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Conference

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1-2 July 2026 | Online

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The 2026 International Online Conference on Tropical Medicine and Infectious Disease

1-2 July 2026 | Online



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Welcome from the Chair

Dear Colleagues and Participants,

It is with great pleasure that I welcome you to the **2026 International Online Conference on Tropical Medicine and Infectious Disease (CTMID 2026)**, which will be held online on 1–2 July 2026.

Organized By **MDPI** and the ***Tropical Medicine and Infectious Disease*** journal, this conference brings together leading researchers, public health professionals, clinicians, and policy-makers from around the world to share advances and challenges in the field of tropical medicine and infectious disease. Our virtual format ensures broad accessibility, allowing global participation without the need for travel.

CTMID 2026 provides a valuable platform to exchange cutting-edge knowledge and foster collaboration in tackling some of the world's most pressing health issues. With sessions dedicated to **Vector-Borne Diseases, One Health and Zoonotic Diseases, Neglected Tropical Diseases, and Antimicrobial Resistance**, the conference reflects the urgent need for interdisciplinary approaches and global cooperation in combating infectious threats.

In addition to engaging presentations and live discussions, we are pleased to offer exciting **publication opportunities**. All accepted abstracts will be published in the **conference report in *Medical Sciences Forum***. Outstanding contributions from each session will be eligible for **conference awards**. Moreover, instead of limiting presentations to a live poster session, all participants have the opportunity to **upload and display their research in the form of a poster via the poster gallery on the conference website**. Therefore, all participants with poster submissions for the poster gallery are now eligible for awards!

I encourage all participants to make the most of this opportunity to connect with peers, contribute to meaningful dialogue, and inspire future research directions.

On behalf of the organizing committee, thank you for your participation and support. I look forward to your valuable contributions and wish you a fruitful and impactful conference.



Prof. Dr. John Freaan
Conference Chair

Pathologist, Parasitology
Reference Lab, Centre for
Emerging Zoonotic and Parasitic
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Tropical Medicine and Infectious Disease

Tropical Medicine and Infectious Disease (ISSN 2414-6366) publishes authoritative and original articles, critical and systematic reviews, editorials, perspectives, short communications, commentaries, book reviews, letters to the editor and Special Issues on all aspects of tropical medicine and infectious disease. Our aim is to encourage scientists to publish their experimental and theoretical results in as much detail as possible. There is no restriction on the maximum length of the papers. The full experimental details must be provided so that the results can be reproduced. There is, in addition, a unique feature of this journal:

We consider studies of high scientific quality that show meaningful but negative results. While there are many journals that focus on tropical medicine and infectious disease studies, none of them actively accept negative results. As a result, most negative data do not end up in the public domain, even if the data were meaningfully negative and the study was well-designed and executed. By accepting such negative results, our journal encourages scientists to share these data, to avoid unnecessary duplication by others.

Impact Factor: 3.1 (2025); **5-Year Impact Factor:** 3.2 (2025)

Keynote Speakers



Professor Cordia Chu

Centre for Environment and
Population Health, Griffith
School of Environment, Griffith
University,
Brisbane, Australia



Prof. Dr. John Russell Stothard

Department of Tropical Disease
Biology, Liverpool School of
Tropical Medicine,
Liverpool, United Kingdom

Invited Speakers



Dr. Gyanendra Gongal

Senior Public Health Officer,
World Health Emergency
Programme, WHO Regional
Office for South-East Asia,
New Delhi, India



Dr. Helen Mayfield

School of Earth and
Environmental Sciences, Faculty
of Science, University of
Queensland, Brisbane, Australia



Dr. Marco Antonio Natal Vigilato

Pan American Health
Organization, Washington, D.C.,
USA



Dr. Matteo Riccò

AUSL-IRCCS di Reggio Emilia,
Servizio di Prevenzione e
Sicurezza Negli Ambienti di
Lavoro (SPSAL), Local Health
Unit of Reggio Emilia,
Reggio Emilia, Italy



Dr. Tina Joshi

School of Medicine, University of
Limerick, Limerick, Ireland



Dr. Veerle Dermaux Msimang

Centre for Emerging Zoonotic
and Parasitic Diseases, National
Institute for Communicable
Diseases, Johannesburg,
South Africa



Dr. Wendy Page

Australasian College of Tropical
Medicine, Brisbane, QLD,
Australia



Prof. Dr. Alfonso Rodríguez-Morales

Faculty of Health Sciences,
Universidad Científica del Sur,
Lima, Peru



Prof. Dr. Tjandra Yoga Aditama

Director, Graduate School,
YARSI University,
Jakarta, Indonesia



Prof. Dr. Toshio Hattori

Emeritus Professor, International
Research Institute of Disaster
Science, Tohoku University,
Miyagi, Japan

Program Overview

	Day 1	Day 2
Morning	Session 1: Vector-Borne Diseases	Session 2: One Health-Zoonotic Diseases
Afternoon	Session 3: Neglected Tropical Disease	Session 4: Antimicrobial Resistance

CTMID 2026 Program

1 July 2026 (Wednesday)

Session 1: Vector - Borne Diseases

Time: 9:00 (CEST, Basel) | 03:00 (EST, New York) | 15:00 (CST Asia, Beijing)

CEST	Speaker	Title
09:00–09:10	<i>Welcome from the Event Chair Prof. Dr. John Frean</i>	
09:10–09:20	<i>Welcome from the Session Chair Prof. Dr. Basil Brooke</i>	
09:20–09:40	Prof. Dr. Alfonso J. Rodríguez-Morales Invited Speaker	To be announced.
09:40–10:00	Prof. Dr. Tashio Hattori Invited Speaker	Understanding Resilience through Biomarkers in Disaster-Related and Tropical Infectious Diseases
10:00–10:20	Dr. Matteo Riccò Invited Speaker	To be announced.
10:20–10:35	Prabir Kumar Sen Selected Oral Speaker	Multisectoral Collaboration and Its Impact on Reducing Japanese Encephalitis (JE)/Acute Encephalitis Syndrome (AES) in India: An Integrated Approach to Global Health Security
10:35–10:50	Ayesha Aswat Selected Oral Speaker	Male Reproductive Transcript Silencing Reduces Fitness in <i>Anopheles funestus</i>
10:50–11:05	Dr. Bhavya H P Selected Oral Speaker	Molecular Characterization and Serotype Distribution of Dengue Virus in Bengaluru Rural
11:05–11:20	Cintia Carolina Palavecino Selected Oral Speaker	Spatial Coupling Between <i>Aedes Aegypti</i> Life Stages and Urban Land Surface Temperature in A Temperate Argentine City
11:20–11:35	Marion Risse Selected Oral Speaker	Identity, Not Sex or Menstrual Cycle, Drives Human Body Odor and Attractiveness to <i>Anopheles Gambiae</i> Mosquitoes
11:35–11:50	Shune V. Oliver Selected Oral Speaker	The Effect of Insecticide Exposure on The Gut Microbial Composition of <i>Anopheles arabiensis</i> (Diptera: Culicidae) from South Africa.
11:50–14:00	BREAK	

Session 3: Neglected Tropical Diseases

Time: 14:00 (CEST, Basel) | 08:00 (EST, New York) | 20:00 (CST Asia, Beijing)

CEST	Speaker	Title
14:00–14:10	<i>Welcome from the Session Chair Prof. Archie Clements</i>	
14:10–14:40	Prof. Dr. Russell Strothard Keynote Speaker	The Changing Epidemiology of Schistosomiasis in Africa: Highlighting Hybrid, Zoonotic and Mixed Species Infections in Malawi
14:40–15:00	Dr. Helen Mayfield Invited speaker	Comparing Human and Vector-Based Indicators of Lymphatic Filariasis Transmission in Samoa
15:00–15:20	Dr. Wendy Page Invited Speaker	Strongyloidiasis - A Neglected, Preventable, Chronic Infectious Disease?
15:20–15:40	Dr. Veerle Dermaux Msimang Invited Speaker	Human Schistosomiasis in South Africa: Laboratory-Based Prevalence, 2019-2024
15:40–15:55	Oladunni Nimota Adekunle Selected Oral Speaker	Hidden in the Dirt: The Persistent Presence and Environmental Drivers of Soil-Transmitted Helminths in parts of Ogun State, Southwestern Nigeria
15:55–16:10	Imrana Muhammad Arzika Selected Oral Speaker	Prevalence of Urinary Schistosomiasis Among School-Age Children In Goronyo Local Government Area, Sokoto State, Nigeria

16:10-16:25	Shivani Sharma Selected Oral Speaker	Field Assessment of Lymphatic Filariasis, Transmission Dynamics, and Intervention Efficacy in Varanasi District (2019-2025).
16:25-16:40	Elizabeth Oluwatoyin Ibikunle Selected Oral Speaker	Prevalence and Intensity of Urogenital Schistosomiasis Among School Children in Spill Way Community of Ikere George Dam, Iseyin LGA, Oyo State, Nigeria.

2 July 2026 (Thursday)**Session 2: One Health–Zoonotic Diseases****Time: 9:00 (CEST, Basel) | 03:00 (EST, New York) | 15:00 (CST Asia, Beijing)**

CEST	Speaker	Title
09:00–09:10	Welcome from the Session Chair Dr. Noore Alam	
09:10–09:40	Prof. Cordia Chu Keynote Speaker	One Health Action for Global Health Security
09:40–10:00	Prof. Dr. Tjandra Yoga Aditama Invited Speaker	Zoonotic Diseases in Indonesia
10:00–10:20	Dr. Gyanendra Gongal Invited Speaker	Hantavirus: What We Know and What We Do Not Know?
10:20–10:35	Maksim Rakovich Selected Oral Speaker	Climate-Driven Environmental Change and Zoonotic Spillover Risk: Implications for One Health Governance
10:35–10:50	Md Rezaul Hasan Selected Oral Speaker	Operationalising One Health for Dengue Prevention: Pathways Toward an Integrated Early Warning System in Bangladesh
10:50–11:05	Onah Isegbe Emmanuel Selected Oral Speaker	Parasitic Contamination of Soil Samples in Primary School Playgrounds in Jos North and South Local Government Areas, Plateau State
11:05–11:20	Rakiliya Sikataril Saril Selected Oral Speaker	Serological Evidence of Bat-Borne and Shrew-Borne Hantavirus Infections in Humans: A Comparative Study from Thailand, Sri Lanka, and Zambia
11:20–11:35	Uttama Acharjee Selected Oral Speaker	Broad-Spectrum Antiviral Activity of 3CLpro Inhibitors against Bat Coronaviruses Utilizing ACE2 or DPP4 Receptors
11:35–11:50	Dr. Marco Antonio Natal Vigilato Invited Speaker	To be announced.
11:50–14:00	BREAK	

Session 4: Antimicrobial Resistance**Time: 14:00 (CEST, Basel) | 08:00 (EST, New York) | 20:00 (CST Asia, Beijing)**

CEST	Speaker	Title
14:00–14:10	Welcome from the Session Chair Dr. Constantinos Tsioutsis & Dr. Josette Raymond	
14:10–14:30	Dr. Tina Joshi Invited Speaker	Antimicrobial Resistance: From Microbial Evolution to Global Health Threat
14:30–14:45	Suryanti Suryanti Selected Oral Speaker	Digital Strategies to Improve Tuberculosis Case Notification in Private Healthcare Facilities: Implications for Antimicrobial Resistance Surveillance in Low- and Middle-Income Countries
14:45–15:00	Shreshtha Singh Selected Oral Speaker	Pathotype Diversity and High ESBL Gene Carriage Among Diarrheagenic Escherichia coli Isolates From Pediatric Diarrhea in North India
15:00–15:15	Aaftab G Pendari Selected Oral Speaker	Longitudinal Impact of Antibigram-Guided Antimicrobial Stewardship on Resistance Patterns and Multidrug-Resistant Organisms in a South Indian Tertiary Care Hospital
15:15–15:30	Prince Kyere Dwaah Selected Oral Speaker	Knowledge, Attitudes, and Practices Related to Antimicrobial Resistance Across the One Health Sector in Ghana: A Cross-Sectional Study
15:30–15:45	Lotgarda Tayao Selected Oral Speaker	Bridging the Diagnostic Gap: Evaluating the Concordance of Genotypic and Phenotypic AMR Detection in a Philippine Tropical Disease Center
15:45–16:00	Jérôme Munyangi Wa Nkola Selected Oral Speaker	Pilot Molecular Investigation of Artemisinin Resistance Markers in Artemisia annua Users for Malaria Treatment/Prevention: First African Follow-Up vs. ACT Controls in DRC

16:00–16:15	Carlos Domínguez-Vargas Selected Oral Speaker	Epidemiology of CTX-M Extended-Spectrum β -Lactamases in Escherichia coli Clinical Isolates in Mexico: A Systematic Review
16:15–16:30	Oumar Abakar Mahamed Selected Oral Speaker	Prevalence and Determinants of Drug-Resistant Pulmonary Tuberculosis in the MENA Region: A Systematic Review and Meta-analysis

Session 1. Vector-Borne Diseases

sciforum-175666: Climate-Driven Expansion of *Aedes aegypti* and Its Impact on the Changing Epidemiology of Dengue Fever

Maria Crina Isac

Department of Biology, Faculty of Biology, Alexandru Ioan Cuza University of Iași, Iași, 700506, Romania

Climate change has emerged as a major determinant of vector-borne disease dynamics worldwide. Rising temperatures, altered precipitation patterns, and increasing frequency of extreme weather events have significantly influenced the geographic distribution and seasonal activity of *Aedes aegypti*, the primary vector of dengue fever. This systematic review synthesizes global evidence on the relationship between climate variability and the spatial expansion of *A. aegypti*, and its impact on dengue epidemiology. A structured literature search was conducted in PubMed, Scopus, and Web of Science for studies published between 2010 and 2026, including epidemiological analyses, climate-model projections, entomological surveys, and outbreak reports examining associations between climatic factors and vector distribution or disease incidence. Findings demonstrate a poleward and altitudinal expansion of *A. aegypti*, with the vector now reported at altitudes of 1000–1500 m and in over 50 countries previously considered non-endemic. Increased mean temperatures and extended warm seasons were associated with higher vector survival, shorter viral incubation periods, and prolonged transmission seasons. Globally, dengue infections affect approximately 390 million people annually, of which ~96 million are symptomatic, and recent data show a 30–50% increase in reported cases in Asia and Latin America over the past decade. Climate variability has contributed to dengue emergence in temperate zones and intensification of outbreaks in endemic regions. Predictive models suggest that by 2050, the population at risk could increase by ~1.2 billion worldwide. These results highlight that climate-driven expansion of *Aedes aegypti* is reshaping dengue epidemiology, increasing both geographic spread and transmission intensity. Strengthened climate-informed surveillance, integrated vector management, and adaptive public health strategies are urgently needed to mitigate the growing global burden of dengue.



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sciforum-177411: Malaria Epidemiology in Forest-Fringe Villages of Block Korchi, District Gadchiroli, India

Dr. Lankesh Yashwant Bhaisare ^{1,*}, Dr. Vinod Vishnuji Madavi ¹ and Dr. Desh Deepak Chaudhary ²

¹ Block Public Health Unit, Taluka Health Office, Block Korchi, District Gadchiroli, Maharashtra, India

² Department of Zoology, Indira Gandhi National Tribal University, Amarkantak, Madhya Pradesh, India

Malaria is one of the most prevalent infectious parasitic diseases worldwide, placing well over 216 million people at risk of infection. India contributes a substantial share of malaria cases in Southeast Asia, particularly in forested and tribal regions where ecological conditions favor vector breeding and transmission. Gadchiroli district in eastern Maharashtra is predominantly forest-covered and inhabited largely by tribal communities living near forest ecosystems, making it highly vulnerable to malaria transmission. Among the 12 blocks in the *district*, Korchi block is considered one of the most malaria-prone areas. The present study analyzed malaria surveillance data from two Primary Health Centers (PHCs), Kotgul and Botekasa, in the Korchi block to assess seasonal, demographic, parasitological, and spatial patterns of malaria incidence. A total of 443 cases were reported at Kotgul PHC and 130 cases at Botekasa PHC. Malaria incidence remained low during the pre-monsoon months (January–May) but increased sharply with the onset of the monsoon, peaking in July and declining gradually from August to December. Individuals aged ≥ 15 years accounted for the majority of cases, likely due to occupational exposure related to agriculture and forest activities. *Plasmodium falciparum* was the predominant parasite species. Spatial analysis revealed focal transmission with several hotspot villages contributing disproportionately to the disease burden. These findings highlight the importance of pre-monsoon vector control, strengthened surveillance, and hotspot-based interventions for effective malaria control.



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sciforum-175491: Predicting the Future Distribution of Japanese Encephalitis Vectors in India Using MaxEnt Species Distribution Modeling

Aditya Shankar Katak

School of Biodiversity, One Health and Veterinary Medicine, Department of Zoology, University of Glasgow, Glasgow, Scotland, United Kingdom

Introduction: Japanese encephalitis (JE) remains a major public health concern in India, particularly in rural and peri-urban regions where environmental conditions favor vector proliferation. The primary vectors, especially *Culex* species, are highly sensitive to climatic and land-use changes. Predicting future vector distribution under changing environmental scenarios is critical for proactive surveillance and disease prevention. This study proposes the use of a species distribution modeling approach to map the current and future distribution of Japanese encephalitis vectors in India and to estimate potential vector abundance and associated disease risk by 2030. **Methods:** Occurrence records of confirmed JE mosquito vectors, including *Culex tritaeniorhynchus*, will be compiled from entomological surveys, literature reviews, and published databases across India. Environmental predictors such as temperature, precipitation, vegetation indices, elevation, and land-use variables will be incorporated. Species distribution models will be developed using MaxEnt, which applies a maximum entropy algorithm to estimate habitat suitability from presence-only data. Future projections for 2030 will be generated using climate scenarios derived from global climate models (GCMs). Habitat suitability outputs will be integrated with human population density and historical case data to model potential changes in vector abundance and projected JE risk. **Results:** The model is expected to identify high-suitability zones in endemic states and predict geographic expansion or shifts in vector distribution by 2030. Areas with increasing climatic suitability may correspond to higher projected vector abundance and elevated JE transmission risk. **Conclusion:** MaxEnt-based predictive modeling offers a robust tool for forecasting JE vector distribution and future disease risk. Integrating ecological suitability with epidemiological data can support targeted vector control, vaccination planning, and early warning systems for Japanese encephalitis in India.



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sciforum-175674: Spatial coupling between *Aedes aegypti* life stages and urban land surface temperature in a temperate Argentine city

Cintia Carolina Palavecino ^{1,2,*}, **Santiago Tomás Rodríguez** ^{1,2}, **Julio Alberto Galarza** ¹, **Luis Adrian Diaz** ^{2,3} and **Maria Soledad López** ^{1,2}

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² National Scientific and Technical Research Council (CONICET), Buenos Aires, C1033AAJ, Argentina

³ Institute of Virology "Dr. J. M. Vanella", National University of Cordoba, Cordoba, X5000, Argentina

Understanding how *Aedes aegypti* eggs and gravid female are spatially structured, and how they relate to urban temperature heterogeneity, is essential in improving vector surveillance. This study analyzed the spatial distribution patterns of egg and gravid female abundance of *Ae. aegypti* in the city of Reconquista (Argentina) during the 2024–2025 epidemiological season and assessed spatial associations between life stages and with land surface temperature (LST). Data obtained between December 2024 and March 2025 during monitoring using ovitraps and gravid *Aedes* traps were analyzed. The mean abundance of eggs (EG) and gravid female (GF) (adjusted by active devices) was calculated. Spatial autocorrelation and the association between both stages were assessed using global univariate and bivariate Moran's I statistics. Mean abundance was aggregated into a 600 m hexagonal grid, and bivariate LISA was used to identify local spatial clusters. Both EG and GF exhibited significant positive spatial autocorrelation, with clusters of high reproductive activity concentrated in specific sectors of the city. There was a significant positive global spatial association between EG abundance and GF female abundance. However, local LISA analysis showed that this association was spatially heterogeneous, with most areas not exhibiting significant local coupling. These results indicate that egg and gravid female distributions are spatially coupled at the urban scale, although this relationship is spatially heterogeneous and restricted to specific sectors of the city. We found a positive spatial association between EG and GF with LST, with nearly half of the study area exhibiting concordant High EG/GF–High LST or Low EG/GF–Low LST patterns. EG and GF abundance show clear spatial structuring across the evaluated life stages. Urban LST appears spatially coupled with EG and GF abundance, supporting a strong thermo-biological linkage in the urban landscape.



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sciforum-175667: The effects of low heavy metal concentrations of in *Anopheles arabiensis* (Diptera: Culicidae)

Caitlin de Winnaar ^{1,*} and Shüné Oliver ^{1,2}

¹ Wits Research Institute for Malaria, Faculty of Health Sciences, University of the Witwatersrand, Johannesburg, South Africa

² Centre for Emerging Zoonotic & Parasitic Diseases, National Institute for Communicable Diseases, a Division of the National Health Laboratory Service, Johannesburg, South Africa

Anopheles arabiensis is a major malaria vector in Southern Africa. This vector displays plastic behaviour in terms of feeding and resting behaviour. It is also one of the members of the *An. gambiae* complex adapting to breeding in polluted waters. Heavy metal pollution is a common effect of anthropogenic activities. This is prevalent in both rural and urban areas. While heavy metals are toxic in high concentrations, some serve as critical micronutrients. These include iron, copper, nickel, zinc and cobalt. Zinc is essential for enzyme activity and cobalt is involved in vitamin synthesis. These metals contribute to insect development, reproduction, and immunity, often interacting with the insect's microbiota in a complex manner. There can be a variety of concentrations of these pollutants in both urban and rural bodies. This study aimed to determine whether zinc and cobalt could have positive effects at lower concentration on the major malaria vector *Anopheles arabiensis*. Sublethal concentrations were assessed for zinc and cobalt for the insecticide susceptible *An. arabiensis* strain SENN and the insecticide resistant strain SENN-DDT. Although these strains did not differ significantly in their tolerance at first instar, these low doses did become cumulatively toxic. Low doses of zinc and cobalt had differential effects on the two strains. Zinc had a positive effect on the development of SENN, while cobalt has a positive effect on the larval development of SENN-DDT. Similarly, these low doses increased longevity in both strains. These larval exposures also had variable effects on the oxidative stress response and gut microbial composition and diversity of both strains. KEGG analysis also indicated a variability between strains in response to the metal exposure. These findings highlight that heavy metal exposure is not necessarily negative, but dependent on concentration. This has implications for the potential expansion of *An. arabiensis* into urban areas.



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sciforum-178224: Acute-on-Chronic Liver Failure Triggered by Dengue Infection in a Patient with Probable Autoimmune Hepatitis

Maylin Abigail Matienzo Rafael ¹, Orlando Paul Quishpe Guafía ², Michelle Denise Brito Gomez ³, Beatriz Chumacero Llanquipacha ⁴ and Paolo Augusto Romero Merino ^{5,*}

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This clinical case report describes the complex management of autoimmune hepatitis (AIH), a chronic inflammatory liver disease of idiopathic origin that can progress to cirrhosis or liver failure if not diagnosed and treated promptly. In tropical regions, infections such as dengue may worsen the course of liver diseases. We report the case of a 48-year-old woman with a history of mammary tuberculosis, type 2 diabetes, confirmed dengue infection, fever, and intermittent use of herbal infusions. She presented with dark urine, acholia, jaundice, and right upper quadrant pain lasting 17 days. Laboratory tests showed elevated liver enzymes, coagulation abnormalities, positive antinuclear antibodies (ANA), and abdominal imaging findings consistent with chronic liver disease and cirrhosis. Despite corticosteroid treatment, she progressed to fulminant hepatic failure and passed away. AIH was considered the main contributing factor, given its higher prevalence in women and its interaction with triggers such as viral infections. Dengue, particularly serotypes DENV1 and DENV3, has high liver tropism and may cause anything from asymptomatic transaminase elevation to fulminant liver failure. The diagnosis of AIH relies on serology and clinical criteria; in this case, only ANA with a speckled pattern was detected, and specific autoantibodies like anti-LC1 could not be tested due to resource limitations. Initial treatment was based on corticosteroids. An integrated diagnostic approach, including liver biopsy, is essential, as is health education to raise awareness of AIH as a potential cause of liver failure in patients with recent viral infections.



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sciforum-175593: Clinical Phenotypes, Temporal Dynamics, and Early Cardiac Risk in Orally Transmitted Acute Chagas Disease: A Longitudinal Outbreak Cohort from Colombia

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Introduction

Orally transmitted acute Chagas disease has emerged in Latin America as a severe outbreak-associated presentation characterized by high parasite inoculum, systemic inflammation, and frequent early cardiac involvement. However, longitudinal evidence describing clinical phenotypes, temporal progression, and predictors of early cardiac risk remains limited. This study aimed to characterize phenotype-defined trajectories and identify determinants of severe cardiac involvement in outbreak-associated acute Chagas disease in Colombia.

Methods

This longitudinal cohort study included 104 patients diagnosed with orally transmitted acute *Trypanosoma cruzi* infection between 2000 and 2023. Patients were classified into predefined clinical phenotypes based on systemic severity and cardiac involvement. Temporal intervals from symptom onset to diagnosis and treatment initiation were measured. Serial electrocardiography was performed during the acute phase and at approximately 6 and 12 months. Multivariable regression models evaluated predictors of severe cardiac phenotype and intensive care admission.

Results

Three phenotypes were identified: mild systemic (28%), inflammatory non-cardiac (29%), and severe cardiac (43%). Acute myocarditis occurred in 43% of patients and electrocardiographic abnormalities in 63%. The hospitalization rate reached 82% among severe cardiac cases, and intensive care admission occurred exclusively in this group (18%). Early mortality was 2.9%, confined to fulminant myocarditis. Diagnostic delay exceeding 10 days independently predicted severe cardiac phenotype (adjusted OR 2.4; 95% CI 1.1–5.3). At 12 months, electrocardiographic abnormalities were resolved in 67% of affected individuals, while 33% had persistent alterations, predominantly among severe cardiac phenotypes.

Conclusions

Orally transmitted acute Chagas disease follows distinct phenotype-defined trajectories with markedly different early cardiac risks and recovery patterns. Severe cardiac involvement identifies a high-risk clinical course. Early diagnosis and structured cardiac follow-up are essential to reduce morbidity in outbreak settings.



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sciforum-178165: Clinical Spectrum and Healthcare Burden of Autochthonous Neuroinvasive West Nile Virus: A Six-Case Series from a Tertiary Center in Western Romania (2024–2026)

Ana Maria Mihai ^{1,2,*} and Florina Lucaciu ^{1,2}

¹ The Infectious Diseases Department, “Victor Babes” University of Medicine and Pharmacy, Timisoara, Romania

² “Victor Babes” Infectious Diseases Hospital, Timisoara, Romania

Introduction: Western Romania, the Banat region, has emerged a significant endemic hub for West Nile Virus (WNV). The ecosystem, characterized by hot, humid summers and extensive river basins, provides a high-receptive environment for the *Culex* mosquito vector. As global thermal anomalies increase, the transmission window in these latitudes is expanding. This study analyzes the clinical trajectory and healthcare resource utilization of six confirmed cases, emphasizing the risk posed by shifting ecological dynamics in non-tropical region.

Methods: We performed a retrospective clinical audit of six laboratory-confirmed WNV patients admitted between October 2024–February 2026. Diagnosis was established via ELISA detection of WNV-specific IgM in serum and cerebrospinal fluid (CSF). Analysis focused on clinical phenotyping, therapeutic interventions and hospitalization duration.

Results: The cohort (median age: 57.5 years; 1:1 sex ratio) demonstrated a high prevalence of neuroinvasive syndromes (66.7%), specifically meningoencephalitis. All cases were autochthonous, with no recent history of travel, confirming active regional circulation. Clinical severity was high: 50% of patients required Intensive Care Unit admission and mechanical ventilation. Advanced interventions, including TPE and intravenous immunoglobulin were utilized to manage progressive neurological decline. The healthcare burden was characterized by extensively prolonged hospitalizations, with a median LOS of 38.5 days (range: 10–69 days). The case fatality rate was 16.7% (n=1), associated with multiorgan failure, while surviving WNND patients exhibited significant neurological sequelae.

Conclusions: Our series underscores the severe clinical impact of endemic WNV in Western Romania, characterized by high ICU utilization and prolonged recovery periods. The identification of cases outside the traditional summer window suggests shifting vector dynamics. Early clinical suspicion and a multimodal therapeutic approach are essential for managing autochthonous neuroinvasive disease in emerging European hotspots.



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sciforum-175731: Diversity and Insecticide Susceptibility of *Anopheles* Mosquitoes in Bushbuckridge, a Residual Malaria Transmission Setting in South Africa

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Introduction:

Bushbuckridge subdistrict, located in the northeastern lowveld of South Africa, lies within the country's malaria-endemic belt and borders Kruger National Park, as well as being near Mozambique and Eswatini. Despite significant progress toward malaria elimination, the area remains vulnerable to residual and cross-border transmission. Understanding local *Anopheles* vector dynamics and insecticide susceptibility is therefore essential for sustaining malaria control. This study assessed *Anopheles* species diversity and insecticide susceptibility to inform entomological surveillance priorities aligned with the WHO Entomological Surveillance Planning Tool (ESPT).

Methods:

Larval *Anopheles* mosquitoes were collected from natural habitats between June 2022 and April 2024 and reared to adulthood. Adult males and females underwent WHO tube bioassays with deltamethrin (0.05%), DDT (4%), and pirimiphos-methyl (0.25%). Species were identified using morphological keys and PCR assays.

Results:

A total of 4454 adults emerged (45.1% males, 54.9% females), representing 18 taxa, including primary, secondary, and non-vector species, highlighting ecological complexity. *Anopheles pretoriensis* was most abundant (33.4%), followed by *An. quadriannulatus* (20.7%) and *An. rufipes* (20.0%). The primary malaria vector *An. arabiensis* represented 7.1%, demonstrating its persistence in residual transmission areas and the need for targeted control. Two specimens indicated potential hybridisation between *An. arabiensis* and *An. quadriannulatus*. PCR identification failed in 3% of *An. gambiae* complex and 16% of *An. funestus* group specimens. Bioassays showed high susceptibility overall, but *An. funestus* group males exposed to DDT had 94.6% mortality, suggesting possible resistance.

Conclusions:

This study highlights a diverse *Anopheles* community in a residual transmission setting. While susceptibility remains high, emerging resistance and hybridisation underscore the need for continued species-specific, ESPT-informed surveillance to guide adaptive malaria vector control strategies.



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sciforum-177334: Ecological Aspects of Anophelines, Malaria Vectors, in Endemic Areas of Santo Antônio do Içá, Upper Solimões River – Amazonas

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Introduction

Malaria remains a public health problem in the Brazilian Amazon. Understanding the spatiotemporal dynamics of vectors is essential for identifying areas at higher risk of transmission. This study evaluated ecological aspects of anopheline populations in two endemic communities in the municipality of Santo Antônio do Içá, Amazonas.

Methods

The study was conducted in the communities of Vila Alterosa Juí (Juí) and Vila Pinheiro Palestina do Juí (Pinheiro). Entomological collections were carried out in 2025 using protected human landing catches (PHLC) in intra- and peridomiliary environments. The total sampling effort was 720 hours of collection. Indicators were analyzed, including abundance, human biting rate (HBR), and hematophagic activity, as well as their relationship with environmental variables and local epidemiological data.

Results

A total of 13,070 mosquitoes of the genus *Anopheles* were collected, with predominance of *Anopheles darlingi* (99.97%). Heterogeneity between communities was observed despite the short geographic distance. The highest mosquito abundance was recorded in Pinheiro, whereas Juí showed lower and more stable densities during the collections. The mean human biting rate was 18.15 mosquitoes/person-hour, reaching values above 28 mosquitoes/person-hour in the peridomile of Pinheiro. Hematophagic activity showed a distinct pattern between the localities. In Pinheiro, a bimodal pattern was observed, with peaks during the early evening and around midnight, whereas in Juí the activity was more homogeneous.

Conclusions

The results highlight spatial heterogeneity in vector abundance and biting intensity between nearby communities, reinforcing the focal nature of malaria transmission in the region. The predominance of *Anopheles darlingi* and the pattern of hematophagic activity indicate critical periods of human exposure. This study helps reduce knowledge gaps on vector ecology in the Upper Solimões and provides support for strengthening entomological surveillance and guiding control strategies adapted to Amazonian communities.



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sciforum-155886: Evaluation of a novel RT-PCR test for *Plasmodium falciparum* detection

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Abstract

The effort to eliminate malaria is hampered not only by the lack of effective drugs, but also by the lack of sensitive diagnostic tools to detect infections with low parasite density. As a result, more sensitive and specific high-throughput molecular diagnostic approaches are needed for accurate malaria diagnosis in order to destroy potential *Plasmodium* reservoirs.

In the present study, the performance of the EXP1 based RT-PCR assay was evaluated for the detection of *Plasmodium falciparum* infection. After obtaining ethical clearance N° 2018/09/1104/CE/CNERSH/SP from the Research Ethics Committee for Human health and Authorization of Academic Research N°810/ARA/JO5-02/SP from the Divisional officer of Esse subdivision, 134 Samples were taken in three government schools at Esse from children aged between five and fifteen suspected of having malaria for the population screening, and a parasite culture at the Malaria Research Unit of Centre Pasteur of Cameroon for analytical testing.

The detection limit of the test RT-PCR in terms of Concentration and in terms of parasitaemia is 1415×10^{-7} ng and 0.0012 parasites/ μ l respectively. For the PCR multiplex, the limit of detection in terms of concentration is 1815×10^{-6} ng and in terms of parasitaemia 1.2 parasites/ μ l. *Plasmodium falciparum* was detected in 125 individuals (93.28%) by RT-PCR and in 122 individuals (91.04%) by PCR multiplex. In comparison to the PCR multiplex test, the RT-PCR test has a sensitivity of 90.35%, a specificity of 5.00%, a Positive Predictive Value of 84.43% and a Negative Predictive Value of 8.33%.

These results demonstrate the importance of using the EXP1 based RT-PCR assay as a tool for the rapid diagnosis and early detection of malaria. The test uses primers specific to *Plasmodium falciparum*. It is reliable, simple, rapid and highly sensitive. It can be used on the field in malaria-endemic areas with limited resources.



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sciforum-173452: Identity, not sex or menstrual cycle, drives human body odor and attractiveness to *Anopheles gambiae* mosquitoes

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Introduction

Mosquito host-seeking behavior is a key driver of malaria transmission, yet the biological factors underlying variation in human attractiveness remain unclear. Physiological states such as pregnancy and menstrual cycle have been proposed to increase of human odor variability and modify attractiveness to mosquitoes, but evidence remains inconsistent. These assumptions have raised concerns about variability in female odor cues limiting the inclusion of women in research and the generalizability of findings. To address this gap, we investigated whether sex and menstrual cycle consistently influence human body odor and attractiveness to *Anopheles gambiae*, a primary malaria vector.

Methods

We conducted two longitudinal studies in which body odor samples were repeatedly collected from women at three menstrual cycle phases across up to four cycles, and from men at matched intervals. Skin volatile profiles were analyzed using gas chromatography, and mosquito attraction was assessed using a uniport olfactometer assay with worn nylon sleeves and socks.

Results

Mosquito attraction did not differ between male and female participants at any timepoint. Attraction levels and volatile profiles remained stable within individuals across repeated measurements. Individual-level differences explained most of the variation observed in both mosquito attraction and odor chemistry, accounting for up to 64% of the variance in foot volatiles and 59% in arm volatiles. In contrast, sex and menstrual cycle phases showed only marginal effects.

Conclusion

Our findings refine and challenge assumptions from prior studies by demonstrating no consistent effect of sex or menstrual cycle phase on mosquito attraction. Instead, stable, individual specific odor signatures were the primary determinants of both volatile composition and attractiveness to *Anopheles gambiae*. These results highlight the intrinsic stability of human body odor and emphasize the importance of interindividual variation, rather than sex-related physiology, in shaping host attractiveness.



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sciforum-169138: Impact of Climate Change on the Global Expansion, Severity, and Transmission Dynamics of Dengue: A Systematic Review and Meta-Analysis

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Introduction

Dengue is the most prevalent arboviral disease worldwide, with rapidly increasing incidence driven by climate change, urbanization, and global mobility. Rising temperatures, altered precipitation patterns, and extreme weather events have expanded the geographic range of *Aedes* mosquitoes, modifying dengue transmission dynamics and disease burden. We conducted a systematic review and meta-analysis to evaluate the impact of climate variables on dengue incidence, severity, and spatial expansion.

Methods

A systematic search of PubMed, Embase, Web of Science, and Scopus was conducted from January 2000 to December 2025, following PRISMA guidelines. Eligible studies included observational, ecological, and modeling studies assessing associations between climatic factors and dengue transmission, incidence, outbreaks, or severity. Primary outcomes were changes in dengue incidence and geographic expansion. Secondary outcomes included outbreak frequency and disease severity. Random-effects meta-analyses were performed when appropriate, and heterogeneity was assessed using the I^2 statistic.

Results

A total of 52 studies comprising data from over 45 countries were included. Increased ambient temperature, rainfall variability, and humidity were consistently associated with higher dengue incidence. Each 1 °C increase in mean temperature was associated with a pooled 12% increase in dengue risk (RR 1.12; 95% CI 1.08–1.16). Regions previously considered non-endemic demonstrated sustained autochthonous transmission, particularly in temperate and high-altitude areas. Climate-driven changes were also linked to longer transmission seasons, increased outbreak intensity, and expansion of hyperendemic zones. Significant heterogeneity reflected regional ecological variability.

Conclusions

Climate change is a major driver of the global expansion and intensification of dengue transmission. These findings underscore the urgency of integrating climate-informed surveillance, vector control strategies, and public health preparedness into global dengue prevention policies. Anticipatory models incorporating climate projections are essential to mitigate future epidemic risks.



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sciforum-175677: Malaria Transmission Dynamics and Vector Ecology in Mpumalanga Province, South Africa: A Comparative Analysis of April-March 2024/2025 to April to March 2025/2026

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Introduction: Malaria remains a significant public health concern in Mpumalanga Province, South Africa, despite sustained vector control interventions. *Anopheles arabiensis* is the primary malaria vector in the province. Understanding the relationship between malaria case trends and mosquito vector ecology is essential to guide elimination strategies. This study compared malaria incidence and vector patterns over two consecutive seasons, from April 2024 to March 2026.

Methods: An analysis of confirmed malaria cases reported to the District Health Information System (DHIS2) was conducted for April 2024–March 2025 and April 2025–March 2026. Entomological surveillance included routine mosquito collections at randomly selected sites using larval habitat sampling, clay pots, pit traps, house searches, direct catches, and baited nets. Vector species composition and density were analysed in relation to malaria case data using Microsoft Excel and DHIS2.

Results: In 2024/25, 1,068 total malaria cases were reported, including 66 local cases and three deaths. In 2025/26, total cases increased to 1,174, with 95 local cases and six deaths reported by the end of February 2026, reflecting a 10% increase in incidence. More than 90% of cases occurred in Ehlanzeni District, while Nkangala and Gert Sibande districts reported only imported cases. Imported infections accounted for most overall cases.

A total of 1,442 mosquitoes were collected in 2024/25, including 199 *Anopheles gambiae* complex larvae and 76 adults (84 *An. arabiensis*, 69 *An. merus* and 66 *An. quadriannulatus*). In 2025/26, 1,415 mosquitoes were collected, with 255 *An. gambiae* complex larvae and 21 adults (83 *An. arabiensis*, 165 *An. merus* and 24 *An. quadriannulatus*). *Anopheles arabiensis* remained the dominant vector, comprising 6% of collections in 2024/25 and 6% in 2025/26. *Anopheles merus* increased proportionally from 5% to 12% respectively.

Conclusion: Malaria incidence increased over the two-year period, coinciding with reduced *An. arabiensis* density and a relative rise in *An. merus*. The suspected shifts toward outdoor biting and the increasing proportion of *An. merus* suggest persistent residual transmission risk. Strengthened integrated vector management targeting outdoor transmission may reduce local cases and support elimination efforts.



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sciforum-175342: Malaria vector surveillance in the endemic areas in South Africa over a five-year period: a retrospective study

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Malaria in South Africa is seasonal and primarily occurs in the endemic provinces of Limpopo, Mpumalanga and KwaZulu-Natal. Malaria transmission depends on the occurrence of mosquito vector populations and thus malaria control relies heavily on the implementation of vector control interventions. Vector surveillance is essential for optimal vector control, and, as the country moves towards malaria elimination, enhanced vector surveillance is necessary to obtain comprehensive information on those primary and potential vectors that are responsible in varying degrees for ongoing residual transmission.

This retrospective study collated *Anopheles* mosquito collections from sentinel sites in the three endemic provinces from 01 March 2017 to 28 February 2022. Field-collected specimens were identified to species by morphology and polymerase chain reaction assays.

A total of 32,955 *Anopheles* mosquitoes were collected and identified from sentinel sites in the KwaZulu-Natal (n=25,359; 77.0%), Limpopo (14.5%) and Mpumalanga (8.6%) provinces. Of the collected *Anopheles* specimens, 73.7% (n= 24,304) were identified as members of vector species/populations in South Africa, i.e., *Anopheles arabiensis* (58.8%), *An. parensis* (6.7%), *An. vaneedeni* (2.2%), and *An. merus* (6.1%). Furthermore, the collections included species implicated as vectors in other countries (11.9%). *Anopheles arabiensis* (major vector) was the predominant species collected through all seasons in KwaZulu-Natal and in autumn in Mpumalanga. *Anopheles pretoriensis* and *An. rufipes* (potential vectors) were the most abundant species in spring and summer in Limpopo. In Mpumalanga, *An. merus* (potential vector) predominated the collection in winter, spring and summer.

The occurrence of major and potential vector species in all malaria-endemic districts under vector surveillance shows that these regions remain receptive to malaria transmission, but to varying degrees and at different times/seasons. This supports ongoing implementation of vector control strategies in each endemic province. We recommend ongoing vector surveillance and the collection of insecticide susceptibility data for vector populations in endemic districts.



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sciforum-175200: Male Reproductive Transcript Silencing Reduces Fitness in *Anopheles funestus*

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Male mosquito biology remains underrepresented in studies of host traits influencing vector populations and parasite transmission. *Anopheles funestus* is a major African malaria vector, yet the molecular basis of male reproductive function in this species is poorly understood. Transcript *EZ976679* is strongly male-biased and shares high sequence identity with a juvenile hormone esterase-like gene, suggesting a potential role in reproductive physiology.

In this study, *EZ976679* expression was profiled across developmental stages, sexes, and dissected tissues using quantitative PCR. Functional characterisation was performed using dsRNA-mediated knockdown in adult males, with transcript abundance assessed at multiple time points post-injection. Reproductive and longevity assays were conducted to evaluate the effects of *EZ976679* knockdown on mating success, fecundity, fertility and adult male survival.

EZ976679 expression was age-dependent and highly enriched in the testes and accessory glands of 3–5-day-old males, with minimal expression in females and immature stages. RNA interference knockdown reduced transcript levels by more than 80% for up to five days, followed by partial recovery at later time points. Knockdown males exhibited significantly reduced mating success, decreased female fecundity and reduced adult male survival compared with controls, while fertility remained unaffected.

These findings identify *EZ976679* as a male-specific host factor required for optimal reproductive performance in *An. funestus*. By modulating male survival, mating success and female reproductive output, this transcript may influence vector population dynamics. Targeting male reproductive biology represents a complementary and underexplored avenue for innovative malaria vector control strategies.



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sciforum-178877: Molecular Characterization and Serotype Distribution of Dengue Virus in Bengaluru Rural

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Introduction

Dengue is one of the largest prevailing mosquito-borne viral infections, with an increasing load in India due to fast development and low regulation of vectors. Dengue virus circulates as four distinct serotypes (DENV-1 to DENV-4) with significant genetic variability influencing disease epidemiology. Identification of circulating serotypes and their genotypes is essential to understand viral evolution and transmission patterns.

Objectives

This study had the following objectives:

To detect Dengue serotypes DENV-1, DENV-2, DENV-3, and DENV-4 among positive RT-PCR samples. To sequence genotypes among the serotypes detected.

Methods

ELISA-positive dengue samples (n = 380) collected from clinically suspected patients between 2021 and 2023 were subjected to real-time RT-PCR for detection of viral RNA. Positive samples were further analyzed for serotype identification and selected samples among different serotypes for gene sequencing. Phylogenetic analysis was performed to determine genotypic distribution.

Results

Out of 380 samples, 275 (75.9%) were RT-PCR positive. Serotyping revealed DENV-2 as the predominant serotype (56.7%), followed by DENV-1 (36.7%) and DENV-3 (6.5%), while DENV-4 was not detected. Phylogenetic analysis showed that DENV-1 belonged to Genotype III and DENV-2 to the Cosmopolitan Genotype IV, indicating circulation of multiple genetic lineages

Conclusion

The study demonstrates the predominance of DENV-2 along with co-circulation of other serotypes in Bengaluru Rural. The presence of distinct genotypes highlights ongoing viral evolution. Continuous molecular surveillance is crucial for tracking dengue dynamics and supporting effective control strategies.



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sciforum-175294: Multisectoral Collaboration and Its Impact on Reducing Japanese Encephalitis (JE)/Acute Encephalitis Syndrome (AES) in India: An Integrated Approach to Global Health Security

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Introduction:

Acute Encephalitis Syndrome (AES) in India reflects complex interplay of factors at the agent–host–environment interface, involving Japanese Encephalitis (JE) and other zoonotic pathogens such as scrub typhus, West Nile virus, *Leptospira* etc. The interconnected risks underscore the critical need for a robust coordinated multisectoral approach.

This presentation examines how multisectoral collaboration contributed to the decline of AES/JE and how improved understanding of AES aetiology reshaped program strategies.

Methods:

A qualitative synthesis of national program interventions using a multisectoral collaborative implementation model. Methods included on-the-spot field visits by health workers, strengthened program-manager supervision, periodic reviews, and rigorous monitoring and evaluation. Inputs were drawn from cross-sectoral partners—Health, Animal Husbandry, Rural Development, Education, Tribal Health, Panchayati Raj Institutions, national and international agencies like BMGF, PATH, medical colleges, and research agencies (ICMR, NIMHANS). Importantly, GHSA–CDC-supported laboratories and surveillance platforms significantly strengthened AES/JE diagnostic capacity and case confirmation.

Results:

Serological and molecular evidence identified scrub typhus as responsible for nearly half of AES cases, with dengue, malaria, and other pathogens contributing substantially. Only 10–15% were JE, challenging earlier assumptions. Targeted interventions for these etiologies, combined with JE vaccination, vector control, and improved diagnostics, led to substantial reductions in AES cases and deaths.

Conclusion:

The study highlights how evidence-driven governance and cross-sector coordination can transform policy, strengthen practice, and advance sustainable AES/JE control.



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sciforum-175648: Physiological and environmental factors affecting thermal tolerance in the major malaria vector *Anopheles arabiensis* (Diptera: Culicidae)

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Thermal tolerance is a key determinant of mosquito survival and vectorial capacity under rising global temperatures. Understanding how physiological and environmental factors influence heat tolerance is therefore essential for predicting the impacts of climate change on malaria transmission. *Anopheles arabiensis* is a major malaria vector in Southern Africa. This species is difficult to control due to its plastic behaviour. This species is typically found in hot, arid areas, and its thermal tolerance may play a role in its capacity to invade new regions, particularly in the context of climate change. This study investigated the effects of humidity, blood-feeding status, age, sex, and strain on the thermal tolerance of *Anopheles arabiensis*. Temperature knockdown assays were conducted in which adult male and female mosquitoes of different strains and ages were exposed to a sublethal heat stress at 41 °C for 5 hours under controlled-humidity conditions. This is a proxy for resilience under stressful conditions. Females from all strains were more heat-tolerant than males in the 5-hour heat shock assays. In adult females, heat tolerance decreases with age, but this can be rescued by the provision of multiple blood meals. Crucially, insecticide resistant *An. arabiensis* had a distinct advantage under these conditions. These findings suggest that *An. arabiensis* is remarkably adaptable to heat stressed conditions with insecticide resistant females being particularly suited for conditions of current climatic conditions. This could have important implications for mosquito population dynamics and malaria risk in a warming climate.



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sciforum-159573: Seasonal Dynamics and Population Genetic Structure of *Plasmodium falciparum* in North-Central Nigeria: Implications for Malaria Surveillance and Control

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Malaria remains a major public health challenge in Nigeria, with parasite genetic diversity posing significant obstacles to effective control and vaccine development. This study investigated the seasonal variation in prevalence and genetic diversity of *Plasmodium falciparum* isolates in Kogi State, North-Central Nigeria, using polymorphic markers of merozoite surface protein 1 (MSP-1) and merozoite surface protein 2 (MSP-2).

A total of 3,669 participants were enrolled between 2021 and 2023 across selected Local Government Areas in the three geopolitical zones of Kogi State. Of these, 1,834 (50.0%) tested positive for *P. falciparum* by rapid diagnostic test and microscopy. Malaria prevalence was higher during the wet season (52.9%) compared to the dry season (47.0%), with Kogi East recording the highest burden across seasons. Children aged 1–10 years exhibited the highest prevalence (75.4%), and infection rates varied significantly across Local Government Areas.

Genotyping revealed the presence of all three MSP-1 allelic families (K1, MAD20, and RO33) and two MSP-2 families (FC27 and 3D7). FC27 and 3D7 were the predominant MSP-2 alleles across zones and seasons. Multiplicity of infection ranged from 1.0 to 1.3, indicating low to moderate clonal diversity. The expected heterozygosity (H_e) was 0.56 for MSP-1 and 0.84 for MSP-2, demonstrating greater genetic diversity at the MSP-2 locus.

The findings reveal seasonal and geographical variation in malaria prevalence and substantial genetic diversity of circulating *P. falciparum* strains in Kogi State. These population-based genetic data provide valuable insights for malaria control strategies and vaccine development efforts in North-Central Nigeria.



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sciforum-178646: Temporal dynamics of *Aedes aegypti* in a semi-arid urban environment in Northeastern Brazil

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Introduction: *Aedes aegypti* is the main urban mosquito vector of several arboviruses responsible for outbreaks and epidemics. Its adaptability to diverse environmental conditions promotes dispersal and challenges vector control. Understanding oviposition dynamics in relation to climatic factors is essential for improving entomological surveillance.

Objective: To relate the density of eggs from female *A. aegypti* with climatic variables (temperature, relative humidity, and rainfall) at the Teacher Training Center of the Federal University of Campina Grande, located in Cajazeiras, Paraíba, a region characterized by a hot and dry semi-arid climate in Brazil.

Materials and Methods: Fifty-one ovitraps were installed across the campus, distributed according to the mosquito's environmental preferences, and remained in the field from June 2019 to March 2020. During this period, 39 weekly inspections were carried out, recording the number of eggs and larvae present in the traps. Rainfall, temperature, and relative humidity data were obtained from the National Institute of Meteorology and the Executive Agency for Water Management of the State of Paraíba.

Results and Conclusion: A total of 6,296 eggs and 759 larvae of *A. aegypti* were collected. The highest values of the Ovitrap Positivity Index occurred between January and March, while the Egg Density Index was highest in February, March and June. Among the climatic variables evaluated, rainfall had the greatest influence on the increase in egg density in the traps, suggesting a strong influence of water availability on the vector's reproductive activity. The maintenance of oviposition during periods of drought may be related to the eggs' resistance to desiccation, the presence of cryptic breeding sites, and the skip oviposition behavior of females—strategies that allow reproductive continuity even in environmental conditions with low water availability. These findings reinforce the importance of continuous entomological monitoring in semi-arid regions to guide more effective vector control strategies.



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sciforum-175553: The effect of insecticide exposure on the gut microbial composition of *Anopheles arabiensis* (Diptera: Culicidae) from South Africa

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Insecticide intervention is still the major vector control tool of South Africa. However, despite low levels of resistance, it is notable that low levels of resistance have been detected in two of the country's endemic provinces, KwaZulu-Natal and Mpumalanga. Currently, no increased levels of detoxification enzyme activity have been detected in adults from either province. However, survivors of insecticide exposure have been detected. To determine whether gut microbiota could potentially play a role in this survivorship, the gut microbial composition of survivors from both provinces was compared to unexposed controls of F1 *Anopheles arabiensis*, the major malaria vector of South Africa. Deltamethrin, permethrin and bendiocarb survivors were examined from KwaZulu-Natal and deltamethrin survivors were examined from Mpumalanga. There were both notable similarities and differences in the provinces. While untreated samples had the most unique species in Mpumalanga, more unique species were recorded after deltamethrin and bendiocarb exposure in KwaZulu-Natal. *Asaia* was the dominant genus in KwaZulu-Natal, regardless of treatment. There was a marked reduction in *Pseudomonas* in all survivors. In this province, the number of differentially abundant genera was reduced after permethrin exposure but increased after deltamethrin and bendiocarb exposure. In Mpumalanga, *Asaia* and *Rhanella* were the dominant genera, with *Asaia* dominating in the deltamethrin treatments. There was less of a change in differential abundance in Mpumalanga, with only *Klebsiella* and *Asaia* differentially abundant after deltamethrin exposure. These findings highlight different microbial responses in the provinces, with variable region differences. The dominance of *Asaia* in both provinces, particularly after deltamethrin exposure, is notable. This genus is associated with both pyrethroid resistance and reduced *Plasmodium* transmission. These findings suggest a potential selection for microbial resistance in both provinces. This could also underlie disease transmission patterns in South Africa, with the potential for leveraging this information for future paratransgenesis interventions.



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sciforum-178384: Vertical habitat use and larvitrapping efficiency for arbovirus vector mosquitoes (Diptera: Culicidae) in an Amazonian rural settlement

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Mosquito species exhibit preferences for different vertical forest strata, which may influence arbovirus transmission dynamics in tropical environments. Arboreal mosquitoes such as *Haemagogus* and *Sabethes* are strongly associated with forest canopies and play an important role in the sylvatic transmission cycle of yellow fever virus (YFV). This study evaluated the diversity and abundance of acrodendrophilic Culicidae and assessed the efficiency of different larvitrapping types for sampling immature mosquitoes in preserved and anthropized forest fragments in the Amazon. Field collections were conducted in the Rio Pardo rural settlement, municipality of Presidente Figueiredo, Amazonas, Brazil, between January and September 2021 during six sampling campaigns covering both dry and rainy seasons. Larvitrap made of bamboo internodes, plastic containers, and tires were installed in the forest canopy at approximately 12 m height and remained in the field for 15 days during each sampling period. A total of 160 immature specimens belonging to nine mosquito species of medical and veterinary importance were recorded. *Haemagogus janthinomys*, the primary vector of sylvatic yellow fever virus, was the most abundant species, followed by *Limatus flavisetosus* and *Aedes albopictus*, a secondary vector of dengue virus. Tire traps showed the highest colonization rates, whereas plastic containers exhibited greater species diversity and evenness. Community analyses did not reveal significant differences between areas with contrasting levels of deforestation. However, *Hg. janthinomys* and *Sabethes* spp. were predominantly associated with bamboo traps, reflecting their affinity for natural phytotelmata in the canopy. In contrast, *Ae. albopictus* was more frequent in anthropized environments and associated with artificial containers. Its occurrence in canopy traps suggests ecological plasticity in vertically stratified habitats under environmental disturbance. These findings contribute to the understanding of canopy mosquito ecology and provide relevant information for arbovirus surveillance strategies in the Amazon.



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Session 2. One Health – Zoonotic Diseases

sciforum-174581: *Neisseria macacae* isolated in a patient's peritoneal dialysate effluent

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Introduction

Neisseria macacae is a gram-negative diplococcus colonized in the oral cavity of monkeys. Finding *N. macacae* in patients' specimens may cause suspicion of patients' exposure to monkeys. We encountered a case of *N. macacae* isolated in a patient's peritoneal dialysate effluent that demonstrated how the *Neisseria* taxonomy can be misleading.

Methods

The 31-year-old male is a previous anabolic steroid user who was diagnosed as having end-stage renal disease secondary to biopsy-proven focal segmental glomerulosclerosis. Fifty days after his peritoneal dialysis catheter insertion, he complained of one-day history of cloudy dialysate effluent, which was sent for laboratory analysis. The effluent's total nucleated count (TNC) was $13504 \times 10^6/L$, with 0.97 neutrophil and 0.03 monocyte/macrophage. The effluent was inoculated in an aerobic blood culture bottle which showed growth after 30 hours of incubation. Gram staining of the culture fluid showed moderate polymorphonuclear leukocytes in addition to gram-negative diplococci under 1000x magnification (Figure 1 https://drive.google.com/file/d/1p_Y0fWzDhLq2H18bcWMbeuCDoa2KyzzZ/view?usp=sharing). He received one intraperitoneal dose of ceftazidime 1.5 g and vancomycin 2 g.

Results

After 24-hour incubation, this microorganism was identified as *Neisseria macacae* by matrix-assisted laser desorption/ionization time-of-flight (MALDI-TOF) mass spectrometry (score >2.0). Subsequently, 16S ribosomal RNA testing identified this microorganism as *Neisseria macacae/perflava*. *N. macacae/perflava* are usually non-pathogenic commensal flora in the oropharynx of rhesus macaques. However, the patient denied exposure to monkeys. A review of the Bruker manufacturer MALDI-TOF library showed limitations in differentiating between *Neisseria macacae* and *Neisseria sicca*, a commensal flora. In three days, his dialysate effluent TNC decreased to $93 \times 10^6/L$. He subsequently received 18 intraperitoneal doses of ceftriaxone 1 g daily and clinically improved.

Conclusions

This case demonstrated the importance of clinical correlation in interpreting test results and diagnosing zoonotic diseases.



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sciforum-174816: Clinical and Epidemiological Profile of Human Brucellosis in Sétif, Algeria: A 4-Year Hospital-Based Study (2021–2024)

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Introduction: Brucellosis remains a major public health concern in Algeria, particularly in agro-pastoral regions like Sétif. This study aims to describe the clinical, epidemiological, and microbiological characteristics of human brucellosis cases managed at the University Hospital of Sétif. **Methods:** A retrospective descriptive study was conducted on 37 patients hospitalized at the Infectious Diseases Department between 2021 and 2024. All cases were confirmed by the isolation of *Brucella spp.* from blood cultures or localized samples. Statistical analysis included 95% confidence intervals (CIs) for key proportions, Fisher's exact test for categorical variables and the Binomial test for gender distribution. A p-value 0.05 was considered statistically significant. **Results:** A total of 37 patients were included. A significant male predominance was confirmed (78.4% vs. 21.6%; $p = 0.001$), with a mean age of 43 years ($SD \pm 15.6$). The temporal distribution showed a peak in 2022 (32.4%), followed by a fluctuation in annual incidence without a linear trend ($p > 0.05$). The hallmark clinical sign was undulant fever (97%), frequently associated with arthralgia (19%) and headache (11%). Focal osteoarticular complications were identified in 10.8% of the cohort ($n=4$), specifically spondylodiscitis ($n=2$) and sacroiliitis ($n=2$). Notably, all complicated cases occurred in male patients; however, this association did not reach statistical significance (Fisher's exact test, $p = 0.55$), likely due to the limited sample size. **Conclusion:** Human brucellosis in Sétif is characterized by a high burden among middle-aged men and significant osteoarticular morbidity. The lack of a declining trend over four years underlines the urgency of an integrated "One Health" surveillance system to control the animal reservoir and improve early clinical detection.



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sciforum-178333: Rabies Virus Diagnostic Testing – Evidence towards updating tissue sampling DFA testing

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Introduction/Background

Rabies is a fatal zoonotic disease of public health concern. The direct fluorescent antibody (DFA) test is internationally recognized as the gold standard for postmortem rabies diagnosis with some variations in sampling recommendations depending on the reference standard used. The United States National Rabies Diagnostic protocol recommends sampling both the brainstem and cerebellum for testing. Our study aimed to assess whether brainstem tissue alone is sufficient for reliable DFA diagnosis by comparing brainstem and cerebellar results from routine case submissions.

Methods

We reviewed 437 DFA-positive rabies cases submitted between January 2013 and January 2026 from multiple species [skunks (323), cats (41), bovines (41), horses (10), dogs (9), foxes (7), raccoons (2), sheep (1), goat (1), donkey (1), and llama (1)]. Brainstem and cerebellar impression smears were fixed in cold acetone, stained with fluorescein isothiocyanate, and examined for apple-green fluorescence indicating rabies antigen. Antigen distribution was graded on a scale of 1 to 4 based on abundance. Tissue scores were statistically compared using paired student t-tests and Pearson correlation.

Results

Brainstem and cerebellum scores demonstrated a high correlation ($r = 0.93$; $N = 437$; $t = 52.40$; $DF = 435$; $P = 4.98 \times 10^{-190}$). The paired (two-tailed) Student's t-test showed a small but significant difference ($P = 0.0005$; $t = 3.48$; $DF = 436$; mean difference = 0.03; 95% CI: 0.01–0.05) between brainstem (3.87 ± 0.39) and cerebellum (3.84 ± 0.51) scores.

Conclusions

Brainstem and cerebellum scores show a strong positive correlation indicative of consistent antigen detection. Brainstem showed higher mean scores compared to cerebellum. These findings provide supporting evidence towards revising minimum tissue sampling standards to allow for independent brainstem testing when optimal tissue collection is not feasible. This will improve diagnostic efficiency and biosafety without compromising diagnostic accuracy or public health protection.



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sciforum-173416: "Effectiveness of Participatory Strategies for Prevention of Dengue and Leptospirosis: A Two-Year Controlled Community Trial in Santa Fe, Argentina"

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Introduction: The city of Santa Fe (Argentina) is highly exposed to environmental conditions that favor outbreaks of dengue and leptospirosis. Official public health campaigns often rely on top-down compliance-based approaches, underestimating the potential of community participation. This study aimed to quantify the effectiveness of participatory strategies compared to conventional methods through controlled community trials in four riverside neighborhoods with similar socio-environmental conditions.

Methodology: In 2024/2025, two intervention sectors (Vuelta del Paraguay / Manzana 2) and two control sectors (Colastiné / Boca) were established (n=80 households per site). The intervention involved training cycles for health promoters based on popular education and participatory action research (PAR), promoting community dialogue and territorial planning. Control areas received traditional, non-participatory campaigns. A longitudinal pre-post design was used. Indicators included: knowledge, attitudes, practices, and perceptions (KAPP); abundance of *Aedes aegypti* adults, larvae, and breeding sites; and rodent activity monitored through hair traps. Data were analyzed using generalized linear mixed models (GLMM) and logistic regressions to assess the interaction effect between treatment condition (participatory vs. control) and time in both trials.

Results: Significant interaction effects were found (p 0.05). The probability of finding potential larval breeding sites was reduced by 39% (OR: 0.61), larval breeding sites by 41% (OR: 0.59), and *Ae. aegypti* adults by 31% (OR: 0.69) compared to control groups (p 0.05). Additionally, rodent activity was reduced by 44% (OR: 0.56). Furthermore, a significant increase in risk knowledge and perception was observed.

Conclusion: Participatory methods demonstrate greater efficacy than traditional approaches in reducing biological risk indicators. Community empowerment acts as a cost-effective strategy by fostering social sustainability, reducing dependence on recurring chemical interventions, and mitigating the risk of zoonotic disease transmission in vulnerable settings



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sciforum-175546: Climate-Driven Environmental Change and Zoonotic Spillover Risk: Implications for One Health Governance

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Introduction:

Climate change functions as a pervasive ecological driver reshaping the dynamics of infectious disease emergence. Rising temperatures, altered precipitation patterns, and extreme weather events increasingly affect vector ecology, wildlife migration, and human land use, intensifying interactions at the human–animal–environment interface. These processes collectively elevate the likelihood of zoonotic spillover events. Recognising climate change as a cross-sectoral threat highlights the urgency of strengthening One Health governance frameworks to integrate environmental, veterinary, and public health perspectives within a unified risk management system.

Methods:

A structured narrative review was conducted to examine evidence linking climate-driven environmental change to zoonotic spillover risk. The literature published between 2015 and 2026 was systematically identified through PubMed and Web of Science databases. Eligible studies addressed associations between climatic or ecological changes—such as temperature rise, extreme weather, land-use modification, or biodiversity loss—and zoonotic disease emergence or transmission dynamics. Data were synthesised thematically to elucidate recurrent ecological mechanisms and governance implications; no formal risk-of-bias scoring was applied due to the review’s integrative scope.

Results:

The synthesis identified three primary environmental drivers of spillover: temperature-driven vector expansion (notably *Aedes albopictus* related to dengue and West Nile virus), extreme weather events triggering vector proliferation or waterborne outbreaks (as in Rift Valley fever following heavy rainfall), and anthropogenic land-use alterations contributing to biodiversity disruption and viral spillover (e.g., Ebola virus disease). Mechanistic patterns included altered vector suitability, wildlife host redistribution, and intensified human–animal contact. Governance analysis revealed fragmented surveillance systems, inadequate integration of climate and health data, and reliance on reactive rather than anticipatory response frameworks.

Conclusions:

Climate change amplifies zoonotic spillover risk by restructuring ecological and epidemiological interactions. Effective prevention necessitates integrated, climate-informed One Health governance that unites environmental, veterinary, and human health sectors. Strengthened transdisciplinary surveillance and predictive modelling are critical for anticipatory risk management in an era of accelerating climate variability.



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sciforum-174692: Epidemiology of human Brucellosis in rural South Africa: Household survey of seroprevalence and risk factors, 2022–2023

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Introduction: Brucellosis, caused by *Brucella* spp., is a globally prevalent zoonotic disease and a significant cause of febrile illness, yet it often remains underdiagnosed. This study assessed brucellosis seroprevalence in a rural South African community and examined associated exposure factors among livestock-owning and non-livestock households.

Methods: A cross-sectional random cluster household survey was conducted in 2022–2023 in uMkhanyakude District, KwaZulu-Natal Province, South Africa. Household interviews were conducted, and serum samples from 688 participants were tested for anti-*Brucella* IgG antibodies using a commercial ELISA. Risk factors for seropositivity were assessed using Fisher's Exact test, with $p < 0.05$ considered significant.

Results: Overall, human *Brucella* seroprevalence was 4.4% (30/688; 95% CI: 3.0–6.3%) after adjusting for household clustering. Participants had a median age of 36 years (IQR: 25–53; range: 12–95); 98% identified as Black African and 59% were female. Poultry ownership was common (74% kept chickens), while 12% kept cattle, 16% goats, and 39% both bovids. Univariable analysis showed higher seropositivity among males (7.9% vs. 2.0%; $p = 0.001$), participants older than 36 years (6.3% vs. 2.4%; $p = 0.09$), and those with primary-level or no schooling (6.9% vs. 3.0%; $p = 0.106$). A strong association was observed with household cattle or goat ownership (6.4% vs. 0.4%; $p = 0.001$), whereas associations with livestock slaughter ($p = 0.151$) and abortions ($p = 0.19$) were weaker. Behavioural factors associated with increased seropositivity included consumption of unboiled/raw milk ($p = 0.097$) or fermented milk ($p = 0.077$), eating animals found dead ($p = 0.059$), and frequent hunting of antelopes, small mammals, or birds ($p = 0.085$). No associations were found with the consumption of undercooked meat, employment status or sector, chicken ownership, or keeping cats/dogs as pets (stratified by bovid ownership). Multivariable analysis will be presented.

Conclusions: Brucellosis seroprevalence was associated with multiple demographic and behavioural factors, particularly sex, age and contact with cattle or goats. Strengthening livestock control measures, together with targeted awareness campaigns for high-risk groups, may reduce human *Brucella* exposure.



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sciforum-176122: Serological Evidence of Bat-Borne and Shrew-Borne Hantavirus Infections in Humans: A Comparative Study from Thailand, Sri Lanka, and Zambia

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This study provides the first evidence of human infection with bat-borne hantaviruses and reveals widespread exposure to both bat- and shrew-borne hantaviruses in human and animal populations across Asia and Africa. Traditionally, hantaviruses were known as rodent-borne pathogens causing severe disease in humans. However, numerous novel viruses have been discovered in shrews, moles, and bats, yet their potential to infect humans remained unclear due to a lack of comprehensive serological tools.

Using a newly developed mixed-antigen screening system based on recombinant nucleocapsid proteins, researchers conducted retrospective serological studies on human samples from Thailand and Sri Lanka, as well as bat samples from Zambia. The method proved highly efficient, reducing the number of test wells required by 80%.

In Thailand, among 143 patients initially suspected of leptospirosis, 4.9% showed confirmed seroconversion to bat-borne hantaviruses (Robina virus, Dakrong virus, and Xuan Son virus). Notably, this rate was significantly higher than the prevalence of classical rodent-borne hantavirus infections (1.4%) in the same cohort.

In Sri Lanka, screening of 336 human sera (half healthy, half febrile) revealed that 23.2% of febrile patients had antibodies to either bat-borne or shrew-borne hantaviruses, compared to only 1.2% of healthy controls. Reactivity was detected against a wide range of viruses, including Quezon virus, Robina virus, Asama virus, and Thottapalayam virus.

Among 1,764 bats from 11 species in Zambia, overall seroprevalence reached 28.8%, with reactivity to both bat-borne and shrew-borne antigens. Frugivorous bat species showed higher seropositivity than insectivorous ones.

The findings demonstrate that bat-borne and shrew-borne hantaviruses are capable of infecting humans and may represent emerging zoonotic pathogens with a broader geographic distribution than previously recognized. The study underscores the urgent need for expanded surveillance, virus isolation, reservoir identification, and clinical assessment of these novel viruses to inform public health preparedness.



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sciforum-178840: Bridging Gaps in Antibiotic Stewardship: Knowledge, Attitudes, and Practices of Livestock Farmers in a One Health Context

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Introduction:

Antimicrobial resistance (AMR) is a critical global health challenge driven by inappropriate antibiotic use across human, animal, and environmental sectors (1,2). In livestock farming, irrational antibiotic practices and poor awareness contribute significantly to the emergence and spread of resistant pathogens (3,4). Strengthening antibiotic stewardship at the community level is essential within the One Health framework. This study aimed to assess gaps in knowledge, attitudes, and practices (KAP) related to antibiotic use among livestock farmers.

Methods:

A cross-sectional, questionnaire-based study was conducted among 30 livestock farmers in rural Karnataka. Data was collected using a structured, pre-validated KAP questionnaires covering domains of antibiotic awareness, AMR knowledge, usage practices and environmental factors. Responses were recorded in the local language and analyzed descriptively as proportions.

Results:

Although 70% of participants were aware of antibiotics, only 40% correctly identified their appropriate use for bacterial infections. Awareness of AMR was limited (30%), reflecting trends reported in similar settings (5). Inappropriate practices were prevalent, with over 60% of farmers reporting non-prescription antibiotic use and nearly half discontinuing treatment prematurely, undermining antibiotic stewardship (6). Knowledge gaps regarding withdrawal periods and antibiotic residues in animal products were significant. Environmental dimensions of AMR, including contamination of soil and water, were poorly recognized (7). Despite these gaps, a majority expressed positive attitudes toward improved practices and willingness to participate in stewardship training.

Conclusion:

Substantial gaps in antibiotic stewardship exist among livestock farmers, driven by inadequate knowledge and unsafe practices. Targeted interventions including farmer education, improved veterinary access, and regulatory enforcement are essential. Integrating these strategies into a One Health framework is crucial in mitigating AMR and promoting sustainable antibiotic use (3,8).



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sciforum-178313: Broad-Spectrum Antiviral Activity of 3CLpro Inhibitors against Bat Coronaviruses Utilizing ACE2 or DPP4 Receptors

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Introduction:

Bats are recognized as natural reservoirs of coronaviruses. Major human disease outbreaks caused by SARS-CoV, SARS-CoV-2, and MERS-CoV are presumed to have originated from zoonotic spillover of bat coronaviruses. Multiple bat species harbor SARS-CoV-like (Sarbecovirus) and MERS-CoV-like (Merbecovirus) viruses that use angiotensin-converting enzyme-2 (ACE2) or dipeptidyl peptidase-4 (DPP4) as a host cell receptor, similar to SARS-CoV, SARS-CoV-2, and MERS-CoV. This shared receptor tropism highlights the zoonotic and pandemic potential of bat coronaviruses and underscores the importance of evaluating the antiviral activity of inhibitors against them. Coronavirus 3CLpro cleaves the viral polyprotein into functional nonstructural proteins, essential for the viral replication cycle, and is conserved among coronaviruses, making it an attractive broad-spectrum antiviral target. This study aims to evaluate the antiviral activity of 3CLpro inhibitors against ACE2 or DPP4 utilizing bat coronaviruses.

Methodology:

Ten bat coronaviruses from the Betacoronavirus (Sarbecovirus and Merbecovirus) and Alphacoronavirus genera, along with SARS-CoV, SARS-CoV-2, MERS-CoV, and FIPV (Feline Infectious Peritonitis Virus), were included in this study. Their full-length 3CLpro genes were cloned and expressed. Nine 3CLpro inhibitors, including GC376, its analogs, and Nirmatrelvir, were tested against the expressed 3CLpros in the Fluorescence Resonance Energy Transfer (FRET) assay to determine 50% inhibitory concentrations (IC₅₀). X-ray crystallography of bat coronavirus 3CLpro in complex with GC376 was performed. Additionally, we analyzed approximately 220 bat coronavirus 3CLpro sequences for amino acid homology and phylogeny.

Result:

Sequence analysis of these bat coronavirus 3CLpros revealed high homology within the Sarbecovirus (87-100%) and Merbecovirus (78-100%) subgenera and 41-100% homology within the Alphacoronavirus genus. Fifty percent or less homology was observed among the different coronavirus genera. In the FRET assay, some compounds demonstrated potent broad-spectrum inhibition across all tested coronaviruses, including those utilizing ACE2 or DPP4 receptors.

Conclusion:

These preliminary results highlight the potential of 3CLpro inhibitors as antiviral candidates against bat coronaviruses with zoonotic potential.



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sciforum-178845: Brucellosis Control in the One Health Era: A Systematic Review of Global Evidence with Implications for India

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Background

Brucellosis is a significant public health concern in lower- and middle-income countries (LMICs), predominantly in India, due to close contact with the animal population owing to individuals' occupation. Additionally, families of these groups face a high risk of possible domestic exposure due to the proximity of animals in residential spaces. On account of its complex dynamics spanning across human, animal, and environmental sectors and emerging AMR, Brucellosis is a critical One-Health challenge.¹

Objectives

To systematically review global evidence on brucellosis control and the epidemiological trends under a One Health framework and assess implications for India.

Methods

A systematic review was conducted following PRISMA guidelines. Databases searched included Web of Science, PubMed, Scopus, Cochrane Library, and Embase (from inception to Jan 2025). Studies addressing human brucellosis, antimicrobial resistance, and One Health interventions were included. Two independent reviewers extracted data.

Almost 20 studies were included for qualitative synthesis. A simplified random-effects meta-analysis was performed using Indian prevalence data to estimate pooled seroprevalence and subgroup variation.^{2,3}

Results

The included studies spanned diverse geographical regions in India. Collectively, the findings indicate that brucellosis continues to be a major global public health concern with a pooled prevalence of 4.75% among the general population and 6% among occupationally exposed groups. Environmental and livestock-associated reservoirs and irrational antibiotic use contribute to the transmission of AMR. Key risk factors include direct animal contact and consumption of unpasteurized animal products. From the studies, livestock vaccination consistently emerged as the most effective preventive measure.

Conclusion

Brucellosis persists as a significant zoonosis in India, particularly among high-risk populations. The analysis demonstrates that while overall prevalence in the general population is moderate, high-risk groups bear a substantially higher burden, emphasizing the importance of targeted interventions. Multidisciplinary One Health interventions, including livestock vaccination and antimicrobial stewardship in veterinary and human sectors, are crucial steps towards effective disease mitigation.⁴



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sciforum-170886: Co-circulation of *Chlamydia psittaci*, *C. gallinacea*, and *Chlamydiaceae* DNA in Brazilian Wild Birds and Reptiles

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The *Chlamydiaceae* family includes zoonotic pathogens like *Chlamydia psittaci*, with wild animals acting as reservoirs. As chlamydial diversity expands, surveillance in rehabilitation centers is vital to assess pathogen prevalence and mitigate potential occupational risks under a One Health approach. We analyzed 158 swabs from 105 animals—88 birds (139 swabs) and 17 reptiles (19 swabs)—admitted to CEMPAS (Botucatu, Brazil). Samples were screened using a 23S rRNA *Chlamydiaceae* real-time PCR. Positive samples underwent species-specific qPCRs for *C. psittaci*, *C. avium*, *C. gallinacea*, *C. abortus*, *Ca. C. testudinis*, *C. pecorum*, and *Ca. C. emydidiae*. *Chlamydiaceae* DNA was detected in nine animals, resulting in an overall prevalence of 8.5% (9/105). When analyzed by group, reptiles showed a higher positivity rate of 35.3% (6/17) compared to 3.4% (3/88) in birds. *C. psittaci* was identified in a *Zenaida auriculata* and *C. gallinacea* in a *Ramphastos toco*. All PCR-positive reptile samples tested negative for the targeted species. While this may suggest uncharacterized chlamydial agents—common in chelonians—it could also reflect low DNA load or primer incompatibility; thus, sequencing is required for confirmation. Our findings for birds (3.4%) are below the 16.5% average for South American birds, while the reptile prevalence (35.3%) exceeds the global estimate of 23.5% (Inchuai et al., 2021). The identification of *C. psittaci* and *C. gallinacea* aligns with the emerging diversity reported in wild fauna (Zhang et al., 2021). These results indicate a potential occupational risk for veterinarians and staff. Although no human exposure data was collected, the presence of these pathogens highlights the need for strict biosafety protocols and personal protective equipment (PPE) to prevent spillover at the human–wildlife interface.



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sciforum-175701: Epidemiological profile of human anti-rabies prophylaxis in Southeastern Brazil and cost analysis of inadequate conducts (2014–2023)

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Rabies is a lethal viral zoonosis that requires intensive surveillance and prophylaxis efforts in several countries. Our objective was to describe the epidemiological profile of human anti-rabies consultations recorded in the database of a public regional health division of the most populous state in Brazil between 2014 and 2023, to evaluate the prophylactic measures instituted, and to estimate the direct costs associated with different post-exposure treatment regimens. This is a retrospective, descriptive study based on 54,977 notifications of human anti-rabies consultations from a region comprising approximately 68 municipalities in the State of São Paulo, analyzed using descriptive statistics. The measures were classified as adequate, insufficient, or excessive, according to the guidelines of the Brazilian Ministry of Health. Costs were estimated based on the number of treatments and the average values of the immunobiologicals administered. More than half of the prophylaxis procedures were carried out in situations considered to be low risk. Children between 1 and 19 years of age comprise the age group with the highest number of consultations. Approximately 42.4% of the measures instituted were classified as inadequate, with a predominance of excessive measures in low-risk situations, such as indirect contact and aggressions by healthy animals. Dogs (80.1%) and cats (14.1%) cited as aggressors accounted for nearly all recorded consultations. The measures in severe exposures and those involving wild animals showed greater adherence to the guidelines of the official protocol. Treatment was discontinued in 20.6% of cases, mainly due to abandonment. The total estimated cost was approximately BRL 15.5 million, of which about 20% corresponded to inadequate measures, representing potentially avoidable expenditures. The adoption of measures more aligned with the guidelines may improve clinical effectiveness and the efficiency of public resource use.



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sciforum-178507: Epidemiology of *Cryptosporidium* Infections in Children Under Five Years of Age and Young Livestock in Eastern Ethiopia: A One Health Approach

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Cryptosporidiosis is a significant public health concern in low-income countries, causing diarrhea-related morbidity and mortality. *Cryptosporidium* infection also affects livestock, leading to economic losses, with farm animals potentially serving as reservoirs for human transmission via contaminated food and water. Despite its importance, the epidemiology of cryptosporidiosis in Eastern Ethiopia remains poorly studied. A health facility and community based cross-sectional study was conducted between November 2022 and November 2023 in Dire Dawa Administration and Shinile, Eastern Ethiopia by including 756 children under five years of age with diarrhea, 184 community children, and 628 young livestock. Sociodemographic and other relevant variables were collected using a structured questionnaire and checklist. Fresh fecal specimens from children and livestock were collected, and initial stained by LED fluorescence microscopy, while remaining stool samples were stored at –20 °C for ELISA and molecular analyses. Stool samples tested positive by LED fluorescence microscopy and/or ELISA were processed by PCR targeting the small subunit ribosomal ribonucleic acid and glycoprotein 60 loci. Poisson regression with robust variance and Firth logistic regression were used to assess factors associated with *Cryptosporidium* infection. The prevalence of *Cryptosporidium* infection, as detected by LED-AP microscopy, was 15.2% among diarrheic children, 6.5% among community children, and 4.3% among young livestock. In children, *C. hominis* (64%) and *C. parvum* (36%) were identified, with *gp60* subtype families Ia, Ib, and Id for *C. hominis* and Ile and Ilc for *C. parvum*; the predominant subtypes were *C. hominis* IdA15 and *C. parvum* IleA10G1. Among livestock, *C. ubiquitum*, *C. xiaoi* (subtype XXIIIg), and *C. ryanae* were detected. In children, *Cryptosporidium* infection was significantly associated with season, caregiver educational status, contact with diarrheic individuals, exclusive breastfeeding, handwashing after toileting, and use of toilet paper after defecation. In livestock, herd/flock size, source of drinking water for animal and animal caregiver age were significantly associated with *Cryptosporidium* infection.



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sciforum-175522: Evaluation of Seroprevalence and Periparturient Shedding of *Coxiella burnetii* in a Dairy Herd in Americana, São Paulo, Brazil

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Q fever is a globally distributed zoonosis caused by the obligate intracellular Gram-negative bacterium *Coxiella burnetii*, a highly infectious pathogen with remarkable environmental persistence. Domestic ruminants are the primary source of human infection through inhalation of contaminated aerosols. Clinical manifestations range from acute febrile illness, hepatitis, and pneumonia to severe persistent focalized complications such as endocarditis, osteomyelitis, and vascular infections. Given the limited data available in Brazil, further investigation into the circulation and shedding of *C. burnetii* is needed. Here, we describe a prospective cohort study evaluating the association between pre-parturition serological status and periparturient shedding of *C. burnetii*. For serology, an indirect ELISA (ID Screen® Q fever Indirect Multi-species) was used to detect antibodies in serum samples. Vaginal swabs were collected for DNA extraction and subsequent analysis by real-time PCR (qPCR) using specific primers and a probe targeting the *IS1111* gene of *C. burnetii*. Sixty-five percent (67/103) of the herd was seropositive during the prepartum period, indicating prior exposure to *C. burnetii*. Among the 42 parturient animals, 29 were seropositive, 10 seronegative, and 1 was not serologically evaluated due to logistical constraints. Of the animals that gave birth within 2 months, 28.6% (12/42) were qPCR-positive, with shedding rates of 24.1% (7/29) and 40% (4/10) for seropositive and seronegative animals, respectively. Notably, some animals exhibited Ct values below 25, indicating high bacterial loads and suggesting increased potential for environmental contamination. Shedding in seronegative animals indicates that serology alone underestimates the risk of *C. burnetii* dissemination. Active circulation in a dairy herd near Americana's urban area suggests endemic infection and ongoing zoonotic risk via windborne aerosols. Although limited by single-point sampling and total serology, these findings underscore the need for One Health surveillance to protect workers and neighboring populations at the peri-urban interface.



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sciforum-170386: Extreme Rainfall, Flooding Events and Leptospirosis Incidence: A Decade-Long Ecological Analysis in Southern Brazil

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Introduction

Leptospirosis is a zoonotic disease caused by bacteria of the genus *Leptospira*, prevalent in tropical regions. Transmission is facilitated by heavy rainfall, inundation, and poor sanitation. In 2024, Rio Grande do Sul experienced widespread flooding. Therefore, this study aimed to evaluate socio-demographic distribution and temporal trend of leptospirosis in southern Brazil, with particular attention to the 2024 event.

Methods

A retrospective ecological study was conducted including all confirmed leptospirosis cases in Rio Grande do Sul from January 2014 to December 2024, obtained from TABNET/DATASUS. Analyses were performed in R (v.4.4.2) and RStudio. To compare 2024 with the 2014-2023 period, quasi-Poisson regression with population offset was applied due to overdispersion. Cases were further stratified by educational attainment as a proxy for socioeconomic position. As an ecological study, causal inferences at the individual level cannot be established.

Results

A total of 5,569 cases were analyzed. Annual incidence rates remained stable between 2 and 6 cases/100,000 inhabitants from 2014 to 2023, but increased in 2024, exceeding 10 cases per 100,000. In regression analysis adjusted for population size, incidence in 2024 was higher compared to 2014-2023 (IRR = 4.88; 95% CI: 1.90-12.54; $p = 0.009$). The increase was temporally associated with extreme rainfall and flooding in May 2024. Regarding educational attainment, individuals with primary education consistently represented the majority of cases throughout the decade. Still, the 2024 outbreak was characterized by a substantial increase across all educational levels compared to preceding years.

Conclusions

The increase in leptospirosis incidence in 2024 highlights its sensitivity to extreme flooding events. Although individuals with lower educational attainment accounted for a large proportion of cases, this likely reflects differences in exposure rather than intrinsic risk. Further analytical studies are needed to clarify social and environmental determinants.



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sciforum-178360: Molecular Characterization of Rotavirus strains from humans and some animal species in Calabar, Cross River State, Nigeria

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Background: Rotavirus is a double-stranded RNA virus of the Reoviridae family and the most common cause of diarrhea in children. This study determined the prevalence and genotypes of Rotavirus in humans and animals in Calabar, Nigeria.

Methods: A total of 1000 faecal samples were collected (400 from children ≤ 5 years and 600 from animals - dogs, pigs and cattle). Samples were tested for Rotavirus using ELISA and genotyping was done using Multiplex RT-PCR. Questionnaires were used to obtain demographic data from human participants. Data was analysed using SPSS version 25 and significant variations were determined using the Chi Square test.

Results: Of the 1,000 samples analyzed, 64 tested positive, yielding an overall prevalence of 6.4%. The distribution of PCR-confirmed Rotavirus infection across species included: pigs (20/200, 10.0%); dogs (4/200, 2.0%); cattle (0/200, 0.0%) and humans (40/400, 10.0%). The prevalence of Rotavirus varied markedly among host species with higher rates in humans and pigs ($\chi^2 = 33.12$, $df = 3$, $p = 0.0001$). Eight different Rotavirus A gene (G and P) combinations were detected in humans while only 2 were detected in animals. Of the 64 genotypes, 24 (37.5%) were obtained from animals (pigs and dogs) and 40 (62.5%) from humans. The predominant genotype in humans was (G10,P8) (9, 22.5%) and in animals was (G9,P8) (13, 65%). Meanwhile, two genotypes (G9,P8) and (P8) were common in both humans and animals. Monthly analysis showed that the highest prevalence of Rotavirus was observed in January (26.3%) while the lowest was in June (0%). There was no significant difference in the distribution of rotavirus by month ($\chi^2=0.450$; $P=0.994$).

Conclusion: Rotavirus A is common in both humans and animals in the study area. The presence of similar genotypes highlights the potential for zoonotic transmission to humans. There's need to improve rotavirus vaccine coverage for children in the study area.



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sciforum-173926: Molecular detection of *Coxiella burnetii* in wild birds and the importance of surveillance

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Coxiella burnetii is a Gram-negative bacterium capable of infecting a wide range of hosts. Even though domestic ruminants are the main reservoirs, wild animals can also play this role, being the source of some documented human outbreaks. In farm animals, it is associated with reproductive disorders, while in humans, it causes Q Fever, a febrile illness that can progress to endocarditis, vascular complications, and persistent infections. Although most cases are asymptomatic, it is essential to track infected animals, as even in the absence of clinical signs, they can shed the pathogen, facilitating transmission and posing a significant risk to human and livestock health. This study screened 182 birds from 11 distinct orders at a wildlife rehabilitation center. Oral and cloacal swabs were collected for DNA extraction and subsequent analysis by real-time PCR (qPCR) using specific primers and a probe targeting the *IS1111* gene of *C. burnetii*. Results identified *C. burnetii* DNA in 1.6% (3/182) of the subjects. Positivity was confirmed in oral swabs from two Passeriforms (*Pitangus sulphuratus* and *Gnorimopsar chopi*) and a cloacal swab of an unidentified Cathartiform. In conclusion, these findings underscore that birds can participate actively in the epidemiology of *C. burnetii*, and the presence of bacterial DNA in swabs suggests that wild birds may contribute to environmental dissemination and, due to their high mobility and migratory patterns, may contribute to the long-distance environmental dissemination of *C. burnetii*, potentially infecting wild and domestic animals as well as human populations.



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sciforum-175582: Operationalising One Health for Dengue Prevention: Pathways Toward an Integrated Early Warning System in Bangladesh

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The epidemiology of dengue in Bangladesh is undergoing a fundamental shift, driven by climate variability, rapid urban expansion, and ecological change. Dengue is transforming a historically monsoon-bound disease into a persistent national health crisis. Recent outbreaks demonstrate expanding geographic distribution and altered transmission dynamics driven by rapid and unplanned urbanisation, and mosquito vector adaptation. These changes have reduced the effectiveness of conventional surveillance approaches that rely primarily on hospital-based reporting and reactive response. Addressing this evolving risk requires a predictive early warning system grounded in a One Health framework that integrates human, environmental, and vector surveillance.

A retrospective analysis was conducted using national routine dengue surveillance datasets reported by the Directorate General of Health Services, Bangladesh, for 2024–2025, alongside system-level evidence, to evaluate readiness for a One Health-based Early Warning System (EWS). Data quality, reporting continuity, and operational feasibility were assessed using WHO data-quality assessment approaches.

The datasets demonstrated nationwide reporting coverage but substantial data gaps, with approximately 53.2% of fields missing in 2024 and only 20.8% in 2025. Substantial data gaps, reporting inconsistencies, and limited interoperability constrain early outbreak detection. Current systems capture human clinical outcomes but lack systematic integration with entomological surveillance and ecological drivers such as temperature, rainfall, and humidity. These limitations reduce the ability to generate timely, actionable alerts.

The evolving epidemiology of dengue in Bangladesh necessitates transitioning from conventional surveillance to a predictive One Health early-warning system. Implementing a One Health framework can operationalise multi-sectoral integration, strengthen data systems, and enable anticipatory public health action. Bangladesh represents a critical frontline example of how climate, ecological disruption, and human population dynamics are reshaping dengue transmission. This demands a transition from conventional surveillance toward integrated One Health early warning systems. A coordinated One Health EWS represents a critical pathway for improving climate-sensitive disease preparedness and reducing future dengue burden in Bangladesh.



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sciforum-177624: Parasitic Contamination of Fresh Green Leafy Vegetables Sold in Open Markets in Sri Lanka during the Second Inter-Monsoon Season: A Cross-Sectional Study

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Introduction

Intestinal parasitic infections remain a public health concern in Sri Lanka, where contaminated green leafy vegetables are an important transmission route. This study assessed intestinal parasite prevalence in fresh green leafy vegetables across all nine provinces of Sri Lanka and examined variations in parasitic contamination according to the site of collection in different geographical locations.

Methods

A cross-sectional study was conducted from October 1 to November 30, 2025, during the Second Inter-Monsoon (SIM) season across all nine provinces of Sri Lanka. Ninety open markets were included, with ten per province. Five fresh green leafy vegetable types consumed either raw, steamed, or half-cooked namely; *Centella asiatica* (Gotukola, [n=84]), *Alternanthera sessilis* (Mukunuwenna, [n=86]), *Ipomoea aquatica* (Kankun, [n=83]), *Trianthema portulacastrum* (Sarana, [n=52]), and *Amaranthus viridis* (Thampala, [n=44]) were selected. Approximately 50g of each sample was processed with a Tween 20 (5%) wash followed by overnight sedimentation, and centrifugation (2000×g, 15 min). Microscopic examination of parasites was performed on both the supernatant and sediment of each sample.

Results

The overall parasitic contamination was 22.6% (n=79). *A. sessilis* recorded the highest prevalence (24/86; 27.9%), while *I. aquatica* exhibited the lowest (10/83; 12.1%). Medically important parasites, including protozoans (*Balantidium coli*, *Cystoisospora belli*, coccidian oocysts morphologically consistent with *Toxoplasma gondii*) and helminths (*Ascaris* spp., *Hymenolepis* spp., *Strongyloides* spp., *Capillaria* spp., *Toxocara* spp., hookworm and taeniid eggs) were detected. *Strongyloides* spp. was the most prevalent parasite (31/349; 8.9%). No statistically significant differences were observed in the distribution of parasitic species across vegetable types or in prevalence across provinces ($P > 0.05$).

Conclusions

This study confirms uniform parasitic contamination of fresh green leafy vegetables across all nine provinces of Sri Lanka, regardless of vegetable type or geographical location during the Second Inter-Monsoon season.



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sciforum-177765: Parasitic Contamination of Soil Samples in Primary School Playgrounds in Jos North and South Local Government Areas, Plateau State

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Background: Parasitological contamination of soil in school environments poses a public health risk to school-aged children, particularly in settings with inadequate sanitation. School playgrounds are potential hotspots for parasite transmission among children. This study was conducted to determine the level of parasitic contamination of primary school playground soils in Jos North and Jos South Local Government Areas of Plateau State, Nigeria, and to assess hygiene, sanitation, and behavioural factors that may influence exposure to soil-borne parasites among school-aged children.

Methods: A cross-sectional study was conducted between August 2022 and November 2024. A total of 100 (2–3cm depth) topsoil samples were collected from selected primary school playgrounds using a purposive sampling technique. Collected samples were processed by sucrose flotation technique to detect helminth eggs and larvae. Data were analysed using descriptive statistics and Pearson's Chi-square test, with statistical significance set at $p < 0.05$.

Results: Of the 100 soil samples examined, 19 were positive for at least one STH parasite, giving an overall prevalence of 19.0%. Hookworm larvae were the most frequently encountered parasite with a prevalence of 8.0%, followed by *Ascaris lumbricoides* (3.0%), and larvae of *Strongyloides stercoralis* (2.0%) and *Taenia* spp. (4.0%). There was no statistically significant difference in parasitic contamination of schools' playgrounds between Jos North (20.0%) and Jos South (18.0%) ($\chi^2 = 0.08$, $p = 0.78$).

Conclusion: The detection of STHs in schools' playgrounds in both LGAs is a reflection of environmental contamination by human waste and continued risk of transmission among school-aged children. The presence of infective stages of STHs in primary schools' playgrounds underscores the need for improved sanitation, strengthened school-based deworming programs, and enhanced environmental hygiene practices.



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sciforum-177574: Parasitic helminth stages among companion animals and in soil from selected public and home environments in Gampaha and Colombo Districts, Sri Lanka

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Introduction

Soil contamination with animal excreta is widespread, posing public health risks. The aim was to describe the prevalence of intestinal helminths among cats and dogs and in soil from selected environments in Colombo and Gampaha Districts, Sri Lanka.

Method

Approximately 200g of subsurface soil was collected into zip-lock bags from randomly selected public sites and home gardens from May 2024 to January 2025. Soil samples were processed for helminths using magnesium sulfate flotation and Baermann techniques.

Wet smears prepared from excreta collected from randomly selected cats and dogs attending veterinary clinics in Colombo were examined microscopically for helminth ova and larvae.

Results

A total of 200 soil samples from Colombo (n=108) and Gampaha (n=92) were analyzed. Study sites included parks (n=32), religious places (n=48), university grounds (n=12), side-roads (n=12), beaches (n=12), school grounds (n=28), hospital grounds (n=8), and home gardens (n=48). The overall prevalence of helminth ova in soil by flotation was 14% (28/200), with 16.66% (18/108) and 10.86% (10/92) in Colombo and Gampaha, respectively. Helminth species detected were *Toxocara* spp. 57.14% [16/28], *Ascaris lumbricoides* 14.2% [4/28] and *Ancylostoma* spp. 28.57% [8/28]. The prevalence of parasitic helminth larvae in soil detected using the Baermann technique was 22%, for *Ancylostoma* spp. was 88.63%, and for *Strongyloides* spp. was 11.36%. Soil contamination was highest at religious sites (22.22%) and in parks (11.11%).

Analysis of faecal samples of 17 animals, including 8 feline and 9 canine samples, detected ova of *Toxocara* spp. (12.5%) and *Ancylostoma* spp. (62%) among cats and *Ancylostoma* spp. (55.5%) and *Capilaria* spp. (12.5%) among dogs via direct wet smears. Companion animals at religious sites had the highest parasite prevalence, 88.88% (8/9).

Conclusion

The prevalence of animal hookworms was high among cats and dogs in both Gampaha and Colombo Districts. Zoonotic helminth stages were widespread in soil in both districts, with few areas positive for human STH ova. Religious sites and public parks were the most contaminated. Local incidence rates of zoonotic STHs among humans were unknown. We recommend health education, animal deworming, safe disposal of animal excreta and stray animal control.



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sciforum-178515: Prevalence of *Toxocara canis* Infection in Dogs in Mexico: A Systematic Review

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Introduction. *Toxocara canis* is a zoonotic nematode of global importance that causes visceral and ocular larva migrans in humans. In Mexico, large populations of stray and free-roaming dogs increase environmental contamination with infective eggs, yet no previous systematic synthesis of prevalence data exists. This review aimed to determine the prevalence of *T. canis* infection in dogs across Mexico and identify research gaps.

Methods. Following PRISMA 2020 guidelines, systematic searches were conducted in PubMed and Scopus (up to March 2026) using the terms ("Toxocara canis" OR Toxocara) AND (dog OR dogs OR canine) AND (Mexico OR México) AND (prevalence OR infection OR seroprevalence). Inclusion criteria were original studies reporting quantitative prevalence (coprological, serological, or necropsy) in dogs in any Mexican region. Two independent reviewers screened titles/abstracts and extracted data on location, sample size, diagnostic method, and prevalence.

Results. Of 41 records identified in PubMed (and equivalent in Scopus), only three primary studies met inclusion criteria after duplicate removal and full-text assessment (n=544 dogs total). Prevalence ranged widely: 66.7% (serology, IHAT; stray dogs, Mexico City, 2008; n=141), 15.1% (coprology; stray dogs, Querétaro, 2011; n=378), and 8% (coprology; free-roaming dogs, Tulum, Quintana Roo, 2022; n=25). One additional regional review (2020) reported a broader Latin American range of 0–87%, with the highest values in young stray dogs. No meta-analysis was possible due to high heterogeneity in methods and populations.

Conclusions. *Toxocara canis* prevalence in Mexican dogs varies from 8% to 66.7%, being consistently higher in stray populations. These findings underscore the urgent need for nationwide control programs, routine deworming, and public health education. Future studies should use standardized diagnostics and include owned dogs to better estimate zoonotic risk.



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sciforum-178737: Prevalence of Taeniosis among humans in Mpumalanga Province, South Africa

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Introduction: Taeniosis is a parasitic disease caused by the adult stage of the zoonotic cestode, *Taenia* spp. Humans become infected by eating raw/undercooked beef or pork contaminated with *Taenia saginata* or *T. solium* cysticerci, respectively. *Taenia* infections can result in serious diseases such as neurocysticercosis and lead to major economic losses through the downgrading of cysticerci-infected meat. Although taeniosis is a major risk factor for cysticercosis, there are currently few reports on the prevalence of taeniosis in South Africa. Accordingly, this research aims to determine the prevalence of taeniosis in Mpumalanga Province using morphological and molecular techniques.

Methods: Routine laboratory-submitted stool samples originating from adults were obtained from a private pathology laboratory. Samples were examined for the presence of tapeworm proglottids macroscopically, and the detection of taeniid ova was performed by examining wet mounts of the stool samples using microscopy. Species identification was carried out by injecting adult tapeworm proglottids with Indian ink to highlight morphological differences.

Results: Out of 221 stool samples tested thus far, a 2.26% prevalence of taeniosis has been recorded, with positive samples originating from Nkangala and Ehlanzeni districts of the province. Proglottids observed in the positive samples were all identified to be from *T. saginata*. The preliminary results from this study correlate with published findings in KwaZulu-Natal and the Eastern Cape, with prevalence ranging between 0.78% and 3.8%. Molecular techniques are yet to be conducted to confirm the prevalence of taeniosis in Mpumalanga Province.

Conclusion: South African cases of taeniosis are not mandatorily reportable, despite the clinical and consequential economic impact when livestock become infected. There is a need for targeted public health interventions, improved food safety measures, and enhanced surveillance strategies to mitigate the burden of taeniosis in endemic regions such as South Africa.



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sciforum-169139: Re-emergence of Leptospirosis in Urban Tropical Settings: A Systematic Review of Climate, Environmental, and Socioeconomic Drivers

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Introduction

Leptospirosis is a neglected zoonotic disease with increasing global incidence, particularly in tropical urban environments. Rapid urbanization, climate change, inadequate sanitation, and expanding rodent populations have driven the re-emergence of leptospirosis, leading to recurrent outbreaks and substantial morbidity and mortality. We conducted a systematic review to synthesize current evidence on the climatic, environmental, and socioeconomic determinants of urban leptospirosis.

Methods

A systematic search of PubMed, Embase, Web of Science, and Scopus was conducted from January 2000 to December 2025 following PRISMA guidelines. Eligible studies included observational, ecological, and modeling studies evaluating environmental, climatic, and social drivers of leptospirosis transmission in urban settings. Primary outcomes were incidence, outbreak occurrence, and mortality. Secondary outcomes included environmental risk factors and socioeconomic vulnerability indicators. Qualitative synthesis and random-effects meta-analysis were performed when feasible.

Results

Forty-eight studies from 32 countries were included. Heavy rainfall, flooding events, and elevated temperatures were consistently associated with increased leptospirosis incidence, with pooled relative risks ranging from 1.6 to 3.4 following extreme precipitation events. Informal housing, poor sanitation infrastructure, high rodent density, and occupational exposure were major socioeconomic determinants. Urban slums accounted for a disproportionate burden of severe disease and mortality. Climate anomalies, including El Niño-related rainfall surges, were strongly linked to large-scale outbreaks. Integrative One Health surveillance models demonstrated improved outbreak prediction and early warning capacity.

Conclusions

Leptospirosis is rapidly re-emerging in urban tropical environments due to the synergistic effects of climate change, environmental degradation, and social vulnerability. Integrated One Health approaches combining environmental monitoring, rodent control, infrastructure investment, and climate-adaptive public health policies are urgently needed to reduce disease burden and prevent future epidemics.



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sciforum-175133: Recurrent Multicystic Vertebral Hydatidosis Causing Spinal Cord Compression: Radical Corpectomy and Instrumented Reconstruction in an Endemic Setting

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Background:

Spinal hydatidosis is a rare manifestation of cystic echinococcosis caused by *Echinococcus granulosus*, endemic in Peru and other regions of South America, the Mediterranean, Africa, and Asia. Vertebral involvement accounts for 0.5–2% of cases and is associated with high morbidity, neurological compromise, and frequent recurrence.

Case Presentation:

A 28-year-old woman from Huacho, Peru, with prior T12 hydatid cyst surgery presented with six months of progressive dorsal pain, lower limb paresthesias, urinary retention, and worsening paraparesis. Examination showed paraparesis (MRC 3+/5, left predominance), hyperreflexia, a sensory level at T10, and partial sphincter dysfunction.

MRI revealed a multiloculated cystic lesion at T12 with vertebral body lysis and >50% canal compromise. CT demonstrated ≈80% destruction of the T12 vertebral body with dorsolumbar instability. After one week of albendazole (400 mg twice daily), she underwent T12 corpectomy, cyst excision, decompression, and reconstruction with a titanium mesh cage and T11–L1 fixation. Intraoperative rupture occurred; hypertonic saline irrigation was applied. Histopathology confirmed echinococcosis.

Postoperatively, she completed a 4-month rehabilitation program, achieving recovery of sphincter control and motor improvement to 4/5. At discharge, she could walk short distances with a walker and required partial assistance.

At 12 months post-surgery, she remained stable, with no radiological recurrence. She ambulated with minimal assistance and had functional urinary continence, with mild residual weakness.

Conclusion:

Recurrent spinal hydatidosis requires aggressive surgical resection and prolonged antihelminthic therapy. Multicystic lesions increase the risk of rupture and recurrence. Early diagnosis, radical excision, stabilization, and close follow-up are essential to optimize neurological outcomes.



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sciforum-178475: Severe Mpox in people with advanced HIV disease complicated by disseminated tuberculosis: a report of three cases from Nigeria

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Introduction:

Mpox in PLHIV is associated with severe outcomes, particularly when co-infected with opportunistic pathogens, such as Mycobacterium tuberculosis (MTB).

Aim: We describe three cases of severe mpox in PLHIV, each with CD4 counts under 200 cells/mm³ and laboratory-confirmed disseminated tuberculosis.

Methods:

A retrospective review of three hospitalized patients with mpox and HIV who were also found to have disseminated tuberculosis. The clinical course, management, and outcomes were summarized.

Results:

Case 1: A 44-year-old man with newly diagnosed HIV presented after 14 days of illness with disseminated necrotizing mpox and sepsis, along with severe immunosuppression (CD4 200 cells/mm³). Urine LF-LAM confirmed disseminated TB, and blood culture confirmed Staphylococcus aureus bacteremia. Despite oxygen supplementation and broad-spectrum antibiotics, he died within three days of admission, prior to starting anti-tuberculosis or antiretroviral therapy.

Case 2: A 22-year-old woman with perinatally acquired HIV, virally suppressed on ART, presented after 8 days of illness with nodulopustular and severe genital mpox. Disseminated TB was confirmed via urine LF-LAM. She was started on anti-tuberculosis therapy, continued her ART, improved clinically, and was discharged after 10 days.

Case 3: A 28-year-old woman with HIV who had stopped ART for over a year presented with two weeks of widespread nodulopustular lesions. Initially misdiagnosed as disseminated herpes, she was restarted on ART. She became unconscious and died shortly after starting ART, raising concerns for unmasking IRIS.

Conclusion:

Mpox in PLHIV with severe immunosuppression is associated with high morbidity and mortality, especially when combined with disseminated TB and delayed ART initiation or reinitiation. Early recognition, integrated HIV/TB/mpox assessment, and careful timing of ART are crucial in high-burden settings to improve clinical outcomes.



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Session 3. Neglected Tropical Diseases

sciforum-175706: Prognostic factors associated with recurrence in patients undergoing surgery for hepatic cystic echinococcosis. A systematic review

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Background:

Hepatic cystic echinococcosis (HCE) is a neglected zoonotic disease with a substantial burden in endemic regions. Surgery remains the most frequently employed therapeutic approach; however, recurrence rates range from 8% to 10% and are associated with increased morbidity and healthcare costs. Identifying prognostic factors (PFs) may enable risk stratification and optimization of clinical management.

Objective:

To identify prognostic factors associated with recurrence in patients undergoing surgery for HCE.

Methods:

A systematic review was conducted (PROSPERO: CRD42024538005). Observational and experimental studies were searched in MEDLINE, Scopus, Embase, Web of Science, BIREME-BVS, and SciELO up to January 2026. Studies evaluating preoperative or surgical characteristics associated with recurrence were included. Risk of bias was assessed using the QUIPS tool, and certainty of evidence was evaluated with a modified GRADE approach for prognostic factors. Random-effects meta-analyses (REML) were performed when appropriate.

Results:

Nineteen studies were included (3,849 patients; 334 recurrences, 8.7%). Twenty-eight PFs were identified. In unadjusted analyses, prior recurrence (OR: 2.4), extrahepatic cysts (OR: 2.5), cyst rupture (OR: 11.1), multiple cysts (OR: 2.9), and cyst diameter >9 cm (OR: 2.1) were associated with increased recurrence risk. In multivariable analyses, prior recurrence (aOR: 2.7), ≥ 2 cysts (aHR up to 3.8), and larger cyst size (aOR up to 4.0) showed consistent independent associations. Evidence regarding surgical factors was limited and highly imprecise. Overall certainty of evidence ranged from low to very low due to clinical heterogeneity, lack of standardized recurrence definitions, and risk of confounding.

Conclusions:

Parasitic burden and intraoperative dissemination appear to be the primary drivers of recurrence after HCE surgery. Well-designed prospective multicenter cohorts with standardized definitions and robust multivariable adjustment are needed to strengthen prognostic evidence.



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sciforum-176727: National epidemiological patterns and clinical characteristics of leprosy in Brazil: a population-based analysis of surveillance data from 2001 to 2025

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Introduction

Leprosy remains a major neglected tropical disease and a persistent public health challenge in endemic regions. Brazil accounts for a substantial proportion of global cases, reflecting ongoing transmission and structural inequalities that affect early detection and disease control. Understanding national epidemiological and clinical patterns is essential for guiding public health strategies.

Methods

A nationwide ecological study was conducted using secondary data from the Brazilian Notifiable Diseases Information System (SINAN), accessed through the DATASUS platform. All confirmed leprosy cases reported between 2001 and 2025 were included. Variables analyzed comprised sex, age group, geographic region, operational classification, and clinical form. Descriptive epidemiological analyses were performed using absolute and relative frequencies.

Results

During the study period, 998,774 cases of leprosy were reported in Brazil. A slight predominance among males was observed (56.0%). Most cases occurred in individuals aged 15 years or older (93.5%), while 6.5% were detected in children under 15 years, indicating continued transmission. The Northeast region accounted for the largest proportion of cases (40.2%), followed by the North (20.0%) and Central-West (18.4%) regions, demonstrating marked regional disparities. Multibacillary disease represented 65.7% of cases, suggesting late diagnosis and sustained transmission chains. The dimorphic clinical form was the most frequently reported presentation (40.0%).

Conclusions

Leprosy remains widely distributed across Brazil and disproportionately affects highly endemic regions. The predominance of multibacillary disease and the persistence of cases among children reinforce the need to strengthen early diagnosis, active case detection, and public health surveillance in endemic settings.



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sciforum-175603: Snake envenomation and acute kidney injury: asystematic review and meta-analysis

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Background

Snakebite envenomation remains a health problem in tropical regions and is a recognized cause of acute kidney injury (AKI). Despite numerous regional studies, the global burden and predictors of snakebite-induced AKI have not been systematically quantified. This review aimed to estimate the pooled incidence of AKI following snake envenomation, identify key clinical and laboratory features, and determine the mortality rate and proportion of patients requiring renal replacement therapy (RRT).

Methods

A systematic search of PubMed, Embase, and Cochrane Library was conducted for studies published between 2015 and 2025 that reported AKI in snakebite patients. Eligible studies included observational and interventional designs with ≥ 10 participants. Data were extracted on study characteristics, incidence of AKI, need for RRT, mortality rate and associated clinical and laboratory features.

Results

Thirty (30) studies comprising 8,612 participants met the inclusion criteria. The pooled incidence of AKI following snake envenomation was 23% (95% CI: 17–33%; $I^2 = 97.2\%$), and among these, 28% (95% CI: 17–43%; $I^2 = 86.9\%$) required RRT and the pooled mortality rate was 10% (95% CI 4–21%), with substantial heterogeneity ($I^2 = 85\%$). A high incidence was observed among Russell's viper victims, 37% (95% CI: 21–57%), and 23% (95% CI: 15–34%) in non-Russell's viper victims. Common clinical predictors of AKI included older age, male sex, comorbidities (hypertension, diabetes mellitus), local swelling, cellulitis, bleeding, hypotension, oliguria/anuria, and delayed presentation. Laboratory features included incoagulable 20-min whole blood clotting test (WBCT), prolonged prothrombin time/ international normalized ratio (PT/INR), elevated serum creatinine and blood urea and nitrogen (BUN), thrombocytopenia, and proteinuria. Biomarkers such as urinary neutrophil gelatinase-associated lipocalin (NGAL), cystatin C, and β -2 microglobulin were associated with early renal injury.

Conclusion

Approximately one-third of snakebite victims develop AKI, and nearly one in three affected patients requires dialysis. Clinical manifestations such as coagulopathy and local tissue injury are commonly observed. Early recognition, prompt antivenom therapy, and supportive renal management are critical to improving outcomes.



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sciforum-176683: Temporal and demographic trends of American tegumentary leishmaniasis in Brazil: a nationwide analysis from 2007 to 2025

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Introduction

American tegumentary leishmaniasis (ATL) remains a major neglected tropical disease in Latin America. Brazil accounts for a substantial proportion of cases worldwide, with transmission strongly influenced by ecological and socioeconomic factors. Investigating temporal and demographic trends is essential to better understand the current epidemiological dynamics of the disease.

Methods

A nationwide ecological study was conducted using secondary data from the Brazilian Notifiable Diseases Information System (SINAN), available through the DATASUS platform. Confirmed ATL cases reported between 2007 and 2025 were analyzed. Variables included sex, age group, and region of residence. Descriptive epidemiological analyses were performed to evaluate demographic patterns and geographic distribution.

Results

Between 2007 and 2025, 351,267 confirmed ATL cases were reported in Brazil. A pronounced male predominance was observed (72.9% of cases), suggesting occupational or environmental exposure patterns. Adults aged 20–39 years represented the most affected group (38.9%), followed by individuals aged 40–59 years (25.1%), indicating higher incidence among economically active populations. Geographically, the North region concentrated the largest share of cases (43.5%), followed by the Northeast (28.4%), reflecting the persistence of endemic transmission in tropical and Amazonian areas.

Conclusions

The epidemiological profile of ATL in Brazil reveals strong demographic and geographic disparities, with higher incidence among adult males and populations living in northern tropical regions. These findings highlight the continued need for targeted surveillance and control strategies in endemic areas and reinforce the importance of strengthening public health interventions in high-transmission settings.



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sciforum-177760: Assessing Essential Diagnostic Availability for Neglected Tropical Diseases in India: A Burden-Informed Analysis

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India bears a substantial burden of neglected tropical diseases (NTDs), yet the availability of essential diagnostic services across public health facilities may not adequately reflect local epidemiological needs. This study aimed to assess the availability of diagnostics for major NTDs and examine their alignment with disease burden across different levels of the public health system.

A cross-sectional assessment was conducted in 332 public health facilities across seven states and one union territory in India, including sub-centres, primary health centres, community health centres, and district hospitals. Diagnostic availability for malaria, dengue, Japanese encephalitis, chikungunya, lymphatic filariasis, leishmaniasis, helminthic infections, and HIV was evaluated based on the Indian Council of Medical Research National Essential Diagnostics List (2019). A Diagnostic Readiness Index (DRI) was calculated at facility, district, and state levels to measure diagnostic capacity.

Diagnostic readiness increased with higher levels of healthcare facilities but showed limited concordance with reported disease burden. Malaria diagnostics demonstrated the highest availability across all tiers of care (mean district DRI: 84.34%), reflecting sustained national programmatic prioritization. In contrast, diagnostic availability for dengue (40.36%), lymphatic filariasis (29.22%), helminthic infections (25.30%), Japanese encephalitis (8.13%), and leishmaniasis (5.72%) remained limited, even in districts reporting considerable disease burden. The most pronounced gaps between disease burden and diagnostic availability were observed at sub-centres and primary health centres, while district hospitals showed relatively better alignment.

These findings highlight a persistent mismatch between NTD burden and diagnostic readiness within India's public health system. Strengthening decentralized, burden-informed deployment of point-of-care diagnostics—particularly at peripheral and primary care levels—will be critical to improve early case detection, enhance surveillance accuracy, and accelerate progress toward national NTD control and elimination goals.



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sciforum-174832: Clinical vulnerability patterns in human *Cochliomyia hominivorax* myiasis in Southern Mexico: an exploratory analytical study

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Introduction: Human myiasis caused by *Cochliomyia hominivorax* remains a neglected tropical zoonosis in Latin America despite regional eradication programs targeting the New World screwworm. Contemporary epidemiological and vulnerability patterns in Mexico are poorly characterized. We conducted an analytical exploratory study to describe clinical distribution and identify factors associated with complicated outcomes in confirmed human cases reported in Southern Mexico.

Methods: A retrospective observational exploratory study was conducted, including 33 laboratory-confirmed human cases reported in the National Epidemiological Surveillance System (epidemiological week 29, 2025). Variables analyzed included age, sex, anatomical location, comorbidities, and clinical outcomes. Comorbidity was defined as documented chronic clinical conditions in the registry (e.g., diabetes mellitus, neoplasms, vascular disease, chronic kidney disease, malnutrition, alcohol use disorder). Age was summarized using the median and interquartile range (IQR). Proportions were calculated with 95% confidence intervals (95% CIs) using the Wilson method. Associations were assessed using Fisher's exact test and crude odds ratios (ORs) with Haldane correction.

Results: The median age was 60 years (IQR 48–74; range 17–87), and 63.6% were male (95% CI 46.6–77.8). Cephalic involvement was the most frequent presentation (45.5%; 95% CI 29.8–62.0). At least one comorbidity was present in 75.8% (95% CI 59.0–87.2), and ≥ 2 in 21.2%. Six patients (18.2%) had neoplastic disease, including skin cancer, basal cell carcinoma, lip cancer, tongue cancer, and parietal neoplastic lesions; all were located in the cephalic region (100%). Complicated outcomes occurred in 15.2% (95% CI 6.7–30.9), and case fatality was 3.0% (95% CI 0.5–15.3). One death occurred in a patient with multiple comorbidities; the specific cause of death was not publicly available.

Conclusions: Human *Cochliomyia hominivorax* myiasis in Southern Mexico predominantly affects patients with comorbidities and conditions favoring tissue exposure. The observed association between cephalic neoplasms and infestation suggests that exposed tumor lesions may play a key role in pathogenesis. These findings provide clinical evidence of vulnerability factors in this neglected zoonosis.



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sciforum-176502: Community-Level Profiling of Gut Bacteria in Sand Flies from a Human Leishmaniasis-Endemic Region: Implications for Disease Transmission and Control

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Introduction: Leishmaniasis is a neglected tropical disease affecting millions worldwide, and Sri Lanka has reported increasing human cases annually. The interaction between sand fly vectors, their gut microbiota, and *Leishmania* parasites influences human disease transmission. Understanding vector gut bacterial communities in disease-endemic areas is therefore important for developing novel strategies to interrupt human infection cycles.

Methods: Sand flies were collected from Mihintale, a confirmed leishmaniasis-endemic region with active human cases, to investigate gut bacterial profiles relevant to human disease transmission. Light traps were placed in peridomestic environments (buffalo cattle sheds) adjacent to human dwellings between 18:00-06:00 hours. Following morphological identification, 50 male and 50 female *Phlebotomus argentipes* and *Sergentomyia punjabensis* were surface-sterilized and dissected. Pooled male and female gut samples were subjected to next-generation sequencing of the 16S rRNA gene (V1-V9 regions) to characterize bacterial communities.

Results: Analysis revealed 75 bacterial genera in males and 53 in females across both *Phlebotomus argentipes* and *Sergentomyia punjabensis* populations collected from this disease-endemic region. Across both species, *Methylobacterium* was the most abundant genus in males (27.01%) and females (28.04%). Thirty bacterial genera constituted a core microbiota shared between sexes. *Wolbachia* was detected exclusively in female sand flies.

Conclusions: This culture-independent profiling provides baseline data on the gut bacterial communities associated with sand fly vectors in a Sri Lankan endemic region. The abundance of *Methylobacterium* merits further investigation to determine its suitability as a candidate for paratransgenesis. The detection of *Wolbachia* exclusively in females requires cautious interpretation, as it may reflect acquisition during blood feeding from other hosts rather than a stable endosymbiotic association. Future studies should focus on confirming the origin and heritability of *Wolbachia* in *Phlebotomus argentipes* and evaluating the functional role of core microbiota in vector competence to inform the development of microbiome-based intervention strategies.



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sciforum-175272: Detection, Isolation, and *In Vitro* Cultivation of *Balamuthia mandrillaris*: A Systematic Review of Current Laboratory Approaches and Evidence

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Introduction: *Balamuthia mandrillaris* is an opportunistic free-living amoeba that causes granulomatous amoebic encephalitis, a rare but often fatal disease with delayed diagnosis. Laboratory identification is challenging because of low organism burden, slow growth, and morphological similarity to other free-living amoebae. Consequently, several laboratory techniques have been developed for detection, isolation, or cultivation, though their performance and feasibility vary across studies. This systematic review evaluates and compares these methods. **Methods:** Following PRISMA 2020 guidelines, a systematic search (24/09/2025) was conducted in Medline, Web of Science, ScienceDirect, and ProQuest using “*Balamuthia mandrillaris*” combined with “Detection”, “Isolation”, “Culture Techniques”, and “*In Vitro* Techniques”. Experimental and observational laboratory studies assessing detection, isolation, or cultivation methods in clinical, veterinary, or environmental samples were included. Outcomes comprised methodological performance, feasibility, and cultivation success. **Results:** Of 350 articles screened, 10 studies met the inclusion criteria. Molecular methods, particularly PCR, demonstrated the highest analytical performance, with sensitivities up to 84% in formalin-fixed tissues and limits of detection as low as ~1 amoeba per sample. In environmental studies, PCR showed higher detection rates than culture (e.g., 47.4% vs 18.4% for free-living amoebae). Culture-based methods enabled isolation but required prolonged incubation (up to 60 days) and showed low recovery (e.g., 4.5% in water samples). Multi-step protocols combining environmental culture, mammalian cell co-culture, and axenization improved isolation but remained technically demanding. *In vitro* cultivation advances demonstrated sustained growth in human fibroblast and endothelial cell lines and axenic media, achieving yields up to 1.3×10^6 amoebae/mL with long-term viability. Immunological assays were useful for exposure assessment but insufficient as standalone diagnostics. **Conclusions:** Molecular methods provide the most sensitive detection, while culture remains essential for isolation despite low efficiency. Integrated workflows and standardized protocols are needed to improve diagnostic reliability and support future research.



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sciforum-174046: Empowering Rural Communities for Neglected Tropical Disease Prevention: Outcomes of a Participatory Vector Surveillance System for Chagas Disease

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Introduction: Chagas disease (CD), a neglected tropical disease caused by *Trypanosoma cruzi*, disproportionately affects socially and economically vulnerable populations in the Gran Chaco ecoregion. Despite regional advances in vector control, persistent structural inequalities, geographic dispersion, and limited health resources challenge the sustainability of traditional top-down strategies. Innovative, community-centered approaches are needed to enhance surveillance, equity, and long-term control.

Methods: A longitudinal mixed-methods community intervention was conducted between April 2021 and November 2023 in a rural locality of Santa Fe Province, Argentina. A participatory collaborative social network was co-constructed through stakeholder mapping, intersectoral workshops, school-based activities, and sustained communication using information and communication technologies. Community members were trained to identify and report suspected triatomine bugs, while institutional partners performed entomological confirmation and focal insecticide spraying. Infestation data from 2023 were compared with those from the last Ministry of Health inspection in 2018.

Results: In 2023, four households with triatomine infestation were detected through community-based surveillance. All specimens were identified as *Triatoma infestans* and tested negative for *T. cruzi*. Focal fumigation was implemented within the same week through coordinated municipal action. The number of infested houses matched the 2018 institutional findings; however, the participatory strategy required fewer external resources, reduced logistical costs, and enabled faster response. The intervention strengthened local awareness, inter-institutional articulation, and collective responsibility for prevention.

Conclusions: Embedding vector surveillance within a participatory community network represents a feasible and sustainable complementary strategy for Chagas disease control in underserved rural settings. By addressing social determinants, promoting local ownership, and reinforcing intersectoral collaboration, this approach aligns with current global strategies for neglected tropical diseases and may contribute to more equitable and resilient control programs.



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sciforum-174733: Field Assessment of Lymphatic Filariasis, Transmission Dynamics, and Intervention Efficacy in Varanasi District (2019-2025).

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Background

Lymphatic Filariasis (LF) is a neglected tropical disease that affects millions of people worldwide and impacts mental, physical, and socioeconomic health globally. India carries a significant portion of this burden, with cases endemic in 21 states and union territories. The Government of India had a nationwide Mass Drug Administration/IDA (triple drug therapy) across various districts, which includes Varanasi, as part of the Global Programme to Eliminate Lymphatic Filariasis.

Objective

This study aims to assess administration, transmission, and intervention outcomes in the Varanasi district from the years 2019 to 2025. This comprises MDA/IDA coverage for the duration from 2019 to 2021 and was evaluated for its impact on LF transmission through night blood surveys and Transmission Assessment Surveys conducted in 2022. The coverage of MDA/IDA was recorded, and administration and evaluation were repeated in regions with more than 1% Mf rate.

Results

Mf rates were observed to have decreased in sentinel sites from 0.94% to 0.15% and in spot check sites from 0.46% to 0.10% from 2019 to 2021. The TAS conducted in 2022 with 19,852 eligible participants revealed an overall Mf rate of 0.1%. After the successful completion and evaluation of TAS, areas like Jaitpura (urban) and Chhapra (rural) exhibited Mf rates greater than 1% and thus continued MDA/IDA for two more years. By 2025, the prevalence of Mf in both regions was less than 1%, signifying a prolonged cessation of transmission.

Conclusion

This study shows that the MDA/IDA successfully lowered LF transmission in areas with high infection rates in the Varanasi district, but ongoing monitoring and strategic interventions are still needed to reach and maintain LF elimination goals through 2027.



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sciforum-175594: Foodborne Chagas Disease as an Emerging Transmission Pathway: A One Health Analysis of Outbreak Preparedness in Colombia

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Introduction

Foodborne transmission of *Trypanosoma cruzi* is an increasingly recognized cause of acute Chagas disease outbreaks in Latin America. Unlike classical vector-borne transmission, these events involve high parasite inocula, severe clinical presentations, and rapid clustering of cases. In Colombia, outbreaks associated with contaminated beverages and artisanal food production reveal vulnerabilities that extend beyond clinical detection into surveillance, food safety, and intersectoral coordination. This study aimed to evaluate public health preparedness for foodborne *T. cruzi* transmission in Colombia using a One Health and systems-thinking framework.

Methods

A qualitative institutional case study was conducted using a One Health and systems-thinking framework. Sixty-two official documents issued between 2000 and 2024—including surveillance guidelines, outbreak reports, regulatory instruments, and response protocols—were reviewed. Structured consultations were performed with stakeholders from health, food safety, agricultural, and territorial authorities. Data were analyzed using hybrid deductive–inductive thematic analysis focusing on surveillance integration, regulatory clarity, territorial response capacity, and intersectoral coordination.

Results

Preparedness for foodborne Chagas disease was limited by fragmented institutional responsibilities and delayed cross-sector activation. Surveillance systems operated in parallel, often linking food safety investigations only after clinical confirmation of acute cases. Upstream prevention was constrained by unclear mandates for identifying contamination pathways. Territorial capacity varied widely, and coordination mechanisms functioned mainly during outbreaks rather than prevention phases. These factors produced response delays and hindered early containment.

Conclusions

Foodborne Chagas disease represents a distinct epidemiological scenario requiring integrated surveillance beyond vector control frameworks. Strengthening preparedness requires interoperable surveillance systems, defined cross-sector responsibilities, and institutionalized One Health coordination. Addressing governance gaps is essential to prevent recurrent outbreaks and to adapt Chagas disease control strategies to emerging transmission pathways.



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sciforum-168061: Hidden in the Dirt: The Persistent Presence and Environmental Drivers of Soil-Transmitted Helminths in parts of Ogun State, Southwestern Nigeria

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Introduction: Soil-transmitted helminths (STHs) remain a significant public health challenge in Nigeria, particularly in areas with inadequate sanitation and environmental conditions that favor parasite persistence. This study investigated the prevalence of STHs in soil samples from three Local Government Areas in Ogun State, Nigeria, and evaluated the influence of selected soil physicochemical parameters on helminth occurrence.

Methods: One hundred and sixty-four (164) soil samples were collected from public locations, including dumpsites, markets, schools and roadsides, across 35 communities. In situ measurements of soil temperature, pH and moisture were obtained using a soil survey probe inserted vertically to a depth of approximately 5 cm. Parasitological examination of soil samples was performed using the sedimentation technique. Data analysis was conducted using R software. Descriptive statistics were used to summarize parasite distribution, while inferential statistics were applied to assess associations between STH occurrence and environmental variables, with statistical significance set at p 0.05.

Results: Results revealed that out of the 164 samples, 152 (92.7%) were contaminated with at least one parasite species. The most frequently detected helminths were *Taenia* spp. (76%) and *Ascaris lumbricoides* (61%), followed by *Trichuris trichiura* (12%), Hookworms (8%), *Toxocara canis* (5%), *Enterobius vermicularis* (4%) and *Strongyloides stercoralis* (2%). There was no significant relationship between the intestinal parasites found in the soil samples and the study locations ($p > 0.05$). Soil physicochemical analysis indicated more dry soils (66%), with a mean temperature of 37°C and a mean pH of 6.89. No significant associations ($p > 0.05$) were observed between STH occurrence and moisture content, soil temperature and pH.

Conclusion: The widespread soil contamination observed highlights substantial environmental exposure risk and underscores the importance of integrated control measures, including environmental sanitation, routine deworming and continuous public health surveillance to reduce STH transmission in endemic settings such as in the studied area.



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sciforum-175382: Impact of Intestinal Helminth Infections on Iron Deficiency Anemia during Pregnancy

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Iron deficiency anemia (IDA) remains a major public health challenge among pregnant women, particularly in low- and middle-income countries where intestinal parasitic infections (IPIs) are highly endemic. Evidence from cross-sectional, case-control, cohort studies, and systematic reviews consistently demonstrates a strong association between helminthic infections and maternal anemia. In rural Chad, anemia affected 53% of pregnant women, with high rates of intestinal parasitism. Similarly, in Southern Ethiopia, 38.7% of pregnant women were infected with intestinal parasites, and anemia prevalence was significantly higher among infected women (55.6%) compared to non-infected counterparts (16.4%), with a sixfold increased odds of anemia (AOR=6.14). Helminth-specific studies in East Wollega, Ethiopia, reported a 24.7% prevalence of intestinal helminths, predominantly hookworm (15.1%), and confirmed significant associations between helminth infection and anemia. A global meta-analysis further estimated pooled prevalences of hookworm (19%), *Ascaris lumbricoides* (17%), and *Trichuris trichiura* (11%) among pregnant women, demonstrating a 2.65-fold increased risk of anemia in infected individuals. Prospective cohort data showed significant reductions in hemoglobin and hematocrit levels among infected pregnant women, particularly with hookworm and *Schistosoma mansoni* infections. Mechanistically, helminths contribute to chronic intestinal blood loss, impaired iron absorption, reduced appetite, and inflammation-mediated nutrient malabsorption, exacerbating iron deficiency during pregnancy. Co-infections amplify severity, increasing risks of miscarriage, low birth weight, and small-for-gestational-age outcomes. Evidence from randomized trials indicates that second-trimester deworming may reduce maternal anemia prevalence. Collectively, these findings underscore the dual burden of IPIs and IDA in pregnancy and highlight the importance of routine screening, deworming strategies, iron supplementation, and improved water, sanitation, and hygiene interventions to mitigate adverse maternal and neonatal outcomes.



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sciforum-172696: Impact of Mass Treatment with Praziquantel Among Students of Tsangaya Schools in Kura Local Government, Kano State

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Introduction: Schistosomiasis is reported to be one of the most important worm infestations of mankind and is widely distributed over three continents, affecting more than 200 million people. Mass administration of praziquantel has taken place in many centers focusing only on children attending public schools. The purpose of this study was to assess the impact of mass treatment with praziquantel among students of Tsangaya School (Almajiri Schools) in Kura Local Government, Kano State. **Methods:** The study is a cross-sectional prospective interventional study involving four Tsangaya Schools named Tsangaya A, Tsangaya B, Tsangaya C, and Tsangaya D, from which 181 Almajiri students were recruited and questionnaires administered. Urine and blood samples were collected before and after drug intervention for macroscopic and microscopic examination for detection of *Schistosoma* eggs and assessment of packed cell volume (PCV) for possible risk of anemia. **Results:** The majority of the Almajiri students (90.6%) were infected with *Schistosoma haematobium* only, while 1.7% were co-infected with *S. mansoni*, given the overall prevalence of 92.3%. Tsangaya A has the highest prevalence of 32.0%, while Tsangaya B has the lowest of 14.9%. Tsangaya C has a prevalence of 24.9%, while that of Tsangaya D has 20.4%. The prevalence dropped to 12.7% after intervention. The mean PCV (M=34.80%, SD=5.75) of the participant was found to be significantly lower than the PCV among participants after treatment (M=35.57%, SD=5.48), $t=-4.923$, $df=166$, $P=0.001$. The binary logistic regression model predicted a high (OR=2.65) risk of developing schistosomiasis when staying for a duration of more than 10 years. **Conclusion:** This study showed that urinary schistosomiasis was prevalent among students of Tsangaya schools and that praziquantel is effective. There is a need for health education in this community.



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sciforum-171916: Imported Human African Trypanosomiasis in a Non-Endemic Setting: A Ten-Year Laboratory Review at the National Institute for Communicable Diseases, South Africa

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Background

Human African trypanosomiasis (HAT) occurs in two forms, caused by *Trypanosoma brucei gambiense* in West and Central Africa and *Trypanosoma brucei rhodesiense* in Eastern and Southern Africa. Although substantial progress toward elimination has been achieved in endemic regions, *T. brucei* infections continue to pose diagnostic challenges in non-endemic countries in people arriving from affected areas. South Africa is not endemic for HAT and all detected cases are imported or travel-associated. Reference laboratories therefore play a critical role in confirmatory diagnosis.

Methods

We conducted a retrospective laboratory-based review of samples submitted for trypanosomiasis testing at the National Institute for Communicable Diseases (NICD) between 2016 and 2025, evaluating diagnostic outcomes, specimen characteristics, and referral patterns. All specimens referred for suspected or confirmatory *T. brucei* infection were included, and demographic, referral and laboratory data were analysed.

Results

A total of 38 patients with submitted samples were included; 69% were male and 29% female, with a median age of 45 years (range 12–87). Whole blood (81.8%) and cerebrospinal fluid (CSF) (10.9%) were the most frequently submitted specimen types. Whole blood demonstrated a positivity rate of 23.6%, while none of the CSF samples tested positive. A real-time PCR for detection of *Trypanosoma brucei* species complemented microscopy and enabled analysis of additional specimen types; notably, one case was diagnosed from serum using PCR. Most submissions (92%) originated from the private health sector, primarily in Gauteng Province, of which 25% tested positive. Confirmed cases reported travel or residence in Zambia, Malawi, Tanzania, and the Democratic Republic of the Congo.

Conclusions

This review highlights the importance of centralised reference laboratory services for detecting imported HAT in non-endemic countries. Expanded molecular diagnostic capacity and sustained clinical awareness remain essential for timely detection. Implementation of multiplex PCR capable of distinguishing *T. brucei subspecies*, currently under development at the PRL, will enhance surveillance sensitivity and support ongoing elimination efforts in the African region.



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sciforum-172168: Improved and customized dengue serodiagnostics through combined NS1/IgM testing and novel dual-cut-off IgG ELISA

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Introduction

Accurate diagnostics of dengue virus (DENV) infection are essential for patient management, outbreak control, and vaccine implementation. Serological testing plays a key role, especially when molecular assays are unavailable or viremia subsides; yet, cross-reactivity with other flaviviruses remains a challenge. This study examined the diagnostic accuracy of four Euroimmun ELISAs, including a newly developed dual-cut-off Anti-DENV IgG ELISA.

Methods

The Dengue Virus NS1 ELISA, Anti-Dengue Virus Type 1-4 ELISA (IgM), Anti-Dengue Virus Type 1-4 ELISA (IgG; native antigen/gE-based), and the novel Anti-Dengue Virus NS1 ELISA 2.0 (IgG; recombinant NS1-based, with an alternative higher cut-off for flavivirus-endemic regions) were analyzed. Sensitivity was determined using sera from 22 Vietnamese patients with RT-PCR-confirmed DENV infection, collected during acute (t1, 1-6dpo), early convalescent (t2, 4-9dpo), and late convalescent (t3, 13-19dpo) phases. Specificity was assessed with samples from 500 healthy German blood donors (HBD) and 40 patients each with West Nile virus (WNV) or Zika virus (ZIKV) infection, all serologically positive for the respective virus.

Results

Sensitivities were 90.5%/70.0%/0% (t1/t2/t3) for NS1, 33.3%/85.0%/77.3% for IgM, 66.7%/100%/100% for IgG, and 33.3%/65.0%/100% vs. 19.1%/50.0%/100% for IgG 2.0 (standard vs. alternative cut-off). Combined NS1/IgM testing achieved 100% sensitivity in single acute-phase samples. Overall specificity was 85.7% (HBD/WNV/ZIKV: 95.0%/50.0%/5.0%) for IgG, compared to 95.7% (98.2%/95.0%/65.0%) vs. 99.5% (99.8%/97.5%/97.5%) for IgG 2.0 (standard vs. alternative cut-off).

Conclusion

Euroimmun ELISAs support customized, highly accurate and versatile diagnostic strategies applicable to various dengue testing contexts. Combining NS1 and IgM ELISAs offers an alternative to molecular assays during the acute phase of infection. The native antigen/gE-based IgG ELISA enables early sensitive IgG detection, although with limited specificity. With minimal cross-reactivity, the NS1-based dual-cut-off ELISA 2.0 (IgG) reliably captures DENV-specific IgG dynamics and enhances differentiation from other flaviviruses, which could provide an advantage in the use for convalescent-phase diagnostics, surveillance, and pre-vaccination serostatus determination.



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sciforum-180745: Malacological and Parasitological Determinants of Human and Bovine Schistosomiasis at Bwanje Valley Irrigation Scheme in Dedza District, Malawi

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This mixed-method cross-sectional study was conducted in 2024 to assess the burden and determinants of schistosomiasis in snails, cattle, and humans. Snail habitats were mapped using Quantum GIS and sampled using purposive and simple random sampling. Snails were collected, identified, and examined for schistosomes via cercariae shedding and microscopy. A structured questionnaire was administered. Urine and stool samples were collected using cluster and systematic random sampling, and analyzed by means of microscopy. Cattle postmortem inspection was performed using convenience sampling. Data entry, descriptive statistics, Chi-square test, binary logistic regression analysis, and Pearson correlation were performed using SPSS at P 0.05. Out of the 385 snails, *Bulinus globosus* snails (n=362, 94.0%) were more abundant than *Bulinus pfeifferi* (n=14, 4.0%) and *Bulinus africanus* (n=9, 2.0%). Only *Bulinus globosus* (n=104) snails were shedding Cercariae, registering a 27.01% infection rate. Of the samples, 168/406 were positive for urinary schistosomiasis, registering 45.81% prevalence. In addition, 13/180 stool samples were positive for bovine schistosomiasis, registering 7.22% prevalence. All postmortem samples were negative for bovine schistosomes. Gender, age, occupation, history of Mass Drug Administration (MDA), use of PPE, and water source were associated with urinary schistosomiasis (P<0.005). Respondents who did not receive Praziquantel (COR= 2.481, 95%, CI: 1.020- 6.031) were 2.48 times more at risk of schistosomiasis. Lack of PPE usage (COR= 0.524, 95%, CI: 0.309-0.889), open water source (COR= 0.455, 95%, CI: 0.181-1.143), and men (COR=0.467, 95%, CI: 0.299-0.730) had reduced odds of being infected than their counterparts. We recommended MDA for residents and livestock, vector control, and health education.



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sciforum-178171: Molecular analysis of individually laser-dissected microfilariae reveals *Acanthocheilonema reconditum* disguised as *Dirofilaria immitis*

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Introduction

Canine filarial parasites, including *Dirofilaria immitis* and *Acanthocheilonema reconditum*, can cause zoonotic infections in humans. *Dirofilaria immitis* and *Acanthocheilonema reconditum*, however, respond differently to drug treatments and, therefore, it is necessary to discriminate between these two parasites during diagnosis.

Methods

Light microscope blood surveys of canines were used to identify the presence of *D. immitis* and *A. reconditum* infections and co-infections in dogs that were life-long residents of Manaus (Amazonas, Brazil). The ITS-1 and 5S nuclear ribosomal DNA sequences and the mitochondrial CO1 and 12S gene sequences of filarial parasites were amplified by PCR and then Sanger sequenced for the molecular taxonomic classification of 20 individual microfilariae. These 20 individual microfilariae were isolated by laser dissection from a single canine blood sample, which morphological analysis of microfilariae suggested contained both *D. immitis* and *A. reconditum* parasites.

Results

A total of 20 individual microfilariae, which all morphologically appeared as *Dirofilaria immitis*, had two or more taxonomically informative PCR fragments amplified and Sanger sequenced. More than five ITS-1, 5S, 12S and CO1 DNA sequences were recovered from the twenty individual microfilariae. All recovered sequences showed 100% identity to database reference sequences matching *A. reconditum*.

Conclusions

Acanthocheilonema reconditum is present in the state of Amazonas and indeed the city of Manaus. *Acanthocheilonema reconditum* microfilariae are more difficult to distinguish from *D. immitis* than has previously been reported and it may, in fact, not be possible to reliably discriminate between these two species by the morphological features of their microfilariae alone. Although the possibility that *A. reconditum* and *D. immitis* form hybrids cannot be ruled out by this work, no evidence of hybrids or gene flow between these parasites was detected in our study.



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sciforum-169517: Morbidity and Mortality from Visceral Leishmaniasis in Brazil: An Ecological Study Based on DATASUS

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Visceral leishmaniasis is a neglected zoonotic disease in Brazil, occurring predominantly in tropical and subtropical areas. It is a chronic disease with systemic involvement, associated with high morbidity and mortality. Analyzing the epidemiological behavior of this disease is essential for planning effective prevention and control strategies.

This was a retrospective ecological study based on secondary data obtained from the Department of Informatics of the Brazilian Unified Health System (DATASUS). Records of cases and deaths due to visceral leishmaniasis in Brazil from 2015 to 2025 were analyzed. The variables evaluated included year of occurrence, geographic region, sex, and age group. A descriptive analysis was performed to assess temporal and regional distribution.

During the study period, a total of 28,553 cases and 2,295 deaths due to visceral leishmaniasis were recorded in Brazil. The highest frequencies of cases and deaths were observed in the Northeast and Southeast regions. Males and individuals aged 20 to 39 years were the most affected. A variable temporal pattern was observed, with periods of increased mortality in certain regions of the country.

Therefore, visceral leishmaniasis, as a neglected disease, represents a major public health challenge in Brazil, with significant regional and demographic inequalities. The findings highlight the need to strengthen epidemiological surveillance, promote early diagnosis, and implement public policies targeted at areas with the highest disease burden.



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sciforum-159529: Prevalence and Intensity of Soil-Transmitted Helminthiasis in Urban and Peri-Urban Dumpsites in Ibadan, Southwestern Nigeria: A Cross-Sectional Study

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Background Soil-Transmitted Helminthiasis (STHs) remains a major public health burden in developing countries, with contaminated soil acting as reservoirs of transmission. Here, we assessed the prevalence and intensity of STHs in soil samples collected from selected dumpsites across four areas in Ibadan, Oyo State, Nigeria.

Method: A total of 312 soil samples were collected across 12 dumpsites (26 per site) across four local government areas. Parasite eggs or larva recovered using sedimentation and modified Baermann techniques. Identification was done using standard microscopy. Data was analyzed using SPSS version 22. Prevalence and intensity of STHs was computed across study sites, with chi-square test, ANOVA used logistic regression used to assess association respectively. Statistical significance was set at p0.05.

Result: Overall STH prevalence was 43.9%, with *Strongyloides* spp. been the most common (28.2%), followed by hookworms (13.8%) and *Ascaris* spp. (1.9%). Mean infection intensity was highest for *Strongyloides* (0.59 ± 0.95), followed by hookworms (0.22 ± 0.56) and *Ascaris* (0.03 ± 0.19). Prevalence was slightly higher in peri-urban (43.9%) than urban areas (40.4%) without statistical significance ($p = 0.10$). However, urbanity (AOR: 6.11, 95% CI: 2.24–18.00, $p = 0.001$) and in Ido LGA (AOR: 8.72, 95% CI: 4.29–18.60, $p = 0.001$) were significantly associated with contamination.

Conclusion: Our findings show that dumpsites in urban and peri-urban areas could serve as important reservoirs for STH parasites. This calls for urgent need for environmental and health educational interventions targeted at improving waste management, dissuading open defecation and scavenging practices on dumpsites.



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sciforum-175373: Prevalence of Urinary Schistosomiasis Among School-Age Children in Goronyo Local Government Area, Sokoto State, Nigeria

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Introduction: Urinary schistosomiasis remains a significant public health challenge in Nigeria, affecting millions of people, particularly school-age children. A cross-sectional study was conducted to determine the prevalence and risk factors associated with urinary schistosomiasis among school-age children in Goronyo Local Government Area, Sokoto State, Nigeria. **Methods:** A total of 200 urine samples were collected and analyzed using standard filtration technique. Chi-square statistical analysis was used to determine significant association between occurrence of urinary schistosomiasis and gender, age, and wards of the pupils. **Results:** Out of the 200 samples analyzed, 48 (24%) were found to be infected with *Schistosoma haematobium*. Males were more often infected (14%) than females (10%). The highest prevalence was recorded in the Sabon-Gari ward (8%) settlement, followed by Bazza (7%) and Taloka (5%), while the lowest prevalence was recorded in Kwakwazo (4%). The prevalence of infection was highest among pupils in Primary 4 (9%), followed by Primary 5 pupils (8%) and pupils in Primary 3 (5%), while the lowest prevalence was observed in Primary 2 pupils (2%). No infections were recorded in Primary 6 pupils. Results of chi-square analysis revealed a significant association between the occurrence of urinary schistosomiasis and the age of the pupils. **Conclusion:** It is concluded that urinary schistosomiasis remains a public health challenge in the Goronyo Local Government Area, Sokoto. Therefore, it is recommended that local authorities should prioritize improving sanitation infrastructures in schools and communities and health education campaigns, especially in high-prevalence settlements like Sabon-Gari and Bazza.



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sciforum-159848: Prevalence and intensity of Urogenital Schistosomiasis among school children in Spill way community in Spill way community of Ikere George Dam, Iseyin LGA, Oyo State, Nigeria

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Urogenital schistosomiasis, a neglected tropical disease, remains endemic in Nigeria and continues to pose a significant public health challenge, especially among school-aged children in rural communities. Many areas with active transmission remain unmapped for intervention. This study investigated the prevalence, intensity, and risk factors associated with urogenital schistosomiasis among primary school children in Spill Way community, Ikere George Dam, Oyo State, Nigeria, a remote area where residents frequently contact dam water. A total of 109 school-aged children (53 females and 56 males; aged 2–20 years) voluntarily participated. A pretested questionnaire was administered to collect sociodemographic data and water contact behaviours. Urine samples were collected and examined for *Schistosoma haematobium* eggs using standard parasitological sedimentation techniques. Hematuria was screened using chemical reagent strips. Overall, 21 (19.3%) participants were positive for *S. haematobium* eggs, with the 6–10-year age group showing the highest prevalence (21.1%). Two (9.5%) of the infected participants had heavy infections (≥ 50 eggs/10 ml of urine). There was no statistically significant difference ($P > 0.05$) in infection rates between males and females. Additionally, 42 (38.5%) participants exhibited hematuria. The findings indicate ongoing transmission of urogenital schistosomiasis within the community. All infected children were treated with praziquantel (40mg/kg) by the Local Government Area Neglected Tropical Disease (NTD) coordinators. This study highlights the urgent need for sustained community-based interventions, including mass drug administration, improved water, sanitation, and hygiene (WASH) practices, and health education, to reduce transmission and safeguard the health of school-aged children in endemic rural settings.



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sciforum-174911: Safety Profile and Pharmacokinetic Considerations of Moxidectin in Human Onchocerciasis: A Systematic Review

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Introduction: Moxidectin is approved for the treatment of *Onchocerca volvulus* infection and represents a potential advancement over ivermectin in mass drug administration (MDA) programs. Its prolonged elimination half-life and sustained microfilarial suppression may enhance control strategies. A comprehensive synthesis of safety and pharmacokinetic (PK) data is essential to inform large-scale implementation, including use in pediatric and special populations.

Methods: A systematic PubMed search was performed using the MeSH terms “moxidectin” AND “onchocerciasis.” Human clinical trials reporting safety and/or PK outcomes were eligible. Seven studies (Phase 2–3 randomized controlled trials and dedicated PK investigations) were included. Data were narratively synthesized.

Results: Across Phase 3 trials (≈2,400 participants), single-dose moxidectin 8 mg demonstrated a safety profile comparable to ivermectin. Adverse events were predominantly Mazzotti-type reactions associated with microfilarial clearance. In the pivotal superiority trial (n=978 moxidectin recipients), 99% experienced Mazzotti reactions, serious adverse events occurred in 4%, and no drug-related deaths were reported. Severe postural hypotension (~5%) was generally transient. Ocular adverse events (~12%) reflected parasite kill rather than intrinsic toxicity. No QT prolongation signal was detected in studies incorporating ECG monitoring. Dose-ranging Phase 2 studies (2–8 mg) showed dose-proportional exposure, median T_{max} ≈4 h, and a prolonged elimination half-life (~17–23 days). Pediatric PK data (4–17 years) demonstrated weight-dependent clearance with exposure comparable to adults and no exposure–adverse event association. Lactation modeling predicted low infant exposure (relative infant dose ~8.7%), below established safety thresholds. No clinically relevant CYP3A4 interaction signal was identified.

Conclusions: Moxidectin exhibits predictable, linear pharmacokinetics and sustained systemic exposure supportive of MDA strategies. Its safety profile is primarily driven by expected Mazzotti reactions and remains comparable to ivermectin, without evidence of intrinsic ocular, neurologic, or cardiac toxicity. These findings support its expanding role in onchocerciasis control programs.



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sciforum-175494: Serum-based untargeted metabolomics to investigate possible indicators of asymptomatic Lymphatic Filariasis

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Abstract

Introduction

Lymphatic filariasis (LF), a devastating tropical disease caused by the parasitic filarial worms *Wuchereria bancrofti*, *Brugia malayi*, and *Brugia timori*, continues to pose a substantial public health challenge in endemic tropical and subtropical regions. After malaria, it is the second most prevalent vector-borne illness. A wide range of clinical manifestations are associated with LF. The clinical symptoms of LF are varied, ranging from asymptomatic or subclinical infections with circulating microfilariae to pronounced pathologies such as lymphedema, elephantiasis, and hydrocele. The diagnosis of asymptomatic LF infections can be challenging since microscopy, serological tests, and antigen detection tests may exhibit decreased sensitivity in certain instances.

Methods

Serum samples were collected from 84 microfilaremic individuals and 48 healthy volunteers residing in the endemic districts of Eastern Uttar Pradesh. The serum samples were processed, and the metabolites were extracted and identified via High-Resolution Accurate Mass Spectrometry (HRAMS)-based metabolomics. Metabolomic data analysis was conducted using the default parameters of "Compound Discoverer 3.3.3.20" software. A two-tailed Student's t-test was employed to assess feature differences between healthy and microfilaremic groups. The p-value was adjusted using the Benjamini-Hochberg correction for false discovery rate (FDR). A p-value of 0.05 was regarded as statistically significant. The "MetaboAnalyst 6.0" platform was utilized for pathway and network analyses.

Results

A total of 161 metabolites were uncovered, with 24 exhibiting significant upregulation and 137 exhibiting significant downregulation. Multivariate and univariate statistical analysis demonstrated significant metabolic differences distinguishing microfilaremic individuals from healthy controls. Additionally, pathway analysis of the metabolites showed changes in the metabolism of arachidonic acid and unsaturated fatty acid synthesis. Network analysis identified metabolites that had significant clinical implications.

Conclusions

The findings indicate an alteration in the host serum metabolome during the microfilaremic stage of lymphatic filariasis, which could function as possible biomarkers for early disease detection, surveillance, and therapeutic intervention.



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sciforum-172419: Sustaining Lymphatic Filariasis Elimination: A Systematic Review of Post-Intervention and Post-Validation Challenges

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Background:

The Global Programme to Eliminate Lymphatic Filariasis (GPELF) has made substantial progress, with 21 countries confirmed as having eliminated lymphatic filariasis (LF) as a public health problem and 14 under surveillance. However, sustaining elimination following mass drug administration (MDA) and during post-validation phases remains a major challenge. This review aimed to systematically identify and characterize challenges affecting the sustainability of LF elimination globally.

Methods:

A systematic review was conducted in accordance with the PRISMA guidelines. PubMed/MEDLINE, Europe PubMed Central, DOAJ, and Scopus were searched (July–October 2025) without time restrictions. Search terms combined LF-related keywords (e.g., lymphatic filariasis, *Wuchereria bancrofti*, *Brugia malayi*) with post-elimination concepts (e.g., post-MDA, surveillance, recrudescence) and challenges. Studies reporting challenges were included and categorized into biological, vector-related, socio-behavioural, and health system domains. Data were extracted and synthesized thematically.

Results:

Fourteen studies from eight countries met the inclusion criteria, spanning three WHO regions: African (57%), South-East Asia (36%), and Western Pacific (7%). Most studies evaluated post-intervention settings (79%). Biological challenges were most frequently reported (86%), including persistent microfilaremia and circulating filarial antigen (CFA) positivity following MDA cessation, suggesting ongoing transmission. Limited post-validation evidence indicated possible persistence, with CFA prevalence around 2.2% up to seven years after validation. Health system challenges (86%), particularly surveillance gaps and operational weaknesses, were also prominent. Socio-behavioural (50%) and vector-related (43%) factors further contributed to continued transmission risk.

Conclusion:

Sustained LF elimination is hindered by persistent infection reservoirs, surveillance gaps, and socio-behavioural barriers. Regional variation highlights the need for context-specific strategies. Strengthening surveillance and response systems is essential to prevent recrudescence and ensure long-term elimination.



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sciforum-175088: Therapeutic Strategies for Lobomycosis (*Lacazia loboi*): A Systematic Review of Clinical Evidence and Management Outcomes

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Introduction.

Lobomycosis (lacaziosis), caused by *Lacazia loboi*, is a chronic cutaneous–subcutaneous mycosis endemic to the Amazon basin and other tropical regions. Due to an inability to culture the organism in vitro and the rarity of cases, standardized treatment guidelines are lacking. Therapeutic decisions rely primarily on case reports and small case series. This systematic review aims to synthesize available evidence regarding medical and surgical treatment outcomes for lobomycosis.

Methods.

A systematic search of PubMed/MEDLINE, Scopus-indexed sources, and open-access repositories was conducted through February 2026 using the terms “lobomycosis,” “lacaziosis,” “*Lacazia loboi*,” and “treatment.” Eligible studies included case reports, case series, and narrative reviews reporting therapeutic interventions and clinical outcomes. Extracted variables included type of intervention, antifungal regimen and duration, clinical response, recurrence, and follow-up time. Due to heterogeneity and absence of controlled trials, a qualitative synthesis was performed.

Results.

Evidence is limited to observational data, predominantly individual case reports and small series. Surgical excision remains the most frequently employed treatment for localized disease but is associated with recurrence, particularly in multifocal or extensive lesions. Systemic antifungal therapy with itraconazole has demonstrated variable responses, often requiring prolonged administration. Combination therapy with itraconazole and clofazimine has been associated with clinical remission in selected cases. Posaconazole has shown promising outcomes in refractory or extensive disease, with sustained remission reported after long-term therapy (≥12 months). However, treatment duration, dosing regimens, and follow-up periods vary considerably across reports.

Conclusions.

No standardized or evidence-based therapeutic protocol exists for lobomycosis. Combined surgical and prolonged systemic antifungal therapy appears to offer better outcomes than monotherapy. Posaconazole represents a promising option for extensive disease, although cost and limited evidence remain constraints. Prospective multicenter studies and regional registries are urgently needed to establish optimal management strategies for this neglected tropical disease.



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Session 4. Antimicrobial Resistance

sciforum-178295: Bacterial spectrum and proportion of multidrug-resistant bacteria in clinical samples from a secondary hospital in Lambaréné, Gabon

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Background: Antimicrobial resistance (AMR) remains a pressing global health challenge, disproportionately affecting low- and middle-income countries (LMICs). This study investigates the spectrum and proportion of multidrug-resistant (MDR) bacteria isolated from clinical samples processed at the Microbiology lab of the Centre de Recherches Médicales de Lambaréné, Lambaréné, Gabon.

Methods: Microbiological laboratory results from 2017 to 2023 were retrospectively analysed to assess the non-susceptibility rates of the most common isolates from seven major types of clinical specimens (urine, blood, stool, wound swabs, urethral swabs, ear swabs, and throat swabs). Standard cultures and interpretation of results were done according to Clinical Laboratory Standards Institute (CLSI) guidelines.

Results: A total of 5,401 were clinically relevant bacterial isolates. The most frequently identified pathogens were *Escherichia coli* (273/1050; 26%), *Staphylococcus aureus* (192/1050; 18%), β -hemolytic *Streptococci* (160/1050; 15%), and *Klebsiella pneumoniae* (69/1050; 6.6%). Urine samples predominantly yielded *E. coli* and *K. pneumoniae*, while *S. aureus* was most common in wound and blood cultures. Overall, (242/1050; 23%) of isolates were classified as MDR, with *E. coli* accounting for 40%(96/1050;) of these cases. The proportion of ESBL producers among Enterobacterales was 10.5% (55/522). Resistance to third-generation cephalosporins was notably high, especially among *K. pneumoniae* (28/69; 41%) and *E. coli* (34/273; 13%). Methicillin-resistant *S. aureus* (MRSA) represented 12% (22/192) of *S. aureus* isolates. According to the WHO 2024 bacterial priority pathogen list, 58/1050 (5.5%) of isolates including carbapenem-resistant *Acinetobacter baumannii*(3) and ESBL-producing Enterobacterales(55).

Conclusion: This study highlighted the spectrum of bacteria leading causes of clinical infections, in Lambaréné, with urinary isolates dominated by *E. coli* and wound/blood cultures by *S. aureus*. Antimicrobial resistance is widespread, with nearly one-quarter of isolates classified as multidrug resistant, including ESBL-producing Enterobacterales and MRSA. The presence of WHO “Critical Priority” pathogens highlights an urgent need for strengthened surveillance, antimicrobial stewardship, and infection-control strategies to curb the growing threat of resistance.



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sciforum-178285: Beyond “Resistant or Susceptible”: A Framework for Heteroresistance and Within-Host Evolution of *Pseudomonas aeruginosa* in Cystic Fibrosis

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Introduction: Chronic *Pseudomonas aeruginosa* infection remains a leading driver of morbidity in cystic fibrosis (CF) and is tightly linked to antimicrobial resistance (AMR). However, treatment failure often occurs even when routine susceptibility testing suggests activity. Emerging evidence indicates that CF airways can act as an evolutionary niche where *P. aeruginosa* diversifies into co-existing subpopulations with distinct resistance and tolerance profiles. This abstract proposes a framework describing how within-host diversity and heteroresistance contribute to persistent infection and recurrent antibiotic exposure.

Methods: We developed a conceptual framework by synthesizing established mechanisms in CF microbiology and AMR research and mapping them to clinical decision points. The model integrates (i) spatially structured biofilms and mucus-associated microenvironments, (ii) adaptive evolution under repeated antibiotic selection, and (iii) phenotypic heterogeneity (including heteroresistance and tolerant subpopulations) that may be under-detected by single-colony testing. We outline measurable indicators suitable for evaluation, including longitudinal culture patterns, multi-isolate susceptibility profiles, genomic diversity signals, and recurrence-related outcomes.

Results: The framework identifies three mechanisms that can sustain apparent “discordance” between lab susceptibility and clinical response: (1) coexistence of minority resistant subpopulations that expand during therapy, (2) biofilm-associated tolerance reducing effective antibiotic killing despite susceptibility in planktonic assays, and (3) rapid adaptive shifts during repeated treatment cycles. These processes may increase antibiotic burden, promote selection pressure, and accelerate progression to difficult-to-treat phenotypes in CF.

Conclusions: CF-associated *P. aeruginosa* AMR is not solely a single-strain resistance problem but a dynamic within-host ecosystem challenge. Incorporating within-host diversity into diagnostics and stewardship such as multi-isolate testing and longitudinal surveillance may better align therapy with real-world AMR biology and reduce treatment failure.



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sciforum-176599: Bridging the Diagnostic Gap: Evaluating the Concordance of Genotypic and Phenotypic AMR Detection in a Philippine Tropical Disease Center

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Background: Antimicrobial resistance (AMR) is a critical public health threat in the Philippines, necessitating rapid diagnostic tools for effective stewardship. This study evaluates the concordance between multiplex PCR resistance gene detection and conventional phenotypic culture-based susceptibility testing.

Methods: A cross-sectional analytical study was conducted at San Lazaro Hospital (June 2023 – April 2025) involving 109 patients. Resistance markers identified via multiplex PCR (including NDM, IMP, VIM, KPC, and CTX-M) were compared against culture-based resistance profiles.

Results: Concordance between AMR gene detection and phenotypic resistance patterns was notably low at 31.57%. Despite this, PCR enabled the rapid identification of critical carbapenemase and ESBL genes. In the 90 days prior to admission, 3rd and 4th generation cephalosporins were the most frequently used antibiotics, a trend that continued during hospitalization (utilized in 69% of cases), alongside carbapenems (29.8%).

Conclusion: The identification of resistance genes like NDM and KPC through molecular methods is critical for AMR surveillance and antimicrobial stewardship. While multiplex PCR provides rapid genotypic data essential for surveillance, its limited concordance with phenotypic susceptibility indicates it should complement, not replace, conventional culture. PCR may detect resistance genes that are not phenotypically expressed, or vice-versa, necessitating careful clinical interpretation. These findings emphasize the need for integrated diagnostic approaches to optimize antimicrobial stewardship in resource-limited settings.



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sciforum-177543: Digital Strategies to Improve Tuberculosis Case Notification in Private Healthcare Facilities: Implications for Antimicrobial Resistance Surveillance in Low- and Middle-Income Countries

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Background: Tuberculosis (TB) remains a leading infectious cause of death globally and a major contributor to antimicrobial resistance through multidrug-resistant TB (MDR-TB). In many low- and middle-income countries (LMICs), particularly in low-income countries (LICs), a substantial proportion of individuals with TB first seek care in private healthcare facilities. Incomplete notification from these providers contributes to under-reporting, weakens national surveillance systems, and may delay detection of drug-resistant TB. While digital innovations have been proposed to address these gaps, their feasibility in resource-constrained settings remains uncertain.

Methods: A structured literature review was conducted using multiple international databases and gray literature sources, focusing on studies published within the past five years. Evidence was extracted on digital reporting systems, electronic case-based notification platforms, laboratory information exchange, interoperability, and mobile applications. Implementation context and feasibility-related factors were also assessed.

Results: Digital reporting platforms improved TB notification completeness and timeliness in several LMIC settings, particularly where baseline infrastructure and policy support were present. Integration with public-private mix (PPM) strategies and provider engagement strengthened linkages with national TB programs. However, feasibility remains a key challenge. Evidence from LICs is limited, and implementation is constrained by inadequate infrastructure, limited technical capacity, fragmented data governance, and variable provider participation, affecting scalability and sustainability.

Conclusion: Digital reporting systems can enhance TB surveillance and support earlier detection of drug-resistant TB in LMICs with enabling conditions. However, they are not a standalone solution, particularly in LICs. Context-adapted, phased, and hybrid approaches, combining digital tools with health system strengthening and sustained provider engagement, are essential to ensure feasible and sustainable implementation.



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sciforum-178514: Epidemiology of CTX-M Extended-Spectrum β -Lactamases in *Escherichia coli* Clinical Isolates in Mexico: A Systematic Review

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Introduction

The global spread of extended-spectrum β -lactamase (ESBL)-producing *Escherichia coli*, particularly those harboring CTX-M enzymes, represents a major public health concern due to their association with multidrug resistance and limited therapeutic options. In Mexico, increasing reports of CTX-M-producing *E. coli* have been documented in both hospital and community settings. However, the epidemiological and molecular characteristics of these isolates remain fragmented across individual studies. This study aimed to review the available evidence on the prevalence and molecular features of CTX-M-producing *E. coli* in clinical isolates from Mexico.

Methods

A systematic review was conducted in PubMed and Scopus to identify studies reporting ESBL or CTX-M-producing *E. coli* in Mexico. Eligible studies included original research articles describing clinical human isolates. Studies focusing exclusively on animals, food, environmental sources, or non-*E. coli* organisms were excluded. Data extracted included study location, infection type, number of isolates, prevalence of CTX-M genes, and molecular characteristics such as sequence types or plasmid profiles.

Results

Nine studies met the inclusion criteria, encompassing clinical isolates obtained from hospitals and outpatient settings across several regions of Mexico. The majority of studies reported CTX-M enzymes as the predominant ESBL type among *E. coli* isolates. CTX-M-15, CTX-M-14, and CTX-M-27 were the most frequently identified variants. Several studies also reported the presence of high-risk clones such as sequence type ST131 and plasmids belonging to the IncF family, highlighting the role of mobile genetic elements in the dissemination of resistance. Uropathogenic *E. coli* was commonly associated with multidrug resistance phenotypes and multiple virulence determinants.

Conclusions

CTX-M-producing *Escherichia coli* are widely distributed among clinical isolates in Mexico and represent a significant contributor to antimicrobial resistance in both hospital and community infections. The predominance of CTX-M variants and the circulation of high-risk clones underscore the importance of molecular surveillance and antimicrobial stewardship programs to limit the spread of resistant strains.



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sciforum-177010: Knowledge, Attitudes, and Practices Related to Antimicrobial Resistance Across the One Health Sector in Ghana: A Cross-Sectional Study

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Introduction:

Antimicrobial resistance (AMR) is a growing public health threat that spans human, animal, and environmental health systems. In Ghana, limited multisectoral evidence exists on how knowledge, attitudes, and practices related to AMR vary across these interconnected sectors. This study assessed AMR-related knowledge, attitudes, and practices across the One Health sectors in selected districts of Ghana and examined factors associated with appropriate antimicrobial-related behaviours.

Methods:

A cross-sectional analytical study was conducted among adults working in human health, animal health, and environmental health sectors in Sunyani West Municipality, Techiman Metropolitan Area, and Offinso North District. A stratified random sampling approach was used to recruit 450 participants, of whom 448 completed a structured questionnaire. Data on sociodemographic characteristics and AMR-related knowledge, attitudes, and practices were collected through face-to-face interviews. Descriptive statistics summarized outcomes, while chi-square tests and multivariable logistic regression identified factors associated with good knowledge and appropriate practices.

Results:

Overall, 63% of participants demonstrated good knowledge of AMR, with significant variation across sectors ($p < 0.001$). Positive attitudes toward prudent antimicrobial use were reported by 85% of respondents; however, only 40% exhibited appropriate practices. Good knowledge was significantly associated with tertiary education (adjusted odds ratio [aOR] = 2.8; 95% CI: 1.7–4.6) and employment in the human health sector (aOR = 2.5; 95% CI: 1.4–4.4). Appropriate practices were independently predicted by good knowledge (aOR = 3.6; 95% CI: 2.2–5.9) and positive attitudes toward antimicrobial stewardship (aOR = 2.1; 95% CI: 1.3–3.2).

Conclusion:

Knowledge and practices related to antimicrobial resistance vary substantially across One Health sectors in Ghana, with notable gaps between awareness and behaviour. Strengthening multisectoral training, regulation of antimicrobial use, and district-level stewardship interventions are essential to promote responsible antimicrobial use and reduce AMR risks.



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sciforum-177597: Longitudinal Impact of Antibigram-Guided Antimicrobial Stewardship on Resistance Patterns and Multidrug-Resistant Organisms in a South Indian Tertiary Care Hospital

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Introduction

Antimicrobial resistance (AMR) is a major global health threat driven by inappropriate antibiotic use. Antimicrobial stewardship programs (ASPs) aim to optimize prescribing and limit the spread of multidrug-resistant organisms (MDROs). This study evaluated the impact of an antibiogram-guided antimicrobial stewardship intervention on antimicrobial susceptibility patterns, MDRO prevalence, and antibiotic consumption in a tertiary care hospital in South India.

Methods

longitudinal observational study was conducted from January 2022 to December 2024 in a tertiary care hospital. A total of 3092 clinical specimens were processed, of which 1144 yielded bacterial growth. Antimicrobial susceptibility testing was performed using the Kirby–Bauer disk diffusion method as per CLSI guidelines. A cumulative antibiogram (2022) was used to formulate and implement an institutional antibiotic policy in January 2023, supported by clinician education and prescription audits as part of the ASP. Resistance trends were compared across three periods: pre-implementation (OYB), one year post-implementation (OYA), and two years post-implementation (TYA). Statistical analysis was performed using Chi-square/Fisher's exact test, with $p < 0.05$ considered significant. Antibiotic consumption was assessed using DDD/1000 patients.

Results

Following implementation, modest but significant improvements in antimicrobial susceptibility were observed. Mean susceptibility of *Escherichia coli* increased from 65.6% to 68.5%, with significant improvement in doxycycline susceptibility ($p < 0.05$). *Pseudomonas aeruginosa* showed improved ciprofloxacin susceptibility ($p < 0.05$). The prevalence of ESBL-producing *E. coli* declined from 63% to 51%, and ESBL-producing *Klebsiella* from 60% to 52%. MRSA prevalence decreased from 24% to 22%. A significant reduction in β -lactam/ β -lactamase inhibitor consumption was observed ($p < 0.05$).

Conclusion

Antibiogram-guided antimicrobial stewardship, incorporating policy implementation, clinician education, and audit feedback, was associated with improved susceptibility patterns and reduced MDRO burden. Sustained surveillance and policy reinforcement are essential to combat AMR.



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sciforum-178430: Pathotype Diversity and High ESBL Gene Carriage Among Diarrheagenic *Escherichia coli* Isolates From Pediatric Diarrhea in North India

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Introduction: Diarrheagenic *Escherichia coli* (DEC) remains one of the leading bacterial causes of pediatric diarrhea in developing countries. The increasing emergence of extended-spectrum β -lactamase (ESBL)-producing strains has further complicated the management of enteric infections and raised significant concerns regarding antimicrobial resistance (AMR). This study aimed to investigate the distribution of DEC pathotypes and the prevalence of ESBL-associated resistance genes among clinical *E. coli* isolates obtained from pediatric diarrheal patients.

Methodology: A total of 350 *E. coli* isolates from pediatric stool samples were analyzed from secondary and tertiary healthcare settings in India from November 2024–December 2025 of acute and persistent cases. Pathotype identification was performed using PCR targeting virulence genes associated with the major DEC pathotypes: EPEC, EAEC, ETEC, EIEC, and DAEC. Phenotypic detection of ESBL production was carried out using the Double Disk Synergy Test (DDST). Molecular detection of ESBL genes blaCTX-M-15 and blaTEM was performed using PCR, and antimicrobial susceptibility testing was conducted using the VITEK® 2 Compact system.

Results: A diverse distribution of DEC pathotypes was observed, including EPEC (9%), EAEC (13%), ETEC (14%), EIEC (7%), and DAEC (15%), with isolates demonstrating hybrid virulence gene combinations (10%), highlighting the dynamic genetic landscape of circulating strains. Notably, 66% of isolates were confirmed as ESBL producers by DDST, indicating widespread phenotypic resistance to β -lactam antibiotics. Molecular analysis revealed a strikingly high prevalence of blaCTX-M-15 (78%), while blaTEM genes were detected in 62% of isolates, suggesting the dissemination of ESBL determinants within the bacterial population. Higher ESBL carriage was observed in secondary settings.

Conclusions: These findings highlight the convergence of virulence diversity and antimicrobial resistance among diarrheagenic *E. coli*, with the high ESBL prevalence in pediatric isolates likely reflecting early-life antibiotic exposure and increasing community circulation of resistant strains. This underscores the need for continuous molecular surveillance and strengthened antimicrobial stewardship to mitigate the growing threat of resistant enteric pathogens in pediatric populations.



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sciforum-176106: Prevalence and determinants of drug-resistant pulmonary tuberculosis in the MENA region: a systematic review and meta-analysis

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Background: Multidrug-Resistant Tuberculosis (MDR-TB) is a constraining challenge for tuberculosis (TB) control worldwide. The MENA region accounts for a large part of the global MDR-TB burden.

Aim: To estimate the prevalence of MDR-TB and associated factors in the MENA region.

Methods: We searched for studies published in English and French on the subject up to 31st January 2026 on Web of Science, PubMed, Scopus, and Cochrane, without time restriction. Original studies reporting data on the prevalence of MDR-TB (resistance to rifampicin and isoniazid simultaneously) in individuals living in the MENA region were selected. The random effects model was used to perform the meta-analysis, considering the heterogeneity among the included studies, and the I² statistic was used to assess heterogeneity.

Results: A total of 1239 articles were identified, and 25 studies from 6 countries were included in this review. The prevalence of MDR-TB in the MENA region ranged from 0% (95% CI: 0 - 4.1%) to 17.1% (95% CI: 10.6 - 25.4%). The estimated pooled prevalence was 3.54% (95% CI: 2.18 - 5.72%) with a high heterogeneity, I² = 95.6%; 95% CI: 94.4 - 96.5%. Previous TB treatment, HIV infection, smoking and the presence of comorbidities were the most reported associated factors.

Conclusion: This review underscores the persistence of MDR-TB in the MENA region, suggesting insufficiency in TB control. Multisectoral interventions integrating strong prevention measures, standardized treatment protocols and measures to enhance treatment adherence should be implemented.



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sciforum-177652: Title: Pilot Molecular Investigation of Artemisinin Resistance Markers in *Artemisia annua* Users for Malaria Treatment/Prevention: First African Follow-Up vs. ACT Controls in DRC
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Abstract:

Artemisia annua tea is widely used for uncomplicated malaria treatment and prevention in the Democratic Republic of Congo (DRC) despite WHO contraindications against non-pharmaceutical forms, creating urgent need for molecular surveillance of potential resistance emergence. This pioneering African pilot study investigates artemisinin resistance markers among *A. annua* consumers versus artemisinin-based combination therapy (ACT) controls from Kalima Health Zone (Maniema Province), specifically Kakutya 1, Bobela, and Lubile health areas consultations (CONS-LUB).

High-quality genomic DNA was extracted from 144 clinical samples using a CTAB-optimized protocol adapted for low-parasitemia specimens (yield: 150-250 ng/μL, A260/280: 1.8-2.0). Nested PCR targeting the *P. falciparum* 18S rRNA gene detected infection in 57/144 cases (39.6% prevalence): 44.7% (42/94) in CONS-LUB versus 30.0% (15/50) in controls. Preliminary therapeutic monitoring (n=32 *A. annua* users) demonstrated >95% parasitemia clearance within 72 hours, comparable to standard ACT regimens. Sequencing of key artemisinin resistance markers (*Pfkelch13*, *Pfmdr1*, *Pfcr1*) in all PCR-positive cases is currently ongoing—the first such molecular follow-up of *A. annua* consumers across Africa.

A parallel cross-sectional health worker survey (n=320) revealed 72% acceptability due to accessibility and cultural fit. This study bridges molecular validation with public health perceptions, supporting One Health approaches for vector-borne diseases amid rising resistance threats. CTMID 2026 presentation underscores urgent need for evidence on traditional therapies in global malaria control.



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