the promise of medicinal plants as natural antifungal agents and provide molecular-level insights into their mechanisms of action

Genital schistosomiasis, a neglected sexual reproductive and health crisis in men, women and girls: challenges, progress, and path towards their elimination in Kenya.

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Pathology of Urogenital schistosomiasis is associated with the immunological response to *Schistosoma haematobium* eggs lodged in the pelvic region. Genital schistosomiasis is rarely routinely diagnosed in the field after a positive urine test. Consequently, it contributes to high prevalence in endemic regions. Patients presenting with symptoms such as blood in urine, genital discharge, and pain during intercourse or ejaculation are frequently misdiagnosed and treated for sexually transmitted infections, resulting in incorrect diagnosis and management.

Lack of awareness, topic missing in curriculum, limited access to safe water, sanitation facilities, and colposcopy services in endemic areas, hinder elimination efforts.

There are efforts in Kenya to integrate female genital schistosomiasis in sexual and reproductive health services, through community awareness, FGS health literacy, and training healthcare professionals. Guidelines in addressing genital schistomiasis in men and boys are lacking in other endemic parts where they are exposed while engaging in economic and recreational activities.

Therefore, an inclusive intervention strategy is required to achieve the World Health Organisation's 2030 goal of eliminating schistosomiasis.

Keywords: Genital schistosomiasis, neglected tropical disease, sexual and reproductive health Kenya

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